Two Achilles' Heels of the Ebolavirus Glycoprotein? Supplementary Materials

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List of Tables

Supporting Material

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EBO	A_LYS_14	NZ	A_GLU_10	OE2	3.109
1EBO	A_ARG_79	NH1	A_ASP_113	OD1	3.914
1EBO	A_LYS_87	NZ	C_ASP_106	OD2	3.887
1EBO	A_HIS_112	ND1	B_GLU_77	OE1	3.658
1EBO	A_HIS_112	ND1	B_GLU_77	OE2	3.104
1EBO	A_LYS_116	NZ	A_ASP_120	OD1	3.258
1EBO	A_HIS_127	ND1	A_ASP_128	OD1	2.733
1EBO	B_LYS_14	NZ	B_GLU_10	OE2	3.661
1EBO	B_ARG_79	NH1	B_ASP_113	OD1	3.995
1EBO	B_HIS_112	ND1	C_GLU_77	OE1	3.068
1EBO	B_HIS_112	ND1	C_GLU_77	OE2	2.658
1EBO	B_LYS_116	NZ	B_ASP_120	OD1	3.905
1EBO	B_LYS_116	NZ	B_ASP_120	OD2	3.784
1EBO	B_HIS_127	ND1	B_ASP_128	OD1	2.787
1EBO	C_LYS_7	NZ	B_GLU_9	OE1	3.472
1EBO	C_LYS_14	NZ	C_GLU_10	OE2	3.363
1EBO	C_HIS_17	NE2	C_GLU_21	OE2	3.656
1EBO	C_LYS_26	NZ	A_GLU_21	OE1	2.847
1EBO	C_LYS_26	NZ	A_GLU_21	OE2	3.880
1EBO	C_ARG_79	NH1	C_ASP_113	OD1	3.945
1EBO	C_ARG_79	NH2	C_GLU_110	OE2	3.323
1EBO	C_LYS_87	NZ	B_ASP_106	OD2	3.920
1EBO	C_LYS_116	NZ	C_ASP_120	OD1	3.226
1EBO	C_HIS_127	ND1	C_ASP_128	OD1	3.507
1EBO	D_ARG_24	NH1	D_GLU_21	OE2	3.453
1EBO	D_HIS_112	ND1	E_GLU_77	OE1	3.490
1EBO	D_HIS_112	ND1	E_GLU_77	OE2	2.696
1EBO	D_HIS_127	ND1	D_ASP_128	OD1	2.959
1EBO	E_LYS_26	NZ	F_GLU_21	OE2	3.162
1EBO	E_ARG_79	NH2	E_GLU_110	OE1	3.971
1EBO	E_LYS_87	NZ	D_ASP_106	OD2	3.925
1EBO	E_LYS_116	NZ	E_ASP_120	OD1	3.470
1EBO	E_HIS_127	ND1	E_ASP_128	OD1	2.619
1EBO	F_LYS_26	NZ	D_GLU_21	OE1	3.927
1EBO	F_LYS_87	NZ	E_ASP_106	OD2	3.651
1EBO	F_HIS_112	ND1	D_GLU_77	OE2	3.188
1EBO	F_HIS_127	ND1	F_ASP_128	OD1	2.746
2EBO	A_HIS_613	ND1	B_GLU_578	OE1	3.396
2EBO	A_HIS_613	ND1	B_GLU_578	OE2	3.211
2EBO	A_LYS_617	NZ	A_ASP_621	OD2	2.696
2EBO	B_ARG_580	NH1	B_ASP_614	OD2	3.885
2EBO	B_HIS_613	ND1	C_GLU_578	OE1	3.346
2EBO	B_HIS_613	ND1	C_GLU_578	OE2	2.789
2EBO	C_HIS_628	ND1	C_ASP_629	OD1	2.824
2QHR	H_ARG_38	NH1	H_GLU_46	OE1	2.994
2QHR	H_ARG_38	NH1	H_GLU_46	OE2	3.872
2QHR	H_ARG_38	NH1	H_ASP_86	OD1	3.831
2QHR	H_ARG_38	NH2	H_ASP_86	OD1	2.870
2QHR	H_ARG_66	NH1	H_ASP_86	OD1	3.110
2QHR	H_ARG_66	NH1	H_ASP_86	OD2	3.628
2QHR	H_ARG_66	NH2	H_ASP_86	OD1	3.793
2QHR	H_ARG_66	NH2	H_ASP_86	OD2	2.806
2QHR	H_ARG_94	NH2	H_ASP_101	OD1	3.235
2QHR	H_ARG_94	NH2	H_ASP_101	OD2	2.743
2QHR	H_LYS_143	NZ	L_GLU_125	OE2	2.743
2QHR	H_HIS_164	ND1	L_GLU_168	OE1	3.446
2QHR	H_HIS_164	ND1	L_GLU_168	OE2	2.691

2QHR	H_LYS_205	NZ	H_ASP_207	OD2	3.730
2QHR	H_LYS_208	NZ	L_GLU_124	OE1	3.025
2QHR	H_LYS_208	NZ	L_GLU_124	OE2	3.278
2QHR	L_ARG_61	NH1	L_ASP_82	OD1	3.738
2QHR	L_ARG_61	NH1	L_ASP_82	OD2	2.709
2QHR	L_ARG_61	NH2	L_ASP_82	OD1	3.238
2QHR	L_ARG_61	NH2	L_ASP_82	OD2	3.549
2QHR	L_LYS_111	NZ	L_ASP_200	OD2	3.160
2QHR	L_LYS_150	NZ	L_GLU_203	OE2	3.712
2QHR	L_LYS_167	NZ	L_GLU_83	OE1	3.792
2QHR	L_HIS_179	ND1	L_ASP_161	OD2	3.673
2QHR	L_LYS_204	NZ	H_ASP_130	OD1	2.837
2QHR	L_LYS_204	NZ	H_ASP_130	OD2	3.813
2QHR	P_HIS_407	ND1	L_ASP_92	OD1	3.553
2QHR	P_ARG_409	NH1	H_ASP_33	OD2	2.967
2QHR	P_ARG_410	NH1	P_ASP_414	OD1	3.195
2QHR	P_ARG_410	NH1	P_ASP_414	OD2	3.569
2Y6S	C_ARG_65	NH1	C_GLU_83	OE1	3.999
2Y6S	C_ARG_65	NH1	C_GLU_85	OE2	3.669
2Y6S	C_ARG_65	NH1	C_ASP_86	OD1	2.662
2Y6S	C_ARG_65	NH1	C_ASP_86	OD2	2.895
2Y6S	C_ARG_65	NH2	C_GLU_83	OE1	3.359
2Y6S	C_ARG_65	NH2	C_GLU_83	OE2	2.893
2Y6S	C_ARG_65	NH2	C_GLU_85	OE2	3.603
2Y6S	C_ARG_100	NH1	D_GLU_50	OE1	2.758
2Y6S	C_LYS_107	NZ	C_GLU_109	OE2	3.166
2Y6S	C_LYS_107	NZ	C_ASP_169	OD1	3.905
2Y6S	C_LYS_146	NZ	C_GLU_109	OE1	2.925
2Y6S	C_LYS_146	NZ	C_GLU_109	OE2	3.794
2Y6S	C_LYS_153	NZ	C_GLU_199	OE2	3.238
2Y6S	C_ARG_159	NH2	C_GLU_189	OE1	2.973
2Y6S	C_LYS_187	NZ	C_GLU_191	OE1	3.081
2Y6S	C_LYS_187	NZ	C_GLU_191	OE2	3.018
2Y6S	C_HIS_193	ND1	C_ASP_155	OD2	3.103
2Y6S	C_LYS_203	NZ	C_ASP_114	OD2	2.593
2Y6S	D_ARG_67	NH1	D_ASP_90	OD1	2.837
2Y6S	D_ARG_67	NH1	D_ASP_90	OD2	2.696
2Y6S	D_LYS_74	NZ	D_ASP_56	OD1	3.129
2Y6S	D_LYS_74	NZ	D_ASP_56	OD2	3.876
2Y6S	D_LYS_208	NZ	C_GLU_127	OE1	3.225
2Y6S	H_ARG_67	NH1	H_ASP_90	OD1	2.838
2Y6S	H_ARG_67	NH1	H_ASP_90	OD2	2.694
2Y6S	H_LYS_74	NZ	H_ASP_56	OD1	3.138
2Y6S	H_LYS_74	NZ	H_ASP_56	OD2	3.860
2Y6S	H_LYS_208	NZ	L_GLU_127	OE1	3.152
2Y6S	L_ARG_65	NH1	L_GLU_85	OE2	3.674
2Y6S	L_ARG_65	NH1	L_ASP_86	OD1	2.664
2Y6S	L_ARG_65	NH1	L_ASP_86	OD2	2.893
2Y6S	L_ARG_65	NH2	L_GLU_83	OE1	3.384
2Y6S	L_ARG_65	NH2	L_GLU_83	OE2	2.916
2Y6S	L_ARG_65	NH2	L_GLU_85	OE2	3.600
2Y6S	L_ARG_100	NH1	H_GLU_50	OE1	2.759
2Y6S	L_ARG_100	NH2	H_GLU_50	OE1	3.945
2Y6S	L_LYS_107	NZ	L_GLU_109	OE2	3.165
2Y6S	L_LYS_107	NZ	L_ASP_169	OD1	3.901
2Y6S	L_LYS_146	NZ	L_GLU_109	OE1	2.917
2Y6S	L_LYS_146	NZ	L_GLU_109	OE2	3.793
2Y6S	L_LYS_153	NZ	L_GLU_199	OE2	3.234

2Y6S	L_ARG_159	NH2	L_GLU_189	OE1	2.963
2Y6S	L_LYS_187	NZ	L_GLU_191	OE1	3.077
2Y6S	L_LYS_187	NZ	L_GLU_191	OE2	3.017
2Y6S	L_HIS_193	ND1	L_ASP_155	OD2	3.115
2Y6S	L_LYS_203	NZ	L_ASP_114	OD2	2.587
3CSY	A_ARG_33	NH1	A_GLU_95	OE1	3.330
3CSY	A_ARG_33	NH1	A_GLU_95	OE2	3.449
3CSY	A_ARG_38	NH1	A_GLU_46	OE2	2.868
3CSY	A_ARG_38	NH2	A_ASP_86	OD1	2.786
3CSY	A_ARG_66	NH1	A_ASP_86	OD1	3.738
3CSY	A_ARG_66	NH1	A_ASP_86	OD2	2.985
3CSY	A_ARG_66	NH2	A_ASP_86	OD1	3.541
3CSY	A_ARG_94	NH2	A_ASP_101	OD1	3.102
3CSY	A_ARG_94	NH2	A_ASP_101	OD2	3.588
3CSY	A_ARG_98	NH1	A_ASP_100F	OD1	2.690
3CSY	A_ARG_98	NH1	A_ASP_100F	OD2	3.265
3CSY	A_LYS_145	NZ	A_ASP_146	OD1	3.667
3CSY	A_LYS_145	NZ	A_ASP_146	OD2	3.424
3CSY	A_LYS_221	NZ	B_GLU_123	OE1	3.090
3CSY	A_LYS_221	NZ	B_GLU_123	OE2	3.307
3CSY	A_LYS_222	NZ	A_GLU_226	OE1	3.338
3CSY	B_LYS_24	NZ	B_ASP_70	OD1	3.112
3CSY	B_LYS_24	NZ	B_ASP_70	OD2	3.834
3CSY	B_ARG_61	NH2	B_GLU_81	OE1	3.999
3CSY	B_ARG_61	NH2	B_ASP_82	OD1	3.114
3CSY	B_ARG_61	NH2	B_ASP_82	OD2	3.791
3CSY	B_ARG_142	NH2	B_GLU_165	OE1	3.547
3CSY	B_LYS_149	NZ	B_GLU_195	OE1	2.968
3CSY	B_LYS_188	NZ	B_ASP_185	OD1	3.323
3CSY	B_HIS_189	ND1	B_ASP_151	OD1	3.608
3CSY	B_HIS_189	ND1	B_ASP_151	OD2	2.713
3CSY	C_ARG_33	NH2	C_GLU_95	OE1	3.005
3CSY	C_ARG_33	NH2	C_GLU_95	OE2	3.100
3CSY	C_ARG_38	NH1	C_GLU_46	OE2	3.062
3CSY	C_ARG_38	NH2	C_ASP_86	OD1	2.925
3CSY	C_ARG_66	NH1	C_ASP_86	OD1	3.795
3CSY	C_ARG_66	NH1	C_ASP_86	OD2	3.175
3CSY	C_ARG_66	NH2	C_ASP_86	OD1	3.757
3CSY	C_ARG_94	NH2	C_ASP_101	OD1	2.980
3CSY	C_ARG_94	NH2	C_ASP_101	OD2	3.244
3CSY	C_ARG_98	NH1	C_ASP_100F	OD1	2.963
3CSY	C_ARG_98	NH1	C_ASP_100F	OD2	3.539
3CSY	C_LYS_145	NZ	C_ASP_146	OD1	3.956
3CSY	C_HIS_172	NE2	D_ASP_167	OD2	3.885
3CSY	C_LYS_221	NZ	D_GLU_123	OE1	3.258
3CSY	C_LYS_221	NZ	D_GLU_123	OE2	3.282
3CSY	C_LYS_222	NZ	C_GLU_226	OE1	3.372
3CSY	D_LYS_24	NZ	D_ASP_70	OD1	3.251
3CSY	D_LYS_24	NZ	D_ASP_70	OD2	3.569
3CSY	D_ARG_61	NH2	D_ASP_82	OD1	3.121
3CSY	D_ARG_61	NH2	D_ASP_82	OD2	3.757
3CSY	D_ARG_142	NH2	D_GLU_165	OE1	3.115
3CSY	D_LYS_149	NZ	D_GLU_195	OE1	3.045
3CSY	D_HIS_189	ND1	D_ASP_151	OD1	3.792
3CSY	D_HIS_189	ND1	D_ASP_151	OD2	2.842
3CSY	E_ARG_33	NH2	E_GLU_95	OE1	3.422
3CSY	E_ARG_33	NH2	E_GLU_95	OE2	3.409
3CSY	E_ARG_38	NH1	E_GLU_46	OE2	2.948

3CSY	E_ARG_38	NH2	E_ASP_86	OD1	3.088
3CSY	E_ARG_66	NH1	E_ASP_86	OD2	2.937
3CSY	E_ARG_66	NH2	E_ASP_86	OD1	3.488
3CSY	E_ARG_66	NH2	E_ASP_86	OD2	3.575
3CSY	E_ARG_94	NH2	E_ASP_101	OD1	3.133
3CSY	E_ARG_94	NH2	E_ASP_101	OD2	3.533
3CSY	E_ARG_98	NH1	E_ASP_100F	OD1	3.332
3CSY	E_ARG_98	NH1	E_ASP_100F	OD2	3.049
3CSY	E_LYS_145	NZ	E_ASP_146	OD2	3.678
3CSY	E_LYS_221	NZ	F_GLU_123	OE1	3.238
3CSY	E_LYS_221	NZ	F_GLU_123	OE2	3.205
3CSY	E_LYS_222	NZ	E_GLU_226	OE1	3.405
3CSY	F_LYS_24	NZ	F_ASP_70	OD1	3.269
3CSY	F_LYS_24	NZ	F_ASP_70	OD2	3.477
3CSY	F_ARG_61	NH2	F_GLU_81	OE1	3.492
3CSY	F_ARG_61	NH2	F_ASP_82	OD1	3.832
3CSY	F_ARG_142	NH2	F_GLU_165	OE1	3.343
3CSY	F_LYS_149	NZ	F_GLU_195	OE1	3.168
3CSY	F_LYS_188	NZ	F_ASP_185	OD1	3.831
3CSY	F_HIS_189	ND1	F_ASP_151	OD2	3.133
3CSY	G_ARG_33	NH2	G_GLU_95	OE1	3.360
3CSY	G_ARG_33	NH2	G_GLU_95	OE2	3.356
3CSY	G_ARG_38	NH1	G_GLU_46	OE1	3.934
3CSY	G_ARG_38	NH1	G_GLU_46	OE2	3.037
3CSY	G_ARG_38	NH2	G_ASP_86	OD1	2.730
3CSY	G_ARG_66	NH1	G_ASP_86	OD2	2.862
3CSY	G_ARG_66	NH2	G_ASP_86	OD1	3.483
3CSY	G_ARG_66	NH2	G_ASP_86	OD2	3.538
3CSY	G_ARG_94	NH2	G_ASP_101	OD1	3.059
3CSY	G_ARG_98	NH1	G_ASP_100F	OD1	2.838
3CSY	G_ARG_98	NH1	G_ASP_100F	OD2	3.524
3CSY	G_LYS_145	NZ	G_ASP_146	OD2	3.536
3CSY	G_HIS_172	NE2	H_ASP_167	OD2	3.733
3CSY	G_LYS_221	NZ	H_GLU_123	OE1	3.440
3CSY	G_LYS_221	NZ	H_GLU_123	OE2	3.445
3CSY	G_LYS_222	NZ	G_GLU_226	OE1	3.676
3CSY	H_LYS_24	NZ	H_ASP_70	OD1	3.595
3CSY	H_LYS_24	NZ	H_ASP_70	OD2	3.439
3CSY	H_ARG_61	NH2	H_GLU_81	OE1	3.520
3CSY	H_ARG_61	NH2	H_ASP_82	OD1	3.815
3CSY	H_ARG_61	NH2	H_ASP_82	OD2	3.245
3CSY	H_ARG_142	NH2	H_GLU_165	OE1	3.557
3CSY	H_LYS_149	NZ	H_GLU_195	OE1	3.085
3CSY	H_HIS_189	ND1	H_ASP_151	OD1	3.553
3CSY	H_HIS_189	ND1	H_ASP_151	OD2	2.707
3CSY	I_ARG_64	NH1	I_GLU_100	OE2	2.693
3CSY	I_ARG_85	NH2	I_GLU_178	OE1	2.760
3CSY	I_ARG_85	NH2	I_GLU_178	OE2	2.883
3CSY	I_LYS_114	NZ	I_GLU_120	OE2	3.520
3CSY	I_ARG_130	NH2	I_ASP_163	OD2	2.701
3CSY	I_ARG_134	NH1	J_GLU_545	OE2	3.043
3CSY	I_ARG_136	NH1	I_GLU_106	OE2	3.755
3CSY	I_HIS_154	NE2	I_GLU_178	OE2	2.796
3CSY	I_ARG_164	NH2	I_ASP_163	OD1	3.175
3CSY	I_ARG_164	NH2	I_ASP_163	OD2	3.157
3CSY	J_ARG_559	NH2	I_GLU_103	OE1	3.261
3CSY	J_ARG_559	NH2	I_GLU_103	OE2	3.005
3CSY	K_ARG_64	NH1	K_GLU_100	OE2	3.248

3CSY	K_ARG_85	NH2	K_GLU_178	OE1	2.723
3CSY	K_ARG_85	NH2	K_GLU_178	OE2	3.019
3CSY	K_LYS_114	NZ	K_GLU_120	OE1	3.499
3CSY	K_ARG_130	NH1	K_ASP_163	OD2	2.845
3CSY	K_ARG_134	NH1	L_GLU_545	OE2	3.181
3CSY	K_ARG_136	NH1	K_GLU_106	OE2	3.184
3CSY	K_HIS_154	NE2	K_GLU_178	OE2	2.720
3CSY	K_ARG_164	NH2	K_ASP_163	OD1	3.547
3CSY	K_ARG_164	NH2	K_ASP_163	OD2	3.244
3CSY	L_ARG_559	NH2	K_GLU_103	OE1	3.317
3CSY	L_ARG_559	NH2	K_GLU_103	OE2	3.156
3CSY	M_ARG_64	NH1	M_GLU_100	OE2	2.845
3CSY	M_ARG_85	NH2	M_GLU_178	OE1	2.759
3CSY	M_ARG_85	NH2	M_GLU_178	OE2	3.004
3CSY	M_ARG_130	NH1	M_ASP_163	OD2	2.888
3CSY	M_ARG_134	NH1	N_GLU_545	OE2	2.894
3CSY	M_ARG_136	NH1	M_GLU_106	OE2	3.351
3CSY	M_HIS_154	NE2	M_GLU_178	OE2	2.684
3CSY	M_ARG_164	NH2	M_ASP_163	OD1	3.214
3CSY	M_ARG_164	NH2	M_ASP_163	OD2	3.477
3CSY	N_ARG_559	NH2	M_GLU_103	OE1	2.925
3CSY	N_ARG_559	NH2	M_GLU_103	OE2	3.048
3CSY	O_ARG_64	NH1	O_GLU_100	OE2	2.902
3CSY	O_ARG_85	NH2	O_GLU_178	OE1	3.008
3CSY	O_ARG_85	NH2	O_GLU_178	OE2	3.292
3CSY	O_ARG_130	NH1	O_ASP_163	OD2	2.770
3CSY	O_ARG_130	NH2	O_ASP_163	OD2	3.071
3CSY	O_ARG_134	NH1	P_GLU_545	OE2	3.026
3CSY	O_ARG_136	NH1	O_GLU_106	OE2	3.514
3CSY	O_HIS_154	NE2	O_GLU_178	OE2	2.770
3CSY	O_ARG_164	NH2	O_ASP_163	OD1	3.340
3CSY	O_ARG_164	NH2	O_ASP_163	OD2	3.003
3CSY	P_ARG_559	NH2	O_GLU_103	OE1	3.054
3CSY	P_ARG_559	NH2	O_GLU_103	OE2	2.808
3VE0	I_LYS_64	NZ	I_GLU_100	OE1	3.434
3VE0	I_ARG_85	NH2	I_GLU_178	OE1	3.938
3VE0	I_ARG_85	NH2	I_GLU_178	OE2	2.598
3VE0	I_ARG_130	NH1	I_ASP_163	OD2	3.227
3VE0	I_HIS_154	NE2	I_GLU_178	OE1	2.497
3VE0	I_ARG_164	NH1	I_ASP_163	OD1	2.966
3VE0	I_ARG_164	NH1	I_ASP_163	OD2	2.614
3VE0	I_ARG_164	NH2	I_ASP_163	OD2	3.976
3VE0	I_ARG_172	NH1	I_GLU_112	OE1	3.788
3VE0	I_ARG_172	NH1	I_GLU_112	OE2	3.022
3VE0	I_ARG_172	NH1	I_GLU_120	OE1	3.786
3VE0	J_HIS_516	ND1	J_GLU_545	OE1	3.938
3VE0	J_ARG_559	NH1	I_GLU_103	OE1	3.852
3VE0	J_ARG_559	NH1	I_GLU_103	OE2	3.848
3VE0	J_ARG_559	NH2	I_GLU_103	OE1	2.444
3VE0	J_ARG_559	NH2	I_GLU_103	OE2	2.766
3VE0	J_ARG_595	NH1	J_ASP_591	OD2	3.637
3VE0	J_ARG_595	NH2	I_ASP_49	OD2	3.842
3VE0	J_ARG_596	NH1	I_ASP_55	OD1	3.003
3VE0	A_ARG_38	NH1	A_ASP_90	OD2	2.796
3VE0	A_ARG_38	NH2	A_GLU_46	OE1	2.957
3VE0	A_ARG_38	NH2	A_ASP_90	OD2	3.833
3VE0	A_ARG_67	NH1	A_ASP_90	OD1	2.638
3VE0	A_ARG_67	NH1	A_ASP_90	OD2	3.818

3VE0	A_ARG_67	NH2	A_ASP_90	OD1	3.519
3VE0	A_ARG_67	NH2	A_ASP_90	OD2	3.251
3VE0	A_ARG_87	NH2	A_GLU_89	OE1	3.633
3VE0	A_ARG_98	NH2	I_GLU_44	OE1	3.137
3VE0	A_ARG_98	NH2	I_GLU_44	OE2	3.008
3VE0	A_ARG_98	NH2	A_ASP_107	OD1	3.467
3VE0	A_LYS_214	NZ	B_GLU_123	OE1	3.666
3VE0	A_LYS_214	NZ	B_GLU_123	OE2	2.624
3VE0	A_ARG_219	NH1	A_ASP_220	OD1	3.088
3VE0	B_ARG_54	NH2	B_ASP_60	OD1	3.562
3VE0	B_ARG_61	NH1	B_GLU_81	OE1	3.512
3VE0	B_ARG_61	NH1	B_ASP_82	OD2	3.714
3VE0	B_ARG_61	NH2	B_GLU_81	OE1	3.757
3VE0	B_ARG_61	NH2	B_GLU_81	OE2	3.987
3VE0	B_LYS_103	NZ	B_GLU_105	OE1	3.337
3VE0	B_LYS_149	NZ	B_GLU_195	OE1	3.446
3VE0	B_LYS_149	NZ	B_GLU_195	OE2	2.550
3VE0	B_ARG_155	NH1	B_GLU_185	OE1	2.325
3VE0	B_ARG_155	NH1	B_GLU_185	OE2	3.974
3VE0	B_ARG_155	NH2	B_GLU_185	OE1	3.539
3VE0	B_ARG_155	NH2	B_GLU_185	OE2	3.905
3VE0	B_HIS_189	ND1	B_ASP_151	OD1	3.017
5F1B	A_HIS_39	NE2	A_ASP_55	OD1	3.999
5F1B	A_ARG_64	NH1	A_GLU_100	OE1	3.273
5F1B	A_ARG_64	NH1	A_GLU_100	OE2	3.876
5F1B	A_ARG_85	NH2	A_GLU_178	OE1	2.662
5F1B	A_ARG_85	NH2	A_GLU_178	OE2	3.814
5F1B	A_ARG_130	NH2	A_ASP_163	OD2	3.180
5F1B	A_ARG_134	NH1	B_GLU_545	OE2	3.659
5F1B	A_HIS_154	NE2	A_GLU_178	OE2	2.611
5F1B	A_ARG_164	NH2	A_ASP_163	OD1	3.605
5F1B	A_ARG_164	NH2	A_ASP_163	OD2	3.318
5F1B	B_HIS_516	NE2	B_GLU_545	OE1	3.961
5F1B	B_ARG_559	NH1	A_GLU_103	OE1	3.219
5F1B	B_ARG_559	NH1	A_GLU_103	OE2	3.449
5F1B	B_ARG_559	NH2	A_GLU_103	OE1	3.928
5F1B	B_ARG_559	NH2	A_GLU_103	OE2	2.697
5F1B	B_LYS_588	NZ	A_ASP_47	OD1	3.551
5F1B	B_LYS_588	NZ	A_ASP_47	OD2	3.521
5F1B	C_ARG_32	NH1	C_GLU_34	OE1	3.894
5F1B	C_ARG_32	NH1	C_GLU_212	OE2	3.039
5F1B	C_ARG_32	NH2	C_GLU_212	OE2	3.122
5F1B	C_HIS_69	NE2	C_ASP_124	OD1	2.595
5F1B	C_HIS_69	NE2	C_ASP_124	OD2	3.426
5F1B	C_HIS_120	NE2	C_ASP_73	OD1	3.129
5F1B	C_HIS_125	ND1	C_ASP_159	OD1	3.361
5F1B	C_HIS_125	ND1	C_ASP_159	OD2	2.705
5F1B	C_HIS_138	ND1	C_ASP_136	OD1	3.569
5F1B	C_HIS_138	ND1	C_ASP_136	OD2	2.668
5F1B	C_HIS_140	ND1	C_ASP_153	OD2	2.612
5F1B	C_LYS_204	NZ	C_ASP_201	OD2	2.921
5F1B	C_ARG_207	NH2	C_ASP_86	OD2	3.888
5F1B	C_ARG_207	NH2	C_GLU_88	OE1	2.527
5F1B	C_ARG_207	NH2	C_GLU_88	OE2	3.562
5FHC	J_ARG_559	NH2	K_GLU_103	OE1	3.531
5FHC	J_ARG_559	NH2	K_GLU_103	OE2	3.399
5FHC	K_ARG_64	NH1	K_GLU_100	OE2	3.218
5FHC	K_ARG_85	NH2	K_GLU_178	OE1	2.651

5FHC	K_ARG_85	NH2	K_GLU_178	OE2	3.046
5FHC	K_LYS_114	NZ	K_GLU_112	OE1	3.499
5FHC	K_LYS_114	NZ	K_GLU_120	OE1	3.155
5FHC	K_ARG_130	NH1	K_ASP_163	OD2	2.715
5FHC	K_ARG_134	NH1	J_GLU_545	OE2	2.861
5FHC	K_ARG_136	NH1	K_GLU_106	OE2	3.301
5FHC	K_HIS_154	NE2	K_GLU_178	OE2	2.716
5FHC	K_ARG_164	NH2	K_ASP_163	OD1	3.639
5FHC	K_ARG_164	NH2	K_ASP_163	OD2	3.655
5FHC	A_ARG_38	NH1	A_ASP_86	OD1	2.921
5FHC	A_ARG_38	NH2	A_GLU_46	OE1	3.040
5FHC	A_ARG_38	NH2	A_GLU_46	OE2	3.982
5FHC	A_ARG_38	NH2	A_ASP_86	OD1	3.615
5FHC	A_ARG_66	NH1	A_ASP_86	OD1	3.508
5FHC	A_ARG_66	NH2	A_ASP_86	OD1	3.465
5FHC	A_ARG_66	NH2	A_ASP_86	OD2	2.756
5FHC	A_ARG_94	NH2	A_ASP_101	OD1	3.473
5FHC	A_ARG_94	NH2	A_ASP_101	OD2	3.241
5FHC	A_LYS_143	NZ	B_GLU_124	OE2	2.678
5FHC	A_LYS_209	NZ	B_GLU_123	OE1	2.702
5FHC	A_LYS_209	NZ	B_GLU_123	OE2	3.358
5FHC	B_ARG_39	NH2	B_ASP_82	OD1	3.944
5FHC	B_ARG_61	NH1	B_ASP_82	OD1	3.826
5FHC	B_ARG_61	NH1	B_ASP_82	OD2	2.658
5FHC	B_ARG_61	NH2	B_ASP_82	OD1	2.976
5FHC	B_ARG_61	NH2	B_ASP_82	OD2	3.232
5FHC	B_LYS_103	NZ	B_ASP_85	OD1	2.875
5FHC	B_LYS_103	NZ	B_ASP_85	OD2	3.594
5FHC	B_LYS_149	NZ	B_GLU_203	OE1	3.331
5FHC	B_LYS_149	NZ	B_GLU_203	OE2	3.999
5FHC	L_ARG_61	NH1	L_GLU_81	OE2	3.402
5FHC	L_ARG_61	NH1	L_ASP_82	OD1	2.944
5FHC	L_ARG_61	NH1	L_ASP_82	OD2	3.402
5FHC	L_LYS_103	NZ	L_GLU_165	OE2	3.468
5FHC	L_LYS_149	NZ	L_GLU_195	OE2	2.669
5FHC	L_LYS_183	NZ	L_GLU_187	OE2	2.948
5FHC	L_HIS_189	ND1	L_ASP_151	OD2	3.045
5FHC	H_ARG_38	NH1	H_ASP_86	OD1	2.743
5FHC	H_ARG_38	NH2	H_GLU_46	OE1	3.708
5FHC	H_ARG_38	NH2	H_GLU_46	OE2	3.194
5FHC	H_ARG_38	NH2	H_ASP_86	OD1	3.696
5FHC	H_LYS_64	NZ	H_ASP_61	OD1	3.953
5FHC	H_ARG_66	NH1	H_ASP_86	OD1	3.816
5FHC	H_ARG_66	NH1	H_ASP_86	OD2	2.875
5FHC	H_ARG_66	NH2	H_ASP_86	OD1	3.199
5FHC	H_ARG_66	NH2	H_ASP_86	OD2	3.692
5FHC	H_LYS_75	NZ	H_GLU_72	OE1	3.342
5FHC	H_LYS_75	NZ	H_GLU_72	OE2	3.694
5FHC	H_ARG_94	NH2	H_ASP_101	OD1	3.811
5FHC	H_ARG_94	NH2	H_ASP_101	OD2	3.111
5FHC	H_LYS_143	NZ	H_ASP_144	OD1	3.605
5FHC	H_LYS_209	NZ	L_GLU_123	OE1	3.238
5FHC	H_LYS_209	NZ	L_GLU_123	OE2	3.173
5FHC	H_LYS_210	NZ	H_GLU_212	OE1	3.977
5FHC	H_LYS_210	NZ	H_GLU_212	OE2	2.157
5HJ3	C_HIS_39	NE2	C_ASP_55	OD1	3.393
5HJ3	C_ARG_64	NH1	C_GLU_100	OE2	3.438
5HJ3	C_ARG_85	NH1	C_GLU_178	OE1	3.195

5HJ3	C_ARG_85	NH2	C_GLU_178	OE1	2.394
5HJ3	C_ARG_85	NH2	C_GLU_178	OE2	2.812
5HJ3	C_ARG_130	NH2	C_ASP_163	OD2	3.561
5HJ3	C_ARG_136	NH2	C_GLU_106	OE2	3.743
5HJ3	C_HIS_154	NE2	C_GLU_178	OE2	2.920
5HJ3	C_ARG_164	NH2	C_ASP_163	OD1	3.508
5HJ3	C_ARG_164	NH2	C_ASP_163	OD2	2.651
5HJ3	D_LYS_510	NZ	J_GLU_55	OE1	3.743
5HJ3	D_LYS_510	NZ	J_GLU_55	OE2	3.493
5HJ3	D_HIS_516	NE2	D_GLU_545	OE1	2.622
5HJ3	D_ARG_559	NH2	C_GLU_103	OE1	2.496
5HJ3	D_ARG_559	NH2	C_GLU_103	OE2	2.573
5HJ3	E_ARG_33	NH1	E_GLU_95	OE1	3.015
5HJ3	E_ARG_33	NH1	E_GLU_95	OE2	3.055
5HJ3	E_ARG_38	NH1	E_GLU_46	OE1	3.787
5HJ3	E_ARG_38	NH1	E_GLU_46	OE2	2.695
5HJ3	E_ARG_38	NH2	E_ASP_86	OD1	2.624
5HJ3	E_ARG_66	NH1	E_ASP_86	OD1	3.916
5HJ3	E_ARG_66	NH1	E_ASP_86	OD2	2.722
5HJ3	E_ARG_66	NH2	E_ASP_86	OD1	3.391
5HJ3	E_ARG_66	NH2	E_ASP_86	OD2	3.561
5HJ3	E_ARG_94	NH2	E_ASP_101	OD1	3.948
5HJ3	E_ARG_94	NH2	E_ASP_101	OD2	2.561
5HJ3	E_ARG_98	NH1	E_ASP_100F	OD1	3.696
5HJ3	E_ARG_98	NH1	E_ASP_100F	OD2	2.997
5HJ3	E_LYS_145	NZ	E_ASP_146	OD1	2.852
5HJ3	E_LYS_145	NZ	E_ASP_146	OD2	2.810
5HJ3	E_LYS_221	NZ	F_GLU_123	OE2	3.658
5HJ3	F_ARG_61	NH2	F_ASP_82	OD1	3.037
5HJ3	F_ARG_61	NH2	F_ASP_82	OD2	3.919
5HJ3	F_ARG_142	NH2	F_GLU_105	OE1	2.744
5HJ3	G_HIS_39	NE2	G_ASP_55	OD1	3.217
5HJ3	G_ARG_64	NH1	G_GLU_100	OE2	3.233
5HJ3	G_ARG_85	NH1	G_GLU_178	OE1	3.267
5HJ3	G_ARG_85	NH2	G_GLU_178	OE1	2.478
5HJ3	G_ARG_85	NH2	G_GLU_178	OE2	2.771
5HJ3	G_ARG_130	NH2	G_ASP_163	OD2	3.392
5HJ3	G_HIS_154	NE2	G_GLU_178	OE2	2.990
5HJ3	G_ARG_164	NH2	G_ASP_163	OD1	3.521
5HJ3	G_ARG_164	NH2	G_ASP_163	OD2	2.692
5HJ3	H_LYS_510	NZ	F_GLU_55	OE2	3.815
5HJ3	H_HIS_516	NE2	H_GLU_545	OE1	2.614
5HJ3	H_ARG_559	NH2	G_GLU_103	OE1	2.521
5HJ3	H_ARG_559	NH2	G_GLU_103	OE2	2.719
5HJ3	I_ARG_33	NH1	I_GLU_95	OE1	2.790
5HJ3	I_ARG_33	NH1	I_GLU_95	OE2	3.012
5HJ3	I_ARG_38	NH1	I_GLU_46	OE1	3.771
5HJ3	I_ARG_38	NH1	I_GLU_46	OE2	2.572
5HJ3	I_ARG_38	NH2	I_ASP_86	OD1	2.596
5HJ3	I_ARG_66	NH1	I_ASP_86	OD2	2.716
5HJ3	I_ARG_66	NH2	I_ASP_86	OD1	3.241
5HJ3	I_ARG_66	NH2	I_ASP_86	OD2	3.167
5HJ3	I_ARG_94	NH2	I_ASP_101	OD1	3.512
5HJ3	I_ARG_94	NH2	I_ASP_101	OD2	2.751
5HJ3	I_ARG_98	NH1	I_ASP_100F	OD1	3.834
5HJ3	I_ARG_98	NH1	I_ASP_100F	OD2	3.081
5HJ3	I_LYS_145	NZ	I_ASP_146	OD1	2.788
5HJ3	I_LYS_145	NZ	I_ASP_146	OD2	2.739

5HJ3	I_HIS_172	NE2	J_ASP_167	OD2	3.705
5HJ3	I_LYS_221	NZ	J_GLU_123	OE1	3.253
5HJ3	I_LYS_221	NZ	J_GLU_123	OE2	2.800
5HJ3	J_ARG_61	NH2	J_ASP_82	OD1	2.701
5HJ3	J_ARG_61	NH2	J_ASP_82	OD2	3.572
5HJ3	J_ARG_142	NH2	J_GLU_105	OE1	2.682
5HJ3	J_LYS_145	NZ	J_GLU_161	OE2	3.678
5HJ3	J_LYS_149	NZ	J_GLU_195	OE1	2.603
5HJ3	J_LYS_188	NZ	J_ASP_185	OD2	3.757
5HJ3	J_HIS_189	ND1	J_ASP_151	OD1	3.934
5HJ3	J_HIS_189	ND1	J_ASP_151	OD2	2.742
5HJ3	K_HIS_39	NE2	K_ASP_55	OD1	3.802
5HJ3	K_ARG_64	NH1	K_GLU_100	OE2	3.581
5HJ3	K_ARG_85	NH1	K_GLU_178	OE1	3.179
5HJ3	K_ARG_85	NH2	K_GLU_178	OE1	2.573
5HJ3	K_ARG_85	NH2	K_GLU_178	OE2	2.682
5HJ3	K_ARG_130	NH2	K_ASP_163	OD2	3.783
5HJ3	K_HIS_154	NE2	K_GLU_178	OE2	3.079
5HJ3	K_ARG_164	NH2	K_ASP_163	OD1	3.726
5HJ3	K_ARG_164	NH2	K_ASP_163	OD2	2.770
5HJ3	L_HIS_516	NE2	L_GLU_545	OE1	2.683
5HJ3	L_ARG_559	NH2	K_GLU_103	OE1	2.680
5HJ3	L_ARG_559	NH2	K_GLU_103	OE2	2.484
5HJ3	L_HIS_602	ND1	H_GLU_611	OE1	3.679
5HJ3	L_HIS_602	NE2	H_GLU_611	OE1	3.945
5HJ3	M_ARG_33	NH1	M_GLU_95	OE1	2.923
5HJ3	M_ARG_33	NH1	M_GLU_95	OE2	2.923
5HJ3	M_ARG_38	NH1	M_ASP_86	OD1	3.188
5HJ3	M_ARG_38	NH2	M_GLU_46	OE1	3.623
5HJ3	M_ARG_38	NH2	M_GLU_46	OE2	2.841
5HJ3	M_ARG_66	NH1	M_ASP_86	OD1	3.810
5HJ3	M_ARG_66	NH1	M_ASP_86	OD2	2.388
5HJ3	M_ARG_66	NH2	M_ASP_86	OD1	2.897
5HJ3	M_ARG_66	NH2	M_ASP_86	OD2	2.965
5HJ3	M_ARG_94	NH2	M_ASP_101	OD1	3.853
5HJ3	M_ARG_94	NH2	M_ASP_101	OD2	2.629
5HJ3	M_ARG_98	NH1	M_ASP_100F	OD1	3.630
5HJ3	M_ARG_98	NH1	M_ASP_100F	OD2	2.969
5HJ3	M_LYS_145	NZ	M_ASP_146	OD1	3.782
5HJ3	M_LYS_145	NZ	M_ASP_146	OD2	3.675
5HJ3	M_LYS_221	NZ	N_GLU_123	OE1	3.397
5HJ3	M_LYS_221	NZ	N_GLU_123	OE2	3.011
5HJ3	N_ARG_61	NH2	N_ASP_82	OD1	3.282
5HJ3	N_ARG_142	NH2	N_GLU_105	OE1	2.640
5HJ3	N_LYS_149	NZ	N_GLU_195	OE1	2.786
5HJ3	O_HIS_39	NE2	O_ASP_55	OD1	3.321
5HJ3	O_ARG_64	NH1	O_GLU_100	OE2	3.235
5HJ3	O_ARG_85	NH1	O_GLU_178	OE1	3.339
5HJ3	O_ARG_85	NH2	O_GLU_178	OE1	2.457
5HJ3	O_ARG_85	NH2	O_GLU_178	OE2	2.948
5HJ3	O_ARG_130	NH2	O_ASP_163	OD2	3.468
5HJ3	O_ARG_136	NH2	O_GLU_106	OE2	3.955
5HJ3	O_HIS_154	NE2	O_GLU_178	OE2	2.840
5HJ3	O_ARG_164	NH2	O_ASP_163	OD1	3.663
5HJ3	O_ARG_164	NH2	O_ASP_163	OD2	2.780
5HJ3	P_LYS_510	NZ	B_GLU_55	OE1	3.843
5HJ3	P_LYS_510	NZ	B_GLU_55	OE2	3.553
5HJ3	P_HIS_516	NE2	P_GLU_545	OE1	2.882

5HJ3	P_ARG_559	NH2	O_GLU_103	OE1	2.547
5HJ3	P_ARG_559	NH2	O_GLU_103	OE2	2.625
5HJ3	P_HIS_602	NE2	L_GLU_611	OE1	3.277
5HJ3	A_ARG_33	NH1	A_GLU_95	OE1	2.660
5HJ3	A_ARG_33	NH1	A_GLU_95	OE2	3.038
5HJ3	A_ARG_38	NH1	A_GLU_46	OE1	3.725
5HJ3	A_ARG_38	NH1	A_GLU_46	OE2	2.619
5HJ3	A_ARG_38	NH2	A_ASP_86	OD1	2.771
5HJ3	A_ARG_66	NH1	A_ASP_86	OD1	3.710
5HJ3	A_ARG_66	NH1	A_ASP_86	OD2	2.544
5HJ3	A_ARG_66	NH2	A_ASP_86	OD1	3.134
5HJ3	A_ARG_66	NH2	A_ASP_86	OD2	3.423
5HJ3	A_ARG_94	NH2	A_ASP_101	OD1	3.718
5HJ3	A_ARG_94	NH2	A_ASP_101	OD2	2.938
5HJ3	A_ARG_98	NH1	A_ASP_100F	OD1	3.722
5HJ3	A_ARG_98	NH1	A_ASP_100F	OD2	2.936
5HJ3	A_LYS_145	NZ	A_ASP_146	OD1	2.925
5HJ3	A_LYS_145	NZ	A_ASP_146	OD2	2.830
5HJ3	A_LYS_221	NZ	B_GLU_123	OE1	3.583
5HJ3	A_LYS_221	NZ	B_GLU_123	OE2	3.404
5HJ3	B_ARG_61	NH2	B_ASP_82	OD1	3.154
5HJ3	B_ARG_142	NH2	B_GLU_105	OE1	3.025
5HJ3	B_LYS_188	NZ	B_ASP_185	OD2	3.880
5HJ3	B_HIS_189	ND1	B_ASP_151	OD2	2.951
5JNX	A_LYS_38	NZ	A_ASP_37	OD1	3.268
5JNX	A_LYS_84	NZ	A_GLU_61	OE1	2.923
5JNX	A_LYS_84	NZ	A_GLU_61	OE2	2.871
5JNX	A_LYS_142	NZ	A_GLU_127	OE1	2.943
5JNX	A_LYS_171	NZ	A_GLU_164	OE2	3.483
5JNX	A_ARG_389	NH1	A_GLU_393	OE2	3.992
5JNX	A_LYS_392	NZ	A_ASP_396	OD1	3.754
5JNX	A_ARG_404	NH1	A_GLU_606	OE1	3.028
5JNX	A_ARG_404	NH1	A_GLU_606	OE2	3.947
5JNX	A_ARG_404	NH2	A_GLU_584	OE1	3.703
5JNX	A_HIS_441	ND1	A_ASP_496	OD1	3.845
5JNX	A_HIS_441	NE2	A_ASP_496	OD1	2.206
5JNX	A_HIS_441	NE2	A_ASP_496	OD2	3.645
5JNX	A_HIS_492	NE2	A_ASP_445	OD1	3.105
5JNX	A_HIS_510	ND1	A_ASP_508	OD2	3.286
5JNX	A_HIS_512	ND1	A_ASP_525	OD2	2.862
5JNX	A_ARG_579	NH2	A_ASP_466	OD2	3.380
5JNX	A_ARG_607	NH1	A_ASP_611	OD2	3.972
5JNX	A_ARG_1059	NH2	A_GLU_391	OE1	2.950
5JNX	A_ARG_1059	NH2	A_GLU_391	OE2	3.638
5JNX	A_ARG_1059	NH2	A_GLU_1089	OE1	3.854
5JNX	A_ARG_1059	NH2	A_GLU_1089	OE2	3.604
5JNX	A_HIS_1170	ND1	A_GLU_1166	OE1	3.445
5JNX	A_HIS_1170	NE2	A_GLU_688	OE2	2.924
5JNX	C_HIS_39	NE2	C_ASP_55	OD1	3.998
5JNX	C_ARG_64	NH1	C_GLU_100	OE1	3.273
5JNX	C_ARG_64	NH1	C_GLU_100	OE2	3.875
5JNX	C_ARG_85	NH2	C_GLU_178	OE1	2.663
5JNX	C_ARG_85	NH2	C_GLU_178	OE2	3.814
5JNX	C_ARG_130	NH2	C_ASP_163	OD2	3.179
5JNX	C_ARG_134	NH1	D_GLU_545	OE2	3.659
5JNX	C_HIS_154	NE2	C_GLU_178	OE2	2.610
5JNX	C_ARG_164	NH2	C_ASP_163	OD1	3.605
5JNX	C_ARG_164	NH2	C_ASP_163	OD2	3.318

5JNX	D_HIS_516	NE2	D_GLU_545	OE1	3.961
5JNX	D_ARG_559	NH1	C_GLU_103	OE1	3.220
5JNX	D_ARG_559	NH1	C_GLU_103	OE2	3.450
5JNX	D_ARG_559	NH2	C_GLU_103	OE1	3.927
5JNX	D_ARG_559	NH2	C_GLU_103	OE2	2.697
5JNX	D_LYS_588	NZ	C_ASP_47	OD1	3.551
5JNX	D_LYS_588	NZ	C_ASP_47	OD2	3.521
5JNX	E_HIS_39	NE2	E_ASP_55	OD1	3.998
5JNX	E_ARG_64	NH1	E_GLU_100	OE1	3.272
5JNX	E_ARG_64	NH1	E_GLU_100	OE2	3.876
5JNX	E_ARG_85	NH2	E_GLU_178	OE1	2.403
5JNX	E_ARG_85	NH2	E_GLU_178	OE2	3.424
5JNX	E_ARG_130	NH2	E_ASP_163	OD2	3.179
5JNX	E_ARG_134	NH1	F_GLU_545	OE2	3.660
5JNX	E_HIS_154	NE2	E_GLU_178	OE2	2.610
5JNX	E_LYS_155	NZ	A_ASP_502	OD2	3.701
5JNX	E_ARG_164	NH2	E_ASP_163	OD1	3.605
5JNX	E_ARG_164	NH2	E_ASP_163	OD2	3.317
5JNX	F_HIS_516	NE2	F_GLU_545	OE1	3.961
5JNX	F_ARG_559	NH1	E_GLU_103	OE1	3.219
5JNX	F_ARG_559	NH1	E_GLU_103	OE2	3.448
5JNX	F_ARG_559	NH2	E_GLU_103	OE1	3.927
5JNX	F_ARG_559	NH2	E_GLU_103	OE2	2.697
5JNX	F_LYS_588	NZ	E_ASP_47	OD1	3.552
5JNX	F_LYS_588	NZ	E_ASP_47	OD2	3.520
5JNX	G_HIS_39	NE2	G_ASP_55	OD1	3.998
5JNX	G_ARG_64	NH1	G_GLU_100	OE1	3.273
5JNX	G_ARG_64	NH1	G_GLU_100	OE2	3.876
5JNX	G_ARG_85	NH2	G_GLU_178	OE1	2.663
5JNX	G_ARG_85	NH2	G_GLU_178	OE2	3.813
5JNX	G_ARG_130	NH2	G_ASP_163	OD2	3.180
5JNX	G_ARG_134	NH1	H_GLU_545	OE2	3.659
5JNX	G_HIS_154	NE2	G_GLU_178	OE2	2.610
5JNX	G_ARG_164	NH2	G_ASP_163	OD1	3.606
5JNX	G_ARG_164	NH2	G_ASP_163	OD2	3.318
5JNX	H_HIS_516	NE2	H_GLU_545	OE1	3.961
5JNX	H_ARG_559	NH1	G_GLU_103	OE1	3.221
5JNX	H_ARG_559	NH1	G_GLU_103	OE2	3.449
5JNX	H_ARG_559	NH2	G_GLU_103	OE1	3.928
5JNX	H_ARG_559	NH2	G_GLU_103	OE2	2.697
5JNX	H_LYS_588	NZ	G_ASP_47	OD1	3.552
5JNX	H_LYS_588	NZ	G_ASP_47	OD2	3.522
5JQ3	A_HIS_39	NE2	A_ASP_55	OD1	2.911
5JQ3	A_HIS_39	NE2	A_ASP_55	OD2	3.472
5JQ3	A_ARG_85	NH1	A_GLU_178	OE1	3.536
5JQ3	A_ARG_85	NH1	A_GLU_178	OE2	2.746
5JQ3	A_LYS_114	NZ	A_GLU_120	OE1	3.849
5JQ3	A_LYS_114	NZ	A_GLU_120	OE2	3.453
5JQ3	A_ARG_130	NH2	A_ASP_163	OD1	3.021
5JQ3	A_HIS_154	NE2	A_GLU_178	OE1	2.776
5JQ3	A_ARG_164	NH1	A_ASP_163	OD1	3.056
5JQ3	A_ARG_164	NH1	A_ASP_163	OD2	3.532
5JQ3	A_ARG_266	NH2	A_ASP_237	OD2	3.203
5JQ3	B_HIS_516	NE2	B_GLU_545	OE1	2.971
5JQ3	B_ARG_559	NH1	A_GLU_103	OE1	2.754
5JQ3	B_ARG_559	NH1	A_GLU_103	OE2	3.830
5JQ3	B_ARG_559	NH2	A_GLU_103	OE1	3.362
5JQ3	B_ARG_559	NH2	A_GLU_103	OE2	2.945

5JQ7	A_HIS_39	NE2	A_ASP_55	OD1	3.302
5JQ7	A_HIS_39	NE2	A_ASP_55	OD2	2.805
5JQ7	A_ARG_85	NH1	A_GLU_178	OE1	3.344
5JQ7	A_ARG_85	NH1	A_GLU_178	OE2	2.714
5JQ7	A_LYS_114	NZ	A_GLU_120	OE2	3.552
5JQ7	A_ARG_130	NH2	A_ASP_163	OD1	2.926
5JQ7	A_HIS_154	NE2	A_GLU_178	OE1	2.770
5JQ7	A_ARG_164	NH1	A_ASP_163	OD1	2.933
5JQ7	A_ARG_164	NH1	A_ASP_163	OD2	3.613
5JQ7	A_ARG_247	NH1	A_GLU_245	OE1	3.700
5JQ7	A_ARG_247	NH1	A_GLU_245	OE2	3.859
5JQ7	A_ARG_266	NH2	A_ASP_237	OD2	3.168
5JQ7	B_LYS_510	NZ	A_GLU_292	OE1	3.131
5JQ7	B_HIS_516	NE2	B_GLU_545	OE1	2.658
5JQ7	B_ARG_559	NH1	A_GLU_103	OE1	2.800
5JQ7	B_ARG_559	NH1	A_GLU_103	OE2	3.720
5JQ7	B_ARG_559	NH2	A_GLU_103	OE1	3.375
5JQ7	B_ARG_559	NH2	A_GLU_103	OE2	2.748
5JQ7	B_HIS_613	NE2	B_ASP_614	OD1	3.865
5JQB	A_ARG_85	NH1	A_GLU_178	OE1	3.533
5JQB	A_ARG_85	NH1	A_GLU_178	OE2	2.805
5JQB	A_LYS_114	NZ	A_GLU_120	OE2	3.275
5JQB	A_ARG_130	NH2	A_ASP_163	OD1	3.034
5JQB	A_HIS_154	NE2	A_GLU_178	OE1	2.801
5JQB	A_ARG_164	NH1	A_ASP_163	OD1	2.868
5JQB	A_ARG_164	NH1	A_ASP_163	OD2	3.537
5JQB	A_ARG_247	NH1	A_GLU_245	OE1	3.146
5JQB	A_ARG_266	NH2	A_ASP_237	OD2	3.033
5JQB	B_LYS_510	NZ	A_GLU_292	OE1	2.746
5JQB	B_LYS_510	NZ	A_GLU_292	OE2	3.918
5JQB	B_HIS_516	NE2	B_GLU_545	OE1	2.749
5JQB	B_ARG_559	NH1	A_GLU_103	OE1	2.703
5JQB	B_ARG_559	NH1	A_GLU_103	OE2	3.788
5JQB	B_ARG_559	NH2	A_GLU_103	OE1	3.188
5JQB	B_ARG_559	NH2	A_GLU_103	OE2	2.857
5JQB	B_LYS_588	NZ	A_ASP_47	OD1	3.558
5JQB	B_LYS_588	NZ	A_ASP_47	OD2	3.148
5JQB	B_LYS_617	NZ	B_ASP_614	OD1	3.955
5KEL	A_ARG_85	NH2	A_GLU_178	OE1	2.875
5KEL	A_ARG_85	NH2	A_GLU_178	OE2	3.676
5KEL	A_LYS_114	NZ	A_GLU_120	OE2	2.853
5KEL	A_ARG_130	NH1	B_GLU_540	OE2	3.053
5KEL	A_ARG_130	NH2	A_ASP_163	OD1	3.103
5KEL	A_ARG_164	NH2	A_GLU_100	OE1	3.728
5KEL	A_ARG_164	NH2	A_GLU_100	OE2	2.804
5KEL	A_ARG_172	NH1	A_GLU_120	OE1	2.760
5KEL	A_ARG_172	NH2	A_GLU_112	OE1	3.171
5KEL	A_ARG_172	NH2	A_GLU_120	OE1	2.755
5KEL	A_ARG_219	NH1	A_GLU_235	OE2	2.800
5KEL	A_ARG_219	NH2	A_GLU_235	OE2	3.004
5KEL	A_ARG_247	NH1	A_GLU_245	OE2	3.112
5KEL	A_ARG_247	NH2	A_GLU_245	OE2	3.134
5KEL	A_LYS_272	NZ	C_ASP_54	OD2	3.464
5KEL	A_LYS_272	NZ	C_ASP_56	OD2	2.595
5KEL	A_ARG_299	NH2	A_GLU_304	OE1	3.032
5KEL	A_ARG_299	NH2	A_GLU_304	OE2	3.954
5KEL	A_ARG_302	NH1	A_GLU_304	OE2	3.084
5KEL	A_ARG_302	NH2	A_GLU_258	OE2	2.817

5KEL	B_HIS_516	NE2	B_GLU_545	OE1	2.855
5KEL	B_ARG_559	NH1	A_GLU_103	OE2	3.831
5KEL	B_ARG_559	NH2	A_GLU_103	OE1	3.279
5KEL	B_ARG_559	NH2	A_GLU_103	OE2	3.801
5KEL	B_ARG_596	NH2	B_ASP_607	OD1	3.037
5KEL	H_ARG_38	NH1	H_ASP_86	OD1	3.058
5KEL	H_ARG_38	NH2	H_GLU_46	OE2	2.878
5KEL	H_ARG_52	NH1	H_GLU_50	OE2	3.140
5KEL	H_LYS_64	NZ	H_GLU_61	OE1	3.895
5KEL	H_LYS_64	NZ	H_GLU_61	OE2	2.690
5KEL	H_ARG_66	NH1	H_ASP_86	OD1	3.110
5KEL	H_ARG_66	NH1	H_ASP_86	OD2	3.688
5KEL	H_ARG_66	NH2	H_ASP_86	OD1	3.615
5KEL	H_ARG_66	NH2	H_ASP_86	OD2	2.807
5KEL	H_ARG_71	NH2	H_ASP_73	OD1	2.936
5KEL	H_ARG_71	NH2	H_ASP_73	OD2	3.775
5KEL	H_ARG_83	NH1	H_GLU_85	OE1	3.189
5KEL	H_ARG_83	NH2	H_GLU_85	OE1	3.016
5KEL	L_ARG_61	NH1	L_ASP_82	OD2	2.735
5KEL	L_ARG_61	NH2	L_GLU_81	OE2	3.025
5KEL	L_ARG_61	NH2	L_ASP_82	OD1	3.676
5KEL	L_ARG_61	NH2	L_ASP_82	OD2	2.981
5KEL	L_LYS_107	NZ	L_GLU_17	OE1	2.902
5KEL	L_LYS_107	NZ	L_GLU_17	OE2	3.185
5KEL	C_LYS_3	NZ	C_ASP_1	OD1	2.754
5KEL	C_LYS_3	NZ	C_ASP_1	OD2	3.442
5KEL	C_ARG_38	NH1	C_ASP_86	OD1	3.057
5KEL	C_ARG_38	NH2	C_GLU_46	OE1	3.665
5KEL	C_ARG_38	NH2	C_GLU_46	OE2	3.228
5KEL	C_ARG_38	NH2	C_ASP_86	OD1	3.984
5KEL	C_LYS_71	NZ	C_ASP_55	OD1	2.808
5KEL	C_ARG_75	NH2	C_ASP_72	OD2	2.896
5KEL	D_LYS_24	NZ	D_ASP_70	OD1	2.745
5KEL	D_LYS_24	NZ	D_ASP_70	OD2	3.810
5KEL	D_ARG_61	NH1	D_GLU_81	OE2	3.962
5KEL	D_ARG_61	NH2	D_GLU_81	OE2	2.780
5KEL	D_ARG_61	NH2	D_ASP_82	OD1	2.856
5KEL	D_ARG_61	NH2	D_ASP_82	OD2	3.346
5KEL	D_ARG_107	NH1	D_GLU_105	OE2	2.791
5KEL	E_ARG_85	NH2	E_GLU_178	OE1	2.875
5KEL	E_ARG_85	NH2	E_GLU_178	OE2	3.677
5KEL	E_LYS_114	NZ	E_GLU_120	OE2	2.853
5KEL	E_ARG_130	NH1	G_GLU_540	OE2	3.054
5KEL	E_ARG_130	NH2	E_ASP_163	OD1	3.104
5KEL	E_ARG_164	NH2	E_GLU_100	OE1	3.728
5KEL	E_ARG_164	NH2	E_GLU_100	OE2	2.804
5KEL	E_ARG_172	NH1	E_GLU_120	OE1	2.760
5KEL	E_ARG_172	NH2	E_GLU_112	OE1	3.171
5KEL	E_ARG_172	NH2	E_GLU_120	OE1	2.755
5KEL	E_ARG_219	NH1	E_GLU_235	OE2	2.800
5KEL	E_ARG_219	NH2	E_GLU_235	OE2	3.003
5KEL	E_ARG_247	NH1	E_GLU_245	OE2	3.112
5KEL	E_ARG_247	NH2	E_GLU_245	OE2	3.134
5KEL	E_LYS_272	NZ	J_ASP_54	OD2	3.464
5KEL	E_LYS_272	NZ	J_ASP_56	OD2	2.596
5KEL	E_ARG_299	NH2	E_GLU_304	OE1	3.031
5KEL	E_ARG_299	NH2	E_GLU_304	OE2	3.954
5KEL	E_ARG_302	NH1	E_GLU_304	OE2	3.085

5KEL	E_ARG_302	NH2	E_GLU_258	OE2	2.816
5KEL	G_HIS_516	NE2	G_GLU_545	OE1	2.855
5KEL	G_ARG_559	NH1	E_GLU_103	OE2	3.832
5KEL	G_ARG_559	NH2	E_GLU_103	OE1	3.279
5KEL	G_ARG_559	NH2	E_GLU_103	OE2	3.802
5KEL	G_ARG_596	NH2	G_ASP_607	OD1	3.038
5KEL	P_ARG_38	NH1	P_ASP_86	OD1	3.058
5KEL	P_ARG_38	NH2	P_GLU_46	OE2	2.878
5KEL	P_ARG_52	NH1	P_GLU_50	OE2	3.140
5KEL	P_LYS_64	NZ	P_GLU_61	OE1	3.894
5KEL	P_LYS_64	NZ	P_GLU_61	OE2	2.690
5KEL	P_ARG_66	NH1	P_ASP_86	OD1	3.110
5KEL	P_ARG_66	NH1	P_ASP_86	OD2	3.688
5KEL	P_ARG_66	NH2	P_ASP_86	OD1	3.615
5KEL	P_ARG_66	NH2	P_ASP_86	OD2	2.807
5KEL	P_ARG_71	NH2	P_ASP_73	OD1	2.936
5KEL	P_ARG_71	NH2	P_ASP_73	OD2	3.775
5KEL	P_ARG_83	NH1	P_GLU_85	OE1	3.188
5KEL	P_ARG_83	NH2	P_GLU_85	OE1	3.017
5KEL	T_ARG_61	NH1	T_ASP_82	OD2	2.735
5KEL	T_ARG_61	NH2	T_GLU_81	OE2	3.025
5KEL	T_ARG_61	NH2	T_ASP_82	OD1	3.676
5KEL	T_ARG_61	NH2	T_ASP_82	OD2	2.981
5KEL	T_LYS_107	NZ	T_GLU_17	OE1	2.903
5KEL	T_LYS_107	NZ	T_GLU_17	OE2	3.186
5KEL	J_LYS_3	NZ	J_ASP_1	OD1	2.754
5KEL	J_LYS_3	NZ	J_ASP_1	OD2	3.442
5KEL	J_ARG_38	NH1	J_ASP_86	OD1	3.057
5KEL	J_ARG_38	NH2	J_GLU_46	OE1	3.665
5KEL	J_ARG_38	NH2	J_GLU_46	OE2	3.228
5KEL	J_ARG_38	NH2	J_ASP_86	OD1	3.983
5KEL	J_LYS_71	NZ	J_ASP_55	OD1	2.808
5KEL	J_ARG_75	NH2	J_ASP_72	OD2	2.896
5KEL	N_LYS_24	NZ	N_ASP_70	OD1	2.744
5KEL	N_LYS_24	NZ	N_ASP_70	OD2	3.810
5KEL	N_ARG_61	NH1	N_GLU_81	OE2	3.962
5KEL	N_ARG_61	NH2	N_GLU_81	OE2	2.781
5KEL	N_ARG_61	NH2	N_ASP_82	OD1	2.855
5KEL	N_ARG_61	NH2	N_ASP_82	OD2	3.346
5KEL	N_ARG_107	NH1	N_GLU_105	OE2	2.791
5KEL	F_ARG_85	NH2	F_GLU_178	OE1	2.875
5KEL	F_ARG_85	NH2	F_GLU_178	OE2	3.677
5KEL	F_LYS_114	NZ	F_GLU_120	OE2	2.853
5KEL	F_ARG_130	NH1	I_GLU_540	OE2	3.053
5KEL	F_ARG_130	NH2	F_ASP_163	OD1	3.103
5KEL	F_ARG_164	NH2	F_GLU_100	OE1	3.728
5KEL	F_ARG_164	NH2	F_GLU_100	OE2	2.804
5KEL	F_ARG_172	NH1	F_GLU_120	OE1	2.760
5KEL	F_ARG_172	NH2	F_GLU_112	OE1	3.170
5KEL	F_ARG_172	NH2	F_GLU_120	OE1	2.755
5KEL	F_ARG_219	NH1	F_GLU_235	OE2	2.799
5KEL	F_ARG_219	NH2	F_GLU_235	OE2	3.003
5KEL	F_ARG_247	NH1	F_GLU_245	OE2	3.112
5KEL	F_ARG_247	NH2	F_GLU_245	OE2	3.134
5KEL	F_LYS_272	NZ	M_ASP_54	OD2	3.463
5KEL	F_LYS_272	NZ	M_ASP_56	OD2	2.596
5KEL	F_ARG_299	NH2	F_GLU_304	OE1	3.032
5KEL	F_ARG_299	NH2	F_GLU_304	OE2	3.954

5KEL	F_ARG_302	NH1	F_GLU_304	OE2	3.084
5KEL	F_ARG_302	NH2	F_GLU_258	OE2	2.816
5KEL	I_HIS_516	NE2	I_GLU_545	OE1	2.855
5KEL	I_ARG_559	NH1	F_GLU_103	OE2	3.831
5KEL	I_ARG_559	NH2	F_GLU_103	OE1	3.279
5KEL	I_ARG_559	NH2	F_GLU_103	OE2	3.801
5KEL	I_ARG_596	NH2	I_ASP_607	OD1	3.037
5KEL	Q_ARG_38	NH1	Q_ASP_86	OD1	3.058
5KEL	Q_ARG_38	NH2	Q_GLU_46	OE2	2.878
5KEL	Q_ARG_52	NH1	Q_GLU_50	OE2	3.140
5KEL	Q_LYS_64	NZ	Q_GLU_61	OE1	3.895
5KEL	Q_LYS_64	NZ	Q_GLU_61	OE2	2.690
5KEL	Q_ARG_66	NH1	Q_ASP_86	OD1	3.110
5KEL	Q_ARG_66	NH1	Q_ASP_86	OD2	3.688
5KEL	Q_ARG_66	NH2	Q_ASP_86	OD1	3.615
5KEL	Q_ARG_66	NH2	Q_ASP_86	OD2	2.807
5KEL	Q_ARG_71	NH2	Q_ASP_73	OD1	2.936
5KEL	Q_ARG_71	NH2	Q_ASP_73	OD2	3.774
5KEL	Q_ARG_83	NH1	Q_GLU_85	OE1	3.189
5KEL	Q_ARG_83	NH2	Q_GLU_85	OE1	3.016
5KEL	U_ARG_61	NH1	U_ASP_82	OD2	2.734
5KEL	U_ARG_61	NH2	U_GLU_81	OE2	3.025
5KEL	U_ARG_61	NH2	U_ASP_82	OD1	3.676
5KEL	U_ARG_61	NH2	U_ASP_82	OD2	2.981
5KEL	U_LYS_107	NZ	U_GLU_17	OE1	2.903
5KEL	U_LYS_107	NZ	U_GLU_17	OE2	3.186
5KEL	M_LYS_3	NZ	M_ASP_1	OD1	2.754
5KEL	M_LYS_3	NZ	M_ASP_1	OD2	3.442
5KEL	M_ARG_38	NH1	M_ASP_86	OD1	3.057
5KEL	M_ARG_38	NH2	M_GLU_46	OE1	3.665
5KEL	M_ARG_38	NH2	M_GLU_46	OE2	3.228
5KEL	M_ARG_38	NH2	M_ASP_86	OD1	3.984
5KEL	M_LYS_71	NZ	M_ASP_55	OD1	2.808
5KEL	M_ARG_75	NH2	M_ASP_72	OD2	2.896
5KEL	O_LYS_24	NZ	O_ASP_70	OD1	2.745
5KEL	O_LYS_24	NZ	O_ASP_70	OD2	3.811
5KEL	O_ARG_61	NH1	O_GLU_81	OE2	3.961
5KEL	O_ARG_61	NH2	O_GLU_81	OE2	2.780
5KEL	O_ARG_61	NH2	O_ASP_82	OD1	2.855
5KEL	O_ARG_61	NH2	O_ASP_82	OD2	3.346
5KEL	O_ARG_107	NH1	O_GLU_105	OE2	2.791
5KEM	C_ARG_24	NH1	C_GLU_70	OE1	3.169
5KEM	C_ARG_24	NH2	C_GLU_70	OE1	2.965
5KEM	C_ARG_61	NH1	C_ASP_82	OD1	3.729
5KEM	C_ARG_61	NH1	C_ASP_82	OD2	2.658
5KEM	C_ARG_61	NH2	C_GLU_81	OE2	3.360
5KEM	C_ARG_61	NH2	C_ASP_82	OD1	3.084
5KEM	C_ARG_61	NH2	C_ASP_82	OD2	3.287
5KEM	C_ARG_103	NH1	C_GLU_105	OE1	2.773
5KEM	C_ARG_103	NH2	C_GLU_105	OE1	2.948
5KEM	B_LYS_12	NZ	B_GLU_10	OE1	3.650
5KEM	B_LYS_12	NZ	B_GLU_10	OE2	2.758
5KEM	B_LYS_19	NZ	B_ASP_81	OD2	2.772
5KEM	B_ARG_38	NH1	B_GLU_46	OE1	2.905
5KEM	B_ARG_38	NH1	B_ASP_86	OD1	3.520
5KEM	B_ARG_38	NH1	B_ASP_86	OD2	3.245
5KEM	B_ARG_38	NH2	B_ASP_86	OD1	2.958
5KEM	B_ARG_38	NH2	B_ASP_86	OD2	3.504

5KEM	B_LYS_53	NZ	B_ASP_31	OD1	2.921
5KEM	B_ARG_64	NH1	B_GLU_46	OE1	3.725
5KEM	B_ARG_64	NH1	B_GLU_46	OE2	2.926
5KEM	B_ARG_64	NH2	B_GLU_46	OE1	3.105
5KEM	B_ARG_64	NH2	B_GLU_46	OE2	3.585
5KEM	B_LYS_83	NZ	B_ASP_85	OD1	3.656
5KEM	B_LYS_83	NZ	B_ASP_85	OD2	2.787
5KEM	D_LYS_3	NZ	D_ASP_1	OD2	2.842
5KEM	D_LYS_43	NZ	D_GLU_46	OE2	2.896
5KEM	D_LYS_57	NZ	D_ASP_55	OD1	3.976
5KEM	D_LYS_57	NZ	D_ASP_55	OD2	2.638
5KEM	D_LYS_71	NZ	D_ASP_56	OD1	2.855
5KEM	D_LYS_71	NZ	D_ASP_56	OD2	3.526
5KEM	D_ARG_75	NH2	D_ASP_72	OD2	2.852
5KEM	D_ARG_94	NH1	D_ASP_96	OD1	3.169
5KEM	D_ARG_94	NH2	D_ASP_96	OD1	3.069
5KEM	E_LYS_24	NZ	E_ASP_70	OD1	3.824
5KEM	E_ARG_54	NH1	E_ASP_60	OD1	2.684
5KEM	E_ARG_54	NH2	E_ASP_60	OD1	2.959
5KEM	E_ARG_61	NH1	E_ASP_82	OD2	3.854
5KEM	E_ARG_107	NH1	E_GLU_105	OE1	2.926
5KEM	E_ARG_107	NH1	E_GLU_105	OE2	3.400
5KEM	A_ARG_85	NH1	A_GLU_178	OE1	2.986
5KEM	A_ARG_85	NH1	A_GLU_178	OE2	3.588
5KEM	A_ARG_85	NH2	A_GLU_178	OE1	3.598
5KEM	A_ARG_85	NH2	A_GLU_178	OE2	2.771
5KEM	A_LYS_114	NZ	A_GLU_112	OE2	2.902
5KEM	A_LYS_114	NZ	A_GLU_120	OE1	2.734
5KEM	A_ARG_172	NH2	A_GLU_112	OE1	2.757
5KEM	A_ARG_219	NH1	A_GLU_235	OE1	3.033
5KEM	A_ARG_247	NH1	A_ASP_282	OD2	3.763
5KEM	A_ARG_247	NH2	A_ASP_282	OD2	3.187
5KEM	A_LYS_272	NZ	D_ASP_54	OD1	2.876
5KEM	A_LYS_272	NZ	D_ASP_54	OD2	3.185
5KEM	A_LYS_272	NZ	A_GLU_235	OE2	2.870
5KEM	H_ARG_24	NH1	H_GLU_70	OE1	3.169
5KEM	H_ARG_24	NH2	H_GLU_70	OE1	2.966
5KEM	H_ARG_61	NH1	H_ASP_82	OD1	3.730
5KEM	H_ARG_61	NH1	H_ASP_82	OD2	2.658
5KEM	H_ARG_61	NH2	H_GLU_81	OE2	3.360
5KEM	H_ARG_61	NH2	H_ASP_82	OD1	3.084
5KEM	H_ARG_61	NH2	H_ASP_82	OD2	3.287
5KEM	H_ARG_103	NH1	H_GLU_105	OE1	2.774
5KEM	H_ARG_103	NH2	H_GLU_105	OE1	2.948
5KEM	G_LYS_12	NZ	G_GLU_10	OE1	3.649
5KEM	G_LYS_12	NZ	G_GLU_10	OE2	2.758
5KEM	G_LYS_19	NZ	G_ASP_81	OD2	2.772
5KEM	G_ARG_38	NH1	G_GLU_46	OE1	2.905
5KEM	G_ARG_38	NH1	G_ASP_86	OD1	3.521
5KEM	G_ARG_38	NH1	G_ASP_86	OD2	3.246
5KEM	G_ARG_38	NH2	G_ASP_86	OD1	2.960
5KEM	G_ARG_38	NH2	G_ASP_86	OD2	3.505
5KEM	G_LYS_53	NZ	G_ASP_31	OD1	2.921
5KEM	G_ARG_64	NH1	G_GLU_46	OE1	3.725
5KEM	G_ARG_64	NH1	G_GLU_46	OE2	2.925
5KEM	G_ARG_64	NH2	G_GLU_46	OE1	3.106
5KEM	G_ARG_64	NH2	G_GLU_46	OE2	3.585
5KEM	G_LYS_83	NZ	G_ASP_85	OD1	3.656

5KEM	G_LYS_83	NZ	G_ASP_85	OD2	2.788
5KEM	I_LYS_3	NZ	I_ASP_1	OD2	2.842
5KEM	I_LYS_43	NZ	I_GLU_46	OE2	2.897
5KEM	I_LYS_57	NZ	I_ASP_55	OD1	3.976
5KEM	I_LYS_57	NZ	I_ASP_55	OD2	2.638
5KEM	I_LYS_71	NZ	I_ASP_56	OD1	2.856
5KEM	I_LYS_71	NZ	I_ASP_56	OD2	3.527
5KEM	I_ARG_75	NH2	I_ASP_72	OD2	2.852
5KEM	I_ARG_94	NH1	I_ASP_96	OD1	3.167
5KEM	I_ARG_94	NH2	I_ASP_96	OD1	3.069
5KEM	J_LYS_24	NZ	J_ASP_70	OD1	3.825
5KEM	J_ARG_54	NH1	J_ASP_60	OD1	2.683
5KEM	J_ARG_54	NH2	J_ASP_60	OD1	2.960
5KEM	J_ARG_61	NH1	J_ASP_82	OD2	3.854
5KEM	J_ARG_107	NH1	J_GLU_105	OE1	2.925
5KEM	J_ARG_107	NH1	J_GLU_105	OE2	3.399
5KEM	F_ARG_85	NH1	F_GLU_178	OE1	2.987
5KEM	F_ARG_85	NH1	F_GLU_178	OE2	3.589
5KEM	F_ARG_85	NH2	F_GLU_178	OE1	3.598
5KEM	F_ARG_85	NH2	F_GLU_178	OE2	2.771
5KEM	F_LYS_114	NZ	F_GLU_112	OE2	2.902
5KEM	F_LYS_114	NZ	F_GLU_120	OE1	2.734
5KEM	F_ARG_172	NH2	F_GLU_112	OE1	2.756
5KEM	F_ARG_219	NH1	F_GLU_235	OE1	3.032
5KEM	F_ARG_247	NH1	F_ASP_282	OD2	3.762
5KEM	F_ARG_247	NH2	F_ASP_282	OD2	3.186
5KEM	F_LYS_272	NZ	I_ASP_54	OD1	2.876
5KEM	F_LYS_272	NZ	I_ASP_54	OD2	3.185
5KEM	F_LYS_272	NZ	F_GLU_235	OE2	2.870
5KEN	A_ARG_54	NH2	A_ASP_55	OD2	3.882
5KEN	A_ARG_85	NH2	A_GLU_178	OE1	3.646
5KEN	A_ARG_85	NH2	A_GLU_178	OE2	2.914
5KEN	A_ARG_130	NH2	A_ASP_163	OD1	3.381
5KEN	A_ARG_134	NH2	B_GLU_545	OE1	2.859
5KEN	A_ARG_136	NH1	A_GLU_106	OE2	2.734
5KEN	A_LYS_140	NZ	A_GLU_112	OE2	3.961
5KEN	A_HIS_154	NE2	A_GLU_178	OE1	2.777
5KEN	A_ARG_164	NH2	A_GLU_100	OE1	3.828
5KEN	A_ARG_164	NH2	A_GLU_100	OE2	3.033
5KEN	A_ARG_172	NH2	A_GLU_112	OE1	3.530
5KEN	B_LYS_510	NZ	D_GLU_56	OE1	3.639
5KEN	B_LYS_510	NZ	D_GLU_56	OE2	2.773
5KEN	B_HIS_549	NE2	C_ASP_52	OD1	3.874
5KEN	B_ARG_559	NH1	A_GLU_103	OE1	3.709
5KEN	B_ARG_559	NH1	A_GLU_103	OE2	2.818
5KEN	B_ARG_559	NH2	A_GLU_103	OE1	3.114
5KEN	B_ARG_559	NH2	A_GLU_103	OE2	3.662
5KEN	B_ARG_596	NH2	B_ASP_607	OD1	3.053
5KEN	C_LYS_38	NZ	C_GLU_46	OE1	2.804
5KEN	C_LYS_38	NZ	C_GLU_46	OE2	3.887
5KEN	D_ARG_61	NH2	D_GLU_81	OE2	2.826
5KEN	D_ARG_61	NH2	D_ASP_82	OD1	3.556
5KEN	D_ARG_61	NH2	D_ASP_82	OD2	2.823
5KEN	D_LYS_107	NZ	D_GLU_17	OE1	3.537
5KEN	D_LYS_107	NZ	D_GLU_17	OE2	2.886
5KEN	E_HIS_39	ND1	E_ASP_55	OD1	2.715
5KEN	E_HIS_39	ND1	E_ASP_55	OD2	3.363
5KEN	E_ARG_85	NH2	E_GLU_178	OE1	3.714

5KEN	E_ARG_85	NH2	E_GLU_178	OE2	3.034
5KEN	E_ARG_130	NH1	E_ASP_163	OD1	2.771
5KEN	E_ARG_136	NH1	E_GLU_106	OE2	2.733
5KEN	E_LYS_140	NZ	E_GLU_112	OE2	2.756
5KEN	E_HIS_154	NE2	E_GLU_178	OE1	2.772
5KEN	E_ARG_164	NH2	E_GLU_100	OE1	3.488
5KEN	E_ARG_164	NH2	E_GLU_100	OE2	3.760
5KEN	E_LYS_272	NZ	J_ASP_54	OD2	3.722
5KEN	E_LYS_272	NZ	J_ASP_56	OD1	3.736
5KEN	E_LYS_272	NZ	J_ASP_56	OD2	2.765
5KEN	E_LYS_276	NZ	E_GLU_245	OE1	3.431
5KEN	E_LYS_276	NZ	E_GLU_245	OE2	2.793
5KEN	E_ARG_299	NH1	E_GLU_304	OE1	2.918
5KEN	E_ARG_299	NH1	E_GLU_305	OE2	3.083
5KEN	E_ARG_299	NH2	E_GLU_305	OE2	2.937
5KEN	E_ARG_302	NH1	E_GLU_304	OE2	2.810
5KEN	E_ARG_302	NH2	E_GLU_258	OE2	2.806
5KEN	F_LYS_510	NZ	H_GLU_56	OE2	2.720
5KEN	F_HIS_516	NE2	F_GLU_545	OE1	2.865
5KEN	F_HIS_549	NE2	G_ASP_52	OD1	3.491
5KEN	F_ARG_559	NH1	E_GLU_103	OE1	3.868
5KEN	F_ARG_559	NH1	E_GLU_103	OE2	2.947
5KEN	F_ARG_559	NH2	E_GLU_103	OE1	3.043
5KEN	F_ARG_559	NH2	E_GLU_103	OE2	3.542
5KEN	F_ARG_596	NH2	F_ASP_607	OD1	2.978
5KEN	F_HIS_613	ND1	F_ASP_614	OD2	3.831
5KEN	G_LYS_38	NZ	G_GLU_46	OE1	2.811
5KEN	G_LYS_38	NZ	G_GLU_46	OE2	3.954
5KEN	G_LYS_62	NZ	H_ASP_1	OD2	2.735
5KEN	H_ARG_61	NH2	H_GLU_81	OE2	2.864
5KEN	H_ARG_61	NH2	H_ASP_82	OD1	3.570
5KEN	H_ARG_61	NH2	H_ASP_82	OD2	2.811
5KEN	H_LYS_107	NZ	H_GLU_17	OE1	3.562
5KEN	H_LYS_107	NZ	H_GLU_17	OE2	2.967
5KEN	I_LYS_24	NZ	I_ASP_70	OD1	2.714
5KEN	I_LYS_24	NZ	I_ASP_70	OD2	3.786
5KEN	I_ARG_54	NH1	I_ASP_60	OD1	3.072
5KEN	I_ARG_61	NH1	I_GLU_81	OE2	3.750
5KEN	I_ARG_61	NH2	I_GLU_81	OE2	2.708
5KEN	I_ARG_61	NH2	I_ASP_82	OD1	2.808
5KEN	I_ARG_61	NH2	I_ASP_82	OD2	3.337
5KEN	I_LYS_103	NZ	I_GLU_105	OE2	2.881
5KEN	I_ARG_107	NH2	I_GLU_105	OE1	2.726
5KEN	J_LYS_3	NZ	J_ASP_1	OD1	2.794
5KEN	J_LYS_3	NZ	J_ASP_1	OD2	3.424
5KEN	J_ARG_38	NH1	J_ASP_86	OD1	3.024
5KEN	J_ARG_38	NH2	J_GLU_46	OE1	3.864
5KEN	J_ARG_38	NH2	J_GLU_46	OE2	3.398
5KEN	J_ARG_38	NH2	J_ASP_86	OD1	3.399
5KEN	J_LYS_71	NZ	J_ASP_55	OD1	2.827
5KEN	J_ARG_75	NH2	J_ASP_72	OD2	2.956
5KEN	K_HIS_39	ND1	K_ASP_55	OD1	2.793
5KEN	K_HIS_39	ND1	K_ASP_55	OD2	3.278
5KEN	K_ARG_85	NH2	K_GLU_178	OE1	3.673
5KEN	K_ARG_85	NH2	K_GLU_178	OE2	3.020
5KEN	K_LYS_115	NZ	K_ASP_150	OD1	3.600
5KEN	K_ARG_130	NH2	K_ASP_163	OD1	3.177
5KEN	K_ARG_130	NH2	K_ASP_163	OD2	3.766

5KEN	K_ARG_136	NH1	K_GLU_106	OE2	2.803
5KEN	K_LYS_140	NZ	K_GLU_112	OE2	2.762
5KEN	K_HIS_154	NE2	K_GLU_178	OE1	2.705
5KEN	K_ARG_164	NH2	K_GLU_100	OE1	3.437
5KEN	K_ARG_164	NH2	K_GLU_100	OE2	3.533
5KEN	K_ARG_219	NH1	K_GLU_235	OE2	2.859
5KEN	K_ARG_219	NH2	K_GLU_235	OE2	2.957
5KEN	K_LYS_272	NZ	K_GLU_235	OE1	3.796
5KEN	K_LYS_272	NZ	Q_ASP_54	OD2	3.814
5KEN	K_LYS_272	NZ	Q_ASP_56	OD1	3.710
5KEN	K_LYS_272	NZ	Q_ASP_56	OD2	2.769
5KEN	K_ARG_299	NH1	K_GLU_304	OE1	2.978
5KEN	K_ARG_299	NH1	K_GLU_305	OE2	3.152
5KEN	K_ARG_299	NH2	K_GLU_305	OE2	2.878
5KEN	K_ARG_302	NH1	K_GLU_304	OE2	2.982
5KEN	K_ARG_302	NH2	K_GLU_258	OE2	2.830
5KEN	M_LYS_510	NZ	O_GLU_56	OE2	2.667
5KEN	M_HIS_516	NE2	M_GLU_545	OE1	2.888
5KEN	M_ARG_559	NH1	K_GLU_103	OE1	3.708
5KEN	M_ARG_559	NH1	K_GLU_103	OE2	2.824
5KEN	M_ARG_559	NH2	K_GLU_103	OE1	3.090
5KEN	M_ARG_559	NH2	K_GLU_103	OE2	3.645
5KEN	M_ARG_596	NH2	M_ASP_607	OD1	2.995
5KEN	N_LYS_38	NZ	N_ASP_86	OD1	3.887
5KEN	N_LYS_62	NZ	O_ASP_1	OD2	2.793
5KEN	O_ARG_61	NH2	O_GLU_81	OE2	3.700
5KEN	O_ARG_61	NH2	O_ASP_82	OD1	3.662
5KEN	O_ARG_61	NH2	O_ASP_82	OD2	2.905
5KEN	O_LYS_107	NZ	O_GLU_17	OE1	3.531
5KEN	O_LYS_107	NZ	O_GLU_17	OE2	2.981
5KEN	P_LYS_24	NZ	P_ASP_70	OD1	2.736
5KEN	P_LYS_24	NZ	P_ASP_70	OD2	3.714
5KEN	P_ARG_54	NH1	P_ASP_60	OD1	2.965
5KEN	P_ARG_61	NH1	P_GLU_81	OE2	3.801
5KEN	P_ARG_61	NH2	P_GLU_81	OE2	2.727
5KEN	P_ARG_61	NH2	P_ASP_82	OD1	2.822
5KEN	P_ARG_61	NH2	P_ASP_82	OD2	3.338
5KEN	P_ARG_107	NH1	P_GLU_105	OE2	2.824
5KEN	Q_LYS_3	NZ	Q_ASP_1	OD1	2.773
5KEN	Q_LYS_3	NZ	Q_ASP_1	OD2	3.470
5KEN	Q_ARG_38	NH1	Q_ASP_86	OD1	3.016
5KEN	Q_ARG_38	NH2	Q_GLU_46	OE1	3.835
5KEN	Q_ARG_38	NH2	Q_GLU_46	OE2	3.412
5KEN	Q_ARG_38	NH2	Q_ASP_86	OD1	3.365
5KEN	Q_LYS_71	NZ	Q_ASP_55	OD1	2.819
5KEN	Q_ARG_75	NH2	Q_ASP_72	OD2	2.942
5T42-13	A_LYS_633	NZ	A_ASP_642	OD2	2.906
5T42-5	A_LYS_633	NZ	A_ASP_642	OD2	3.987
5T42-8	A_LYS_633	NZ	A_ASP_642	OD2	2.592
6DZL	A_ARG_85	NH2	A_GLU_178	OE1	3.930
6DZL	J_ARG_61	NH2	J_ASP_82	OD2	3.985
6DZL	G_ARG_38	NH1	G_ASP_86	OD1	2.843
6DZL	G_ARG_38	NH2	G_GLU_46	OE1	3.120
6DZL	G_ARG_38	NH2	G_GLU_46	OE2	3.080
6DZL	G_ARG_66	NH2	G_ASP_86	OD2	3.660
6DZL	G_HIS_96	ND1	J_GLU_55	OE2	3.342
6DZL	G_HIS_96	NE2	J_GLU_55	OE1	3.570
6DZL	G_HIS_96	NE2	J_GLU_55	OE2	3.728

6DZL	B_ARG_85	NH2	B_GLU_178	OE1	3.931
6DZL	K_ARG_61	NH2	K_ASP_82	OD2	3.984
6DZL	H_ARG_38	NH1	H_ASP_86	OD1	2.845
6DZL	H_ARG_38	NH2	H_GLU_46	OE1	3.120
6DZL	H_ARG_38	NH2	H_GLU_46	OE2	3.080
6DZL	H_ARG_66	NH2	H_ASP_86	OD2	3.660
6DZL	H_HIS_96	ND1	K_GLU_55	OE2	3.341
6DZL	H_HIS_96	NE2	K_GLU_55	OE1	3.571
6DZL	H_HIS_96	NE2	K_GLU_55	OE2	3.727
6DZL	C_ARG_85	NH2	C_GLU_178	OE1	3.930
6DZL	L_ARG_61	NH2	L_ASP_82	OD2	3.984
6DZL	I_ARG_38	NH1	I_ASP_86	OD1	2.844
6DZL	I_ARG_38	NH2	I_GLU_46	OE1	3.120
6DZL	I_ARG_38	NH2	I_GLU_46	OE2	3.080
6DZL	I_ARG_66	NH2	I_ASP_86	OD2	3.660
6DZL	I_HIS_96	ND1	L_GLU_55	OE2	3.341
6DZL	I_HIS_96	NE2	L_GLU_55	OE1	3.571
6DZL	I_HIS_96	NE2	L_GLU_55	OE2	3.727
6EA7	A_ARG_64	NH1	A_GLU_100	OE1	2.585
6EA7	A_ARG_64	NH1	A_GLU_100	OE2	2.698
6EA7	A_ARG_85	NH1	A_GLU_178	OE2	3.995
6EA7	A_LYS_114	NZ	A_GLU_120	OE2	3.917
6EA7	A_ARG_136	NH1	A_GLU_106	OE1	3.638
6EA7	A_HIS_154	NE2	A_GLU_178	OE1	2.817
6EA7	A_ARG_164	NH1	A_ASP_163	OD1	3.751
6EA7	A_ARG_164	NH1	A_ASP_163	OD2	3.561
6EA7	A_ARG_172	NH1	A_GLU_120	OE2	3.778
6EA7	B_HIS_516	NE2	B_GLU_545	OE1	3.238
6EA7	B_ARG_559	NH1	A_GLU_103	OE1	2.641
6EA7	B_ARG_559	NH1	A_GLU_103	OE2	3.432
6EA7	B_ARG_559	NH2	A_GLU_103	OE2	3.686
6EA7	B_HIS_602	ND1	F_GLU_611	OE1	3.135
6EA7	C_HIS_39	NE2	C_ASP_55	OD1	3.559
6EA7	C_ARG_85	NH1	C_GLU_178	OE1	3.607
6EA7	C_ARG_85	NH1	C_GLU_178	OE2	3.196
6EA7	C_LYS_114	NZ	C_GLU_120	OE2	3.697
6EA7	C_ARG_130	NH2	C_ASP_163	OD2	2.578
6EA7	C_ARG_164	NH1	C_ASP_163	OD1	3.787
6EA7	C_ARG_172	NH1	C_GLU_120	OE2	3.868
6EA7	D_HIS_516	NE2	D_GLU_545	OE1	3.935
6EA7	D_ARG_559	NH1	C_GLU_103	OE1	2.573
6EA7	D_ARG_559	NH1	C_GLU_103	OE2	3.488
6EA7	D_ARG_559	NH2	C_GLU_103	OE1	3.832
6EA7	D_ARG_559	NH2	C_GLU_103	OE2	3.318
6EA7	D_HIS_602	ND1	B_GLU_611	OE1	3.062
6EA7	E_ARG_85	NH1	E_GLU_178	OE1	3.412
6EA7	E_ARG_85	NH1	E_GLU_178	OE2	3.298
6EA7	E_ARG_130	NH2	E_ASP_163	OD2	2.654
6EA7	E_HIS_154	NE2	E_GLU_178	OE1	3.949
6EA7	E_ARG_164	NH1	E_ASP_163	OD1	3.520
6EA7	E_ARG_164	NH1	E_ASP_163	OD2	3.465
6EA7	E_ARG_172	NH2	E_GLU_120	OE2	3.923
6EA7	F_ARG_559	NH1	E_GLU_103	OE1	2.812
6EA7	F_ARG_559	NH1	E_GLU_103	OE2	3.584
6EA7	F_ARG_559	NH2	E_GLU_103	OE2	3.608
6EA7	F_ARG_596	NH2	E_ASP_55	OD1	2.483
6EA7	F_ARG_596	NH2	E_ASP_55	OD2	3.342
6EA7	F_HIS_602	ND1	D_GLU_611	OE1	3.253

6EA7	H_ARG_38	NH1	H_GLU_46	OE1	3.611
6EA7	H_ARG_38	NH1	H_ASP_90	OD1	3.414
6EA7	H_ARG_38	NH2	H_GLU_46	OE1	2.876
6EA7	H_ARG_38	NH2	H_GLU_46	OE2	3.020
6EA7	H_HIS_100	ND1	H_ASP_110	OD2	3.934
6EA7	H_HIS_100	ND1	L_GLU_55	OE1	3.325
6EA7	H_HIS_100	NE2	L_GLU_55	OE1	3.655
6EA7	H_HIS_108	NE2	L_ASP_50	OD1	2.912
6EA7	H_HIS_173	ND1	L_ASP_166	OD1	3.947
6EA7	H_HIS_173	ND1	L_ASP_166	OD2	3.590
6EA7	H_LYS_218	NZ	L_GLU_122	OE1	2.826
6EA7	L_LYS_39	NZ	L_GLU_42	OE1	3.713
6EA7	L_LYS_39	NZ	L_ASP_81	OD1	3.700
6EA7	L_ARG_61	NH2	L_ASP_82	OD1	2.764
6EA7	L_ARG_61	NH2	L_ASP_82	OD2	3.165
6EA7	L_LYS_102	NZ	L_GLU_164	OE1	3.631
6EA7	L_LYS_148	NZ	L_GLU_194	OE1	3.419
6EA7	M_ARG_38	NH1	M_GLU_46	OE1	3.632
6EA7	M_ARG_38	NH2	M_GLU_46	OE1	2.819
6EA7	M_ARG_38	NH2	M_GLU_46	OE2	3.086
6EA7	M_ARG_67	NH1	M_ASP_90	OD1	3.655
6EA7	M_ARG_67	NH1	M_ASP_90	OD2	3.008
6EA7	M_ARG_67	NH2	M_ASP_90	OD1	2.976
6EA7	M_ARG_67	NH2	M_ASP_90	OD2	2.990
6EA7	M_HIS_100	ND1	N_GLU_55	OE1	3.446
6EA7	M_HIS_100	ND1	N_GLU_55	OE2	3.681
6EA7	M_HIS_108	ND1	N_ASP_50	OD1	3.757
6EA7	M_HIS_108	NE2	N_ASP_50	OD1	3.718
6EA7	M_HIS_173	ND1	N_ASP_166	OD2	3.701
6EA7	M_LYS_219	NZ	M_GLU_221	OE1	3.040
6EA7	N_LYS_39	NZ	N_ASP_81	OD1	3.604
6EA7	N_ARG_61	NH2	N_ASP_82	OD1	2.680
6EA7	N_ARG_61	NH2	N_ASP_82	OD2	3.258
6EA7	N_LYS_102	NZ	N_GLU_164	OE1	3.534
6EA7	N_LYS_148	NZ	N_GLU_194	OE1	3.192
6EA7	N_HIS_188	ND1	N_ASP_150	OD2	3.491
6EA7	Q_ARG_38	NH1	Q_GLU_46	OE1	3.581
6EA7	Q_ARG_38	NH2	Q_GLU_46	OE1	3.006
6EA7	Q_ARG_38	NH2	Q_GLU_46	OE2	3.019
6EA7	Q_ARG_67	NH1	Q_ASP_90	OD1	3.489
6EA7	Q_ARG_67	NH1	Q_ASP_90	OD2	2.319
6EA7	Q_ARG_67	NH2	Q_ASP_90	OD1	3.689
6EA7	Q_ARG_67	NH2	Q_ASP_90	OD2	3.153
6EA7	Q_HIS_108	NE2	R_ASP_50	OD1	3.227
6EA7	Q_HIS_173	ND1	R_ASP_166	OD1	3.817
6EA7	Q_HIS_173	ND1	R_ASP_166	OD2	3.600
6EA7	R_ARG_24	NH1	R_GLU_70	OE1	2.987
6EA7	R_ARG_24	NH1	R_GLU_70	OE2	2.873
6EA7	R_LYS_39	NZ	R_GLU_42	OE1	3.837
6EA7	R_LYS_39	NZ	R_ASP_81	OD1	3.859
6EA7	R_ARG_61	NH2	R_ASP_82	OD1	2.608
6EA7	R_ARG_61	NH2	R_ASP_82	OD2	3.334
6EA7	R_LYS_102	NZ	R_GLU_164	OE1	3.378
6EA7	R_LYS_106	NZ	R_GLU_104	OE1	3.728
6EA7	R_LYS_148	NZ	R_GLU_194	OE1	3.641
6F5U	A_HIS_39	NE2	A_ASP_55	OD1	3.607
6F5U	A_HIS_39	NE2	A_ASP_55	OD2	3.205
6F5U	A_ARG_85	NH1	A_GLU_178	OE1	3.593

6F5U	A_ARG_85	NH1	A_GLU_178	OE2	2.633
6F5U	A_LYS_114	NZ	A_GLU_120	OE2	3.481
6F5U	A_ARG_130	NH2	A_ASP_163	OD2	3.086
6F5U	A_HIS_154	NE2	A_GLU_178	OE1	2.646
6F5U	A_ARG_164	NH1	A_ASP_163	OD1	3.541
6F5U	A_ARG_164	NH1	A_ASP_163	OD2	3.126
6F5U	A_ARG_247	NH2	A_GLU_245	OE1	3.242
6F5U	A_ARG_266	NH2	A_ASP_237	OD2	3.400
6F5U	B_LYS_510	NZ	A_GLU_292	OE1	3.345
6F5U	B_HIS_516	NE2	B_GLU_545	OE1	2.737
6F5U	B_ARG_559	NH1	A_GLU_103	OE1	2.631
6F5U	B_ARG_559	NH1	A_GLU_103	OE2	3.833
6F5U	B_ARG_559	NH2	A_GLU_103	OE1	3.290
6F5U	B_ARG_559	NH2	A_GLU_103	OE2	2.992
6F6I	A_ARG_85	NH1	A_GLU_178	OE1	3.391
6F6I	A_ARG_85	NH1	A_GLU_178	OE2	2.492
6F6I	A_LYS_114	NZ	A_GLU_120	OE2	3.662
6F6I	A_ARG_130	NH2	A_ASP_163	OD1	3.094
6F6I	A_LYS_140	NZ	A_GLU_112	OE2	3.920
6F6I	A_HIS_154	NE2	A_GLU_178	OE1	2.814
6F6I	A_ARG_164	NH1	A_ASP_163	OD1	3.155
6F6I	A_ARG_164	NH1	A_ASP_163	OD2	3.520
6F6I	A_ARG_247	NH2	A_GLU_245	OE2	2.546
6F6I	A_ARG_266	NH2	A_ASP_237	OD2	3.974
6F6I	B_LYS_510	NZ	A_GLU_292	OE1	3.377
6F6I	B_HIS_516	NE2	B_GLU_545	OE1	2.567
6F6I	B_ARG_559	NH1	A_GLU_103	OE1	3.800
6F6I	B_ARG_559	NH1	A_GLU_103	OE2	2.815
6F6I	B_ARG_559	NH2	A_GLU_103	OE1	3.096
6F6I	B_ARG_559	NH2	A_GLU_103	OE2	3.529
6F6I	B_HIS_628	ND1	B_ASP_629	OD1	3.915
6F6I	B_HIS_628	NE2	B_ASP_629	OD1	3.799
6F6N	A_LYS_50	NZ	A_ASP_49	OD1	3.536
6F6N	A_LYS_50	NZ	A_ASP_49	OD2	3.944
6F6N	A_ARG_85	NH1	A_GLU_178	OE1	3.489
6F6N	A_ARG_85	NH1	A_GLU_178	OE2	2.503
6F6N	A_LYS_114	NZ	A_GLU_120	OE2	3.710
6F6N	A_ARG_130	NH2	A_ASP_163	OD2	3.005
6F6N	A_HIS_154	NE2	A_GLU_178	OE1	2.727
6F6N	A_ARG_164	NH1	A_ASP_163	OD1	3.435
6F6N	A_ARG_164	NH1	A_ASP_163	OD2	2.950
6F6N	A_ARG_247	NH1	A_GLU_245	OE1	3.669
6F6N	A_ARG_266	NH2	A_ASP_237	OD2	3.429
6F6N	A_LYS_276	NZ	A_GLU_245	OE2	2.564
6F6N	B_LYS_510	NZ	A_GLU_292	OE1	2.639
6F6N	B_HIS_516	NE2	B_GLU_545	OE1	2.799
6F6N	B_ARG_559	NH1	A_GLU_103	OE1	2.593
6F6N	B_ARG_559	NH1	A_GLU_103	OE2	3.789
6F6N	B_ARG_559	NH2	A_GLU_103	OE1	3.215
6F6N	B_ARG_559	NH2	A_GLU_103	OE2	2.904
6F6N	B_LYS_588	NZ	A_ASP_47	OD1	3.696
6F6N	B_LYS_588	NZ	A_ASP_47	OD2	2.975
6F6S	A_ARG_85	NH1	A_GLU_178	OE1	3.259
6F6S	A_ARG_85	NH1	A_GLU_178	OE2	2.372
6F6S	A_LYS_114	NZ	A_GLU_120	OE2	3.380
6F6S	A_ARG_130	NH2	A_ASP_163	OD1	3.014
6F6S	A_HIS_154	NE2	A_GLU_178	OE1	3.039
6F6S	A_ARG_164	NH1	A_ASP_163	OD1	2.810

6F6S	A_ARG_164	NH1	A_ASP_163	OD2	3.556
6F6S	B_LYS_510	NZ	A_GLU_292	OE1	2.331
6F6S	B_LYS_510	NZ	A_GLU_292	OE2	3.397
6F6S	B_HIS_516	NE2	B_GLU_545	OE1	2.731
6F6S	B_ARG_559	NH1	A_GLU_103	OE1	2.656
6F6S	B_ARG_559	NH1	A_GLU_103	OE2	3.920
6F6S	B_ARG_559	NH2	A_GLU_103	OE1	3.146
6F6S	B_ARG_559	NH2	A_GLU_103	OE2	2.951
6F6S	B_LYS_588	NZ	A_ASP_47	OD1	2.944
6F6S	B_LYS_588	NZ	A_ASP_47	OD2	2.772
6F6S	B_LYS_617	NZ	B_ASP_614	OD1	3.893
6G95	A_HIS_39	NE2	A_ASP_55	OD1	2.899
6G95	A_HIS_39	NE2	A_ASP_55	OD2	3.064
6G95	A_ARG_85	NH1	A_GLU_178	OE1	3.522
6G95	A_ARG_85	NH1	A_GLU_178	OE2	2.681
6G95	A_LYS_114	NZ	A_GLU_120	OE1	3.918
6G95	A_LYS_114	NZ	A_GLU_120	OE2	3.675
6G95	A_ARG_130	NH2	A_ASP_163	OD1	3.040
6G95	A_LYS_140	NZ	A_GLU_112	OE1	3.777
6G95	A_HIS_154	NE2	A_GLU_178	OE1	2.904
6G95	A_ARG_164	NH1	A_ASP_163	OD1	2.830
6G95	A_ARG_164	NH1	A_ASP_163	OD2	3.454
6G95	A_ARG_266	NH2	A_ASP_237	OD2	3.135
6G95	B_HIS_516	NE2	B_GLU_545	OE1	2.525
6G95	B_ARG_559	NH1	A_GLU_103	OE1	2.683
6G95	B_ARG_559	NH1	A_GLU_103	OE2	3.879
6G95	B_ARG_559	NH2	A_GLU_103	OE1	3.249
6G95	B_ARG_559	NH2	A_GLU_103	OE2	2.973
6G9B	A_ARG_85	NH1	A_GLU_178	OE1	3.384
6G9B	A_ARG_85	NH1	A_GLU_178	OE2	2.574
6G9B	A_LYS_114	NZ	A_GLU_120	OE1	3.989
6G9B	A_LYS_114	NZ	A_GLU_120	OE2	3.841
6G9B	A_ARG_130	NH2	A_ASP_163	OD1	3.043
6G9B	A_LYS_140	NZ	A_GLU_112	OE2	3.639
6G9B	A_HIS_154	NE2	A_GLU_178	OE1	2.960
6G9B	A_ARG_164	NH1	A_ASP_163	OD1	2.869
6G9B	A_ARG_164	NH1	A_ASP_163	OD2	3.373
6G9B	A_ARG_172	NH1	A_GLU_120	OE2	3.934
6G9B	A_ARG_247	NH2	A_GLU_245	OE1	3.502
6G9B	A_ARG_266	NH2	A_ASP_237	OD2	3.075
6G9B	B_LYS_510	NZ	A_GLU_292	OE1	3.414
6G9B	B_HIS_516	NE2	B_GLU_545	OE1	2.666
6G9B	B_ARG_559	NH1	A_GLU_103	OE1	2.574
6G9B	B_ARG_559	NH1	A_GLU_103	OE2	3.760
6G9B	B_ARG_559	NH2	A_GLU_103	OE1	3.199
6G9B	B_ARG_559	NH2	A_GLU_103	OE2	2.870
6G9B	B_LYS_588	NZ	A_ASP_47	OD1	3.317
6G9B	B_LYS_588	NZ	A_ASP_47	OD2	2.892
6G9B	B_LYS_617	NZ	B_ASP_614	OD2	3.817
6G9B	B_HIS_628	NE2	B_ASP_629	OD1	3.701
6G9B	B_HIS_628	NE2	B_ASP_629	OD2	3.971
6G9I	A_HIS_39	NE2	A_ASP_55	OD1	3.027
6G9I	A_HIS_39	NE2	A_ASP_55	OD2	2.861
6G9I	A_ARG_85	NH1	A_GLU_178	OE1	3.616
6G9I	A_ARG_85	NH1	A_GLU_178	OE2	2.527
6G9I	A_LYS_114	NZ	A_GLU_120	OE2	3.647
6G9I	A_ARG_130	NH2	A_ASP_163	OD1	3.039
6G9I	A_HIS_154	NE2	A_GLU_178	OE1	2.656

6G9I	A_ARG_164	NH1	A_ASP_163	OD1	3.026
6G9I	A_ARG_164	NH1	A_ASP_163	OD2	3.451
6G9I	A_ARG_266	NH2	A_ASP_237	OD2	3.464
6G9I	B_HIS_516	NE2	B_GLU_545	OE1	2.739
6G9I	B_ARG_559	NH1	A_GLU_103	OE1	2.689
6G9I	B_ARG_559	NH1	A_GLU_103	OE2	3.794
6G9I	B_ARG_559	NH2	A_GLU_103	OE1	3.340
6G9I	B_ARG_559	NH2	A_GLU_103	OE2	2.940
6G9I	B_LYS_622	NZ	B_ASP_621	OD1	2.501
6G9I	B_LYS_622	NZ	B_ASP_621	OD2	3.672
6HRO	A_ARG_85	NH1	A_GLU_178	OE1	3.459
6HRO	A_ARG_85	NH1	A_GLU_178	OE2	2.606
6HRO	A_LYS_114	NZ	A_GLU_120	OE2	3.759
6HRO	A_ARG_130	NH2	A_ASP_163	OD1	2.957
6HRO	A_HIS_154	NE2	A_GLU_178	OE1	3.012
6HRO	A_ARG_164	NH1	A_ASP_163	OD1	3.206
6HRO	A_ARG_164	NH1	A_ASP_163	OD2	3.548
6HRO	A_ARG_266	NH2	A_ASP_237	OD2	3.585
6HRO	B_LYS_510	NZ	A_GLU_292	OE1	3.852
6HRO	B_HIS_516	NE2	B_GLU_545	OE1	2.827
6HRO	B_ARG_559	NH1	A_GLU_103	OE1	2.817
6HRO	B_ARG_559	NH1	A_GLU_103	OE2	3.911
6HRO	B_ARG_559	NH2	A_GLU_103	OE1	3.514
6HRO	B_ARG_559	NH2	A_GLU_103	OE2	3.164
6HRO	B_LYS_588	NZ	A_ASP_47	OD1	3.207
6HRO	B_LYS_588	NZ	A_ASP_47	OD2	2.778
6HS4	A_HIS_39	NE2	A_ASP_55	OD1	3.180
6HS4	A_HIS_39	NE2	A_ASP_55	OD2	2.847
6HS4	A_ARG_85	NH1	A_GLU_178	OE1	3.429
6HS4	A_ARG_85	NH1	A_GLU_178	OE2	2.535
6HS4	A_LYS_114	NZ	A_GLU_120	OE2	3.578
6HS4	A_ARG_130	NH2	A_ASP_163	OD1	3.064
6HS4	A_HIS_154	NE2	A_GLU_178	OE1	2.801
6HS4	A_ARG_164	NH1	A_ASP_163	OD1	3.114
6HS4	A_ARG_164	NH1	A_ASP_163	OD2	3.585
6HS4	A_ARG_266	NH2	A_ASP_237	OD2	3.211
6HS4	B_HIS_516	NE2	B_GLU_545	OE1	2.734
6HS4	B_ARG_559	NH1	A_GLU_103	OE1	2.624
6HS4	B_ARG_559	NH1	A_GLU_103	OE2	3.811
6HS4	B_ARG_559	NH2	A_GLU_103	OE1	3.176
6HS4	B_ARG_559	NH2	A_GLU_103	OE2	2.846
6HS4	B_LYS_588	NZ	A_ASP_47	OD1	3.053
6HS4	B_LYS_588	NZ	A_ASP_47	OD2	2.954
6MAM	A_ARG_38	NH1	A_ASP_92	OD1	3.032
6MAM	A_ARG_38	NH2	A_GLU_46	OE1	3.455
6MAM	A_ARG_38	NH2	A_GLU_46	OE2	3.429
6MAM	A_ARG_50	NH1	A_ASP_61	OD2	2.812
6MAM	A_ARG_50	NH2	A_GLU_116	OE2	2.918
6MAM	A_ARG_69	NH1	A_ASP_92	OD2	2.800
6MAM	A_ARG_69	NH2	A_ASP_92	OD1	3.038
6MAM	A_ARG_69	NH2	A_ASP_92	OD2	2.756
6MAM	A_ARG_74	NH2	A_ASP_76	OD1	3.398
6MAM	A_LYS_78	NZ	A_ASP_75	OD2	3.612
6MAM	A_ARG_106	NH1	A_ASP_56	OD2	3.214
6MAM	A_ARG_106	NH2	A_ASP_56	OD1	3.431
6MAM	A_ARG_106	NH2	A_ASP_56	OD2	2.235
6MAM	A_LYS_161	NZ	A_ASP_162	OD1	2.861
6MAM	A_LYS_227	NZ	B_GLU_125	OE1	3.431

6MAM	A_LYS_228	NZ	A_GLU_230	OE1	2.933
6MAM	A_LYS_228	NZ	A_GLU_230	OE2	2.500
6MAM	B_ARG_3	NH1	B_ASP_1	OD1	3.296
6MAM	B_ARG_3	NH2	B_ASP_1	OD1	3.656
6MAM	B_ARG_24	NH2	B_ASP_70	OD1	3.387
6MAM	B_ARG_24	NH2	B_ASP_70	OD2	3.517
6MAM	B_ARG_61	NH2	B_GLU_81	OE2	3.262
6MAM	B_ARG_61	NH2	B_ASP_82	OD1	3.695
6MAM	B_LYS_105	NZ	B_GLU_167	OE1	2.898
6MAM	B_LYS_105	NZ	B_GLU_167	OE2	3.314
6MAM	B_LYS_151	NZ	B_GLU_197	OE1	2.860
6MAM	C_ARG_38	NH1	C_ASP_92	OD1	2.663
6MAM	C_ARG_38	NH2	C_GLU_46	OE1	3.453
6MAM	C_ARG_38	NH2	C_GLU_46	OE2	3.332
6MAM	C_ARG_38	NH2	C_ASP_92	OD1	3.874
6MAM	C_ARG_50	NH1	C_ASP_61	OD2	3.061
6MAM	C_ARG_69	NH1	C_ASP_92	OD2	2.947
6MAM	C_ARG_69	NH2	C_ASP_92	OD1	3.364
6MAM	C_ARG_69	NH2	C_ASP_92	OD2	2.722
6MAM	C_ARG_74	NH2	C_ASP_76	OD1	3.320
6MAM	C_LYS_78	NZ	C_ASP_75	OD2	3.377
6MAM	C_LYS_89	NZ	C_GLU_91	OE2	3.915
6MAM	C_ARG_106	NH2	C_ASP_56	OD1	3.976
6MAM	C_ARG_106	NH2	C_ASP_56	OD2	2.463
6MAM	C_LYS_161	NZ	C_ASP_162	OD1	2.840
6MAM	C_LYS_161	NZ	C_ASP_162	OD2	3.813
6MAM	C_HIS_182	NE2	D_ASP_169	OD2	3.087
6MAM	C_LYS_227	NZ	D_GLU_125	OE1	3.951
6MAM	D_ARG_3	NH1	D_ASP_1	OD1	3.278
6MAM	D_ARG_3	NH1	D_ASP_1	OD2	3.738
6MAM	D_ARG_3	NH2	D_ASP_1	OD1	2.805
6MAM	D_ARG_3	NH2	D_ASP_1	OD2	3.711
6MAM	D_ARG_61	NH2	D_GLU_81	OE2	3.528
6MAM	D_ARG_61	NH2	D_ASP_82	OD1	2.930
6MAM	D_ARG_61	NH2	D_ASP_82	OD2	3.239
6MAM	D_LYS_105	NZ	D_GLU_167	OE1	2.533
6MAM	D_LYS_105	NZ	D_GLU_167	OE2	3.413
6MAM	D_LYS_151	NZ	D_GLU_197	OE1	2.852
6MAM	D_HIS_191	ND1	D_ASP_153	OD2	2.884
6MAM	E_ARG_38	NH1	E_ASP_92	OD1	2.865
6MAM	E_ARG_38	NH2	E_GLU_46	OE1	3.478
6MAM	E_ARG_38	NH2	E_GLU_46	OE2	3.114
6MAM	E_ARG_38	NH2	E_ASP_92	OD1	3.571
6MAM	E_ARG_50	NH2	E_ASP_61	OD2	2.222
6MAM	E_ARG_69	NH1	E_ASP_92	OD2	3.919
6MAM	E_ARG_74	NH2	E_ASP_76	OD1	3.361
6MAM	E_LYS_78	NZ	E_ASP_75	OD2	3.911
6MAM	E_ARG_106	NH1	E_ASP_56	OD1	3.912
6MAM	E_ARG_106	NH1	E_ASP_56	OD2	2.681
6MAM	E_ARG_106	NH2	E_ASP_56	OD2	2.658
6MAM	E_LYS_161	NZ	E_ASP_162	OD1	2.972
6MAM	F_ARG_24	NH2	F_ASP_70	OD1	3.490
6MAM	F_ARG_24	NH2	F_ASP_70	OD2	3.587
6MAM	F_ARG_61	NH2	F_GLU_81	OE2	3.395
6MAM	F_ARG_61	NH2	F_ASP_82	OD1	2.777
6MAM	F_ARG_61	NH2	F_ASP_82	OD2	3.559
6MAM	F_LYS_105	NZ	F_GLU_167	OE1	3.155
6MAM	F_LYS_105	NZ	F_GLU_167	OE2	3.321

6MAM	F_LYS_128	NZ	F_GLU_125	OE1	3.556
6MAM	F_LYS_128	NZ	F_GLU_125	OE2	3.637
6MAM	F_LYS_151	NZ	F_GLU_197	OE1	2.889
6MAM	F_LYS_190	NZ	F_ASP_187	OD1	3.330
6MAM	G_ARG_85	NH1	G_GLU_178	OE1	3.649
6MAM	G_ARG_85	NH1	G_GLU_178	OE2	2.952
6MAM	G_LYS_114	NZ	G_GLU_120	OE2	3.654
6MAM	G_ARG_130	NH2	G_ASP_163	OD2	3.414
6MAM	G_HIS_154	NE2	G_GLU_178	OE1	2.787
6MAM	G_ARG_164	NH1	G_ASP_163	OD1	2.973
6MAM	G_ARG_164	NH1	G_ASP_163	OD2	3.775
6MAM	G_ARG_164	NH2	G_ASP_163	OD1	3.075
6MAM	G_ARG_164	NH2	G_ASP_163	OD2	2.437
6MAM	G_ARG_172	NH1	G_GLU_120	OE2	3.996
6MAM	H_HIS_516	NE2	H_GLU_545	OE1	2.716
6MAM	H_ARG_559	NH1	G_GLU_103	OE1	2.237
6MAM	H_ARG_559	NH1	G_GLU_103	OE2	3.123
6MAM	H_ARG_559	NH2	G_GLU_103	OE1	3.565
6MAM	H_ARG_559	NH2	G_GLU_103	OE2	2.826
6MAM	I_ARG_85	NH1	I_GLU_178	OE1	3.469
6MAM	I_ARG_85	NH1	I_GLU_178	OE2	2.648
6MAM	I_LYS_114	NZ	I_GLU_120	OE1	3.810
6MAM	I_LYS_114	NZ	I_GLU_120	OE2	3.218
6MAM	I_ARG_130	NH2	I_ASP_163	OD2	3.267
6MAM	I_HIS_154	NE2	I_GLU_178	OE1	2.764
6MAM	I_ARG_164	NH1	I_ASP_163	OD1	3.601
6MAM	I_ARG_164	NH1	I_ASP_163	OD2	2.921
6MAM	I_ARG_172	NH1	I_GLU_120	OE2	3.984
6MAM	J_HIS_516	NE2	J_GLU_545	OE1	2.735
6MAM	J_ARG_559	NH1	I_GLU_103	OE1	2.281
6MAM	J_ARG_559	NH1	I_GLU_103	OE2	3.223
6MAM	J_ARG_559	NH2	I_GLU_103	OE1	3.504
6MAM	J_ARG_559	NH2	I_GLU_103	OE2	2.826
6MAM	K_ARG_85	NH1	K_GLU_178	OE1	3.549
6MAM	K_ARG_85	NH1	K_GLU_178	OE2	2.788
6MAM	K_LYS_114	NZ	K_GLU_120	OE1	3.898
6MAM	K_LYS_114	NZ	K_GLU_120	OE2	3.320
6MAM	K_ARG_130	NH2	K_ASP_163	OD2	3.275
6MAM	K_HIS_154	NE2	K_GLU_178	OE1	3.032
6MAM	K_ARG_164	NH1	K_ASP_163	OD1	3.574
6MAM	K_ARG_164	NH1	K_ASP_163	OD2	2.908
6MAM	K_ARG_172	NH1	K_GLU_120	OE2	3.957
6MAM	L_HIS_516	NE2	L_GLU_545	OE1	2.681
6MAM	L_ARG_559	NH1	K_GLU_103	OE1	2.658
6MAM	L_ARG_559	NH1	K_GLU_103	OE2	3.420
6MAM	L_ARG_559	NH2	K_GLU_103	OE1	3.722
6MAM	L_ARG_559	NH2	K_GLU_103	OE2	2.995
6NAE	A_HIS_39	NE2	A_ASP_55	OD1	2.745
6NAE	A_HIS_39	NE2	A_ASP_55	OD2	3.133
6NAE	A_ARG_85	NH1	A_GLU_178	OE1	3.501
6NAE	A_ARG_85	NH1	A_GLU_178	OE2	2.362
6NAE	A_ARG_130	NH2	A_ASP_163	OD2	3.231
6NAE	A_HIS_154	NE2	A_GLU_178	OE1	2.851
6NAE	A_ARG_164	NH1	A_ASP_163	OD1	3.478
6NAE	A_ARG_164	NH1	A_ASP_163	OD2	2.808
6NAE	A_ARG_172	NH1	A_GLU_120	OE2	3.850
6NAE	A_ARG_266	NH2	A_ASP_237	OD2	3.596
6NAE	B_LYS_510	NZ	A_GLU_292	OE1	2.350

6NAE	B_LYS_510	NZ	A_GLU_292	OE2	3.768
6NAE	B_HIS_516	NE2	B_GLU_545	OE1	2.507
6NAE	B_ARG_559	NH1	A_GLU_103	OE1	2.669
6NAE	B_ARG_559	NH1	A_GLU_103	OE2	3.739
6NAE	B_ARG_559	NH2	A_GLU_103	OE1	3.488
6NAE	B_ARG_559	NH2	A_GLU_103	OE2	3.068
6QD7	L_ARG_45	NH1	L_GLU_81	OE2	3.933
6QD7	L_ARG_61	NH1	L_GLU_79	OE1	3.350
6QD7	L_ARG_61	NH1	L_GLU_79	OE2	2.563
6QD7	L_ARG_61	NH2	L_GLU_79	OE1	3.628
6QD7	L_ARG_61	NH2	L_GLU_79	OE2	3.965
6QD7	L_ARG_61	NH2	L_GLU_81	OE1	3.504
6QD7	L_ARG_91	NH1	D_GLU_502	OE1	3.607
6QD7	L_ARG_91	NH2	L_GLU_50	OE1	3.410
6QD7	H_ARG_38	NH1	H_ASP_87	OD1	2.843
6QD7	H_LYS_65	NZ	D_ASP_552	OD1	3.151
6QD7	H_LYS_65	NZ	D_ASP_552	OD2	3.487
6QD7	H_ARG_67	NH1	H_ASP_87	OD1	3.877
6QD7	H_ARG_67	NH1	H_ASP_87	OD2	2.749
6QD7	H_ARG_67	NH2	H_ASP_87	OD1	3.605
6QD7	H_ARG_67	NH2	H_ASP_87	OD2	3.759
6QD7	H_LYS_95	NZ	H_ASP_106	OD1	2.959
6QD7	H_LYS_95	NZ	H_ASP_106	OD2	3.089
6QD7	H_ARG_101	NH1	D_GLU_564	OE1	3.838
6QD7	H_ARG_101	NH1	D_GLU_564	OE2	2.869
6QD7	H_ARG_101	NH2	D_GLU_502	OE1	3.497
6QD7	H_ARG_101	NH2	D_GLU_502	OE2	3.635
6QD7	H_ARG_101	NH2	D_GLU_564	OE1	3.061
6QD7	H_ARG_101	NH2	D_GLU_564	OE2	3.438
6QD7	A_ARG_64	NH2	A_ASP_192	OD1	3.858
6QD7	A_ARG_85	NH1	A_GLU_178	OE1	3.413
6QD7	A_ARG_85	NH1	A_GLU_178	OE2	3.024
6QD7	A_LYS_114	NZ	A_GLU_120	OE1	3.280
6QD7	A_ARG_130	NH2	A_ASP_163	OD1	3.286
6QD7	A_ARG_134	NH1	B_GLU_545	OE2	3.138
6QD7	A_HIS_154	ND1	A_GLU_156	OE1	3.400
6QD7	A_HIS_154	NE2	A_GLU_178	OE1	2.937
6QD7	A_ARG_164	NH1	A_ASP_163	OD1	3.712
6QD7	A_ARG_164	NH1	A_ASP_163	OD2	3.939
6QD7	B_ARG_559	NH1	A_GLU_103	OE1	2.604
6QD7	B_ARG_559	NH1	A_GLU_103	OE2	3.895
6QD7	B_ARG_559	NH2	A_GLU_103	OE1	3.220
6QD7	B_ARG_559	NH2	A_GLU_103	OE2	3.089
6QD7	B_ARG_587	NH2	B_GLU_578	OE2	3.922
6QD7	B_LYS_588	NZ	A_ASP_47	OD2	3.517
6QD7	B_HIS_602	ND1	F_GLU_611	OE2	2.318
6QD7	B_HIS_628	ND1	B_ASP_624	OD1	3.831
6QD7	B_HIS_628	NE2	B_ASP_624	OD1	2.455
6QD7	C_ARG_64	NH2	C_ASP_192	OD1	3.858
6QD7	C_ARG_85	NH1	C_GLU_178	OE1	3.413
6QD7	C_ARG_85	NH1	C_GLU_178	OE2	3.024
6QD7	C_LYS_114	NZ	C_GLU_120	OE1	3.281
6QD7	C_ARG_130	NH2	C_ASP_163	OD1	3.286
6QD7	C_ARG_134	NH1	D_GLU_545	OE2	3.066
6QD7	C_HIS_154	ND1	C_GLU_156	OE1	3.400
6QD7	C_HIS_154	NE2	C_GLU_178	OE1	2.937
6QD7	C_ARG_164	NH1	C_ASP_163	OD1	3.711
6QD7	C_ARG_164	NH1	C_ASP_163	OD2	3.938

6QD7	E_ARG_64	NH2	E_ASP_192	OD1	3.857
6QD7	E_ARG_85	NH1	E_GLU_178	OE1	3.413
6QD7	E_ARG_85	NH1	E_GLU_178	OE2	3.024
6QD7	E_LYS_114	NZ	E_GLU_120	OE1	3.279
6QD7	E_ARG_130	NH2	E_ASP_163	OD1	3.285
6QD7	E_ARG_134	NH1	F_GLU_545	OE2	2.931
6QD7	E_HIS_154	ND1	E_GLU_156	OE1	3.400
6QD7	E_HIS_154	NE2	E_GLU_178	OE1	2.937
6QD7	E_ARG_164	NH1	E_ASP_163	OD1	3.712
6QD7	E_ARG_164	NH1	E_ASP_163	OD2	3.939
6QD7	D_ARG_559	NH1	C_GLU_103	OE1	2.624
6QD7	D_ARG_559	NH1	C_GLU_103	OE2	3.858
6QD7	D_ARG_559	NH2	C_GLU_103	OE1	3.320
6QD7	D_ARG_559	NH2	C_GLU_103	OE2	3.132
6QD7	D_ARG_587	NH2	D_GLU_578	OE2	3.922
6QD7	D_LYS_588	NZ	C_ASP_47	OD2	3.598
6QD7	D_HIS_602	ND1	B_GLU_611	OE2	2.828
6QD7	D_HIS_628	ND1	D_ASP_624	OD1	3.831
6QD7	D_HIS_628	NE2	D_ASP_624	OD1	2.456
6QD7	F_ARG_559	NH1	E_GLU_103	OE1	2.462
6QD7	F_ARG_559	NH1	E_GLU_103	OE2	3.800
6QD7	F_ARG_559	NH2	E_GLU_103	OE1	3.090
6QD7	F_ARG_559	NH2	E_GLU_103	OE2	2.951
6QD7	F_ARG_587	NH2	F_GLU_578	OE2	3.922
6QD7	F_LYS_588	NZ	E_ASP_47	OD2	3.686
6QD7	F_HIS_602	ND1	D_GLU_611	OE2	2.771
6QD7	F_HIS_628	ND1	F_ASP_624	OD1	3.831
6QD7	F_HIS_628	NE2	F_ASP_624	OD1	2.455
6QD7	X_ARG_38	NH1	X_ASP_87	OD1	2.843
6QD7	X_LYS_65	NZ	F_ASP_552	OD1	3.082
6QD7	X_LYS_65	NZ	F_ASP_552	OD2	3.701
6QD7	X_ARG_67	NH1	X_ASP_87	OD1	3.876
6QD7	X_ARG_67	NH1	X_ASP_87	OD2	2.748
6QD7	X_ARG_67	NH2	X_ASP_87	OD1	3.604
6QD7	X_ARG_67	NH2	X_ASP_87	OD2	3.759
6QD7	X_LYS_95	NZ	X_ASP_106	OD1	2.959
6QD7	X_LYS_95	NZ	X_ASP_106	OD2	3.089
6QD7	X_ARG_101	NH1	F_GLU_564	OE1	3.893
6QD7	X_ARG_101	NH1	F_GLU_564	OE2	2.816
6QD7	X_ARG_101	NH2	F_GLU_502	OE1	3.631
6QD7	X_ARG_101	NH2	F_GLU_502	OE2	3.812
6QD7	X_ARG_101	NH2	F_GLU_564	OE1	3.108
6QD7	X_ARG_101	NH2	F_GLU_564	OE2	3.371
6QD7	U_ARG_38	NH1	U_ASP_87	OD1	2.842
6QD7	U_LYS_65	NZ	B_ASP_552	OD1	2.927
6QD7	U_LYS_65	NZ	B_ASP_552	OD2	3.579
6QD7	U_ARG_67	NH1	U_ASP_87	OD1	3.877
6QD7	U_ARG_67	NH1	U_ASP_87	OD2	2.749
6QD7	U_ARG_67	NH2	U_ASP_87	OD1	3.604
6QD7	U_ARG_67	NH2	U_ASP_87	OD2	3.760
6QD7	U_LYS_95	NZ	U_ASP_106	OD1	2.959
6QD7	U_LYS_95	NZ	U_ASP_106	OD2	3.089
6QD7	U_ARG_101	NH1	B_GLU_564	OE1	3.771
6QD7	U_ARG_101	NH1	B_GLU_564	OE2	2.902
6QD7	U_ARG_101	NH2	B_GLU_502	OE1	3.404
6QD7	U_ARG_101	NH2	B_GLU_502	OE2	3.473
6QD7	U_ARG_101	NH2	B_GLU_564	OE1	3.146
6QD7	U_ARG_101	NH2	B_GLU_564	OE2	3.609

6QD7	Z_ARG_45	NH1	Z_GLU_81	OE2	3.706
6QD7	Z_ARG_45	NH2	Z_GLU_81	OE2	3.775
6QD7	Z_ARG_61	NH1	Z_GLU_79	OE1	3.427
6QD7	Z_ARG_61	NH1	Z_GLU_79	OE2	2.720
6QD7	Z_ARG_61	NH2	Z_GLU_79	OE1	3.521
6QD7	Z_ARG_61	NH2	Z_GLU_81	OE1	3.408
6QD7	Z_ARG_61	NH2	Z_ASP_82	OD1	3.494
6QD7	Z_ARG_61	NH2	Z_ASP_82	OD2	2.754
6QD7	Z_ARG_91	NH1	F_GLU_502	OE1	3.548
6QD7	Z_ARG_91	NH2	Z_GLU_50	OE1	3.368
6QD7	P_ARG_45	NH1	P_GLU_81	OE2	3.704
6QD7	P_ARG_45	NH2	P_GLU_81	OE2	3.711
6QD7	P_ARG_61	NH1	P_GLU_79	OE1	3.312
6QD7	P_ARG_61	NH1	P_GLU_79	OE2	2.568
6QD7	P_ARG_61	NH2	P_GLU_79	OE1	3.625
6QD7	P_ARG_61	NH2	P_GLU_79	OE2	3.928
6QD7	P_ARG_61	NH2	P_GLU_81	OE1	3.239
6QD7	P_ARG_61	NH2	P_ASP_82	OD1	2.611
6QD7	P_ARG_61	NH2	P_ASP_82	OD2	3.516
6QD7	P_ARG_91	NH1	B_GLU_502	OE1	3.467
6QD7	P_ARG_91	NH2	P_GLU_50	OE1	3.343
6QD8	Z_LYS_39	NZ	Z_GLU_81	OE2	3.248
6QD8	Z_ARG_61	NH2	Z_ASP_82	OD1	2.630
6QD8	Z_ARG_61	NH2	Z_ASP_82	OD2	3.110
6QD8	Z_ARG_96	NH1	W_GLU_51	OE1	3.187
6QD8	Z_ARG_96	NH1	W_GLU_51	OE2	3.722
6QD8	A_ARG_64	NH2	B_ASP_522	OD2	3.626
6QD8	A_ARG_85	NH1	A_GLU_178	OE1	3.877
6QD8	A_ARG_85	NH1	A_GLU_178	OE2	3.145
6QD8	A_LYS_114	NZ	A_GLU_112	OE2	2.626
6QD8	A_LYS_114	NZ	A_GLU_120	OE2	3.220
6QD8	A_ARG_130	NH2	A_ASP_163	OD1	3.061
6QD8	A_ARG_134	NH1	B_GLU_545	OE2	3.117
6QD8	A_HIS_154	NE2	A_GLU_178	OE1	2.431
6QD8	A_ARG_266	NH2	A_ASP_237	OD2	3.394
6QD8	Y_LYS_39	NZ	Y_GLU_81	OE2	3.248
6QD8	Y_ARG_61	NH2	Y_ASP_82	OD1	2.630
6QD8	Y_ARG_61	NH2	Y_ASP_82	OD2	3.109
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE1	3.080
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE2	3.529
6QD8	B_ARG_559	NH1	A_GLU_103	OE1	3.695
6QD8	B_ARG_559	NH1	A_GLU_103	OE2	2.598
6QD8	B_ARG_559	NH2	A_GLU_103	OE1	3.315
6QD8	B_ARG_559	NH2	A_GLU_103	OE2	3.288
6QD8	B_HIS_602	ND1	F_GLU_611	OE2	3.837
6QD8	B_HIS_613	NE2	B_ASP_614	OD2	3.771
6QD8	L_LYS_39	NZ	L_GLU_81	OE2	3.248
6QD8	L_ARG_61	NH2	L_ASP_82	OD1	2.630
6QD8	L_ARG_61	NH2	L_ASP_82	OD2	3.110
6QD8	L_ARG_96	NH1	H_GLU_51	OE1	3.060
6QD8	L_ARG_96	NH1	H_GLU_51	OE2	3.554
6QD8	H_ARG_44	NH2	H_GLU_47	OE1	3.870
6QD8	H_ARG_55	NH1	B_GLU_564	OE1	2.303
6QD8	H_ARG_55	NH1	B_GLU_564	OE2	3.666
6QD8	H_LYS_76	NZ	H_ASP_73	OD2	2.834
6QD8	C_ARG_64	NH2	D_ASP_522	OD2	3.747
6QD8	C_ARG_85	NH1	C_GLU_178	OE1	3.878
6QD8	C_ARG_85	NH1	C_GLU_178	OE2	3.144

6QD8	C_LYS_114	NZ	C_GLU_112	OE2	2.626
6QD8	C_LYS_114	NZ	C_GLU_120	OE2	3.220
6QD8	C_ARG_130	NH2	C_ASP_163	OD1	3.061
6QD8	C_ARG_134	NH1	D_GLU_545	OE2	2.972
6QD8	C_HIS_154	NE2	C_GLU_178	OE1	2.430
6QD8	C_ARG_266	NH2	C_ASP_237	OD2	3.393
6QD8	E_ARG_64	NH2	F_ASP_522	OD2	3.901
6QD8	E_ARG_85	NH1	E_GLU_178	OE1	3.877
6QD8	E_ARG_85	NH1	E_GLU_178	OE2	3.145
6QD8	E_LYS_114	NZ	E_GLU_112	OE2	2.626
6QD8	E_LYS_114	NZ	E_GLU_120	OE2	3.220
6QD8	E_ARG_130	NH2	E_ASP_163	OD1	3.061
6QD8	E_ARG_134	NH1	F_GLU_545	OE2	2.891
6QD8	E_HIS_154	NE2	E_GLU_178	OE1	2.431
6QD8	E_ARG_266	NH2	E_ASP_237	OD2	3.393
6QD8	F_ARG_559	NH1	E_GLU_103	OE1	3.653
6QD8	F_ARG_559	NH1	E_GLU_103	OE2	2.383
6QD8	F_ARG_559	NH2	E_GLU_103	OE1	3.116
6QD8	F_ARG_559	NH2	E_GLU_103	OE2	2.960
6QD8	F_HIS_602	ND1	D_GLU_611	OE2	3.980
6QD8	F_HIS_613	NE2	F_ASP_614	OD2	3.772
6QD8	D_ARG_559	NH1	C_GLU_103	OE1	3.634
6QD8	D_ARG_559	NH1	C_GLU_103	OE2	2.515
6QD8	D_ARG_559	NH2	C_GLU_103	OE1	3.283
6QD8	D_ARG_559	NH2	C_GLU_103	OE2	3.254
6QD8	D_HIS_602	ND1	B_GLU_611	OE2	3.920
6QD8	D_HIS_613	NE2	D_ASP_614	OD2	3.772
6QD8	W_ARG_44	NH2	W_GLU_47	OE1	3.870
6QD8	W_ARG_55	NH1	F_GLU_564	OE1	2.296
6QD8	W_ARG_55	NH1	F_GLU_564	OE2	3.607
6QD8	W_LYS_76	NZ	W_ASP_73	OD2	2.835
6QD8	Q_ARG_44	NH2	Q_GLU_47	OE1	3.871
6QD8	Q_ARG_55	NH1	D_GLU_564	OE1	2.265
6QD8	Q_ARG_55	NH1	D_GLU_564	OE2	3.539
6QD8	Q_LYS_76	NZ	Q_ASP_73	OD2	2.836
6S8D	L_LYS_109	NZ	L_ASP_88	OD1	3.182
6S8D	H_ARG_30	NH2	P_ASP_104	OD2	3.844
6S8D	H_ARG_38	NH1	H_ASP_92	OD1	2.379
6S8D	H_LYS_78	NZ	H_ASP_75	OD1	3.645
6S8D	H_LYS_78	NZ	H_ASP_75	OD2	2.608
6S8D	A_ARG_85	NH1	A_GLU_178	OE1	3.862
6S8D	A_ARG_85	NH1	A_GLU_178	OE2	3.009
6S8D	A_ARG_130	NH2	A_ASP_163	OD2	3.703
6S8D	A_ARG_136	NH1	A_GLU_106	OE2	3.841
6S8D	A_HIS_154	NE2	A_GLU_178	OE1	2.356
6S8D	A_ARG_164	NH1	A_ASP_163	OD2	3.715
6S8D	B_ARG_559	NH1	A_GLU_103	OE1	3.375
6S8D	B_ARG_559	NH1	A_GLU_103	OE2	3.357
6S8D	B_ARG_559	NH2	A_GLU_103	OE1	3.329
6S8D	B_ARG_587	NH2	B_GLU_578	OE1	3.148
6S8D	B_ARG_596	NH2	A_ASP_55	OD2	3.730
6S8D	D_ARG_559	NH1	C_GLU_103	OE1	3.344
6S8D	D_ARG_559	NH1	C_GLU_103	OE2	3.304
6S8D	D_ARG_559	NH2	C_GLU_103	OE1	3.261
6S8D	D_ARG_559	NH2	C_GLU_103	OE2	3.986
6S8D	D_ARG_587	NH2	D_GLU_578	OE1	3.148
6S8D	D_ARG_596	NH2	C_ASP_55	OD2	3.794
6S8D	F_ARG_559	NH1	E_GLU_103	OE1	3.445

6S8D	F_ARG_559	NH1	E_GLU_103	OE2	3.366
6S8D	F_ARG_559	NH2	E_GLU_103	OE1	3.372
6S8D	F_ARG_587	NH2	F_GLU_578	OE1	3.148
6S8D	F_ARG_596	NH2	E_ASP_55	OD2	3.605
6S8D	O_LYS_109	NZ	O_ASP_88	OD1	3.182
6S8D	U_LYS_109	NZ	U_ASP_88	OD1	3.181
6S8D	C_ARG_85	NH1	C_GLU_178	OE1	3.862
6S8D	C_ARG_85	NH1	C_GLU_178	OE2	3.008
6S8D	C_ARG_130	NH2	C_ASP_163	OD2	3.703
6S8D	C_ARG_136	NH1	C_GLU_106	OE2	3.842
6S8D	C_HIS_154	NE2	C_GLU_178	OE1	2.356
6S8D	C_ARG_164	NH1	C_ASP_163	OD2	3.715
6S8D	E_ARG_85	NH1	E_GLU_178	OE1	3.862
6S8D	E_ARG_85	NH1	E_GLU_178	OE2	3.008
6S8D	E_LYS_114	NZ	Y_ASP_56	OD2	3.842
6S8D	E_ARG_130	NH2	E_ASP_163	OD2	3.703
6S8D	E_ARG_136	NH1	E_GLU_106	OE2	3.841
6S8D	E_HIS_154	NE2	E_GLU_178	OE1	2.357
6S8D	E_ARG_164	NH1	E_ASP_163	OD2	3.715
6S8D	P_ARG_30	NH2	Y_ASP_104	OD2	3.808
6S8D	P_ARG_38	NH1	P_ASP_92	OD1	2.379
6S8D	P_LYS_78	NZ	P_ASP_75	OD1	3.644
6S8D	P_LYS_78	NZ	P_ASP_75	OD2	2.608
6S8D	Y_ARG_30	NH2	H_ASP_104	OD2	3.626
6S8D	Y_ARG_38	NH1	Y_ASP_92	OD1	2.379
6S8D	Y_LYS_78	NZ	Y_ASP_75	OD1	3.645
6S8D	Y_LYS_78	NZ	Y_ASP_75	OD2	2.608
6S8I	L_ARG_57	NH1	L_ASP_63	OD1	3.936
6S8I	L_ARG_57	NH2	L_ASP_63	OD2	3.681
6S8I	L_ARG_64	NH2	L_ASP_85	OD1	3.247
6S8I	L_LYS_109	NZ	L_ASP_88	OD1	3.092
6S8I	L_LYS_109	NZ	L_ASP_88	OD2	3.761
6S8I	H_ARG_38	NH1	H_ASP_92	OD1	3.736
6S8I	H_ARG_50	NH2	H_GLU_61	OE1	3.922
6S8I	H_ARG_67	NH2	H_GLU_61	OE2	3.135
6S8I	H_ARG_69	NH2	H_ASP_92	OD1	2.684
6S8I	H_ARG_78	NH1	H_ASP_75	OD2	3.325
6S8I	H_ARG_105	NH1	L_GLU_102	OE1	3.601
6S8I	H_ARG_105	NH1	L_GLU_102	OE2	3.239
6S8I	H_ARG_105	NH2	L_GLU_102	OE2	2.950
6S8I	A_ARG_85	NH1	A_GLU_178	OE1	3.349
6S8I	A_ARG_85	NH1	A_GLU_178	OE2	2.593
6S8I	A_LYS_114	NZ	H_ASP_56	OD1	2.454
6S8I	A_LYS_114	NZ	H_ASP_56	OD2	2.783
6S8I	A_LYS_114	NZ	A_GLU_120	OE2	3.868
6S8I	A_ARG_134	NH1	B_GLU_545	OE2	3.078
6S8I	A_ARG_136	NH1	A_GLU_106	OE2	3.794
6S8I	A_LYS_140	NZ	A_GLU_112	OE2	3.972
6S8I	A_HIS_154	NE2	A_GLU_178	OE1	2.780
6S8I	A_ARG_164	NH1	A_ASP_163	OD1	3.922
6S8I	A_ARG_164	NH1	A_ASP_163	OD2	3.313
6S8I	B_ARG_559	NH1	A_GLU_103	OE1	3.895
6S8I	B_ARG_559	NH1	A_GLU_103	OE2	3.783
6S8I	B_ARG_559	NH2	A_GLU_103	OE1	3.282
6S8I	B_ARG_559	NH2	A_GLU_103	OE2	3.928
6S8I	B_ARG_596	NH2	A_ASP_55	OD1	3.671
6S8I	D_ARG_559	NH1	C_GLU_103	OE1	3.877
6S8I	D_ARG_559	NH1	C_GLU_103	OE2	3.822

6S8I	D_ARG_559	NH2	C_GLU_103	OE1	3.248
6S8I	D_ARG_559	NH2	C_GLU_103	OE2	3.953
6S8I	D_ARG_596	NH2	C_ASP_55	OD1	3.743
6S8I	F_ARG_559	NH1	E_GLU_103	OE1	3.975
6S8I	F_ARG_559	NH1	E_GLU_103	OE2	3.796
6S8I	F_ARG_559	NH2	E_GLU_103	OE1	3.335
6S8I	F_ARG_559	NH2	E_GLU_103	OE2	3.908
6S8I	F_ARG_596	NH2	E_ASP_55	OD1	3.553
6S8I	C_ARG_85	NH1	C_GLU_178	OE1	3.349
6S8I	C_ARG_85	NH1	C_GLU_178	OE2	2.593
6S8I	C_LYS_114	NZ	C_GLU_120	OE2	3.868
6S8I	C_LYS_114	NZ	P_ASP_56	OD1	2.515
6S8I	C_LYS_114	NZ	P_ASP_56	OD2	2.783
6S8I	C_ARG_134	NH1	D_GLU_545	OE2	3.135
6S8I	C_ARG_136	NH1	C_GLU_106	OE2	3.793
6S8I	C_LYS_140	NZ	C_GLU_112	OE2	3.972
6S8I	C_HIS_154	NE2	C_GLU_178	OE1	2.781
6S8I	C_ARG_164	NH1	C_ASP_163	OD1	3.921
6S8I	C_ARG_164	NH1	C_ASP_163	OD2	3.312
6S8I	E_ARG_85	NH1	E_GLU_178	OE1	3.349
6S8I	E_ARG_85	NH1	E_GLU_178	OE2	2.594
6S8I	E_LYS_114	NZ	E_GLU_120	OE2	3.868
6S8I	E_LYS_114	NZ	Y_ASP_56	OD1	2.476
6S8I	E_LYS_114	NZ	Y_ASP_56	OD2	2.735
6S8I	E_ARG_134	NH1	F_GLU_545	OE2	3.154
6S8I	E_ARG_136	NH1	E_GLU_106	OE2	3.794
6S8I	E_LYS_140	NZ	E_GLU_112	OE2	3.972
6S8I	E_HIS_154	NE2	E_GLU_178	OE1	2.779
6S8I	E_ARG_164	NH1	E_ASP_163	OD1	3.921
6S8I	E_ARG_164	NH1	E_ASP_163	OD2	3.313
6S8I	O_ARG_57	NH1	O_ASP_63	OD1	3.936
6S8I	O_ARG_57	NH2	O_ASP_63	OD2	3.681
6S8I	O_ARG_64	NH2	O_ASP_85	OD1	3.246
6S8I	O_LYS_109	NZ	O_ASP_88	OD1	3.092
6S8I	O_LYS_109	NZ	O_ASP_88	OD2	3.761
6S8I	U_ARG_57	NH1	U_ASP_63	OD1	3.937
6S8I	U_ARG_57	NH2	U_ASP_63	OD2	3.681
6S8I	U_ARG_64	NH2	U_ASP_85	OD1	3.247
6S8I	U_LYS_109	NZ	U_ASP_88	OD1	3.092
6S8I	U_LYS_109	NZ	U_ASP_88	OD2	3.761
6S8I	P_ARG_38	NH1	P_ASP_92	OD1	3.736
6S8I	P_ARG_50	NH2	P_GLU_61	OE1	3.922
6S8I	P_ARG_67	NH2	P_GLU_61	OE2	3.135
6S8I	P_ARG_69	NH2	P_ASP_92	OD1	2.683
6S8I	P_ARG_78	NH1	P_ASP_75	OD2	3.324
6S8I	P_ARG_105	NH1	O_GLU_102	OE1	3.789
6S8I	P_ARG_105	NH1	O_GLU_102	OE2	3.289
6S8I	P_ARG_105	NH2	O_GLU_102	OE2	3.143
6S8I	Y_ARG_38	NH1	Y_ASP_92	OD1	3.736
6S8I	Y_ARG_50	NH2	Y_GLU_61	OE1	3.922
6S8I	Y_ARG_67	NH2	Y_GLU_61	OE2	3.135
6S8I	Y_ARG_69	NH2	Y_ASP_92	OD1	2.683
6S8I	Y_ARG_78	NH1	Y_ASP_75	OD2	3.325
6S8I	Y_ARG_105	NH1	U_GLU_102	OE1	3.606
6S8I	Y_ARG_105	NH1	U_GLU_102	OE2	3.273
6S8I	Y_ARG_105	NH2	U_GLU_102	OE2	2.978
6S8J	L_ARG_57	NH1	L_ASP_63	OD1	3.597
6S8J	L_ARG_57	NH2	L_ASP_63	OD2	3.474

6S8J	L_ARG_64	NH2	L_ASP_85	OD1	3.929
6S8J	L_LYS_109	NZ	L_ASP_88	OD1	2.806
6S8J	L_LYS_109	NZ	L_ASP_88	OD2	3.179
6S8J	H_ARG_38	NH2	H_GLU_46	OE1	3.358
6S8J	H_ARG_69	NH1	H_ASP_92	OD1	3.693
6S8J	H_ARG_69	NH2	H_ASP_92	OD1	3.149
6S8J	H_ARG_69	NH2	H_ASP_92	OD2	3.494
6S8J	H_ARG_74	NH1	H_ASP_76	OD1	3.838
6S8J	H_ARG_74	NH1	H_ASP_76	OD2	3.202
6S8J	A_ARG_85	NH1	A_GLU_178	OE1	3.872
6S8J	A_ARG_85	NH1	A_GLU_178	OE2	2.923
6S8J	A_LYS_114	NZ	H_ASP_56	OD1	3.168
6S8J	A_LYS_114	NZ	H_ASP_56	OD2	2.312
6S8J	A_LYS_114	NZ	A_GLU_120	OE2	3.844
6S8J	A_ARG_134	NH1	B_GLU_545	OE2	2.814
6S8J	A_ARG_136	NH1	A_GLU_106	OE2	3.658
6S8J	A_HIS_154	NE2	A_GLU_178	OE1	2.462
6S8J	A_ARG_164	NH1	A_ASP_163	OD2	3.447
6S8J	B_ARG_559	NH1	A_GLU_103	OE1	3.955
6S8J	B_ARG_559	NH1	A_GLU_103	OE2	3.604
6S8J	B_ARG_559	NH2	A_GLU_103	OE1	3.443
6S8J	B_ARG_559	NH2	A_GLU_103	OE2	3.830
6S8J	B_ARG_596	NH2	A_ASP_55	OD1	2.986
6S8J	B_ARG_596	NH2	A_ASP_55	OD2	3.529
6S8J	O_ARG_57	NH1	O_ASP_63	OD1	3.597
6S8J	O_ARG_57	NH2	O_ASP_63	OD2	3.473
6S8J	O_ARG_64	NH2	O_ASP_85	OD1	3.931
6S8J	O_LYS_109	NZ	O_ASP_88	OD1	2.805
6S8J	O_LYS_109	NZ	O_ASP_88	OD2	3.179
6S8J	U_ARG_57	NH1	U_ASP_63	OD1	3.597
6S8J	U_ARG_57	NH2	U_ASP_63	OD2	3.473
6S8J	U_ARG_64	NH2	U_ASP_85	OD1	3.930
6S8J	U_LYS_109	NZ	U_ASP_88	OD1	2.806
6S8J	U_LYS_109	NZ	U_ASP_88	OD2	3.179
6S8J	D_ARG_559	NH1	C_GLU_103	OE1	3.872
6S8J	D_ARG_559	NH1	C_GLU_103	OE2	3.635
6S8J	D_ARG_559	NH2	C_GLU_103	OE1	3.272
6S8J	D_ARG_559	NH2	C_GLU_103	OE2	3.792
6S8J	D_ARG_596	NH2	C_ASP_55	OD1	2.928
6S8J	D_ARG_596	NH2	C_ASP_55	OD2	3.762
6S8J	D_HIS_602	ND1	B_GLU_611	OE1	3.866
6S8J	D_HIS_602	NE2	B_GLU_611	OE1	3.805
6S8J	D_HIS_602	NE2	B_GLU_611	OE2	3.737
6S8J	F_ARG_559	NH1	E_GLU_103	OE1	3.993
6S8J	F_ARG_559	NH1	E_GLU_103	OE2	3.748
6S8J	F_ARG_559	NH2	E_GLU_103	OE1	3.468
6S8J	F_ARG_559	NH2	E_GLU_103	OE2	3.952
6S8J	F_ARG_596	NH2	E_ASP_55	OD1	2.985
6S8J	F_ARG_596	NH2	E_ASP_55	OD2	3.707
6S8J	F_HIS_602	ND1	D_GLU_611	OE1	3.880
6S8J	F_HIS_602	NE2	D_GLU_611	OE2	3.765
6S8J	C_ARG_85	NH1	C_GLU_178	OE1	3.872
6S8J	C_ARG_85	NH1	C_GLU_178	OE2	2.922
6S8J	C_LYS_114	NZ	C_GLU_120	OE2	3.844
6S8J	C_LYS_114	NZ	P_ASP_56	OD1	3.173
6S8J	C_LYS_114	NZ	P_ASP_56	OD2	2.252
6S8J	C_ARG_134	NH1	D_GLU_545	OE2	2.837
6S8J	C_ARG_136	NH1	C_GLU_106	OE2	3.658

6S8J	C_HIS_154	NE2	C_GLU_178	OE1	2.463
6S8J	C_ARG_164	NH1	C_ASP_163	OD2	3.447
6S8J	E_ARG_85	NH1	E_GLU_178	OE1	3.872
6S8J	E_ARG_85	NH1	E_GLU_178	OE2	2.923
6S8J	E_LYS_114	NZ	E_GLU_120	OE2	3.844
6S8J	E_LYS_114	NZ	Y_ASP_56	OD1	3.177
6S8J	E_LYS_114	NZ	Y_ASP_56	OD2	2.185
6S8J	E_ARG_134	NH1	F_GLU_545	OE2	2.997
6S8J	E_ARG_136	NH1	E_GLU_106	OE2	3.659
6S8J	E_HIS_154	NE2	E_GLU_178	OE1	2.462
6S8J	E_ARG_164	NH1	E_ASP_163	OD2	3.447
6S8J	P_ARG_38	NH2	P_GLU_46	OE1	3.357
6S8J	P_ARG_69	NH1	P_ASP_92	OD1	3.693
6S8J	P_ARG_69	NH2	P_ASP_92	OD1	3.150
6S8J	P_ARG_69	NH2	P_ASP_92	OD2	3.494
6S8J	P_ARG_74	NH1	P_ASP_76	OD1	3.838
6S8J	P_ARG_74	NH1	P_ASP_76	OD2	3.202
6S8J	Y_ARG_38	NH2	Y_GLU_46	OE1	3.357
6S8J	Y_ARG_69	NH1	Y_ASP_92	OD1	3.693
6S8J	Y_ARG_69	NH2	Y_ASP_92	OD1	3.150
6S8J	Y_ARG_69	NH2	Y_ASP_92	OD2	3.494
6S8J	Y_ARG_74	NH1	Y_ASP_76	OD1	3.838
6S8J	Y_ARG_74	NH1	Y_ASP_76	OD2	3.202

Table 1: Salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

Count	Residue A	Residue B
191	ARG559	GLU103
122	ARG85	GLU178
86	ARG164	ASP163
83	ARG61	ASP82
59	ARG38	GLU46
53	ARG66	ASP86
50	HIS154	GLU178
49	ARG130	ASP163
42	LYS114	GLU120
38	ARG38	ASP86
32	HIS516	GLU545
31	ARG61	GLU81
27	HIS39	ASP55
23	LYS588	ASP47
22	ARG134	GLU545
21	ARG94	ASP101
20	ARG136	GLU106
20	LYS24	ASP70
19	ARG64	GLU100
19	ARG69	ASP92
17	HIS602	GLU611
16	ARG98	ASP100F
16	ARG33	GLU95
16	ARG67	ASP90
15	ARG172	GLU120
15	LYS109	ASP88
15	ARG266	ASP237
15	ARG596	ASP55
15	LYS221	GLU123
13	LYS145	ASP146
13	LYS114	ASP56
13	ARG247	GLU245
12	LYS3	ASP1
12	HIS189	ASP151
12	LYS107	GLU17
12	ARG101	GLU564
12	LYS510	GLU292
12	ARG57	ASP63
12	ARG67	ASP87
12	ARG164	GLU100
11	ARG38	ASP92
11	ARG61	GLU79
10	ARG219	GLU235
9	ARG105	GLU102
9	ARG74	ASP76
9	LYS78	ASP75
9	HIS96	GLU55
9	LYS272	ASP54
9	LYS149	GLU195
9	ARG107	GLU105
9	LYS140	GLU112
8	ARG106	ASP56
8	ARG172	GLU112
8	ARG64	GLU46
8	ARG299	GLU304
7	ARG54	ASP60
7	LYS272	ASP56

7	ARG75	ASP72
7	HIS112	GLU77
6	ARG55	GLU564
6	ARG3	ASP1
6	ARG64	ASP85
6	LYS64	GLU61
6	LYS95	ASP106
6	ARG24	GLU70
6	HIS127	ASP128
6	ARG587	GLU578
6	ARG71	ASP73
6	ARG101	GLU502
6	LYS105	GLU167
6	LYS65	ASP552
6	ARG96	GLU51
6	LYS114	GLU112
6	HIS628	ASP624
6	ARG83	GLU85
6	ARG596	ASP607
5	LYS510	GLU55
5	LYS116	ASP120
5	ARG302	GLU258
5	HIS613	ASP614
5	ARG65	GLU83
5	ARG45	GLU81
5	HIS628	ASP629
5	LYS71	ASP55
5	HIS173	ASP166
5	ARG302	GLU304
4	LYS57	ASP55
4	ARG155	GLU185
4	LYS188	ASP185
4	LYS209	GLU123
4	ARG94	ASP96
4	LYS26	GLU21
4	LYS146	GLU109
4	LYS187	GLU191
4	LYS222	GLU226
4	ARG103	GLU105
4	ARG142	GLU165
4	LYS161	ASP162
4	ARG24	ASP70
4	HIS108	ASP50
4	HIS100	GLU55
4	LYS12	GLU10
4	ARG65	GLU85
4	ARG142	GLU105
4	ARG247	ASP282
4	LYS87	ASP106
4	LYS510	GLU56
4	LYS71	ASP56
4	HIS613	GLU578
4	LYS38	GLU46
4	ARG65	ASP86
4	LYS83	ASP85
4	LYS74	ASP56
4	ARG299	GLU305
3	ARG64	ASP192

3	HIS154	GLU156
3	HIS441	ASP496
3	ARG91	GLU502
3	LYS151	GLU197
3	LYS39	ASP81
3	ARG64	ASP522
3	ARG38	ASP90
3	LYS617	ASP614
3	LYS102	GLU164
3	ARG30	ASP104
3	LYS276	GLU245
3	LYS633	ASP642
3	ARG100	GLU50
3	ARG50	ASP61
3	ARG38	ASP87
3	ARG52	GLU50
3	ARG67	GLU61
3	LYS39	GLU81
3	ARG79	ASP113
3	HIS172	ASP167
3	ARG78	ASP75
3	ARG130	GLU540
3	ARG91	GLU50
3	LYS272	GLU235
3	ARG44	GLU47
3	LYS148	GLU194
3	ARG50	GLU61
3	LYS76	ASP73
3	LYS14	GLU10
2	ARG410	ASP414
2	HIS164	GLU168
2	LYS62	ASP1
2	HIS193	ASP155
2	LYS203	ASP114
2	LYS227	GLU125
2	LYS204	ASP130
2	LYS103	GLU105
2	LYS153	GLU199
2	ARG404	GLU606
2	HIS138	ASP136
2	LYS43	GLU46
2	LYS50	ASP49
2	LYS622	ASP621
2	LYS84	GLU61
2	LYS39	GLU42
2	LYS128	GLU125
2	ARG98	GLU44
2	ARG207	GLU88
2	ARG1059	GLU391
2	LYS228	GLU230
2	LYS210	GLU212
2	LYS103	ASP85
2	ARG79	GLU110
2	HIS125	ASP159
2	HIS69	ASP124
2	LYS208	GLU127
2	LYS208	GLU124
2	ARG32	GLU212

2	LYS214	GLU123
2	LYS19	ASP81
2	LYS75	GLU72
2	LYS107	ASP169
2	LYS149	GLU203
2	ARG1059	GLU1089
2	LYS53	ASP31
2	HIS549	ASP52
2	LYS107	GLU109
2	ARG159	GLU189
1	ARG50	GLU116
1	HIS1170	GLU1166
1	ARG39	ASP82
1	HIS407	ASP92
1	ARG607	ASP611
1	LYS7	GLU9
1	ARG389	GLU393
1	HIS179	ASP161
1	HIS492	ASP445
1	HIS510	ASP508
1	HIS512	ASP525
1	HIS191	ASP153
1	ARG87	GLU89
1	LYS64	ASP61
1	ARG595	ASP591
1	ARG595	ASP49
1	LYS205	ASP207
1	LYS204	ASP201
1	ARG54	ASP55
1	LYS617	ASP621
1	HIS188	ASP150
1	HIS120	ASP73
1	LYS150	GLU203
1	LYS219	GLU221
1	LYS143	GLU125
1	LYS143	GLU124
1	ARG98	ASP107
1	LYS171	GLU164
1	ARG579	ASP466
1	LYS111	ASP200
1	ARG219	ASP220
1	ARG404	GLU584
1	LYS115	ASP150
1	LYS103	GLU165
1	LYS155	ASP502
1	ARG24	GLU21
1	HIS182	ASP169
1	ARG207	ASP86
1	HIS100	ASP110
1	ARG32	GLU34
1	HIS17	GLU21
1	LYS145	GLU161
1	LYS89	GLU91
1	LYS64	GLU100
1	LYS392	ASP396
1	LYS218	GLU122
1	HIS140	ASP153
1	LYS167	GLU83

1	ARG580	ASP614
1	LYS142	GLU127
1	ARG409	ASP33
1	LYS38	ASP86
1	LYS106	GLU104
1	LYS190	ASP187
1	LYS143	ASP144
1	HIS1170	GLU688
1	LYS38	ASP37
1	LYS183	GLU187

Table 2: Counting of salt bridges within the PDB entries in Table 1.

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
2RLJ-1.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.51	1.63	20.85
2RLJ-11.PDB	O, A_TRP_8	N, A_TYR_11	H, A_TYR_11	2.98	2.09	19.25
2RLJ-11.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.62	1.69	14.63
2RLJ-12.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.59	1.69	19.30
2RLJ-13.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.63	1.78	24.81
2RLJ-14.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.62	8.91
2RLJ-15.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.69	20.08
2RLJ-16.PDB	O, A_ILE_9	N, A_GLY_13	H, A_GLY_13	2.99	2.03	10.52
2RLJ-19.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.73	1.89	26.29
2RLJ-2.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.69	19.33
2RLJ-3.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.54	1.66	20.38
2RLJ-4.PDB	O, A_TRP_8	N, A_TYR_11	H, A_TYR_11	2.94	2.08	23.85
2RLJ-5.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.60	1.76	25.80
2RLJ-5.PDB	O, A_PRO_10	N, A_GLY_13	H, A_GLY_13	2.75	1.88	22.12
2RLJ-6.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.54	1.66	20.70
2RLJ-7.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.71	1.84	22.67
2RLJ-9.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.57	1.64	13.83
5HJ3.PDB	O, C_ALA_166	N, C_VAL_97	H, C_VAL_97	2.93	2.10	12.03
5HJ3.PDB	O, C_VAL_97	N, C_ALA_166	H, C_ALA_166	2.88	2.11	22.07
5HJ3.PDB	O, C_LEU_68	N, C_VAL_180	H, C_VAL_180	2.78	1.98	17.26
5HJ3.PDB	O, C_VAL_66	N, C_ALA_182	H, C_ALA_182	2.79	1.96	12.90
5HJ3.PDB	OE1, J_GLN_89	OH, J_TYR_36	HH, J_TYR_36	2.57	1.82	22.55
5HJ3.PDB	O, A_SER_49	N, A_TRP_36	H, A_TRP_36	2.98	2.17	16.41
5HJ3.PDB	O, A_TYR_91	N, A_VAL_37	H, A_VAL_37	2.94	2.09	8.77
5HJ3.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.97	2.16	16.17
5HJ3.PDB	O, A_VAL_37	N, A_TYR_91	H, A_TYR_91	2.58	1.73	5.25
5HJ3.PDB	O, A_ASN_35	N, A_VAL_93	H, A_VAL_93	3.00	2.19	17.25
5T42-1.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.93	1.95	0.17
5T42-1.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.78	19.27
5T42-1.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.87	1.99	20.76
5T42-1.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.56	18.05
5T42-1.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.60	1.70	18.73
5T42-1.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.66	14.81
5T42-10.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.99	2.02	8.43
5T42-10.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.93	2.13	29.57
5T42-10.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.94	2.13	28.24
5T42-10.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.79
5T42-10.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	3.00	2.20	29.07
5T42-10.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.01	29.53
5T42-10.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.58	17.30
5T42-10.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	15.97
5T42-10.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.64	15.53
5T42-11.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.81	1.85	11.13
5T42-11.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.82	1.97	23.92
5T42-11.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.70	1.78	16.16
5T42-11.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	20.64
5T42-11.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.83
5T42-11.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.62	15.58
5T42-12.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.97	2.01	7.30
5T42-12.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.85	1.89	9.61
5T42-12.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.71	1.80	16.55
5T42-12.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.92	2.10	27.43
5T42-12.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.85
5T42-12.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.74	18.61
5T42-12.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.65	23.17
5T42-13.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.59	1.66	14.08
5T42-13.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.78	19.44

5T42-13.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.94	2.05	20.83
5T42-13.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.45	1.56	19.27
5T42-13.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.98
5T42-13.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.62	12.60
5T42-14.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.95	1.98	4.18
5T42-14.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.91	1.94	7.26
5T42-14.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.68	1.76	16.51
5T42-14.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.08	29.84
5T42-14.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.90
5T42-14.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.74	18.08
5T42-14.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.44
5T42-15.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.70	1.74	9.57
5T42-15.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.66	1.78	20.70
5T42-15.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.88	2.00	21.01
5T42-15.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	19.25
5T42-15.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.62	1.73	20.10
5T42-15.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.64	13.08
5T42-16.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.96	2.14	27.44
5T42-16.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.75	1.84	17.63
5T42-16.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.15	27.18
5T42-16.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.86	2.06	29.61
5T42-16.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	20.21
5T42-16.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.73	16.77
5T42-16.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.52	1.56	10.87
5T42-17.PDB	O, A_ASN_641	N, A_TRP_644	H, A_TRP_644	2.88	1.91	6.60
5T42-17.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.78	1.97	27.65
5T42-17.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.63	1.72	16.57
5T42-17.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.02	29.77
5T42-17.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.62	21.02
5T42-17.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.72	18.50
5T42-17.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.66	24.43
5T42-18.PDB	O, A_TRP_644	NH1, A_ARG_649	HH11, A_ARG_649	2.95	2.14	29.60
5T42-18.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.77	1.80	7.61
5T42-18.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.78	1.94	24.62
5T42-18.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.76	1.84	15.74
5T42-18.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.59	19.69
5T42-18.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.18
5T42-18.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.61	13.20
5T42-19.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.79	1.82	5.18
5T42-19.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.49
5T42-19.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.06	28.72
5T42-19.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.50
5T42-19.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.70	15.62
5T42-19.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.60	14.03
5T42-2.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.85	1.99	23.63
5T42-2.PDB	O, A_GLN_650	N, A_VAL_658	H, A_VAL_658	2.89	2.05	24.99
5T42-2.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.80	1.82	2.37
5T42-2.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.75	16.21
5T42-2.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.88	2.06	27.64
5T42-2.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.59	19.13
5T42-2.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.72	16.09
5T42-2.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.86
5T42-20.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.93	1.95	4.32
5T42-20.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.94	2.14	29.59
5T42-20.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.80	1.85	12.29
5T42-20.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.73	1.85	21.16
5T42-20.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.83	1.95	21.15
5T42-20.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	18.76

5T42-20.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.40
5T42-20.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.55	1.62	15.71
5T42-3.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.55	1.77	29.97
5T42-3.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.73	1.82	17.54
5T42-3.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.99	2.18	28.74
5T42-3.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.79	1.98	28.05
5T42-3.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.71
5T42-3.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.66	1.74	16.19
5T42-3.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	14.42
5T42-4.PDB	O, A_GLY_647	N, A_TRP_651	H, A_TRP_651	2.59	1.68	16.69
5T42-4.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.57	1.78	28.87
5T42-4.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.61	1.73	20.44
5T42-4.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.87	1.99	21.34
5T42-4.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.57	17.87
5T42-4.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.72	19.23
5T42-4.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.63	13.71
5T42-5.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.85	1.98	22.54
5T42-5.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.92	1.95	7.59
5T42-5.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.70	1.79	17.07
5T42-5.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.14	26.58
5T42-5.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.96	2.16	29.30
5T42-5.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	20.58
5T42-5.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.66	1.76	19.47
5T42-5.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.64	14.61
5T42-6.PDB	O, A_ASP_642	N, A_THR_646	H, A_THR_646	2.82	1.99	26.68
5T42-6.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.76	1.79	8.30
5T42-6.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.76	1.89	21.67
5T42-6.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.85	1.95	19.14
5T42-6.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.61	21.67
5T42-6.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.95
5T42-6.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.63	1.70	15.13
5T42-7.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.74	1.91	26.39
5T42-7.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.58	1.78	28.20
5T42-7.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.65	1.77	20.26
5T42-7.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.84	1.96	20.50
5T42-7.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.58	18.36
5T42-7.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.60	1.68	15.41
5T42-7.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.63	14.62
5T42-8.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.71	1.91	28.69
5T42-8.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.71	1.80	17.39
5T42-8.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.15	26.89
5T42-8.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.86	2.06	28.83
5T42-8.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.58	18.05
5T42-8.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.73	17.27
5T42-8.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.65	13.58
5T42-9.PDB	OG1, A_THR_634	NZ, A_LYS_633	HZ2, A_LYS_633	2.68	1.67	11.19
5T42-9.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.72	1.81	17.22
5T42-9.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.16	28.57
5T42-9.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.80	2.00	29.42
5T42-9.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.55
5T42-9.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.73	16.82
5T42-9.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.44

Table 3: The side chain and main chain hydrogen bonding networks.In this table, the names of the PDB files correspond to the single NMR structural model split from the NMR ensemble, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5HJ3.PDB	OE1, J_GLN_89	OH, J_TYR_36	HH, J_TYR_36	2.57	1.82	22.55
5T42-9.PDB	OG1, A_THR_634	NZ, A_LYS_633	HZ2, A_LYS_633	2.68	1.67	11.19

Table 4: Side chain hydrogen bonding network analysis. In this table, the names of the PDB files correspond to the single NMR structural model split from the NMR ensemble, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EBO	A_LYS_87	NZ	C_ASP_106	OD2	3.887
1EBO	A_HIS_112	ND1	B_GLU_77	OE1	3.658
1EBO	A_HIS_112	ND1	B_GLU_77	OE2	3.104
1EBO	B_HIS_112	ND1	C_GLU_77	OE1	3.068
1EBO	B_HIS_112	ND1	C_GLU_77	OE2	2.658
1EBO	C_LYS_7	NZ	B_GLU_9	OE1	3.472
1EBO	C_LYS_26	NZ	A_GLU_21	OE1	2.847
1EBO	C_LYS_26	NZ	A_GLU_21	OE2	3.880
1EBO	C_LYS_87	NZ	B_ASP_106	OD2	3.920
1EBO	D_HIS_112	ND1	E_GLU_77	OE1	3.490
1EBO	D_HIS_112	ND1	E_GLU_77	OE2	2.696
1EBO	E_LYS_26	NZ	F_GLU_21	OE2	3.162
1EBO	E_LYS_87	NZ	D_ASP_106	OD2	3.925
1EBO	F_LYS_26	NZ	D_GLU_21	OE1	3.927
1EBO	F_LYS_87	NZ	E_ASP_106	OD2	3.651
1EBO	F_HIS_112	ND1	D_GLU_77	OE2	3.188
2EBO	A_HIS_613	ND1	B_GLU_578	OE1	3.396
2EBO	A_HIS_613	ND1	B_GLU_578	OE2	3.211
2EBO	B_HIS_613	ND1	C_GLU_578	OE1	3.346
2EBO	B_HIS_613	ND1	C_GLU_578	OE2	2.789
2QHR	H_LYS_143	NZ	L_GLU_125	OE2	2.743
2QHR	H_HIS_164	ND1	L_GLU_168	OE1	3.446
2QHR	H_HIS_164	ND1	L_GLU_168	OE2	2.691
2QHR	H_LYS_208	NZ	L_GLU_124	OE1	3.025
2QHR	H_LYS_208	NZ	L_GLU_124	OE2	3.278
2QHR	L_LYS_204	NZ	H_ASP_130	OD1	2.837
2QHR	L_LYS_204	NZ	H_ASP_130	OD2	3.813
2QHR	P_HIS_407	ND1	L_ASP_92	OD1	3.553
2QHR	P_ARG_409	NH1	H_ASP_33	OD2	2.967
2Y6S	C_ARG_100	NH1	D_GLU_50	OE1	2.758
2Y6S	D_LYS_208	NZ	C_GLU_127	OE1	3.225
2Y6S	H_LYS_208	NZ	L_GLU_127	OE1	3.152
2Y6S	L_ARG_100	NH1	H_GLU_50	OE1	2.759
2Y6S	L_ARG_100	NH2	H_GLU_50	OE1	3.945
3CSY	A_LYS_221	NZ	B_GLU_123	OE1	3.090
3CSY	A_LYS_221	NZ	B_GLU_123	OE2	3.307
3CSY	C_HIS_172	NE2	D_ASP_167	OD2	3.885
3CSY	C_LYS_221	NZ	D_GLU_123	OE1	3.258
3CSY	C_LYS_221	NZ	D_GLU_123	OE2	3.282
3CSY	E_LYS_221	NZ	F_GLU_123	OE1	3.238
3CSY	E_LYS_221	NZ	F_GLU_123	OE2	3.205
3CSY	G_HIS_172	NE2	H_ASP_167	OD2	3.733
3CSY	G_LYS_221	NZ	H_GLU_123	OE1	3.440
3CSY	G_LYS_221	NZ	H_GLU_123	OE2	3.445
3CSY	I_ARG_134	NH1	J_GLU_545	OE2	3.043
3CSY	J_ARG_559	NH2	I_GLU_103	OE1	3.261
3CSY	J_ARG_559	NH2	I_GLU_103	OE2	3.005
3CSY	K_ARG_134	NH1	L_GLU_545	OE2	3.181
3CSY	L_ARG_559	NH2	K_GLU_103	OE1	3.317
3CSY	L_ARG_559	NH2	K_GLU_103	OE2	3.156
3CSY	M_ARG_134	NH1	N_GLU_545	OE2	2.894
3CSY	N_ARG_559	NH2	M_GLU_103	OE1	2.925
3CSY	N_ARG_559	NH2	M_GLU_103	OE2	3.048
3CSY	O_ARG_134	NH1	P_GLU_545	OE2	3.026
3CSY	P_ARG_559	NH2	O_GLU_103	OE1	3.054
3CSY	P_ARG_559	NH2	O_GLU_103	OE2	2.808
3VE0	J_ARG_559	NH1	I_GLU_103	OE1	3.852

3VE0	J_ARG_559	NH1	I_GLU_103	OE2	3.848
3VE0	J_ARG_559	NH2	I_GLU_103	OE1	2.444
3VE0	J_ARG_559	NH2	I_GLU_103	OE2	2.766
3VE0	J_ARG_595	NH2	I_ASP_49	OD2	3.842
3VE0	J_ARG_596	NH1	I_ASP_55	OD1	3.003
3VE0	A_ARG_98	NH2	I_GLU_44	OE1	3.137
3VE0	A_ARG_98	NH2	I_GLU_44	OE2	3.008
3VE0	A_LYS_214	NZ	B_GLU_123	OE1	3.666
3VE0	A_LYS_214	NZ	B_GLU_123	OE2	2.624
5F1B	A_ARG_134	NH1	B_GLU_545	OE2	3.659
5F1B	B_ARG_559	NH1	A_GLU_103	OE1	3.219
5F1B	B_ARG_559	NH1	A_GLU_103	OE2	3.449
5F1B	B_ARG_559	NH2	A_GLU_103	OE1	3.928
5F1B	B_ARG_559	NH2	A_GLU_103	OE2	2.697
5F1B	B_LYS_588	NZ	A_ASP_47	OD1	3.551
5F1B	B_LYS_588	NZ	A_ASP_47	OD2	3.521
5FHC	J_ARG_559	NH2	K_GLU_103	OE1	3.531
5FHC	J_ARG_559	NH2	K_GLU_103	OE2	3.399
5FHC	K_ARG_134	NH1	J_GLU_545	OE2	2.861
5FHC	A_LYS_143	NZ	B_GLU_124	OE2	2.678
5FHC	A_LYS_209	NZ	B_GLU_123	OE1	2.702
5FHC	A_LYS_209	NZ	B_GLU_123	OE2	3.358
5FHC	H_LYS_209	NZ	L_GLU_123	OE1	3.238
5FHC	H_LYS_209	NZ	L_GLU_123	OE2	3.173
5HJ3	D_LYS_510	NZ	J_GLU_55	OE1	3.743
5HJ3	D_LYS_510	NZ	J_GLU_55	OE2	3.493
5HJ3	D_ARG_559	NH2	C_GLU_103	OE1	2.496
5HJ3	D_ARG_559	NH2	C_GLU_103	OE2	2.573
5HJ3	E_LYS_221	NZ	F_GLU_123	OE2	3.658
5HJ3	H_LYS_510	NZ	F_GLU_55	OE2	3.815
5HJ3	H_ARG_559	NH2	G_GLU_103	OE1	2.521
5HJ3	H_ARG_559	NH2	G_GLU_103	OE2	2.719
5HJ3	I_HIS_172	NE2	J_ASP_167	OD2	3.705
5HJ3	I_LYS_221	NZ	J_GLU_123	OE1	3.253
5HJ3	I_LYS_221	NZ	J_GLU_123	OE2	2.800
5HJ3	L_ARG_559	NH2	K_GLU_103	OE1	2.680
5HJ3	L_ARG_559	NH2	K_GLU_103	OE2	2.484
5HJ3	L_HIS_602	ND1	H_GLU_611	OE1	3.679
5HJ3	L_HIS_602	NE2	H_GLU_611	OE1	3.945
5HJ3	M_LYS_221	NZ	N_GLU_123	OE1	3.397
5HJ3	M_LYS_221	NZ	N_GLU_123	OE2	3.011
5HJ3	P_LYS_510	NZ	B_GLU_55	OE1	3.843
5HJ3	P_LYS_510	NZ	B_GLU_55	OE2	3.553
5HJ3	P_ARG_559	NH2	O_GLU_103	OE1	2.547
5HJ3	P_ARG_559	NH2	O_GLU_103	OE2	2.625
5HJ3	P_HIS_602	NE2	L_GLU_611	OE1	3.277
5HJ3	A_LYS_221	NZ	B_GLU_123	OE1	3.583
5HJ3	A_LYS_221	NZ	B_GLU_123	OE2	3.404
5JNX	C_ARG_134	NH1	D_GLU_545	OE2	3.659
5JNX	D_ARG_559	NH1	C_GLU_103	OE1	3.220
5JNX	D_ARG_559	NH1	C_GLU_103	OE2	3.450
5JNX	D_ARG_559	NH2	C_GLU_103	OE1	3.927
5JNX	D_ARG_559	NH2	C_GLU_103	OE2	2.697
5JNX	D_LYS_588	NZ	C_ASP_47	OD1	3.551
5JNX	D_LYS_588	NZ	C_ASP_47	OD2	3.521
5JNX	E_ARG_134	NH1	F_GLU_545	OE2	3.660
5JNX	E_LYS_155	NZ	A_ASP_502	OD2	3.701
5JNX	F_ARG_559	NH1	E_GLU_103	OE1	3.219

5JNX	F_ARG_559	NH1	E_GLU_103	OE2	3.448
5JNX	F_ARG_559	NH2	E_GLU_103	OE1	3.927
5JNX	F_ARG_559	NH2	E_GLU_103	OE2	2.697
5JNX	F_LYS_588	NZ	E_ASP_47	OD1	3.552
5JNX	F_LYS_588	NZ	E_ASP_47	OD2	3.520
5JNX	G_ARG_134	NH1	H_GLU_545	OE2	3.659
5JNX	H_ARG_559	NH1	G_GLU_103	OE1	3.221
5JNX	H_ARG_559	NH1	G_GLU_103	OE2	3.449
5JNX	H_ARG_559	NH2	G_GLU_103	OE1	3.928
5JNX	H_ARG_559	NH2	G_GLU_103	OE2	2.697
5JNX	H_LYS_588	NZ	G_ASP_47	OD1	3.552
5JNX	H_LYS_588	NZ	G_ASP_47	OD2	3.522
5JQ3	B_ARG_559	NH1	A_GLU_103	OE1	2.754
5JQ3	B_ARG_559	NH1	A_GLU_103	OE2	3.830
5JQ3	B_ARG_559	NH2	A_GLU_103	OE1	3.362
5JQ3	B_ARG_559	NH2	A_GLU_103	OE2	2.945
5JQ7	B_LYS_510	NZ	A_GLU_292	OE1	3.131
5JQ7	B_ARG_559	NH1	A_GLU_103	OE1	2.800
5JQ7	B_ARG_559	NH1	A_GLU_103	OE2	3.720
5JQ7	B_ARG_559	NH2	A_GLU_103	OE1	3.375
5JQ7	B_ARG_559	NH2	A_GLU_103	OE2	2.748
5JQB	B_LYS_510	NZ	A_GLU_292	OE1	2.746
5JQB	B_LYS_510	NZ	A_GLU_292	OE2	3.918
5JQB	B_ARG_559	NH1	A_GLU_103	OE1	2.703
5JQB	B_ARG_559	NH1	A_GLU_103	OE2	3.788
5JQB	B_ARG_559	NH2	A_GLU_103	OE1	3.188
5JQB	B_ARG_559	NH2	A_GLU_103	OE2	2.857
5JQB	B_LYS_588	NZ	A_ASP_47	OD1	3.558
5JQB	B_LYS_588	NZ	A_ASP_47	OD2	3.148
5KEL	A_ARG_130	NH1	B_GLU_540	OE2	3.053
5KEL	A_LYS_272	NZ	C_ASP_54	OD2	3.464
5KEL	A_LYS_272	NZ	C_ASP_56	OD2	2.595
5KEL	B_ARG_559	NH1	A_GLU_103	OE2	3.831
5KEL	B_ARG_559	NH2	A_GLU_103	OE1	3.279
5KEL	B_ARG_559	NH2	A_GLU_103	OE2	3.801
5KEL	E_ARG_130	NH1	G_GLU_540	OE2	3.054
5KEL	E_LYS_272	NZ	J_ASP_54	OD2	3.464
5KEL	E_LYS_272	NZ	J_ASP_56	OD2	2.596
5KEL	G_ARG_559	NH1	E_GLU_103	OE2	3.832
5KEL	G_ARG_559	NH2	E_GLU_103	OE1	3.279
5KEL	G_ARG_559	NH2	E_GLU_103	OE2	3.802
5KEL	F_ARG_130	NH1	I_GLU_540	OE2	3.053
5KEL	F_LYS_272	NZ	M_ASP_54	OD2	3.463
5KEL	F_LYS_272	NZ	M_ASP_56	OD2	2.596
5KEL	I_ARG_559	NH1	F_GLU_103	OE2	3.831
5KEL	I_ARG_559	NH2	F_GLU_103	OE1	3.279
5KEL	I_ARG_559	NH2	F_GLU_103	OE2	3.801
5KEM	A_LYS_272	NZ	D_ASP_54	OD1	2.876
5KEM	A_LYS_272	NZ	D_ASP_54	OD2	3.185
5KEM	F_LYS_272	NZ	I_ASP_54	OD1	2.876
5KEM	F_LYS_272	NZ	I_ASP_54	OD2	3.185
5KEN	A_ARG_134	NH2	B_GLU_545	OE1	2.859
5KEN	B_LYS_510	NZ	D_GLU_56	OE1	3.639
5KEN	B_LYS_510	NZ	D_GLU_56	OE2	2.773
5KEN	B_HIS_549	NE2	C_ASP_52	OD1	3.874
5KEN	B_ARG_559	NH1	A_GLU_103	OE1	3.709
5KEN	B_ARG_559	NH1	A_GLU_103	OE2	2.818
5KEN	B_ARG_559	NH2	A_GLU_103	OE1	3.114

5KEN	B_ARG_559	NH2	A_GLU_103	OE2	3.662
5KEN	E_LYS_272	NZ	J_ASP_54	OD2	3.722
5KEN	E_LYS_272	NZ	J_ASP_56	OD1	3.736
5KEN	E_LYS_272	NZ	J_ASP_56	OD2	2.765
5KEN	F_LYS_510	NZ	H_GLU_56	OE2	2.720
5KEN	F_HIS_549	NE2	G_ASP_52	OD1	3.491
5KEN	F_ARG_559	NH1	E_GLU_103	OE1	3.868
5KEN	F_ARG_559	NH1	E_GLU_103	OE2	2.947
5KEN	F_ARG_559	NH2	E_GLU_103	OE1	3.043
5KEN	F_ARG_559	NH2	E_GLU_103	OE2	3.542
5KEN	G_LYS_62	NZ	H_ASP_1	OD2	2.735
5KEN	K_LYS_272	NZ	Q_ASP_54	OD2	3.814
5KEN	K_LYS_272	NZ	Q_ASP_56	OD1	3.710
5KEN	K_LYS_272	NZ	Q_ASP_56	OD2	2.769
5KEN	M_LYS_510	NZ	O_GLU_56	OE2	2.667
5KEN	M_ARG_559	NH1	K_GLU_103	OE1	3.708
5KEN	M_ARG_559	NH1	K_GLU_103	OE2	2.824
5KEN	M_ARG_559	NH2	K_GLU_103	OE1	3.090
5KEN	M_ARG_559	NH2	K_GLU_103	OE2	3.645
5KEN	N_LYS_62	NZ	O_ASP_1	OD2	2.793
6DZL	G_HIS_96	ND1	J_GLU_55	OE2	3.342
6DZL	G_HIS_96	NE2	J_GLU_55	OE1	3.570
6DZL	G_HIS_96	NE2	J_GLU_55	OE2	3.728
6DZL	H_HIS_96	ND1	K_GLU_55	OE2	3.341
6DZL	H_HIS_96	NE2	K_GLU_55	OE1	3.571
6DZL	H_HIS_96	NE2	K_GLU_55	OE2	3.727
6DZL	I_HIS_96	ND1	L_GLU_55	OE2	3.341
6DZL	I_HIS_96	NE2	L_GLU_55	OE1	3.571
6DZL	I_HIS_96	NE2	L_GLU_55	OE2	3.727
6EA7	B_ARG_559	NH1	A_GLU_103	OE1	2.641
6EA7	B_ARG_559	NH1	A_GLU_103	OE2	3.432
6EA7	B_ARG_559	NH2	A_GLU_103	OE2	3.686
6EA7	B_HIS_602	ND1	F_GLU_611	OE1	3.135
6EA7	D_ARG_559	NH1	C_GLU_103	OE1	2.573
6EA7	D_ARG_559	NH1	C_GLU_103	OE2	3.488
6EA7	D_ARG_559	NH2	C_GLU_103	OE1	3.832
6EA7	D_ARG_559	NH2	C_GLU_103	OE2	3.318
6EA7	D_HIS_602	ND1	B_GLU_611	OE1	3.062
6EA7	F_ARG_559	NH1	E_GLU_103	OE1	2.812
6EA7	F_ARG_559	NH1	E_GLU_103	OE2	3.584
6EA7	F_ARG_559	NH2	E_GLU_103	OE2	3.608
6EA7	F_ARG_596	NH2	E_ASP_55	OD1	2.483
6EA7	F_ARG_596	NH2	E_ASP_55	OD2	3.342
6EA7	F_HIS_602	ND1	D_GLU_611	OE1	3.253
6EA7	H_HIS_100	ND1	L_GLU_55	OE1	3.325
6EA7	H_HIS_100	NE2	L_GLU_55	OE1	3.655
6EA7	H_HIS_108	NE2	L_ASP_50	OD1	2.912
6EA7	H_HIS_173	ND1	L_ASP_166	OD1	3.947
6EA7	H_HIS_173	ND1	L_ASP_166	OD2	3.590
6EA7	H_LYS_218	NZ	L_GLU_122	OE1	2.826
6EA7	M_HIS_100	ND1	N_GLU_55	OE1	3.446
6EA7	M_HIS_100	ND1	N_GLU_55	OE2	3.681
6EA7	M_HIS_108	ND1	N_ASP_50	OD1	3.757
6EA7	M_HIS_108	NE2	N_ASP_50	OD1	3.718
6EA7	M_HIS_173	ND1	N_ASP_166	OD2	3.701
6EA7	Q_HIS_108	NE2	R_ASP_50	OD1	3.227
6EA7	Q_HIS_173	ND1	R_ASP_166	OD1	3.817
6EA7	Q_HIS_173	ND1	R_ASP_166	OD2	3.600

6F5U	B_LYS_510	NZ	A_GLU_292	OE1	3.345
6F5U	B_ARG_559	NH1	A_GLU_103	OE1	2.631
6F5U	B_ARG_559	NH1	A_GLU_103	OE2	3.833
6F5U	B_ARG_559	NH2	A_GLU_103	OE1	3.290
6F5U	B_ARG_559	NH2	A_GLU_103	OE2	2.992
6F6I	B_LYS_510	NZ	A_GLU_292	OE1	3.377
6F6I	B_ARG_559	NH1	A_GLU_103	OE1	3.800
6F6I	B_ARG_559	NH1	A_GLU_103	OE2	2.815
6F6I	B_ARG_559	NH2	A_GLU_103	OE1	3.096
6F6I	B_ARG_559	NH2	A_GLU_103	OE2	3.529
6F6N	B_LYS_510	NZ	A_GLU_292	OE1	2.639
6F6N	B_ARG_559	NH1	A_GLU_103	OE1	2.593
6F6N	B_ARG_559	NH1	A_GLU_103	OE2	3.789
6F6N	B_ARG_559	NH2	A_GLU_103	OE1	3.215
6F6N	B_ARG_559	NH2	A_GLU_103	OE2	2.904
6F6N	B_LYS_588	NZ	A_ASP_47	OD1	3.696
6F6N	B_LYS_588	NZ	A_ASP_47	OD2	2.975
6F6S	B_LYS_510	NZ	A_GLU_292	OE1	2.331
6F6S	B_LYS_510	NZ	A_GLU_292	OE2	3.397
6F6S	B_ARG_559	NH1	A_GLU_103	OE1	2.656
6F6S	B_ARG_559	NH1	A_GLU_103	OE2	3.920
6F6S	B_ARG_559	NH2	A_GLU_103	OE1	3.146
6F6S	B_ARG_559	NH2	A_GLU_103	OE2	2.951
6F6S	B_LYS_588	NZ	A_ASP_47	OD1	2.944
6F6S	B_LYS_588	NZ	A_ASP_47	OD2	2.772
6G95	B_ARG_559	NH1	A_GLU_103	OE1	2.683
6G95	B_ARG_559	NH1	A_GLU_103	OE2	3.879
6G95	B_ARG_559	NH2	A_GLU_103	OE1	3.249
6G95	B_ARG_559	NH2	A_GLU_103	OE2	2.973
6G9B	B_LYS_510	NZ	A_GLU_292	OE1	3.414
6G9B	B_ARG_559	NH1	A_GLU_103	OE1	2.574
6G9B	B_ARG_559	NH1	A_GLU_103	OE2	3.760
6G9B	B_ARG_559	NH2	A_GLU_103	OE1	3.199
6G9B	B_ARG_559	NH2	A_GLU_103	OE2	2.870
6G9B	B_LYS_588	NZ	A_ASP_47	OD1	3.317
6G9B	B_LYS_588	NZ	A_ASP_47	OD2	2.892
6G9I	B_ARG_559	NH1	A_GLU_103	OE1	2.689
6G9I	B_ARG_559	NH1	A_GLU_103	OE2	3.794
6G9I	B_ARG_559	NH2	A_GLU_103	OE1	3.340
6G9I	B_ARG_559	NH2	A_GLU_103	OE2	2.940
6HRO	B_LYS_510	NZ	A_GLU_292	OE1	3.852
6HRO	B_ARG_559	NH1	A_GLU_103	OE1	2.817
6HRO	B_ARG_559	NH1	A_GLU_103	OE2	3.911
6HRO	B_ARG_559	NH2	A_GLU_103	OE1	3.514
6HRO	B_ARG_559	NH2	A_GLU_103	OE2	3.164
6HRO	B_LYS_588	NZ	A_ASP_47	OD1	3.207
6HRO	B_LYS_588	NZ	A_ASP_47	OD2	2.778
6HS4	B_ARG_559	NH1	A_GLU_103	OE1	2.624
6HS4	B_ARG_559	NH1	A_GLU_103	OE2	3.811
6HS4	B_ARG_559	NH2	A_GLU_103	OE1	3.176
6HS4	B_ARG_559	NH2	A_GLU_103	OE2	2.846
6HS4	B_LYS_588	NZ	A_ASP_47	OD1	3.053
6HS4	B_LYS_588	NZ	A_ASP_47	OD2	2.954
6MAM	A_LYS_227	NZ	B_GLU_125	OE1	3.431
6MAM	C_HIS_182	NE2	D_ASP_169	OD2	3.087
6MAM	C_LYS_227	NZ	D_GLU_125	OE1	3.951
6MAM	H_ARG_559	NH1	G_GLU_103	OE1	2.237
6MAM	H_ARG_559	NH1	G_GLU_103	OE2	3.123

6MAM	H_ARG_559	NH2	G_GLU_103	OE1	3.565
6MAM	H_ARG_559	NH2	G_GLU_103	OE2	2.826
6MAM	J_ARG_559	NH1	I_GLU_103	OE1	2.281
6MAM	J_ARG_559	NH1	I_GLU_103	OE2	3.223
6MAM	J_ARG_559	NH2	I_GLU_103	OE1	3.504
6MAM	J_ARG_559	NH2	I_GLU_103	OE2	2.826
6MAM	L_ARG_559	NH1	K_GLU_103	OE1	2.658
6MAM	L_ARG_559	NH1	K_GLU_103	OE2	3.420
6MAM	L_ARG_559	NH2	K_GLU_103	OE1	3.722
6MAM	L_ARG_559	NH2	K_GLU_103	OE2	2.995
6NAE	B_LYS_510	NZ	A_GLU_292	OE1	2.350
6NAE	B_LYS_510	NZ	A_GLU_292	OE2	3.768
6NAE	B_ARG_559	NH1	A_GLU_103	OE1	2.669
6NAE	B_ARG_559	NH1	A_GLU_103	OE2	3.739
6NAE	B_ARG_559	NH2	A_GLU_103	OE1	3.488
6NAE	B_ARG_559	NH2	A_GLU_103	OE2	3.068
6QD7	L_ARG_91	NH1	D_GLU_502	OE1	3.607
6QD7	H_LYS_65	NZ	D_ASP_552	OD1	3.151
6QD7	H_LYS_65	NZ	D_ASP_552	OD2	3.487
6QD7	H_ARG_101	NH1	D_GLU_564	OE1	3.838
6QD7	H_ARG_101	NH1	D_GLU_564	OE2	2.869
6QD7	H_ARG_101	NH2	D_GLU_502	OE1	3.497
6QD7	H_ARG_101	NH2	D_GLU_502	OE2	3.635
6QD7	H_ARG_101	NH2	D_GLU_564	OE1	3.061
6QD7	H_ARG_101	NH2	D_GLU_564	OE2	3.438
6QD7	A_ARG_134	NH1	B_GLU_545	OE2	3.138
6QD7	B_ARG_559	NH1	A_GLU_103	OE1	2.604
6QD7	B_ARG_559	NH1	A_GLU_103	OE2	3.895
6QD7	B_ARG_559	NH2	A_GLU_103	OE1	3.220
6QD7	B_ARG_559	NH2	A_GLU_103	OE2	3.089
6QD7	B_LYS_588	NZ	A_ASP_47	OD2	3.517
6QD7	B_HIS_602	ND1	F_GLU_611	OE2	2.318
6QD7	C_ARG_134	NH1	D_GLU_545	OE2	3.066
6QD7	E_ARG_134	NH1	F_GLU_545	OE2	2.931
6QD7	D_ARG_559	NH1	C_GLU_103	OE1	2.624
6QD7	D_ARG_559	NH1	C_GLU_103	OE2	3.858
6QD7	D_ARG_559	NH2	C_GLU_103	OE1	3.320
6QD7	D_ARG_559	NH2	C_GLU_103	OE2	3.132
6QD7	D_LYS_588	NZ	C_ASP_47	OD2	3.598
6QD7	D_HIS_602	ND1	B_GLU_611	OE2	2.828
6QD7	F_ARG_559	NH1	E_GLU_103	OE1	2.462
6QD7	F_ARG_559	NH1	E_GLU_103	OE2	3.800
6QD7	F_ARG_559	NH2	E_GLU_103	OE1	3.090
6QD7	F_ARG_559	NH2	E_GLU_103	OE2	2.951
6QD7	F_LYS_588	NZ	E_ASP_47	OD2	3.686
6QD7	F_HIS_602	ND1	D_GLU_611	OE2	2.771
6QD7	X_LYS_65	NZ	F_ASP_552	OD1	3.082
6QD7	X_LYS_65	NZ	F_ASP_552	OD2	3.701
6QD7	X_ARG_101	NH1	F_GLU_564	OE1	3.893
6QD7	X_ARG_101	NH1	F_GLU_564	OE2	2.816
6QD7	X_ARG_101	NH2	F_GLU_502	OE1	3.631
6QD7	X_ARG_101	NH2	F_GLU_502	OE2	3.812
6QD7	X_ARG_101	NH2	F_GLU_564	OE1	3.108
6QD7	X_ARG_101	NH2	F_GLU_564	OE2	3.371
6QD7	U_LYS_65	NZ	B_ASP_552	OD1	2.927
6QD7	U_LYS_65	NZ	B_ASP_552	OD2	3.579
6QD7	U_ARG_101	NH1	B_GLU_564	OE1	3.771
6QD7	U_ARG_101	NH1	B_GLU_564	OE2	2.902

6QD7	U_ARG_101	NH2	B_GLU_502	OE1	3.404
6QD7	U_ARG_101	NH2	B_GLU_502	OE2	3.473
6QD7	U_ARG_101	NH2	B_GLU_564	OE1	3.146
6QD7	U_ARG_101	NH2	B_GLU_564	OE2	3.609
6QD7	Z_ARG_91	NH1	F_GLU_502	OE1	3.548
6QD7	P_ARG_91	NH1	B_GLU_502	OE1	3.467
6QD8	Z_ARG_96	NH1	W_GLU_51	OE1	3.187
6QD8	Z_ARG_96	NH1	W_GLU_51	OE2	3.722
6QD8	A_ARG_64	NH2	B_ASP_522	OD2	3.626
6QD8	A_ARG_134	NH1	B_GLU_545	OE2	3.117
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE1	3.080
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE2	3.529
6QD8	B_ARG_559	NH1	A_GLU_103	OE1	3.695
6QD8	B_ARG_559	NH1	A_GLU_103	OE2	2.598
6QD8	B_ARG_559	NH2	A_GLU_103	OE1	3.315
6QD8	B_ARG_559	NH2	A_GLU_103	OE2	3.288
6QD8	B_HIS_602	ND1	F_GLU_611	OE2	3.837
6QD8	L_ARG_96	NH1	H_GLU_51	OE1	3.060
6QD8	L_ARG_96	NH1	H_GLU_51	OE2	3.554
6QD8	H_ARG_55	NH1	B_GLU_564	OE1	2.303
6QD8	H_ARG_55	NH1	B_GLU_564	OE2	3.666
6QD8	C_ARG_64	NH2	D_ASP_522	OD2	3.747
6QD8	C_ARG_134	NH1	D_GLU_545	OE2	2.972
6QD8	E_ARG_64	NH2	F_ASP_522	OD2	3.901
6QD8	E_ARG_134	NH1	F_GLU_545	OE2	2.891
6QD8	F_ARG_559	NH1	E_GLU_103	OE1	3.653
6QD8	F_ARG_559	NH1	E_GLU_103	OE2	2.383
6QD8	F_ARG_559	NH2	E_GLU_103	OE1	3.116
6QD8	F_ARG_559	NH2	E_GLU_103	OE2	2.960
6QD8	F_HIS_602	ND1	D_GLU_611	OE2	3.980
6QD8	D_ARG_559	NH1	C_GLU_103	OE1	3.634
6QD8	D_ARG_559	NH1	C_GLU_103	OE2	2.515
6QD8	D_ARG_559	NH2	C_GLU_103	OE1	3.283
6QD8	D_ARG_559	NH2	C_GLU_103	OE2	3.254
6QD8	D_HIS_602	ND1	B_GLU_611	OE2	3.920
6QD8	W_ARG_55	NH1	F_GLU_564	OE1	2.296
6QD8	W_ARG_55	NH1	F_GLU_564	OE2	3.607
6QD8	Q_ARG_55	NH1	D_GLU_564	OE1	2.265
6QD8	Q_ARG_55	NH1	D_GLU_564	OE2	3.539
6S8D	H_ARG_30	NH2	P_ASP_104	OD2	3.844
6S8D	B_ARG_559	NH1	A_GLU_103	OE1	3.375
6S8D	B_ARG_559	NH1	A_GLU_103	OE2	3.357
6S8D	B_ARG_559	NH2	A_GLU_103	OE1	3.329
6S8D	B_ARG_596	NH2	A_ASP_55	OD2	3.730
6S8D	D_ARG_559	NH1	C_GLU_103	OE1	3.344
6S8D	D_ARG_559	NH1	C_GLU_103	OE2	3.304
6S8D	D_ARG_559	NH2	C_GLU_103	OE1	3.261
6S8D	D_ARG_559	NH2	C_GLU_103	OE2	3.986
6S8D	D_ARG_596	NH2	C_ASP_55	OD2	3.794
6S8D	F_ARG_559	NH1	E_GLU_103	OE1	3.445
6S8D	F_ARG_559	NH1	E_GLU_103	OE2	3.366
6S8D	F_ARG_559	NH2	E_GLU_103	OE1	3.372
6S8D	F_ARG_596	NH2	E_ASP_55	OD2	3.605
6S8D	E_LYS_114	NZ	Y_ASP_56	OD2	3.842
6S8D	P_ARG_30	NH2	Y_ASP_104	OD2	3.808
6S8D	Y_ARG_30	NH2	H_ASP_104	OD2	3.626
6S8I	H_ARG_105	NH1	L_GLU_102	OE1	3.601
6S8I	H_ARG_105	NH1	L_GLU_102	OE2	3.239

6S8I	H_ARG_105	NH2	L_GLU_102	OE2	2.950
6S8I	A_LYS_114	NZ	H_ASP_56	OD1	2.454
6S8I	A_LYS_114	NZ	H_ASP_56	OD2	2.783
6S8I	A_ARG_134	NH1	B_GLU_545	OE2	3.078
6S8I	B_ARG_559	NH1	A_GLU_103	OE1	3.895
6S8I	B_ARG_559	NH1	A_GLU_103	OE2	3.783
6S8I	B_ARG_559	NH2	A_GLU_103	OE1	3.282
6S8I	B_ARG_559	NH2	A_GLU_103	OE2	3.928
6S8I	B_ARG_596	NH2	A_ASP_55	OD1	3.671
6S8I	D_ARG_559	NH1	C_GLU_103	OE1	3.877
6S8I	D_ARG_559	NH1	C_GLU_103	OE2	3.822
6S8I	D_ARG_559	NH2	C_GLU_103	OE1	3.248
6S8I	D_ARG_559	NH2	C_GLU_103	OE2	3.953
6S8I	D_ARG_596	NH2	C_ASP_55	OD1	3.743
6S8I	F_ARG_559	NH1	E_GLU_103	OE1	3.975
6S8I	F_ARG_559	NH1	E_GLU_103	OE2	3.796
6S8I	F_ARG_559	NH2	E_GLU_103	OE1	3.335
6S8I	F_ARG_559	NH2	E_GLU_103	OE2	3.908
6S8I	F_ARG_596	NH2	E_ASP_55	OD1	3.553
6S8I	C_LYS_114	NZ	P_ASP_56	OD1	2.515
6S8I	C_LYS_114	NZ	P_ASP_56	OD2	2.783
6S8I	C_ARG_134	NH1	D_GLU_545	OE2	3.135
6S8I	E_LYS_114	NZ	Y_ASP_56	OD1	2.476
6S8I	E_LYS_114	NZ	Y_ASP_56	OD2	2.735
6S8I	E_ARG_134	NH1	F_GLU_545	OE2	3.154
6S8I	P_ARG_105	NH1	O_GLU_102	OE1	3.789
6S8I	P_ARG_105	NH1	O_GLU_102	OE2	3.289
6S8I	P_ARG_105	NH2	O_GLU_102	OE2	3.143
6S8I	Y_ARG_105	NH1	U_GLU_102	OE1	3.606
6S8I	Y_ARG_105	NH1	U_GLU_102	OE2	3.273
6S8I	Y_ARG_105	NH2	U_GLU_102	OE2	2.978
6S8J	A_LYS_114	NZ	H_ASP_56	OD1	3.168
6S8J	A_LYS_114	NZ	H_ASP_56	OD2	2.312
6S8J	A_ARG_134	NH1	B_GLU_545	OE2	2.814
6S8J	B_ARG_559	NH1	A_GLU_103	OE1	3.955
6S8J	B_ARG_559	NH1	A_GLU_103	OE2	3.604
6S8J	B_ARG_559	NH2	A_GLU_103	OE1	3.443
6S8J	B_ARG_559	NH2	A_GLU_103	OE2	3.830
6S8J	B_ARG_596	NH2	A_ASP_55	OD1	2.986
6S8J	B_ARG_596	NH2	A_ASP_55	OD2	3.529
6S8J	D_ARG_559	NH1	C_GLU_103	OE1	3.872
6S8J	D_ARG_559	NH1	C_GLU_103	OE2	3.635
6S8J	D_ARG_559	NH2	C_GLU_103	OE1	3.272
6S8J	D_ARG_559	NH2	C_GLU_103	OE2	3.792
6S8J	D_ARG_596	NH2	C_ASP_55	OD1	2.928
6S8J	D_ARG_596	NH2	C_ASP_55	OD2	3.762
6S8J	D_HIS_602	ND1	B_GLU_611	OE1	3.866
6S8J	D_HIS_602	NE2	B_GLU_611	OE1	3.805
6S8J	D_HIS_602	NE2	B_GLU_611	OE2	3.737
6S8J	F_ARG_559	NH1	E_GLU_103	OE1	3.993
6S8J	F_ARG_559	NH1	E_GLU_103	OE2	3.748
6S8J	F_ARG_559	NH2	E_GLU_103	OE1	3.468
6S8J	F_ARG_559	NH2	E_GLU_103	OE2	3.952
6S8J	F_ARG_596	NH2	E_ASP_55	OD1	2.985
6S8J	F_ARG_596	NH2	E_ASP_55	OD2	3.707
6S8J	F_HIS_602	ND1	D_GLU_611	OE1	3.880
6S8J	F_HIS_602	NE2	D_GLU_611	OE2	3.765
6S8J	C_LYS_114	NZ	P_ASP_56	OD1	3.173

6S8J	C_LYS_114	NZ	P_ASP_56	OD2	2.252
6S8J	C_ARG_134	NH1	D_GLU_545	OE2	2.837
6S8J	E_LYS_114	NZ	Y_ASP_56	OD1	3.177
6S8J	E_LYS_114	NZ	Y_ASP_56	OD2	2.185
6S8J	E_ARG_134	NH1	F_GLU_545	OE2	2.997

Table 5: Interfacial salt bridging network analysis within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

Count	Residue A	Residue B
191	ARG559	GLU103
23	LYS588	ASP47
22	ARG134	GLU545
17	HIS602	GLU611
15	ARG596	ASP55
15	LYS221	GLU123
13	LYS114	ASP56
12	ARG101	GLU564
12	LYS510	GLU292
9	LYS272	ASP54
9	ARG105	GLU102
9	HIS96	GLU55
7	LYS272	ASP56
7	HIS112	GLU77
6	ARG55	GLU564
6	LYS65	ASP552
6	ARG96	GLU51
6	ARG101	GLU502
5	LYS510	GLU55
5	HIS173	ASP166
4	LYS510	GLU56
4	LYS209	GLU123
4	HIS100	GLU55
4	LYS26	GLU21
4	HIS108	ASP50
4	LYS87	ASP106
4	HIS613	GLU578
3	ARG100	GLU50
3	ARG130	GLU540
3	ARG64	ASP522
3	HIS172	ASP167
3	ARG91	GLU502
3	ARG30	ASP104
2	HIS164	GLU168
2	LYS208	GLU127
2	LYS208	GLU124
2	LYS214	GLU123
2	HIS549	ASP52
2	LYS227	GLU125
2	ARG98	GLU44
2	LYS204	ASP130
2	LYS62	ASP1
1	HIS407	ASP92
1	LYS155	ASP502
1	ARG409	ASP33
1	LYS218	GLU122
1	HIS182	ASP169
1	LYS143	GLU125
1	LYS143	GLU124
1	ARG595	ASP49
1	LYS7	GLU9

Table 6: Counting of interfacial salt bridges within the PDB entries in Table 5.

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EBO	A_LYS_14	NZ	A_GLU_10	OE2	3.109
1EBO	A_ARG_79	NH1	A_ASP_113	OD1	3.914
1EBO	A_LYS_87	NZ	C_ASP_106	OD2	3.887
1EBO	A_HIS_112	ND1	B_GLU_77	OE1	3.658
1EBO	A_HIS_112	ND1	B_GLU_77	OE2	3.104
1EBO	A_LYS_116	NZ	A_ASP_120	OD1	3.258
1EBO	A_HIS_127	ND1	A_ASP_128	OD1	2.733
1EBO	B_LYS_14	NZ	B_GLU_10	OE2	3.661
1EBO	B_ARG_79	NH1	B_ASP_113	OD1	3.995
1EBO	B_HIS_112	ND1	C_GLU_77	OE1	3.068
1EBO	B_HIS_112	ND1	C_GLU_77	OE2	2.658
1EBO	B_LYS_116	NZ	B_ASP_120	OD1	3.905
1EBO	B_LYS_116	NZ	B_ASP_120	OD2	3.784
1EBO	B_HIS_127	ND1	B_ASP_128	OD1	2.787
1EBO	C_LYS_7	NZ	B_GLU_9	OE1	3.472
1EBO	C_LYS_14	NZ	C_GLU_10	OE2	3.363
1EBO	C_HIS_17	NE2	C_GLU_21	OE2	3.656
1EBO	C_LYS_26	NZ	A_GLU_21	OE1	2.847
1EBO	C_LYS_26	NZ	A_GLU_21	OE2	3.880
1EBO	C_ARG_79	NH1	C_ASP_113	OD1	3.945
1EBO	C_ARG_79	NH2	C_GLU_110	OE2	3.323
1EBO	C_LYS_87	NZ	B_ASP_106	OD2	3.920
1EBO	C_LYS_116	NZ	C_ASP_120	OD1	3.226
1EBO	C_HIS_127	ND1	C_ASP_128	OD1	3.507
1EBO	D_ARG_24	NH1	D_GLU_21	OE2	3.453
1EBO	D_HIS_112	ND1	E_GLU_77	OE1	3.490
1EBO	D_HIS_112	ND1	E_GLU_77	OE2	2.696
1EBO	D_HIS_127	ND1	D_ASP_128	OD1	2.959
1EBO	E_LYS_26	NZ	F_GLU_21	OE2	3.162
1EBO	E_ARG_79	NH2	E_GLU_110	OE1	3.971
1EBO	E_LYS_87	NZ	D_ASP_106	OD2	3.925
1EBO	E_LYS_116	NZ	E_ASP_120	OD1	3.470
1EBO	E_HIS_127	ND1	E_ASP_128	OD1	2.619
1EBO	F_LYS_26	NZ	D_GLU_21	OE1	3.927
1EBO	F_LYS_87	NZ	E_ASP_106	OD2	3.651
1EBO	F_HIS_112	ND1	D_GLU_77	OE2	3.188
1EBO	F_HIS_127	ND1	F_ASP_128	OD1	2.746

Table 7: 1EBO-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2EBO	A_HIS_613	ND1	B_GLU_578	OE1	3.396
2EBO	A_HIS_613	ND1	B_GLU_578	OE2	3.211
2EBO	A_LYS_617	NZ	A_ASP_621	OD2	2.696
2EBO	B_ARG_580	NH1	B_ASP_614	OD2	3.885
2EBO	B_HIS_613	ND1	C_GLU_578	OE1	3.346
2EBO	B_HIS_613	ND1	C_GLU_578	OE2	2.789
2EBO	C_HIS_628	ND1	C_ASP_629	OD1	2.824

Table 8: 2EBO-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QHR	H_ARG_38	NH1	H_GLU_46	OE1	2.994
2QHR	H_ARG_38	NH1	H_GLU_46	OE2	3.872
2QHR	H_ARG_38	NH1	H_ASP_86	OD1	3.831
2QHR	H_ARG_38	NH2	H_ASP_86	OD1	2.870
2QHR	H_ARG_66	NH1	H_ASP_86	OD1	3.110
2QHR	H_ARG_66	NH1	H_ASP_86	OD2	3.628
2QHR	H_ARG_66	NH2	H_ASP_86	OD1	3.793
2QHR	H_ARG_66	NH2	H_ASP_86	OD2	2.806
2QHR	H_ARG_94	NH2	H_ASP_101	OD1	3.235
2QHR	H_ARG_94	NH2	H_ASP_101	OD2	2.743
2QHR	H_LYS_143	NZ	L_GLU_125	OE2	2.743
2QHR	H_HIS_164	ND1	L_GLU_168	OE1	3.446
2QHR	H_HIS_164	ND1	L_GLU_168	OE2	2.691
2QHR	H_LYS_205	NZ	H_ASP_207	OD2	3.730
2QHR	H_LYS_208	NZ	L_GLU_124	OE1	3.025
2QHR	H_LYS_208	NZ	L_GLU_124	OE2	3.278
2QHR	L_ARG_61	NH1	L_ASP_82	OD1	3.738
2QHR	L_ARG_61	NH1	L_ASP_82	OD2	2.709
2QHR	L_ARG_61	NH2	L_ASP_82	OD1	3.238
2QHR	L_ARG_61	NH2	L_ASP_82	OD2	3.549
2QHR	L_LYS_111	NZ	L_ASP_200	OD2	3.160
2QHR	L_LYS_150	NZ	L_GLU_203	OE2	3.712
2QHR	L_LYS_167	NZ	L_GLU_83	OE1	3.792
2QHR	L_HIS_179	ND1	L_ASP_161	OD2	3.673
2QHR	L_LYS_204	NZ	H_ASP_130	OD1	2.837
2QHR	L_LYS_204	NZ	H_ASP_130	OD2	3.813
2QHR	P_HIS_407	ND1	L_ASP_92	OD1	3.553
2QHR	P_ARG_409	NH1	H_ASP_33	OD2	2.967
2QHR	P_ARG_410	NH1	P_ASP_414	OD1	3.195
2QHR	P_ARG_410	NH1	P_ASP_414	OD2	3.569

Table 9: 2QHR-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y6S	C_ARG_65	NH1	C_GLU_83	OE1	3.999
2Y6S	C_ARG_65	NH1	C_GLU_85	OE2	3.669
2Y6S	C_ARG_65	NH1	C_ASP_86	OD1	2.662
2Y6S	C_ARG_65	NH1	C_ASP_86	OD2	2.895
2Y6S	C_ARG_65	NH2	C_GLU_83	OE1	3.359
2Y6S	C_ARG_65	NH2	C_GLU_83	OE2	2.893
2Y6S	C_ARG_65	NH2	C_GLU_85	OE2	3.603
2Y6S	C_ARG_100	NH1	D_GLU_50	OE1	2.758
2Y6S	C_LYS_107	NZ	C_GLU_109	OE2	3.166
2Y6S	C_LYS_107	NZ	C_ASP_169	OD1	3.905
2Y6S	C_LYS_146	NZ	C_GLU_109	OE1	2.925
2Y6S	C_LYS_146	NZ	C_GLU_109	OE2	3.794
2Y6S	C_LYS_153	NZ	C_GLU_199	OE2	3.238
2Y6S	C_ARG_159	NH2	C_GLU_189	OE1	2.973
2Y6S	C_LYS_187	NZ	C_GLU_191	OE1	3.081
2Y6S	C_LYS_187	NZ	C_GLU_191	OE2	3.018
2Y6S	C_HIS_193	ND1	C_ASP_155	OD2	3.103
2Y6S	C_LYS_203	NZ	C_ASP_114	OD2	2.593
2Y6S	D_ARG_67	NH1	D_ASP_90	OD1	2.837
2Y6S	D_ARG_67	NH1	D_ASP_90	OD2	2.696
2Y6S	D_LYS_74	NZ	D_ASP_56	OD1	3.129
2Y6S	D_LYS_74	NZ	D_ASP_56	OD2	3.876
2Y6S	D_LYS_208	NZ	C_GLU_127	OE1	3.225
2Y6S	H_ARG_67	NH1	H_ASP_90	OD1	2.838
2Y6S	H_ARG_67	NH1	H_ASP_90	OD2	2.694
2Y6S	H_LYS_74	NZ	H_ASP_56	OD1	3.138
2Y6S	H_LYS_74	NZ	H_ASP_56	OD2	3.860
2Y6S	H_LYS_208	NZ	L_GLU_127	OE1	3.152
2Y6S	L_ARG_65	NH1	L_GLU_85	OE2	3.674
2Y6S	L_ARG_65	NH1	L_ASP_86	OD1	2.664
2Y6S	L_ARG_65	NH1	L_ASP_86	OD2	2.893
2Y6S	L_ARG_65	NH2	L_GLU_83	OE1	3.384
2Y6S	L_ARG_65	NH2	L_GLU_83	OE2	2.916
2Y6S	L_ARG_65	NH2	L_GLU_85	OE2	3.600
2Y6S	L_ARG_100	NH1	H_GLU_50	OE1	2.759
2Y6S	L_ARG_100	NH2	H_GLU_50	OE1	3.945
2Y6S	L_LYS_107	NZ	L_GLU_109	OE2	3.165
2Y6S	L_LYS_107	NZ	L_ASP_169	OD1	3.901
2Y6S	L_LYS_146	NZ	L_GLU_109	OE1	2.917
2Y6S	L_LYS_146	NZ	L_GLU_109	OE2	3.793
2Y6S	L_LYS_153	NZ	L_GLU_199	OE2	3.234
2Y6S	L_ARG_159	NH2	L_GLU_189	OE1	2.963
2Y6S	L_LYS_187	NZ	L_GLU_191	OE1	3.077
2Y6S	L_LYS_187	NZ	L_GLU_191	OE2	3.017
2Y6S	L_HIS_193	ND1	L_ASP_155	OD2	3.115
2Y6S	L_LYS_203	NZ	L_ASP_114	OD2	2.587

Table 10: 2Y6S-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CSY	A_ARG_33	NH1	A_GLU_95	OE1	3.330
3CSY	A_ARG_33	NH1	A_GLU_95	OE2	3.449
3CSY	A_ARG_38	NH1	A_GLU_46	OE2	2.868
3CSY	A_ARG_38	NH2	A_ASP_86	OD1	2.786
3CSY	A_ARG_66	NH1	A_ASP_86	OD1	3.738
3CSY	A_ARG_66	NH1	A_ASP_86	OD2	2.985
3CSY	A_ARG_66	NH2	A_ASP_86	OD1	3.541
3CSY	A_ARG_94	NH2	A_ASP_101	OD1	3.102
3CSY	A_ARG_94	NH2	A_ASP_101	OD2	3.588
3CSY	A_ARG_98	NH1	A_ASP_100F	OD1	2.690
3CSY	A_ARG_98	NH1	A_ASP_100F	OD2	3.265
3CSY	A_LYS_145	NZ	A_ASP_146	OD1	3.667
3CSY	A_LYS_145	NZ	A_ASP_146	OD2	3.424
3CSY	A_LYS_221	NZ	B_GLU_123	OE1	3.090
3CSY	A_LYS_221	NZ	B_GLU_123	OE2	3.307
3CSY	A_LYS_222	NZ	A_GLU_226	OE1	3.338
3CSY	B_LYS_24	NZ	B_ASP_70	OD1	3.112
3CSY	B_LYS_24	NZ	B_ASP_70	OD2	3.834
3CSY	B_ARG_61	NH2	B_GLU_81	OE1	3.999
3CSY	B_ARG_61	NH2	B_ASP_82	OD1	3.114
3CSY	B_ARG_61	NH2	B_ASP_82	OD2	3.791
3CSY	B_ARG_142	NH2	B_GLU_165	OE1	3.547
3CSY	B_LYS_149	NZ	B_GLU_195	OE1	2.968
3CSY	B_LYS_188	NZ	B_ASP_185	OD1	3.323
3CSY	B_HIS_189	ND1	B_ASP_151	OD1	3.608
3CSY	B_HIS_189	ND1	B_ASP_151	OD2	2.713
3CSY	C_ARG_33	NH2	C_GLU_95	OE1	3.005
3CSY	C_ARG_33	NH2	C_GLU_95	OE2	3.100
3CSY	C_ARG_38	NH1	C_GLU_46	OE2	3.062
3CSY	C_ARG_38	NH2	C_ASP_86	OD1	2.925
3CSY	C_ARG_66	NH1	C_ASP_86	OD1	3.795
3CSY	C_ARG_66	NH1	C_ASP_86	OD2	3.175
3CSY	C_ARG_66	NH2	C_ASP_86	OD1	3.757
3CSY	C_ARG_94	NH2	C_ASP_101	OD1	2.980
3CSY	C_ARG_94	NH2	C_ASP_101	OD2	3.244
3CSY	C_ARG_98	NH1	C_ASP_100F	OD1	2.963
3CSY	C_ARG_98	NH1	C_ASP_100F	OD2	3.539
3CSY	C_LYS_145	NZ	C_ASP_146	OD1	3.956
3CSY	C_HIS_172	NE2	D_ASP_167	OD2	3.885
3CSY	C_LYS_221	NZ	D_GLU_123	OE1	3.258
3CSY	C_LYS_221	NZ	D_GLU_123	OE2	3.282
3CSY	C_LYS_222	NZ	C_GLU_226	OE1	3.372
3CSY	D_LYS_24	NZ	D_ASP_70	OD1	3.251
3CSY	D_LYS_24	NZ	D_ASP_70	OD2	3.569
3CSY	D_ARG_61	NH2	D_ASP_82	OD1	3.121
3CSY	D_ARG_61	NH2	D_ASP_82	OD2	3.757
3CSY	D_ARG_142	NH2	D_GLU_165	OE1	3.115
3CSY	D_LYS_149	NZ	D_GLU_195	OE1	3.045
3CSY	D_HIS_189	ND1	D_ASP_151	OD1	3.792
3CSY	D_HIS_189	ND1	D_ASP_151	OD2	2.842
3CSY	E_ARG_33	NH2	E_GLU_95	OE1	3.422
3CSY	E_ARG_33	NH2	E_GLU_95	OE2	3.409
3CSY	E_ARG_38	NH1	E_GLU_46	OE2	2.948
3CSY	E_ARG_38	NH2	E_ASP_86	OD1	3.088
3CSY	E_ARG_66	NH1	E_ASP_86	OD2	2.937
3CSY	E_ARG_66	NH2	E_ASP_86	OD1	3.488
3CSY	E_ARG_66	NH2	E_ASP_86	OD2	3.575

3CSY	E_ARG_94	NH2	E_ASP_101	OD1	3.133
3CSY	E_ARG_94	NH2	E_ASP_101	OD2	3.533
3CSY	E_ARG_98	NH1	E_ASP_100F	OD1	3.332
3CSY	E_ARG_98	NH1	E_ASP_100F	OD2	3.049
3CSY	E_LYS_145	NZ	E_ASP_146	OD2	3.678
3CSY	E_LYS_221	NZ	F_GLU_123	OE1	3.238
3CSY	E_LYS_221	NZ	F_GLU_123	OE2	3.205
3CSY	E_LYS_222	NZ	E_GLU_226	OE1	3.405
3CSY	F_LYS_24	NZ	F_ASP_70	OD1	3.269
3CSY	F_LYS_24	NZ	F_ASP_70	OD2	3.477
3CSY	F_ARG_61	NH2	F_GLU_81	OE1	3.492
3CSY	F_ARG_61	NH2	F_ASP_82	OD1	3.832
3CSY	F_ARG_142	NH2	F_GLU_165	OE1	3.343
3CSY	F_LYS_149	NZ	F_GLU_195	OE1	3.168
3CSY	F_LYS_188	NZ	F_ASP_185	OD1	3.831
3CSY	F_HIS_189	ND1	F_ASP_151	OD2	3.133
3CSY	G_ARG_33	NH2	G_GLU_95	OE1	3.360
3CSY	G_ARG_33	NH2	G_GLU_95	OE2	3.356
3CSY	G_ARG_38	NH1	G_GLU_46	OE1	3.934
3CSY	G_ARG_38	NH1	G_GLU_46	OE2	3.037
3CSY	G_ARG_38	NH2	G_ASP_86	OD1	2.730
3CSY	G_ARG_66	NH1	G_ASP_86	OD2	2.862
3CSY	G_ARG_66	NH2	G_ASP_86	OD1	3.483
3CSY	G_ARG_66	NH2	G_ASP_86	OD2	3.538
3CSY	G_ARG_94	NH2	G_ASP_101	OD1	3.059
3CSY	G_ARG_98	NH1	G_ASP_100F	OD1	2.838
3CSY	G_ARG_98	NH1	G_ASP_100F	OD2	3.524
3CSY	G_LYS_145	NZ	G_ASP_146	OD2	3.536
3CSY	G_HIS_172	NE2	H_ASP_167	OD2	3.733
3CSY	G_LYS_221	NZ	H_GLU_123	OE1	3.440
3CSY	G_LYS_221	NZ	H_GLU_123	OE2	3.445
3CSY	G_LYS_222	NZ	G_GLU_226	OE1	3.676
3CSY	H_LYS_24	NZ	H_ASP_70	OD1	3.595
3CSY	H_LYS_24	NZ	H_ASP_70	OD2	3.439
3CSY	H_ARG_61	NH2	H_GLU_81	OE1	3.520
3CSY	H_ARG_61	NH2	H_ASP_82	OD1	3.815
3CSY	H_ARG_61	NH2	H_ASP_82	OD2	3.245
3CSY	H_ARG_142	NH2	H_GLU_165	OE1	3.557
3CSY	H_LYS_149	NZ	H_GLU_195	OE1	3.085
3CSY	H_HIS_189	ND1	H_ASP_151	OD1	3.553
3CSY	H_HIS_189	ND1	H_ASP_151	OD2	2.707
3CSY	I_ARG_64	NH1	I_GLU_100	OE2	2.693
3CSY	I_ARG_85	NH2	I_GLU_178	OE1	2.760
3CSY	I_ARG_85	NH2	I_GLU_178	OE2	2.883
3CSY	I_LYS_114	NZ	I_GLU_120	OE2	3.520
3CSY	I_ARG_130	NH2	I_ASP_163	OD2	2.701
3CSY	I_ARG_134	NH1	J_GLU_545	OE2	3.043
3CSY	I_ARG_136	NH1	I_GLU_106	OE2	3.755
3CSY	I_HIS_154	NE2	I_GLU_178	OE2	2.796
3CSY	I_ARG_164	NH2	I_ASP_163	OD1	3.175
3CSY	I_ARG_164	NH2	I_ASP_163	OD2	3.157
3CSY	J_ARG_559	NH2	I_GLU_103	OE1	3.261
3CSY	J_ARG_559	NH2	I_GLU_103	OE2	3.005
3CSY	K_ARG_64	NH1	K_GLU_100	OE2	3.248
3CSY	K_ARG_85	NH2	K_GLU_178	OE1	2.723
3CSY	K_ARG_85	NH2	K_GLU_178	OE2	3.019
3CSY	K_LYS_114	NZ	K_GLU_120	OE1	3.499
3CSY	K_ARG_130	NH1	K_ASP_163	OD2	2.845

3CSY	K_ARG_134	NH1	L_GLU_545	OE2	3.181
3CSY	K_ARG_136	NH1	K_GLU_106	OE2	3.184
3CSY	K_HIS_154	NE2	K_GLU_178	OE2	2.720
3CSY	K_ARG_164	NH2	K_ASP_163	OD1	3.547
3CSY	K_ARG_164	NH2	K_ASP_163	OD2	3.244
3CSY	L_ARG_559	NH2	K_GLU_103	OE1	3.317
3CSY	L_ARG_559	NH2	K_GLU_103	OE2	3.156
3CSY	M_ARG_64	NH1	M_GLU_100	OE2	2.845
3CSY	M_ARG_85	NH2	M_GLU_178	OE1	2.759
3CSY	M_ARG_85	NH2	M_GLU_178	OE2	3.004
3CSY	M_ARG_130	NH1	M_ASP_163	OD2	2.888
3CSY	M_ARG_134	NH1	N_GLU_545	OE2	2.894
3CSY	M_ARG_136	NH1	M_GLU_106	OE2	3.351
3CSY	M_HIS_154	NE2	M_GLU_178	OE2	2.684
3CSY	M_ARG_164	NH2	M_ASP_163	OD1	3.214
3CSY	M_ARG_164	NH2	M_ASP_163	OD2	3.477
3CSY	N_ARG_559	NH2	M_GLU_103	OE1	2.925
3CSY	N_ARG_559	NH2	M_GLU_103	OE2	3.048
3CSY	O_ARG_64	NH1	O_GLU_100	OE2	2.902
3CSY	O_ARG_85	NH2	O_GLU_178	OE1	3.008
3CSY	O_ARG_85	NH2	O_GLU_178	OE2	3.292
3CSY	O_ARG_130	NH1	O_ASP_163	OD2	2.770
3CSY	O_ARG_130	NH2	O_ASP_163	OD2	3.071
3CSY	O_ARG_134	NH1	P_GLU_545	OE2	3.026
3CSY	O_ARG_136	NH1	O_GLU_106	OE2	3.514
3CSY	O_HIS_154	NE2	O_GLU_178	OE2	2.770
3CSY	O_ARG_164	NH2	O_ASP_163	OD1	3.340
3CSY	O_ARG_164	NH2	O_ASP_163	OD2	3.003
3CSY	P_ARG_559	NH2	O_GLU_103	OE1	3.054
3CSY	P_ARG_559	NH2	O_GLU_103	OE2	2.808

Table 11: 3CSY-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3VE0	I_LYS_64	NZ	I_GLU_100	OE1	3.434
3VE0	I_ARG_85	NH2	I_GLU_178	OE1	3.938
3VE0	I_ARG_85	NH2	I_GLU_178	OE2	2.598
3VE0	I_ARG_130	NH1	I_ASP_163	OD2	3.227
3VE0	I_HIS_154	NE2	I_GLU_178	OE1	2.497
3VE0	I_ARG_164	NH1	I_ASP_163	OD1	2.966
3VE0	I_ARG_164	NH1	I_ASP_163	OD2	2.614
3VE0	I_ARG_164	NH2	I_ASP_163	OD2	3.976
3VE0	I_ARG_172	NH1	I_GLU_112	OE1	3.788
3VE0	I_ARG_172	NH1	I_GLU_112	OE2	3.022
3VE0	I_ARG_172	NH1	I_GLU_120	OE1	3.786
3VE0	J_HIS_516	ND1	J_GLU_545	OE1	3.938
3VE0	J_ARG_559	NH1	I_GLU_103	OE1	3.852
3VE0	J_ARG_559	NH1	I_GLU_103	OE2	3.848
3VE0	J_ARG_559	NH2	I_GLU_103	OE1	2.444
3VE0	J_ARG_559	NH2	I_GLU_103	OE2	2.766
3VE0	J_ARG_595	NH1	J_ASP_591	OD2	3.637
3VE0	J_ARG_595	NH2	I_ASP_49	OD2	3.842
3VE0	J_ARG_596	NH1	I_ASP_55	OD1	3.003
3VE0	A_ARG_38	NH1	A_ASP_90	OD2	2.796
3VE0	A_ARG_38	NH2	A_GLU_46	OE1	2.957
3VE0	A_ARG_38	NH2	A_ASP_90	OD2	3.833
3VE0	A_ARG_67	NH1	A_ASP_90	OD1	2.638
3VE0	A_ARG_67	NH1	A_ASP_90	OD2	3.818
3VE0	A_ARG_67	NH2	A_ASP_90	OD1	3.519
3VE0	A_ARG_67	NH2	A_ASP_90	OD2	3.251
3VE0	A_ARG_87	NH2	A_GLU_89	OE1	3.633
3VE0	A_ARG_98	NH2	I_GLU_44	OE1	3.137
3VE0	A_ARG_98	NH2	I_GLU_44	OE2	3.008
3VE0	A_ARG_98	NH2	A_ASP_107	OD1	3.467
3VE0	A_LYS_214	NZ	B_GLU_123	OE1	3.666
3VE0	A_LYS_214	NZ	B_GLU_123	OE2	2.624
3VE0	A_ARG_219	NH1	A_ASP_220	OD1	3.088
3VE0	B_ARG_54	NH2	B_ASP_60	OD1	3.562
3VE0	B_ARG_61	NH1	B_GLU_81	OE1	3.512
3VE0	B_ARG_61	NH1	B_ASP_82	OD2	3.714
3VE0	B_ARG_61	NH2	B_GLU_81	OE1	3.757
3VE0	B_ARG_61	NH2	B_GLU_81	OE2	3.987
3VE0	B_LYS_103	NZ	B_GLU_105	OE1	3.337
3VE0	B_LYS_149	NZ	B_GLU_195	OE1	3.446
3VE0	B_LYS_149	NZ	B_GLU_195	OE2	2.550
3VE0	B_ARG_155	NH1	B_GLU_185	OE1	2.325
3VE0	B_ARG_155	NH1	B_GLU_185	OE2	3.974
3VE0	B_ARG_155	NH2	B_GLU_185	OE1	3.539
3VE0	B_ARG_155	NH2	B_GLU_185	OE2	3.905
3VE0	B_HIS_189	ND1	B_ASP_151	OD1	3.017

Table 12: 3VE0-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5F1B	A_HIS_39	NE2	A_ASP_55	OD1	3.999
5F1B	A_ARG_64	NH1	A_GLU_100	OE1	3.273
5F1B	A_ARG_64	NH1	A_GLU_100	OE2	3.876
5F1B	A_ARG_85	NH2	A_GLU_178	OE1	2.662
5F1B	A_ARG_85	NH2	A_GLU_178	OE2	3.814
5F1B	A_ARG_130	NH2	A_ASP_163	OD2	3.180
5F1B	A_ARG_134	NH1	B_GLU_545	OE2	3.659
5F1B	A_HIS_154	NE2	A_GLU_178	OE2	2.611
5F1B	A_ARG_164	NH2	A_ASP_163	OD1	3.605
5F1B	A_ARG_164	NH2	A_ASP_163	OD2	3.318
5F1B	B_HIS_516	NE2	B_GLU_545	OE1	3.961
5F1B	B_ARG_559	NH1	A_GLU_103	OE1	3.219
5F1B	B_ARG_559	NH1	A_GLU_103	OE2	3.449
5F1B	B_ARG_559	NH2	A_GLU_103	OE1	3.928
5F1B	B_ARG_559	NH2	A_GLU_103	OE2	2.697
5F1B	B_LYS_588	NZ	A_ASP_47	OD1	3.551
5F1B	B_LYS_588	NZ	A_ASP_47	OD2	3.521
5F1B	C_ARG_32	NH1	C_GLU_34	OE1	3.894
5F1B	C_ARG_32	NH1	C_GLU_212	OE2	3.039
5F1B	C_ARG_32	NH2	C_GLU_212	OE2	3.122
5F1B	C_HIS_69	NE2	C_ASP_124	OD1	2.595
5F1B	C_HIS_69	NE2	C_ASP_124	OD2	3.426
5F1B	C_HIS_120	NE2	C_ASP_73	OD1	3.129
5F1B	C_HIS_125	ND1	C_ASP_159	OD1	3.361
5F1B	C_HIS_125	ND1	C_ASP_159	OD2	2.705
5F1B	C_HIS_138	ND1	C_ASP_136	OD1	3.569
5F1B	C_HIS_138	ND1	C_ASP_136	OD2	2.668
5F1B	C_HIS_140	ND1	C_ASP_153	OD2	2.612
5F1B	C_LYS_204	NZ	C_ASP_201	OD2	2.921
5F1B	C_ARG_207	NH2	C_ASP_86	OD2	3.888
5F1B	C_ARG_207	NH2	C_GLU_88	OE1	2.527
5F1B	C_ARG_207	NH2	C_GLU_88	OE2	3.562

Table 13: 5F1B-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5FHC	J_ARG_559	NH2	K_GLU_103	OE1	3.531
5FHC	J_ARG_559	NH2	K_GLU_103	OE2	3.399
5FHC	K_ARG_64	NH1	K_GLU_100	OE2	3.218
5FHC	K_ARG_85	NH2	K_GLU_178	OE1	2.651
5FHC	K_ARG_85	NH2	K_GLU_178	OE2	3.046
5FHC	K_LYS_114	NZ	K_GLU_112	OE1	3.499
5FHC	K_LYS_114	NZ	K_GLU_120	OE1	3.155
5FHC	K_ARG_130	NH1	K_ASP_163	OD2	2.715
5FHC	K_ARG_134	NH1	J_GLU_545	OE2	2.861
5FHC	K_ARG_136	NH1	K_GLU_106	OE2	3.301
5FHC	K_HIS_154	NE2	K_GLU_178	OE2	2.716
5FHC	K_ARG_164	NH2	K_ASP_163	OD1	3.639
5FHC	K_ARG_164	NH2	K_ASP_163	OD2	3.655
5FHC	A_ARG_38	NH1	A_ASP_86	OD1	2.921
5FHC	A_ARG_38	NH2	A_GLU_46	OE1	3.040
5FHC	A_ARG_38	NH2	A_GLU_46	OE2	3.982
5FHC	A_ARG_38	NH2	A_ASP_86	OD1	3.615
5FHC	A_ARG_66	NH1	A_ASP_86	OD1	3.508
5FHC	A_ARG_66	NH2	A_ASP_86	OD1	3.465
5FHC	A_ARG_66	NH2	A_ASP_86	OD2	2.756
5FHC	A_ARG_94	NH2	A_ASP_101	OD1	3.473
5FHC	A_ARG_94	NH2	A_ASP_101	OD2	3.241
5FHC	A_LYS_143	NZ	B_GLU_124	OE2	2.678
5FHC	A_LYS_209	NZ	B_GLU_123	OE1	2.702
5FHC	A_LYS_209	NZ	B_GLU_123	OE2	3.358
5FHC	B_ARG_39	NH2	B_ASP_82	OD1	3.944
5FHC	B_ARG_61	NH1	B_ASP_82	OD1	3.826
5FHC	B_ARG_61	NH1	B_ASP_82	OD2	2.658
5FHC	B_ARG_61	NH2	B_ASP_82	OD1	2.976
5FHC	B_ARG_61	NH2	B_ASP_82	OD2	3.232
5FHC	B_LYS_103	NZ	B_ASP_85	OD1	2.875
5FHC	B_LYS_103	NZ	B_ASP_85	OD2	3.594
5FHC	B_LYS_149	NZ	B_GLU_203	OE1	3.331
5FHC	B_LYS_149	NZ	B_GLU_203	OE2	3.999
5FHC	L_ARG_61	NH1	L_GLU_81	OE2	3.402
5FHC	L_ARG_61	NH1	L_ASP_82	OD1	2.944
5FHC	L_ARG_61	NH1	L_ASP_82	OD2	3.402
5FHC	L_LYS_103	NZ	L_GLU_165	OE2	3.468
5FHC	L_LYS_149	NZ	L_GLU_195	OE2	2.669
5FHC	L_LYS_183	NZ	L_GLU_187	OE2	2.948
5FHC	L_HIS_189	ND1	L_ASP_151	OD2	3.045
5FHC	H_ARG_38	NH1	H_ASP_86	OD1	2.743
5FHC	H_ARG_38	NH2	H_GLU_46	OE1	3.708
5FHC	H_ARG_38	NH2	H_GLU_46	OE2	3.194
5FHC	H_ARG_38	NH2	H_ASP_86	OD1	3.696
5FHC	H_LYS_64	NZ	H_ASP_61	OD1	3.953
5FHC	H_ARG_66	NH1	H_ASP_86	OD1	3.816
5FHC	H_ARG_66	NH1	H_ASP_86	OD2	2.875
5FHC	H_ARG_66	NH2	H_ASP_86	OD1	3.199
5FHC	H_ARG_66	NH2	H_ASP_86	OD2	3.692
5FHC	H_LYS_75	NZ	H_GLU_72	OE1	3.342
5FHC	H_LYS_75	NZ	H_GLU_72	OE2	3.694
5FHC	H_ARG_94	NH2	H_ASP_101	OD1	3.811
5FHC	H_ARG_94	NH2	H_ASP_101	OD2	3.111
5FHC	H_LYS_143	NZ	H_ASP_144	OD1	3.605
5FHC	H_LYS_209	NZ	L_GLU_123	OE1	3.238
5FHC	H_LYS_209	NZ	L_GLU_123	OE2	3.173

5FHC	H_LYS_210	NZ	H_GLU_212	OE1	3.977
5FHC	H_LYS_210	NZ	H_GLU_212	OE2	2.157

Table 14: 5FHC-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HJ3	C_HIS_39	NE2	C_ASP_55	OD1	3.393
5HJ3	C_ARG_64	NH1	C_GLU_100	OE2	3.438
5HJ3	C_ARG_85	NH1	C_GLU_178	OE1	3.195
5HJ3	C_ARG_85	NH2	C_GLU_178	OE1	2.394
5HJ3	C_ARG_85	NH2	C_GLU_178	OE2	2.812
5HJ3	C_ARG_130	NH2	C_ASP_163	OD2	3.561
5HJ3	C_ARG_136	NH2	C_GLU_106	OE2	3.743
5HJ3	C_HIS_154	NE2	C_GLU_178	OE2	2.920
5HJ3	C_ARG_164	NH2	C_ASP_163	OD1	3.508
5HJ3	C_ARG_164	NH2	C_ASP_163	OD2	2.651
5HJ3	D_LYS_510	NZ	J_GLU_55	OE1	3.743
5HJ3	D_LYS_510	NZ	J_GLU_55	OE2	3.493
5HJ3	D_HIS_516	NE2	D_GLU_545	OE1	2.622
5HJ3	D_ARG_559	NH2	C_GLU_103	OE1	2.496
5HJ3	D_ARG_559	NH2	C_GLU_103	OE2	2.573
5HJ3	E_ARG_33	NH1	E_GLU_95	OE1	3.015
5HJ3	E_ARG_33	NH1	E_GLU_95	OE2	3.055
5HJ3	E_ARG_38	NH1	E_GLU_46	OE1	3.787
5HJ3	E_ARG_38	NH1	E_GLU_46	OE2	2.695
5HJ3	E_ARG_38	NH2	E_ASP_86	OD1	2.624
5HJ3	E_ARG_66	NH1	E_ASP_86	OD1	3.916
5HJ3	E_ARG_66	NH1	E_ASP_86	OD2	2.722
5HJ3	E_ARG_66	NH2	E_ASP_86	OD1	3.391
5HJ3	E_ARG_66	NH2	E_ASP_86	OD2	3.561
5HJ3	E_ARG_94	NH2	E_ASP_101	OD1	3.948
5HJ3	E_ARG_94	NH2	E_ASP_101	OD2	2.561
5HJ3	E_ARG_98	NH1	E_ASP_100F	OD1	3.696
5HJ3	E_ARG_98	NH1	E_ASP_100F	OD2	2.997
5HJ3	E_LYS_145	NZ	E_ASP_146	OD1	2.852
5HJ3	E_LYS_145	NZ	E_ASP_146	OD2	2.810
5HJ3	E_LYS_221	NZ	F_GLU_123	OE2	3.658
5HJ3	F_ARG_61	NH2	F_ASP_82	OD1	3.037
5HJ3	F_ARG_61	NH2	F_ASP_82	OD2	3.919
5HJ3	F_ARG_142	NH2	F_GLU_105	OE1	2.744
5HJ3	G_HIS_39	NE2	G_ASP_55	OD1	3.217
5HJ3	G_ARG_64	NH1	G_GLU_100	OE2	3.233
5HJ3	G_ARG_85	NH1	G_GLU_178	OE1	3.267
5HJ3	G_ARG_85	NH2	G_GLU_178	OE1	2.478
5HJ3	G_ARG_85	NH2	G_GLU_178	OE2	2.771
5HJ3	G_ARG_130	NH2	G_ASP_163	OD2	3.392
5HJ3	G_HIS_154	NE2	G_GLU_178	OE2	2.990
5HJ3	G_ARG_164	NH2	G_ASP_163	OD1	3.521
5HJ3	G_ARG_164	NH2	G_ASP_163	OD2	2.692
5HJ3	H_LYS_510	NZ	F_GLU_55	OE2	3.815
5HJ3	H_HIS_516	NE2	H_GLU_545	OE1	2.614
5HJ3	H_ARG_559	NH2	G_GLU_103	OE1	2.521
5HJ3	H_ARG_559	NH2	G_GLU_103	OE2	2.719
5HJ3	I_ARG_33	NH1	I_GLU_95	OE1	2.790
5HJ3	I_ARG_33	NH1	I_GLU_95	OE2	3.012
5HJ3	I_ARG_38	NH1	I_GLU_46	OE1	3.771
5HJ3	I_ARG_38	NH1	I_GLU_46	OE2	2.572
5HJ3	I_ARG_38	NH2	I_ASP_86	OD1	2.596
5HJ3	I_ARG_66	NH1	I_ASP_86	OD2	2.716
5HJ3	I_ARG_66	NH2	I_ASP_86	OD1	3.241
5HJ3	I_ARG_66	NH2	I_ASP_86	OD2	3.167
5HJ3	I_ARG_94	NH2	I_ASP_101	OD1	3.512
5HJ3	I_ARG_94	NH2	I_ASP_101	OD2	2.751

5HJ3	I_ARG_98	NH1	I_ASP_100F	OD1	3.834
5HJ3	I_ARG_98	NH1	I_ASP_100F	OD2	3.081
5HJ3	I_LYS_145	NZ	I_ASP_146	OD1	2.788
5HJ3	I_LYS_145	NZ	I_ASP_146	OD2	2.739
5HJ3	I_HIS_172	NE2	J_ASP_167	OD2	3.705
5HJ3	I_LYS_221	NZ	J_GLU_123	OE1	3.253
5HJ3	I_LYS_221	NZ	J_GLU_123	OE2	2.800
5HJ3	J_ARG_61	NH2	J_ASP_82	OD1	2.701
5HJ3	J_ARG_61	NH2	J_ASP_82	OD2	3.572
5HJ3	J_ARG_142	NH2	J_GLU_105	OE1	2.682
5HJ3	J_LYS_145	NZ	J_GLU_161	OE2	3.678
5HJ3	J_LYS_149	NZ	J_GLU_195	OE1	2.603
5HJ3	J_LYS_188	NZ	J_ASP_185	OD2	3.757
5HJ3	J_HIS_189	ND1	J_ASP_151	OD1	3.934
5HJ3	J_HIS_189	ND1	J_ASP_151	OD2	2.742
5HJ3	K_HIS_39	NE2	K_ASP_55	OD1	3.802
5HJ3	K_ARG_64	NH1	K_GLU_100	OE2	3.581
5HJ3	K_ARG_85	NH1	K_GLU_178	OE1	3.179
5HJ3	K_ARG_85	NH2	K_GLU_178	OE1	2.573
5HJ3	K_ARG_85	NH2	K_GLU_178	OE2	2.682
5HJ3	K_ARG_130	NH2	K_ASP_163	OD2	3.783
5HJ3	K_HIS_154	NE2	K_GLU_178	OE2	3.079
5HJ3	K_ARG_164	NH2	K_ASP_163	OD1	3.726
5HJ3	K_ARG_164	NH2	K_ASP_163	OD2	2.770
5HJ3	L_HIS_516	NE2	L_GLU_545	OE1	2.683
5HJ3	L_ARG_559	NH2	K_GLU_103	OE1	2.680
5HJ3	L_ARG_559	NH2	K_GLU_103	OE2	2.484
5HJ3	L_HIS_602	ND1	H_GLU_611	OE1	3.679
5HJ3	L_HIS_602	NE2	H_GLU_611	OE1	3.945
5HJ3	M_ARG_33	NH1	M_GLU_95	OE1	2.923
5HJ3	M_ARG_33	NH1	M_GLU_95	OE2	2.923
5HJ3	M_ARG_38	NH1	M_ASP_86	OD1	3.188
5HJ3	M_ARG_38	NH2	M_GLU_46	OE1	3.623
5HJ3	M_ARG_38	NH2	M_GLU_46	OE2	2.841
5HJ3	M_ARG_66	NH1	M_ASP_86	OD1	3.810
5HJ3	M_ARG_66	NH1	M_ASP_86	OD2	2.388
5HJ3	M_ARG_66	NH2	M_ASP_86	OD1	2.897
5HJ3	M_ARG_66	NH2	M_ASP_86	OD2	2.965
5HJ3	M_ARG_94	NH2	M_ASP_101	OD1	3.853
5HJ3	M_ARG_94	NH2	M_ASP_101	OD2	2.629
5HJ3	M_ARG_98	NH1	M_ASP_100F	OD1	3.630
5HJ3	M_ARG_98	NH1	M_ASP_100F	OD2	2.969
5HJ3	M_LYS_145	NZ	M_ASP_146	OD1	3.782
5HJ3	M_LYS_145	NZ	M_ASP_146	OD2	3.675
5HJ3	M_LYS_221	NZ	N_GLU_123	OE1	3.397
5HJ3	M_LYS_221	NZ	N_GLU_123	OE2	3.011
5HJ3	N_ARG_61	NH2	N_ASP_82	OD1	3.282
5HJ3	N_ARG_142	NH2	N_GLU_105	OE1	2.640
5HJ3	N_LYS_149	NZ	N_GLU_195	OE1	2.786
5HJ3	O_HIS_39	NE2	O_ASP_55	OD1	3.321
5HJ3	O_ARG_64	NH1	O_GLU_100	OE2	3.235
5HJ3	O_ARG_85	NH1	O_GLU_178	OE1	3.339
5HJ3	O_ARG_85	NH2	O_GLU_178	OE1	2.457
5HJ3	O_ARG_85	NH2	O_GLU_178	OE2	2.948
5HJ3	O_ARG_130	NH2	O_ASP_163	OD2	3.468
5HJ3	O_ARG_136	NH2	O_GLU_106	OE2	3.955
5HJ3	O_HIS_154	NE2	O_GLU_178	OE2	2.840
5HJ3	O_ARG_164	NH2	O_ASP_163	OD1	3.663

5HJ3	O_ARG_164	NH2	O_ASP_163	OD2	2.780
5HJ3	P_LYS_510	NZ	B_GLU_55	OE1	3.843
5HJ3	P_LYS_510	NZ	B_GLU_55	OE2	3.553
5HJ3	P_HIS_516	NE2	P_GLU_545	OE1	2.882
5HJ3	P_ARG_559	NH2	O_GLU_103	OE1	2.547
5HJ3	P_ARG_559	NH2	O_GLU_103	OE2	2.625
5HJ3	P_HIS_602	NE2	L_GLU_611	OE1	3.277
5HJ3	A_ARG_33	NH1	A_GLU_95	OE1	2.660
5HJ3	A_ARG_33	NH1	A_GLU_95	OE2	3.038
5HJ3	A_ARG_38	NH1	A_GLU_46	OE1	3.725
5HJ3	A_ARG_38	NH1	A_GLU_46	OE2	2.619
5HJ3	A_ARG_38	NH2	A_ASP_86	OD1	2.771
5HJ3	A_ARG_66	NH1	A_ASP_86	OD1	3.710
5HJ3	A_ARG_66	NH1	A_ASP_86	OD2	2.544
5HJ3	A_ARG_66	NH2	A_ASP_86	OD1	3.134
5HJ3	A_ARG_66	NH2	A_ASP_86	OD2	3.423
5HJ3	A_ARG_94	NH2	A_ASP_101	OD1	3.718
5HJ3	A_ARG_94	NH2	A_ASP_101	OD2	2.938
5HJ3	A_ARG_98	NH1	A_ASP_100F	OD1	3.722
5HJ3	A_ARG_98	NH1	A_ASP_100F	OD2	2.936
5HJ3	A_LYS_145	NZ	A_ASP_146	OD1	2.925
5HJ3	A_LYS_145	NZ	A_ASP_146	OD2	2.830
5HJ3	A_LYS_221	NZ	B_GLU_123	OE1	3.583
5HJ3	A_LYS_221	NZ	B_GLU_123	OE2	3.404
5HJ3	B_ARG_61	NH2	B_ASP_82	OD1	3.154
5HJ3	B_ARG_142	NH2	B_GLU_105	OE1	3.025
5HJ3	B_LYS_188	NZ	B_ASP_185	OD2	3.880
5HJ3	B_HIS_189	ND1	B_ASP_151	OD2	2.951

Table 15: 5HJ3-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JNX	A_LYS_38	NZ	A_ASP_37	OD1	3.268
5JNX	A_LYS_84	NZ	A_GLU_61	OE1	2.923
5JNX	A_LYS_84	NZ	A_GLU_61	OE2	2.871
5JNX	A_LYS_142	NZ	A_GLU_127	OE1	2.943
5JNX	A_LYS_171	NZ	A_GLU_164	OE2	3.483
5JNX	A_ARG_389	NH1	A_GLU_393	OE2	3.992
5JNX	A_LYS_392	NZ	A_ASP_396	OD1	3.754
5JNX	A_ARG_404	NH1	A_GLU_606	OE1	3.028
5JNX	A_ARG_404	NH1	A_GLU_606	OE2	3.947
5JNX	A_ARG_404	NH2	A_GLU_584	OE1	3.703
5JNX	A_HIS_441	ND1	A_ASP_496	OD1	3.845
5JNX	A_HIS_441	NE2	A_ASP_496	OD1	2.206
5JNX	A_HIS_441	NE2	A_ASP_496	OD2	3.645
5JNX	A_HIS_492	NE2	A_ASP_445	OD1	3.105
5JNX	A_HIS_510	ND1	A_ASP_508	OD2	3.286
5JNX	A_HIS_512	ND1	A_ASP_525	OD2	2.862
5JNX	A_ARG_579	NH2	A_ASP_466	OD2	3.380
5JNX	A_ARG_607	NH1	A_ASP_611	OD2	3.972
5JNX	A_ARG_1059	NH2	A_GLU_391	OE1	2.950
5JNX	A_ARG_1059	NH2	A_GLU_391	OE2	3.638
5JNX	A_ARG_1059	NH2	A_GLU_1089	OE1	3.854
5JNX	A_ARG_1059	NH2	A_GLU_1089	OE2	3.604
5JNX	A_HIS_1170	ND1	A_GLU_1166	OE1	3.445
5JNX	A_HIS_1170	NE2	A_GLU_688	OE2	2.924
5JNX	C_HIS_39	NE2	C_ASP_55	OD1	3.998
5JNX	C_ARG_64	NH1	C_GLU_100	OE1	3.273
5JNX	C_ARG_64	NH1	C_GLU_100	OE2	3.875
5JNX	C_ARG_85	NH2	C_GLU_178	OE1	2.663
5JNX	C_ARG_85	NH2	C_GLU_178	OE2	3.814
5JNX	C_ARG_130	NH2	C_ASP_163	OD2	3.179
5JNX	C_ARG_134	NH1	D_GLU_545	OE2	3.659
5JNX	C_HIS_154	NE2	C_GLU_178	OE2	2.610
5JNX	C_ARG_164	NH2	C_ASP_163	OD1	3.605
5JNX	C_ARG_164	NH2	C_ASP_163	OD2	3.318
5JNX	D_HIS_516	NE2	D_GLU_545	OE1	3.961
5JNX	D_ARG_559	NH1	C_GLU_103	OE1	3.220
5JNX	D_ARG_559	NH1	C_GLU_103	OE2	3.450
5JNX	D_ARG_559	NH2	C_GLU_103	OE1	3.927
5JNX	D_ARG_559	NH2	C_GLU_103	OE2	2.697
5JNX	D_LYS_588	NZ	C_ASP_47	OD1	3.551
5JNX	D_LYS_588	NZ	C_ASP_47	OD2	3.521
5JNX	E_HIS_39	NE2	E_ASP_55	OD1	3.998
5JNX	E_ARG_64	NH1	E_GLU_100	OE1	3.272
5JNX	E_ARG_64	NH1	E_GLU_100	OE2	3.876
5JNX	E_ARG_85	NH2	E_GLU_178	OE1	2.403
5JNX	E_ARG_85	NH2	E_GLU_178	OE2	3.424
5JNX	E_ARG_130	NH2	E_ASP_163	OD2	3.179
5JNX	E_ARG_134	NH1	F_GLU_545	OE2	3.660
5JNX	E_HIS_154	NE2	E_GLU_178	OE2	2.610
5JNX	E_LYS_155	NZ	A_ASP_502	OD2	3.701
5JNX	E_ARG_164	NH2	E_ASP_163	OD1	3.605
5JNX	E_ARG_164	NH2	E_ASP_163	OD2	3.317
5JNX	F_HIS_516	NE2	F_GLU_545	OE1	3.961
5JNX	F_ARG_559	NH1	E_GLU_103	OE1	3.219
5JNX	F_ARG_559	NH1	E_GLU_103	OE2	3.448
5JNX	F_ARG_559	NH2	E_GLU_103	OE1	3.927
5JNX	F_ARG_559	NH2	E_GLU_103	OE2	2.697

5JNX	F_LYS_588	NZ	E_ASP_47	OD1	3.552
5JNX	F_LYS_588	NZ	E_ASP_47	OD2	3.520
5JNX	G_HIS_39	NE2	G_ASP_55	OD1	3.998
5JNX	G_ARG_64	NH1	G_GLU_100	OE1	3.273
5JNX	G_ARG_64	NH1	G_GLU_100	OE2	3.876
5JNX	G_ARG_85	NH2	G_GLU_178	OE1	2.663
5JNX	G_ARG_85	NH2	G_GLU_178	OE2	3.813
5JNX	G_ARG_130	NH2	G_ASP_163	OD2	3.180
5JNX	G_ARG_134	NH1	H_GLU_545	OE2	3.659
5JNX	G_HIS_154	NE2	G_GLU_178	OE2	2.610
5JNX	G_ARG_164	NH2	G_ASP_163	OD1	3.606
5JNX	G_ARG_164	NH2	G_ASP_163	OD2	3.318
5JNX	H_HIS_516	NE2	H_GLU_545	OE1	3.961
5JNX	H_ARG_559	NH1	G_GLU_103	OE1	3.221
5JNX	H_ARG_559	NH1	G_GLU_103	OE2	3.449
5JNX	H_ARG_559	NH2	G_GLU_103	OE1	3.928
5JNX	H_ARG_559	NH2	G_GLU_103	OE2	2.697
5JNX	H_LYS_588	NZ	G_ASP_47	OD1	3.552
5JNX	H_LYS_588	NZ	G_ASP_47	OD2	3.522

Table 16: 5JNX-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQ3	A_HIS_39	NE2	A_ASP_55	OD1	2.911
5JQ3	A_HIS_39	NE2	A_ASP_55	OD2	3.472
5JQ3	A_ARG_85	NH1	A_GLU_178	OE1	3.536
5JQ3	A_ARG_85	NH1	A_GLU_178	OE2	2.746
5JQ3	A_LYS_114	NZ	A_GLU_120	OE1	3.849
5JQ3	A_LYS_114	NZ	A_GLU_120	OE2	3.453
5JQ3	A_ARG_130	NH2	A_ASP_163	OD1	3.021
5JQ3	A_HIS_154	NE2	A_GLU_178	OE1	2.776
5JQ3	A_ARG_164	NH1	A_ASP_163	OD1	3.056
5JQ3	A_ARG_164	NH1	A_ASP_163	OD2	3.532
5JQ3	A_ARG_266	NH2	A_ASP_237	OD2	3.203
5JQ3	B_HIS_516	NE2	B_GLU_545	OE1	2.971
5JQ3	B_ARG_559	NH1	A_GLU_103	OE1	2.754
5JQ3	B_ARG_559	NH1	A_GLU_103	OE2	3.830
5JQ3	B_ARG_559	NH2	A_GLU_103	OE1	3.362
5JQ3	B_ARG_559	NH2	A_GLU_103	OE2	2.945

Table 17: 5JQ3-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQ7	A_HIS_39	NE2	A_ASP_55	OD1	3.302
5JQ7	A_HIS_39	NE2	A_ASP_55	OD2	2.805
5JQ7	A_ARG_85	NH1	A_GLU_178	OE1	3.344
5JQ7	A_ARG_85	NH1	A_GLU_178	OE2	2.714
5JQ7	A_LYS_114	NZ	A_GLU_120	OE2	3.552
5JQ7	A_ARG_130	NH2	A_ASP_163	OD1	2.926
5JQ7	A_HIS_154	NE2	A_GLU_178	OE1	2.770
5JQ7	A_ARG_164	NH1	A_ASP_163	OD1	2.933
5JQ7	A_ARG_164	NH1	A_ASP_163	OD2	3.613
5JQ7	A_ARG_247	NH1	A_GLU_245	OE1	3.700
5JQ7	A_ARG_247	NH1	A_GLU_245	OE2	3.859
5JQ7	A_ARG_266	NH2	A_ASP_237	OD2	3.168
5JQ7	B_LYS_510	NZ	A_GLU_292	OE1	3.131
5JQ7	B_HIS_516	NE2	B_GLU_545	OE1	2.658
5JQ7	B_ARG_559	NH1	A_GLU_103	OE1	2.800
5JQ7	B_ARG_559	NH1	A_GLU_103	OE2	3.720
5JQ7	B_ARG_559	NH2	A_GLU_103	OE1	3.375
5JQ7	B_ARG_559	NH2	A_GLU_103	OE2	2.748
5JQ7	B_HIS_613	NE2	B_ASP_614	OD1	3.865

Table 18: 5JQ7-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQB	A_ARG_85	NH1	A_GLU_178	OE1	3.533
5JQB	A_ARG_85	NH1	A_GLU_178	OE2	2.805
5JQB	A_LYS_114	NZ	A_GLU_120	OE2	3.275
5JQB	A_ARG_130	NH2	A_ASP_163	OD1	3.034
5JQB	A_HIS_154	NE2	A_GLU_178	OE1	2.801
5JQB	A_ARG_164	NH1	A_ASP_163	OD1	2.868
5JQB	A_ARG_164	NH1	A_ASP_163	OD2	3.537
5JQB	A_ARG_247	NH1	A_GLU_245	OE1	3.146
5JQB	A_ARG_266	NH2	A_ASP_237	OD2	3.033
5JQB	B_LYS_510	NZ	A_GLU_292	OE1	2.746
5JQB	B_LYS_510	NZ	A_GLU_292	OE2	3.918
5JQB	B_HIS_516	NE2	B_GLU_545	OE1	2.749
5JQB	B_ARG_559	NH1	A_GLU_103	OE1	2.703
5JQB	B_ARG_559	NH1	A_GLU_103	OE2	3.788
5JQB	B_ARG_559	NH2	A_GLU_103	OE1	3.188
5JQB	B_ARG_559	NH2	A_GLU_103	OE2	2.857
5JQB	B_LYS_588	NZ	A_ASP_47	OD1	3.558
5JQB	B_LYS_588	NZ	A_ASP_47	OD2	3.148
5JQB	B_LYS_617	NZ	B_ASP_614	OD1	3.955

Table 19: 5JQB-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEL	A_ARG_85	NH2	A_GLU_178	OE1	2.875
5KEL	A_ARG_85	NH2	A_GLU_178	OE2	3.676
5KEL	A_LYS_114	NZ	A_GLU_120	OE2	2.853
5KEL	A_ARG_130	NH1	B_GLU_540	OE2	3.053
5KEL	A_ARG_130	NH2	A_ASP_163	OD1	3.103
5KEL	A_ARG_164	NH2	A_GLU_100	OE1	3.728
5KEL	A_ARG_164	NH2	A_GLU_100	OE2	2.804
5KEL	A_ARG_172	NH1	A_GLU_120	OE1	2.760
5KEL	A_ARG_172	NH2	A_GLU_112	OE1	3.171
5KEL	A_ARG_172	NH2	A_GLU_120	OE1	2.755
5KEL	A_ARG_219	NH1	A_GLU_235	OE2	2.800
5KEL	A_ARG_219	NH2	A_GLU_235	OE2	3.004
5KEL	A_ARG_247	NH1	A_GLU_245	OE2	3.112
5KEL	A_ARG_247	NH2	A_GLU_245	OE2	3.134
5KEL	A_LYS_272	NZ	C_ASP_54	OD2	3.464
5KEL	A_LYS_272	NZ	C_ASP_56	OD2	2.595
5KEL	A_ARG_299	NH2	A_GLU_304	OE1	3.032
5KEL	A_ARG_299	NH2	A_GLU_304	OE2	3.954
5KEL	A_ARG_302	NH1	A_GLU_304	OE2	3.084
5KEL	A_ARG_302	NH2	A_GLU_258	OE2	2.817
5KEL	B_HIS_516	NE2	B_GLU_545	OE1	2.855
5KEL	B_ARG_559	NH1	A_GLU_103	OE2	3.831
5KEL	B_ARG_559	NH2	A_GLU_103	OE1	3.279
5KEL	B_ARG_559	NH2	A_GLU_103	OE2	3.801
5KEL	B_ARG_596	NH2	B_ASP_607	OD1	3.037
5KEL	H_ARG_38	NH1	H_ASP_86	OD1	3.058
5KEL	H_ARG_38	NH2	H_GLU_46	OE2	2.878
5KEL	H_ARG_52	NH1	H_GLU_50	OE2	3.140
5KEL	H_LYS_64	NZ	H_GLU_61	OE1	3.895
5KEL	H_LYS_64	NZ	H_GLU_61	OE2	2.690
5KEL	H_ARG_66	NH1	H_ASP_86	OD1	3.110
5KEL	H_ARG_66	NH1	H_ASP_86	OD2	3.688
5KEL	H_ARG_66	NH2	H_ASP_86	OD1	3.615
5KEL	H_ARG_66	NH2	H_ASP_86	OD2	2.807
5KEL	H_ARG_71	NH2	H_ASP_73	OD1	2.936
5KEL	H_ARG_71	NH2	H_ASP_73	OD2	3.775
5KEL	H_ARG_83	NH1	H_GLU_85	OE1	3.189
5KEL	H_ARG_83	NH2	H_GLU_85	OE1	3.016
5KEL	L_ARG_61	NH1	L_ASP_82	OD2	2.735
5KEL	L_ARG_61	NH2	L_GLU_81	OE2	3.025
5KEL	L_ARG_61	NH2	L_ASP_82	OD1	3.676
5KEL	L_ARG_61	NH2	L_ASP_82	OD2	2.981
5KEL	L_LYS_107	NZ	L_GLU_17	OE1	2.902
5KEL	L_LYS_107	NZ	L_GLU_17	OE2	3.185
5KEL	C_LYS_3	NZ	C_ASP_1	OD1	2.754
5KEL	C_LYS_3	NZ	C_ASP_1	OD2	3.442
5KEL	C_ARG_38	NH1	C_ASP_86	OD1	3.057
5KEL	C_ARG_38	NH2	C_GLU_46	OE1	3.665
5KEL	C_ARG_38	NH2	C_GLU_46	OE2	3.228
5KEL	C_ARG_38	NH2	C_ASP_86	OD1	3.984
5KEL	C_LYS_71	NZ	C_ASP_55	OD1	2.808
5KEL	C_ARG_75	NH2	C_ASP_72	OD2	2.896
5KEL	D_LYS_24	NZ	D_ASP_70	OD1	2.745
5KEL	D_LYS_24	NZ	D_ASP_70	OD2	3.810
5KEL	D_ARG_61	NH1	D_GLU_81	OE2	3.962
5KEL	D_ARG_61	NH2	D_GLU_81	OE2	2.780
5KEL	D_ARG_61	NH2	D_ASP_82	OD1	2.856

5KEL	D_ARG_61	NH2	D_ASP_82	OD2	3.346
5KEL	D_ARG_107	NH1	D_GLU_105	OE2	2.791
5KEL	E_ARG_85	NH2	E_GLU_178	OE1	2.875
5KEL	E_ARG_85	NH2	E_GLU_178	OE2	3.677
5KEL	E_LYS_114	NZ	E_GLU_120	OE2	2.853
5KEL	E_ARG_130	NH1	G_GLU_540	OE2	3.054
5KEL	E_ARG_130	NH2	E_ASP_163	OD1	3.104
5KEL	E_ARG_164	NH2	E_GLU_100	OE1	3.728
5KEL	E_ARG_164	NH2	E_GLU_100	OE2	2.804
5KEL	E_ARG_172	NH1	E_GLU_120	OE1	2.760
5KEL	E_ARG_172	NH2	E_GLU_112	OE1	3.171
5KEL	E_ARG_172	NH2	E_GLU_120	OE1	2.755
5KEL	E_ARG_219	NH1	E_GLU_235	OE2	2.800
5KEL	E_ARG_219	NH2	E_GLU_235	OE2	3.003
5KEL	E_ARG_247	NH1	E_GLU_245	OE2	3.112
5KEL	E_ARG_247	NH2	E_GLU_245	OE2	3.134
5KEL	E_LYS_272	NZ	J_ASP_54	OD2	3.464
5KEL	E_LYS_272	NZ	J_ASP_56	OD2	2.596
5KEL	E_ARG_299	NH2	E_GLU_304	OE1	3.031
5KEL	E_ARG_299	NH2	E_GLU_304	OE2	3.954
5KEL	E_ARG_302	NH1	E_GLU_304	OE2	3.085
5KEL	E_ARG_302	NH2	E_GLU_258	OE2	2.816
5KEL	G_HIS_516	NE2	G_GLU_545	OE1	2.855
5KEL	G_ARG_559	NH1	E_GLU_103	OE2	3.832
5KEL	G_ARG_559	NH2	E_GLU_103	OE1	3.279
5KEL	G_ARG_559	NH2	E_GLU_103	OE2	3.802
5KEL	G_ARG_596	NH2	G_ASP_607	OD1	3.038
5KEL	P_ARG_38	NH1	P_ASP_86	OD1	3.058
5KEL	P_ARG_38	NH2	P_GLU_46	OE2	2.878
5KEL	P_ARG_52	NH1	P_GLU_50	OE2	3.140
5KEL	P_LYS_64	NZ	P_GLU_61	OE1	3.894
5KEL	P_LYS_64	NZ	P_GLU_61	OE2	2.690
5KEL	P_ARG_66	NH1	P_ASP_86	OD1	3.110
5KEL	P_ARG_66	NH1	P_ASP_86	OD2	3.688
5KEL	P_ARG_66	NH2	P_ASP_86	OD1	3.615
5KEL	P_ARG_66	NH2	P_ASP_86	OD2	2.807
5KEL	P_ARG_71	NH2	P_ASP_73	OD1	2.936
5KEL	P_ARG_71	NH2	P_ASP_73	OD2	3.775
5KEL	P_ARG_83	NH1	P_GLU_85	OE1	3.188
5KEL	P_ARG_83	NH2	P_GLU_85	OE1	3.017
5KEL	T_ARG_61	NH1	T_ASP_82	OD2	2.735
5KEL	T_ARG_61	NH2	T_GLU_81	OE2	3.025
5KEL	T_ARG_61	NH2	T_ASP_82	OD1	3.676
5KEL	T_ARG_61	NH2	T_ASP_82	OD2	2.981
5KEL	T_LYS_107	NZ	T_GLU_17	OE1	2.903
5KEL	T_LYS_107	NZ	T_GLU_17	OE2	3.186
5KEL	J_LYS_3	NZ	J_ASP_1	OD1	2.754
5KEL	J_LYS_3	NZ	J_ASP_1	OD2	3.442
5KEL	J_ARG_38	NH1	J_ASP_86	OD1	3.057
5KEL	J_ARG_38	NH2	J_GLU_46	OE1	3.665
5KEL	J_ARG_38	NH2	J_GLU_46	OE2	3.228
5KEL	J_ARG_38	NH2	J_ASP_86	OD1	3.983
5KEL	J_LYS_71	NZ	J_ASP_55	OD1	2.808
5KEL	J_ARG_75	NH2	J_ASP_72	OD2	2.896
5KEL	N_LYS_24	NZ	N_ASP_70	OD1	2.744
5KEL	N_LYS_24	NZ	N_ASP_70	OD2	3.810
5KEL	N_ARG_61	NH1	N_GLU_81	OE2	3.962
5KEL	N_ARG_61	NH2	N_GLU_81	OE2	2.781

5KEL	N_ARG_61	NH2	N_ASP_82	OD1	2.855
5KEL	N_ARG_61	NH2	N_ASP_82	OD2	3.346
5KEL	N_ARG_107	NH1	N_GLU_105	OE2	2.791
5KEL	F_ARG_85	NH2	F_GLU_178	OE1	2.875
5KEL	F_ARG_85	NH2	F_GLU_178	OE2	3.677
5KEL	F_LYS_114	NZ	F_GLU_120	OE2	2.853
5KEL	F_ARG_130	NH1	I_GLU_540	OE2	3.053
5KEL	F_ARG_130	NH2	F_ASP_163	OD1	3.103
5KEL	F_ARG_164	NH2	F_GLU_100	OE1	3.728
5KEL	F_ARG_164	NH2	F_GLU_100	OE2	2.804
5KEL	F_ARG_172	NH1	F_GLU_120	OE1	2.760
5KEL	F_ARG_172	NH2	F_GLU_112	OE1	3.170
5KEL	F_ARG_172	NH2	F_GLU_120	OE1	2.755
5KEL	F_ARG_219	NH1	F_GLU_235	OE2	2.799
5KEL	F_ARG_219	NH2	F_GLU_235	OE2	3.003
5KEL	F_ARG_247	NH1	F_GLU_245	OE2	3.112
5KEL	F_ARG_247	NH2	F_GLU_245	OE2	3.134
5KEL	F_LYS_272	NZ	M_ASP_54	OD2	3.463
5KEL	F_LYS_272	NZ	M_ASP_56	OD2	2.596
5KEL	F_ARG_299	NH2	F_GLU_304	OE1	3.032
5KEL	F_ARG_299	NH2	F_GLU_304	OE2	3.954
5KEL	F_ARG_302	NH1	F_GLU_304	OE2	3.084
5KEL	F_ARG_302	NH2	F_GLU_258	OE2	2.816
5KEL	I_HIS_516	NE2	I_GLU_545	OE1	2.855
5KEL	I_ARG_559	NH1	F_GLU_103	OE2	3.831
5KEL	I_ARG_559	NH2	F_GLU_103	OE1	3.279
5KEL	I_ARG_559	NH2	F_GLU_103	OE2	3.801
5KEL	I_ARG_596	NH2	I_ASP_607	OD1	3.037
5KEL	Q_ARG_38	NH1	Q_ASP_86	OD1	3.058
5KEL	Q_ARG_38	NH2	Q_GLU_46	OE2	2.878
5KEL	Q_ARG_52	NH1	Q_GLU_50	OE2	3.140
5KEL	Q_LYS_64	NZ	Q_GLU_61	OE1	3.895
5KEL	Q_LYS_64	NZ	Q_GLU_61	OE2	2.690
5KEL	Q_ARG_66	NH1	Q_ASP_86	OD1	3.110
5KEL	Q_ARG_66	NH1	Q_ASP_86	OD2	3.688
5KEL	Q_ARG_66	NH2	Q_ASP_86	OD1	3.615
5KEL	Q_ARG_66	NH2	Q_ASP_86	OD2	2.807
5KEL	Q_ARG_71	NH2	Q_ASP_73	OD1	2.936
5KEL	Q_ARG_71	NH2	Q_ASP_73	OD2	3.774
5KEL	Q_ARG_83	NH1	Q_GLU_85	OE1	3.189
5KEL	Q_ARG_83	NH2	Q_GLU_85	OE1	3.016
5KEL	U_ARG_61	NH1	U_ASP_82	OD2	2.734
5KEL	U_ARG_61	NH2	U_GLU_81	OE2	3.025
5KEL	U_ARG_61	NH2	U_ASP_82	OD1	3.676
5KEL	U_ARG_61	NH2	U_ASP_82	OD2	2.981
5KEL	U_LYS_107	NZ	U_GLU_17	OE1	2.903
5KEL	U_LYS_107	NZ	U_GLU_17	OE2	3.186
5KEL	M_LYS_3	NZ	M_ASP_1	OD1	2.754
5KEL	M_LYS_3	NZ	M_ASP_1	OD2	3.442
5KEL	M_ARG_38	NH1	M_ASP_86	OD1	3.057
5KEL	M_ARG_38	NH2	M_GLU_46	OE1	3.665
5KEL	M_ARG_38	NH2	M_GLU_46	OE2	3.228
5KEL	M_ARG_38	NH2	M_ASP_86	OD1	3.984
5KEL	M_LYS_71	NZ	M_ASP_55	OD1	2.808
5KEL	M_ARG_75	NH2	M_ASP_72	OD2	2.896
5KEL	O_LYS_24	NZ	O_ASP_70	OD1	2.745
5KEL	O_LYS_24	NZ	O_ASP_70	OD2	3.811
5KEL	O_ARG_61	NH1	O_GLU_81	OE2	3.961

5KEL	O_ARG_61	NH2	O_GLU_81	OE2	2.780
5KEL	O_ARG_61	NH2	O_ASP_82	OD1	2.855
5KEL	O_ARG_61	NH2	O_ASP_82	OD2	3.346
5KEL	O_ARG_107	NH1	O_GLU_105	OE2	2.791

Table 20: 5KEL-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEM	C_ARG_24	NH1	C_GLU_70	OE1	3.169
5KEM	C_ARG_24	NH2	C_GLU_70	OE1	2.965
5KEM	C_ARG_61	NH1	C_ASP_82	OD1	3.729
5KEM	C_ARG_61	NH1	C_ASP_82	OD2	2.658
5KEM	C_ARG_61	NH2	C_GLU_81	OE2	3.360
5KEM	C_ARG_61	NH2	C_ASP_82	OD1	3.084
5KEM	C_ARG_61	NH2	C_ASP_82	OD2	3.287
5KEM	C_ARG_103	NH1	C_GLU_105	OE1	2.773
5KEM	C_ARG_103	NH2	C_GLU_105	OE1	2.948
5KEM	B_LYS_12	NZ	B_GLU_10	OE1	3.650
5KEM	B_LYS_12	NZ	B_GLU_10	OE2	2.758
5KEM	B_LYS_19	NZ	B_ASP_81	OD2	2.772
5KEM	B_ARG_38	NH1	B_GLU_46	OE1	2.905
5KEM	B_ARG_38	NH1	B_ASP_86	OD1	3.520
5KEM	B_ARG_38	NH1	B_ASP_86	OD2	3.245
5KEM	B_ARG_38	NH2	B_ASP_86	OD1	2.958
5KEM	B_ARG_38	NH2	B_ASP_86	OD2	3.504
5KEM	B_LYS_53	NZ	B_ASP_31	OD1	2.921
5KEM	B_ARG_64	NH1	B_GLU_46	OE1	3.725
5KEM	B_ARG_64	NH1	B_GLU_46	OE2	2.926
5KEM	B_ARG_64	NH2	B_GLU_46	OE1	3.105
5KEM	B_ARG_64	NH2	B_GLU_46	OE2	3.585
5KEM	B_LYS_83	NZ	B_ASP_85	OD1	3.656
5KEM	B_LYS_83	NZ	B_ASP_85	OD2	2.787
5KEM	D_LYS_3	NZ	D_ASP_1	OD2	2.842
5KEM	D_LYS_43	NZ	D_GLU_46	OE2	2.896
5KEM	D_LYS_57	NZ	D_ASP_55	OD1	3.976
5KEM	D_LYS_57	NZ	D_ASP_55	OD2	2.638
5KEM	D_LYS_71	NZ	D_ASP_56	OD1	2.855
5KEM	D_LYS_71	NZ	D_ASP_56	OD2	3.526
5KEM	D_ARG_75	NH2	D_ASP_72	OD2	2.852
5KEM	D_ARG_94	NH1	D_ASP_96	OD1	3.169
5KEM	D_ARG_94	NH2	D_ASP_96	OD1	3.069
5KEM	E_LYS_24	NZ	E_ASP_70	OD1	3.824
5KEM	E_ARG_54	NH1	E_ASP_60	OD1	2.684
5KEM	E_ARG_54	NH2	E_ASP_60	OD1	2.959
5KEM	E_ARG_61	NH1	E_ASP_82	OD2	3.854
5KEM	E_ARG_107	NH1	E_GLU_105	OE1	2.926
5KEM	E_ARG_107	NH1	E_GLU_105	OE2	3.400
5KEM	A_ARG_85	NH1	A_GLU_178	OE1	2.986
5KEM	A_ARG_85	NH1	A_GLU_178	OE2	3.588
5KEM	A_ARG_85	NH2	A_GLU_178	OE1	3.598
5KEM	A_ARG_85	NH2	A_GLU_178	OE2	2.771
5KEM	A_LYS_114	NZ	A_GLU_112	OE2	2.902
5KEM	A_LYS_114	NZ	A_GLU_120	OE1	2.734
5KEM	A_ARG_172	NH2	A_GLU_112	OE1	2.757
5KEM	A_ARG_219	NH1	A_GLU_235	OE1	3.033
5KEM	A_ARG_247	NH1	A_ASP_282	OD2	3.763
5KEM	A_ARG_247	NH2	A_ASP_282	OD2	3.187
5KEM	A_LYS_272	NZ	D_ASP_54	OD1	2.876
5KEM	A_LYS_272	NZ	D_ASP_54	OD2	3.185
5KEM	A_LYS_272	NZ	A_GLU_235	OE2	2.870
5KEM	H_ARG_24	NH1	H_GLU_70	OE1	3.169
5KEM	H_ARG_24	NH2	H_GLU_70	OE1	2.966
5KEM	H_ARG_61	NH1	H_ASP_82	OD1	3.730
5KEM	H_ARG_61	NH1	H_ASP_82	OD2	2.658
5KEM	H_ARG_61	NH2	H_GLU_81	OE2	3.360

5KEM	H_ARG_61	NH2	H_ASP_82	OD1	3.084
5KEM	H_ARG_61	NH2	H_ASP_82	OD2	3.287
5KEM	H_ARG_103	NH1	H_GLU_105	OE1	2.774
5KEM	H_ARG_103	NH2	H_GLU_105	OE1	2.948
5KEM	G_LYS_12	NZ	G_GLU_10	OE1	3.649
5KEM	G_LYS_12	NZ	G_GLU_10	OE2	2.758
5KEM	G_LYS_19	NZ	G_ASP_81	OD2	2.772
5KEM	G_ARG_38	NH1	G_GLU_46	OE1	2.905
5KEM	G_ARG_38	NH1	G_ASP_86	OD1	3.521
5KEM	G_ARG_38	NH1	G_ASP_86	OD2	3.246
5KEM	G_ARG_38	NH2	G_ASP_86	OD1	2.960
5KEM	G_ARG_38	NH2	G_ASP_86	OD2	3.505
5KEM	G_LYS_53	NZ	G_ASP_31	OD1	2.921
5KEM	G_ARG_64	NH1	G_GLU_46	OE1	3.725
5KEM	G_ARG_64	NH1	G_GLU_46	OE2	2.925
5KEM	G_ARG_64	NH2	G_GLU_46	OE1	3.106
5KEM	G_ARG_64	NH2	G_GLU_46	OE2	3.585
5KEM	G_LYS_83	NZ	G_ASP_85	OD1	3.656
5KEM	G_LYS_83	NZ	G_ASP_85	OD2	2.788
5KEM	I_LYS_3	NZ	I_ASP_1	OD2	2.842
5KEM	I_LYS_43	NZ	I_GLU_46	OE2	2.897
5KEM	I_LYS_57	NZ	I_ASP_55	OD1	3.976
5KEM	I_LYS_57	NZ	I_ASP_55	OD2	2.638
5KEM	I_LYS_71	NZ	I_ASP_56	OD1	2.856
5KEM	I_LYS_71	NZ	I_ASP_56	OD2	3.527
5KEM	I_ARG_75	NH2	I_ASP_72	OD2	2.852
5KEM	I_ARG_94	NH1	I_ASP_96	OD1	3.167
5KEM	I_ARG_94	NH2	I_ASP_96	OD1	3.069
5KEM	J_LYS_24	NZ	J_ASP_70	OD1	3.825
5KEM	J_ARG_54	NH1	J_ASP_60	OD1	2.683
5KEM	J_ARG_54	NH2	J_ASP_60	OD1	2.960
5KEM	J_ARG_61	NH1	J_ASP_82	OD2	3.854
5KEM	J_ARG_107	NH1	J_GLU_105	OE1	2.925
5KEM	J_ARG_107	NH1	J_GLU_105	OE2	3.399
5KEM	F_ARG_85	NH1	F_GLU_178	OE1	2.987
5KEM	F_ARG_85	NH1	F_GLU_178	OE2	3.589
5KEM	F_ARG_85	NH2	F_GLU_178	OE1	3.598
5KEM	F_ARG_85	NH2	F_GLU_178	OE2	2.771
5KEM	F_LYS_114	NZ	F_GLU_112	OE2	2.902
5KEM	F_LYS_114	NZ	F_GLU_120	OE1	2.734
5KEM	F_ARG_172	NH2	F_GLU_112	OE1	2.756
5KEM	F_ARG_219	NH1	F_GLU_235	OE1	3.032
5KEM	F_ARG_247	NH1	F_ASP_282	OD2	3.762
5KEM	F_ARG_247	NH2	F_ASP_282	OD2	3.186
5KEM	F_LYS_272	NZ	I_ASP_54	OD1	2.876
5KEM	F_LYS_272	NZ	I_ASP_54	OD2	3.185
5KEM	F_LYS_272	NZ	F_GLU_235	OE2	2.870

Table 21: 5KEM-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEN	A_ARG_54	NH2	A_ASP_55	OD2	3.882
5KEN	A_ARG_85	NH2	A_GLU_178	OE1	3.646
5KEN	A_ARG_85	NH2	A_GLU_178	OE2	2.914
5KEN	A_ARG_130	NH2	A_ASP_163	OD1	3.381
5KEN	A_ARG_134	NH2	B_GLU_545	OE1	2.859
5KEN	A_ARG_136	NH1	A_GLU_106	OE2	2.734
5KEN	A_LYS_140	NZ	A_GLU_112	OE2	3.961
5KEN	A_HIS_154	NE2	A_GLU_178	OE1	2.777
5KEN	A_ARG_164	NH2	A_GLU_100	OE1	3.828
5KEN	A_ARG_164	NH2	A_GLU_100	OE2	3.033
5KEN	A_ARG_172	NH2	A_GLU_112	OE1	3.530
5KEN	B_LYS_510	NZ	D_GLU_56	OE1	3.639
5KEN	B_LYS_510	NZ	D_GLU_56	OE2	2.773
5KEN	B_HIS_549	NE2	C_ASP_52	OD1	3.874
5KEN	B_ARG_559	NH1	A_GLU_103	OE1	3.709
5KEN	B_ARG_559	NH1	A_GLU_103	OE2	2.818
5KEN	B_ARG_559	NH2	A_GLU_103	OE1	3.114
5KEN	B_ARG_559	NH2	A_GLU_103	OE2	3.662
5KEN	B_ARG_596	NH2	B_ASP_607	OD1	3.053
5KEN	C_LYS_38	NZ	C_GLU_46	OE1	2.804
5KEN	C_LYS_38	NZ	C_GLU_46	OE2	3.887
5KEN	D_ARG_61	NH2	D_GLU_81	OE2	2.826
5KEN	D_ARG_61	NH2	D_ASP_82	OD1	3.556
5KEN	D_ARG_61	NH2	D_ASP_82	OD2	2.823
5KEN	D_LYS_107	NZ	D_GLU_17	OE1	3.537
5KEN	D_LYS_107	NZ	D_GLU_17	OE2	2.886
5KEN	E_HIS_39	ND1	E_ASP_55	OD1	2.715
5KEN	E_HIS_39	ND1	E_ASP_55	OD2	3.363
5KEN	E_ARG_85	NH2	E_GLU_178	OE1	3.714
5KEN	E_ARG_85	NH2	E_GLU_178	OE2	3.034
5KEN	E_ARG_130	NH1	E_ASP_163	OD1	2.771
5KEN	E_ARG_136	NH1	E_GLU_106	OE2	2.733
5KEN	E_LYS_140	NZ	E_GLU_112	OE2	2.756
5KEN	E_HIS_154	NE2	E_GLU_178	OE1	2.772
5KEN	E_ARG_164	NH2	E_GLU_100	OE1	3.488
5KEN	E_ARG_164	NH2	E_GLU_100	OE2	3.760
5KEN	E_LYS_272	NZ	J_ASP_54	OD2	3.722
5KEN	E_LYS_272	NZ	J_ASP_56	OD1	3.736
5KEN	E_LYS_272	NZ	J_ASP_56	OD2	2.765
5KEN	E_LYS_276	NZ	E_GLU_245	OE1	3.431
5KEN	E_LYS_276	NZ	E_GLU_245	OE2	2.793
5KEN	E_ARG_299	NH1	E_GLU_304	OE1	2.918
5KEN	E_ARG_299	NH1	E_GLU_305	OE2	3.083
5KEN	E_ARG_299	NH2	E_GLU_305	OE2	2.937
5KEN	E_ARG_302	NH1	E_GLU_304	OE2	2.810
5KEN	E_ARG_302	NH2	E_GLU_258	OE2	2.806
5KEN	F_LYS_510	NZ	H_GLU_56	OE2	2.720
5KEN	F_HIS_516	NE2	F_GLU_545	OE1	2.865
5KEN	F_HIS_549	NE2	G_ASP_52	OD1	3.491
5KEN	F_ARG_559	NH1	E_GLU_103	OE1	3.868
5KEN	F_ARG_559	NH1	E_GLU_103	OE2	2.947
5KEN	F_ARG_559	NH2	E_GLU_103	OE1	3.043
5KEN	F_ARG_559	NH2	E_GLU_103	OE2	3.542
5KEN	F_ARG_596	NH2	F_ASP_607	OD1	2.978
5KEN	F_HIS_613	ND1	F_ASP_614	OD2	3.831
5KEN	G_LYS_38	NZ	G_GLU_46	OE1	2.811
5KEN	G_LYS_38	NZ	G_GLU_46	OE2	3.954

5KEN	G_LYS_62	NZ	H_ASP_1	OD2	2.735
5KEN	H_ARG_61	NH2	H_GLU_81	OE2	2.864
5KEN	H_ARG_61	NH2	H_ASP_82	OD1	3.570
5KEN	H_ARG_61	NH2	H_ASP_82	OD2	2.811
5KEN	H_LYS_107	NZ	H_GLU_17	OE1	3.562
5KEN	H_LYS_107	NZ	H_GLU_17	OE2	2.967
5KEN	I_LYS_24	NZ	I_ASP_70	OD1	2.714
5KEN	I_LYS_24	NZ	I_ASP_70	OD2	3.786
5KEN	I_ARG_54	NH1	I_ASP_60	OD1	3.072
5KEN	I_ARG_61	NH1	I_GLU_81	OE2	3.750
5KEN	I_ARG_61	NH2	I_GLU_81	OE2	2.708
5KEN	I_ARG_61	NH2	I_ASP_82	OD1	2.808
5KEN	I_ARG_61	NH2	I_ASP_82	OD2	3.337
5KEN	I_LYS_103	NZ	I_GLU_105	OE2	2.881
5KEN	I_ARG_107	NH2	I_GLU_105	OE1	2.726
5KEN	J_LYS_3	NZ	J_ASP_1	OD1	2.794
5KEN	J_LYS_3	NZ	J_ASP_1	OD2	3.424
5KEN	J_ARG_38	NH1	J_ASP_86	OD1	3.024
5KEN	J_ARG_38	NH2	J_GLU_46	OE1	3.864
5KEN	J_ARG_38	NH2	J_GLU_46	OE2	3.398
5KEN	J_ARG_38	NH2	J_ASP_86	OD1	3.399
5KEN	J_LYS_71	NZ	J_ASP_55	OD1	2.827
5KEN	J_ARG_75	NH2	J_ASP_72	OD2	2.956
5KEN	K_HIS_39	ND1	K_ASP_55	OD1	2.793
5KEN	K_HIS_39	ND1	K_ASP_55	OD2	3.278
5KEN	K_ARG_85	NH2	K_GLU_178	OE1	3.673
5KEN	K_ARG_85	NH2	K_GLU_178	OE2	3.020
5KEN	K_LYS_115	NZ	K_ASP_150	OD1	3.600
5KEN	K_ARG_130	NH2	K_ASP_163	OD1	3.177
5KEN	K_ARG_130	NH2	K_ASP_163	OD2	3.766
5KEN	K_ARG_136	NH1	K_GLU_106	OE2	2.803
5KEN	K_LYS_140	NZ	K_GLU_112	OE2	2.762
5KEN	K_HIS_154	NE2	K_GLU_178	OE1	2.705
5KEN	K_ARG_164	NH2	K_GLU_100	OE1	3.437
5KEN	K_ARG_164	NH2	K_GLU_100	OE2	3.533
5KEN	K_ARG_219	NH1	K_GLU_235	OE2	2.859
5KEN	K_ARG_219	NH2	K_GLU_235	OE2	2.957
5KEN	K_LYS_272	NZ	K_GLU_235	OE1	3.796
5KEN	K_LYS_272	NZ	Q_ASP_54	OD2	3.814
5KEN	K_LYS_272	NZ	Q_ASP_56	OD1	3.710
5KEN	K_LYS_272	NZ	Q_ASP_56	OD2	2.769
5KEN	K_ARG_299	NH1	K_GLU_304	OE1	2.978
5KEN	K_ARG_299	NH1	K_GLU_305	OE2	3.152
5KEN	K_ARG_299	NH2	K_GLU_305	OE2	2.878
5KEN	K_ARG_302	NH1	K_GLU_304	OE2	2.982
5KEN	K_ARG_302	NH2	K_GLU_258	OE2	2.830
5KEN	M_LYS_510	NZ	O_GLU_56	OE2	2.667
5KEN	M_HIS_516	NE2	M_GLU_545	OE1	2.888
5KEN	M_ARG_559	NH1	K_GLU_103	OE1	3.708
5KEN	M_ARG_559	NH1	K_GLU_103	OE2	2.824
5KEN	M_ARG_559	NH2	K_GLU_103	OE1	3.090
5KEN	M_ARG_559	NH2	K_GLU_103	OE2	3.645
5KEN	M_ARG_596	NH2	M_ASP_607	OD1	2.995
5KEN	N_LYS_38	NZ	N_ASP_86	OD1	3.887
5KEN	N_LYS_62	NZ	O_ASP_1	OD2	2.793
5KEN	O_ARG_61	NH2	O_GLU_81	OE2	3.700
5KEN	O_ARG_61	NH2	O_ASP_82	OD1	3.662
5KEN	O_ARG_61	NH2	O_ASP_82	OD2	2.905

5KEN	O_LYS_107	NZ	O_GLU_17	OE1	3.531
5KEN	O_LYS_107	NZ	O_GLU_17	OE2	2.981
5KEN	P_LYS_24	NZ	P_ASP_70	OD1	2.736
5KEN	P_LYS_24	NZ	P_ASP_70	OD2	3.714
5KEN	P_ARG_54	NH1	P_ASP_60	OD1	2.965
5KEN	P_ARG_61	NH1	P_GLU_81	OE2	3.801
5KEN	P_ARG_61	NH2	P_GLU_81	OE2	2.727
5KEN	P_ARG_61	NH2	P_ASP_82	OD1	2.822
5KEN	P_ARG_61	NH2	P_ASP_82	OD2	3.338
5KEN	P_ARG_107	NH1	P_GLU_105	OE2	2.824
5KEN	Q_LYS_3	NZ	Q_ASP_1	OD1	2.773
5KEN	Q_LYS_3	NZ	Q_ASP_1	OD2	3.470
5KEN	Q_ARG_38	NH1	Q_ASP_86	OD1	3.016
5KEN	Q_ARG_38	NH2	Q_GLU_46	OE1	3.835
5KEN	Q_ARG_38	NH2	Q_GLU_46	OE2	3.412
5KEN	Q_ARG_38	NH2	Q_ASP_86	OD1	3.365
5KEN	Q_LYS_71	NZ	Q_ASP_55	OD1	2.819
5KEN	Q_ARG_75	NH2	Q_ASP_72	OD2	2.942

Table 22: 5KEN-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5T42-13	A_LYS_633	NZ	A_ASP_642	OD2	2.906
5T42-5	A_LYS_633	NZ	A_ASP_642	OD2	3.987
5T42-8	A_LYS_633	NZ	A_ASP_642	OD2	2.592

Table 23: 5T42-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DZL	A_ARG_85	NH2	A_GLU_178	OE1	3.930
6DZL	J_ARG_61	NH2	J_ASP_82	OD2	3.985
6DZL	G_ARG_38	NH1	G_ASP_86	OD1	2.843
6DZL	G_ARG_38	NH2	G_GLU_46	OE1	3.120
6DZL	G_ARG_38	NH2	G_GLU_46	OE2	3.080
6DZL	G_ARG_66	NH2	G_ASP_86	OD2	3.660
6DZL	G_HIS_96	ND1	J_GLU_55	OE2	3.342
6DZL	G_HIS_96	NE2	J_GLU_55	OE1	3.570
6DZL	G_HIS_96	NE2	J_GLU_55	OE2	3.728
6DZL	B_ARG_85	NH2	B_GLU_178	OE1	3.931
6DZL	K_ARG_61	NH2	K_ASP_82	OD2	3.984
6DZL	H_ARG_38	NH1	H_ASP_86	OD1	2.845
6DZL	H_ARG_38	NH2	H_GLU_46	OE1	3.120
6DZL	H_ARG_38	NH2	H_GLU_46	OE2	3.080
6DZL	H_ARG_66	NH2	H_ASP_86	OD2	3.660
6DZL	H_HIS_96	ND1	K_GLU_55	OE2	3.341
6DZL	H_HIS_96	NE2	K_GLU_55	OE1	3.571
6DZL	H_HIS_96	NE2	K_GLU_55	OE2	3.727
6DZL	C_ARG_85	NH2	C_GLU_178	OE1	3.930
6DZL	L_ARG_61	NH2	L_ASP_82	OD2	3.984
6DZL	I_ARG_38	NH1	I_ASP_86	OD1	2.844
6DZL	I_ARG_38	NH2	I_GLU_46	OE1	3.120
6DZL	I_ARG_38	NH2	I_GLU_46	OE2	3.080
6DZL	I_ARG_66	NH2	I_ASP_86	OD2	3.660
6DZL	I_HIS_96	ND1	L_GLU_55	OE2	3.341
6DZL	I_HIS_96	NE2	L_GLU_55	OE1	3.571
6DZL	I_HIS_96	NE2	L_GLU_55	OE2	3.727

Table 24: 6DZL-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EA7	A_ARG_64	NH1	A_GLU_100	OE1	2.585
6EA7	A_ARG_64	NH1	A_GLU_100	OE2	2.698
6EA7	A_ARG_85	NH1	A_GLU_178	OE2	3.995
6EA7	A_LYS_114	NZ	A_GLU_120	OE2	3.917
6EA7	A_ARG_136	NH1	A_GLU_106	OE1	3.638
6EA7	A_HIS_154	NE2	A_GLU_178	OE1	2.817
6EA7	A_ARG_164	NH1	A_ASP_163	OD1	3.751
6EA7	A_ARG_164	NH1	A_ASP_163	OD2	3.561
6EA7	A_ARG_172	NH1	A_GLU_120	OE2	3.778
6EA7	B_HIS_516	NE2	B_GLU_545	OE1	3.238
6EA7	B_ARG_559	NH1	A_GLU_103	OE1	2.641
6EA7	B_ARG_559	NH1	A_GLU_103	OE2	3.432
6EA7	B_ARG_559	NH2	A_GLU_103	OE2	3.686
6EA7	B_HIS_602	ND1	F_GLU_611	OE1	3.135
6EA7	C_HIS_39	NE2	C_ASP_55	OD1	3.559
6EA7	C_ARG_85	NH1	C_GLU_178	OE1	3.607
6EA7	C_ARG_85	NH1	C_GLU_178	OE2	3.196
6EA7	C_LYS_114	NZ	C_GLU_120	OE2	3.697
6EA7	C_ARG_130	NH2	C_ASP_163	OD2	2.578
6EA7	C_ARG_164	NH1	C_ASP_163	OD1	3.787
6EA7	C_ARG_172	NH1	C_GLU_120	OE2	3.868
6EA7	D_HIS_516	NE2	D_GLU_545	OE1	3.935
6EA7	D_ARG_559	NH1	C_GLU_103	OE1	2.573
6EA7	D_ARG_559	NH1	C_GLU_103	OE2	3.488
6EA7	D_ARG_559	NH2	C_GLU_103	OE1	3.832
6EA7	D_ARG_559	NH2	C_GLU_103	OE2	3.318
6EA7	D_HIS_602	ND1	B_GLU_611	OE1	3.062
6EA7	E_ARG_85	NH1	E_GLU_178	OE1	3.412
6EA7	E_ARG_85	NH1	E_GLU_178	OE2	3.298
6EA7	E_ARG_130	NH2	E_ASP_163	OD2	2.654
6EA7	E_HIS_154	NE2	E_GLU_178	OE1	3.949
6EA7	E_ARG_164	NH1	E_ASP_163	OD1	3.520
6EA7	E_ARG_164	NH1	E_ASP_163	OD2	3.465
6EA7	E_ARG_172	NH2	E_GLU_120	OE2	3.923
6EA7	F_ARG_559	NH1	E_GLU_103	OE1	2.812
6EA7	F_ARG_559	NH1	E_GLU_103	OE2	3.584
6EA7	F_ARG_559	NH2	E_GLU_103	OE2	3.608
6EA7	F_ARG_596	NH2	E_ASP_55	OD1	2.483
6EA7	F_ARG_596	NH2	E_ASP_55	OD2	3.342
6EA7	F_HIS_602	ND1	D_GLU_611	OE1	3.253
6EA7	H_ARG_38	NH1	H_GLU_46	OE1	3.611
6EA7	H_ARG_38	NH1	H_ASP_90	OD1	3.414
6EA7	H_ARG_38	NH2	H_GLU_46	OE1	2.876
6EA7	H_ARG_38	NH2	H_GLU_46	OE2	3.020
6EA7	H_HIS_100	ND1	H_ASP_110	OD2	3.934
6EA7	H_HIS_100	ND1	L_GLU_55	OE1	3.325
6EA7	H_HIS_100	NE2	L_GLU_55	OE1	3.655
6EA7	H_HIS_108	NE2	L_ASP_50	OD1	2.912
6EA7	H_HIS_173	ND1	L_ASP_166	OD1	3.947
6EA7	H_HIS_173	ND1	L_ASP_166	OD2	3.590
6EA7	H_LYS_218	NZ	L_GLU_122	OE1	2.826
6EA7	L_LYS_39	NZ	L_GLU_42	OE1	3.713
6EA7	L_LYS_39	NZ	L_ASP_81	OD1	3.700
6EA7	L_ARG_61	NH2	L_ASP_82	OD1	2.764
6EA7	L_ARG_61	NH2	L_ASP_82	OD2	3.165
6EA7	L_LYS_102	NZ	L_GLU_164	OE1	3.631
6EA7	L_LYS_148	NZ	L_GLU_194	OE1	3.419

6EA7	M_ARG_38	NH1	M_GLU_46	OE1	3.632
6EA7	M_ARG_38	NH2	M_GLU_46	OE1	2.819
6EA7	M_ARG_38	NH2	M_GLU_46	OE2	3.086
6EA7	M_ARG_67	NH1	M_ASP_90	OD1	3.655
6EA7	M_ARG_67	NH1	M_ASP_90	OD2	3.008
6EA7	M_ARG_67	NH2	M_ASP_90	OD1	2.976
6EA7	M_ARG_67	NH2	M_ASP_90	OD2	2.990
6EA7	M_HIS_100	ND1	N_GLU_55	OE1	3.446
6EA7	M_HIS_100	ND1	N_GLU_55	OE2	3.681
6EA7	M_HIS_108	ND1	N_ASP_50	OD1	3.757
6EA7	M_HIS_108	NE2	N_ASP_50	OD1	3.718
6EA7	M_HIS_173	ND1	N_ASP_166	OD2	3.701
6EA7	M_LYS_219	NZ	M_GLU_221	OE1	3.040
6EA7	N_LYS_39	NZ	N_ASP_81	OD1	3.604
6EA7	N_ARG_61	NH2	N_ASP_82	OD1	2.680
6EA7	N_ARG_61	NH2	N_ASP_82	OD2	3.258
6EA7	N_LYS_102	NZ	N_GLU_164	OE1	3.534
6EA7	N_LYS_148	NZ	N_GLU_194	OE1	3.192
6EA7	N_HIS_188	ND1	N_ASP_150	OD2	3.491
6EA7	Q_ARG_38	NH1	Q_GLU_46	OE1	3.581
6EA7	Q_ARG_38	NH2	Q_GLU_46	OE1	3.006
6EA7	Q_ARG_38	NH2	Q_GLU_46	OE2	3.019
6EA7	Q_ARG_67	NH1	Q_ASP_90	OD1	3.489
6EA7	Q_ARG_67	NH1	Q_ASP_90	OD2	2.319
6EA7	Q_ARG_67	NH2	Q_ASP_90	OD1	3.689
6EA7	Q_ARG_67	NH2	Q_ASP_90	OD2	3.153
6EA7	Q_HIS_108	NE2	R_ASP_50	OD1	3.227
6EA7	Q_HIS_173	ND1	R_ASP_166	OD1	3.817
6EA7	Q_HIS_173	ND1	R_ASP_166	OD2	3.600
6EA7	R_ARG_24	NH1	R_GLU_70	OE1	2.987
6EA7	R_ARG_24	NH1	R_GLU_70	OE2	2.873
6EA7	R_LYS_39	NZ	R_GLU_42	OE1	3.837
6EA7	R_LYS_39	NZ	R_ASP_81	OD1	3.859
6EA7	R_ARG_61	NH2	R_ASP_82	OD1	2.608
6EA7	R_ARG_61	NH2	R_ASP_82	OD2	3.334
6EA7	R_LYS_102	NZ	R_GLU_164	OE1	3.378
6EA7	R_LYS_106	NZ	R_GLU_104	OE1	3.728
6EA7	R_LYS_148	NZ	R_GLU_194	OE1	3.641

Table 25: 6EA7-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F5U	A_HIS_39	NE2	A_ASP_55	OD1	3.607
6F5U	A_HIS_39	NE2	A_ASP_55	OD2	3.205
6F5U	A_ARG_85	NH1	A_GLU_178	OE1	3.593
6F5U	A_ARG_85	NH1	A_GLU_178	OE2	2.633
6F5U	A_LYS_114	NZ	A_GLU_120	OE2	3.481
6F5U	A_ARG_130	NH2	A_ASP_163	OD2	3.086
6F5U	A_HIS_154	NE2	A_GLU_178	OE1	2.646
6F5U	A_ARG_164	NH1	A_ASP_163	OD1	3.541
6F5U	A_ARG_164	NH1	A_ASP_163	OD2	3.126
6F5U	A_ARG_247	NH2	A_GLU_245	OE1	3.242
6F5U	A_ARG_266	NH2	A_ASP_237	OD2	3.400
6F5U	B_LYS_510	NZ	A_GLU_292	OE1	3.345
6F5U	B_HIS_516	NE2	B_GLU_545	OE1	2.737
6F5U	B_ARG_559	NH1	A_GLU_103	OE1	2.631
6F5U	B_ARG_559	NH1	A_GLU_103	OE2	3.833
6F5U	B_ARG_559	NH2	A_GLU_103	OE1	3.290
6F5U	B_ARG_559	NH2	A_GLU_103	OE2	2.992

Table 26: 6F5U-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6I	A_ARG_85	NH1	A_GLU_178	OE1	3.391
6F6I	A_ARG_85	NH1	A_GLU_178	OE2	2.492
6F6I	A_LYS_114	NZ	A_GLU_120	OE2	3.662
6F6I	A_ARG_130	NH2	A_ASP_163	OD1	3.094
6F6I	A_LYS_140	NZ	A_GLU_112	OE2	3.920
6F6I	A_HIS_154	NE2	A_GLU_178	OE1	2.814
6F6I	A_ARG_164	NH1	A_ASP_163	OD1	3.155
6F6I	A_ARG_164	NH1	A_ASP_163	OD2	3.520
6F6I	A_ARG_247	NH2	A_GLU_245	OE2	2.546
6F6I	A_ARG_266	NH2	A_ASP_237	OD2	3.974
6F6I	B_LYS_510	NZ	A_GLU_292	OE1	3.377
6F6I	B_HIS_516	NE2	B_GLU_545	OE1	2.567
6F6I	B_ARG_559	NH1	A_GLU_103	OE1	3.800
6F6I	B_ARG_559	NH1	A_GLU_103	OE2	2.815
6F6I	B_ARG_559	NH2	A_GLU_103	OE1	3.096
6F6I	B_ARG_559	NH2	A_GLU_103	OE2	3.529
6F6I	B_HIS_628	ND1	B_ASP_629	OD1	3.915
6F6I	B_HIS_628	NE2	B_ASP_629	OD1	3.799

Table 27: 6F6I-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6N	A_LYS_50	NZ	A_ASP_49	OD1	3.536
6F6N	A_LYS_50	NZ	A_ASP_49	OD2	3.944
6F6N	A_ARG_85	NH1	A_GLU_178	OE1	3.489
6F6N	A_ARG_85	NH1	A_GLU_178	OE2	2.503
6F6N	A_LYS_114	NZ	A_GLU_120	OE2	3.710
6F6N	A_ARG_130	NH2	A_ASP_163	OD2	3.005
6F6N	A_HIS_154	NE2	A_GLU_178	OE1	2.727
6F6N	A_ARG_164	NH1	A_ASP_163	OD1	3.435
6F6N	A_ARG_164	NH1	A_ASP_163	OD2	2.950
6F6N	A_ARG_247	NH1	A_GLU_245	OE1	3.669
6F6N	A_ARG_266	NH2	A_ASP_237	OD2	3.429
6F6N	A_LYS_276	NZ	A_GLU_245	OE2	2.564
6F6N	B_LYS_510	NZ	A_GLU_292	OE1	2.639
6F6N	B_HIS_516	NE2	B_GLU_545	OE1	2.799
6F6N	B_ARG_559	NH1	A_GLU_103	OE1	2.593
6F6N	B_ARG_559	NH1	A_GLU_103	OE2	3.789
6F6N	B_ARG_559	NH2	A_GLU_103	OE1	3.215
6F6N	B_ARG_559	NH2	A_GLU_103	OE2	2.904
6F6N	B_LYS_588	NZ	A_ASP_47	OD1	3.696
6F6N	B_LYS_588	NZ	A_ASP_47	OD2	2.975

Table 28: 6F6N-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6S	A_ARG_85	NH1	A_GLU_178	OE1	3.259
6F6S	A_ARG_85	NH1	A_GLU_178	OE2	2.372
6F6S	A_LYS_114	NZ	A_GLU_120	OE2	3.380
6F6S	A_ARG_130	NH2	A_ASP_163	OD1	3.014
6F6S	A_HIS_154	NE2	A_GLU_178	OE1	3.039
6F6S	A_ARG_164	NH1	A_ASP_163	OD1	2.810
6F6S	A_ARG_164	NH1	A_ASP_163	OD2	3.556
6F6S	B_LYS_510	NZ	A_GLU_292	OE1	2.331
6F6S	B_LYS_510	NZ	A_GLU_292	OE2	3.397
6F6S	B_HIS_516	NE2	B_GLU_545	OE1	2.731
6F6S	B_ARG_559	NH1	A_GLU_103	OE1	2.656
6F6S	B_ARG_559	NH1	A_GLU_103	OE2	3.920
6F6S	B_ARG_559	NH2	A_GLU_103	OE1	3.146
6F6S	B_ARG_559	NH2	A_GLU_103	OE2	2.951
6F6S	B_LYS_588	NZ	A_ASP_47	OD1	2.944
6F6S	B_LYS_588	NZ	A_ASP_47	OD2	2.772
6F6S	B_LYS_617	NZ	B_ASP_614	OD1	3.893

Table 29: 6F6S-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G95	A_HIS_39	NE2	A_ASP_55	OD1	2.899
6G95	A_HIS_39	NE2	A_ASP_55	OD2	3.064
6G95	A_ARG_85	NH1	A_GLU_178	OE1	3.522
6G95	A_ARG_85	NH1	A_GLU_178	OE2	2.681
6G95	A_LYS_114	NZ	A_GLU_120	OE1	3.918
6G95	A_LYS_114	NZ	A_GLU_120	OE2	3.675
6G95	A_ARG_130	NH2	A_ASP_163	OD1	3.040
6G95	A_LYS_140	NZ	A_GLU_112	OE1	3.777
6G95	A_HIS_154	NE2	A_GLU_178	OE1	2.904
6G95	A_ARG_164	NH1	A_ASP_163	OD1	2.830
6G95	A_ARG_164	NH1	A_ASP_163	OD2	3.454
6G95	A_ARG_266	NH2	A_ASP_237	OD2	3.135
6G95	B_HIS_516	NE2	B_GLU_545	OE1	2.525
6G95	B_ARG_559	NH1	A_GLU_103	OE1	2.683
6G95	B_ARG_559	NH1	A_GLU_103	OE2	3.879
6G95	B_ARG_559	NH2	A_GLU_103	OE1	3.249
6G95	B_ARG_559	NH2	A_GLU_103	OE2	2.973

Table 30: 6G95-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G9B	A_ARG_85	NH1	A_GLU_178	OE1	3.384
6G9B	A_ARG_85	NH1	A_GLU_178	OE2	2.574
6G9B	A_LYS_114	NZ	A_GLU_120	OE1	3.989
6G9B	A_LYS_114	NZ	A_GLU_120	OE2	3.841
6G9B	A_ARG_130	NH2	A_ASP_163	OD1	3.043
6G9B	A_LYS_140	NZ	A_GLU_112	OE2	3.639
6G9B	A_HIS_154	NE2	A_GLU_178	OE1	2.960
6G9B	A_ARG_164	NH1	A_ASP_163	OD1	2.869
6G9B	A_ARG_164	NH1	A_ASP_163	OD2	3.373
6G9B	A_ARG_172	NH1	A_GLU_120	OE2	3.934
6G9B	A_ARG_247	NH2	A_GLU_245	OE1	3.502
6G9B	A_ARG_266	NH2	A_ASP_237	OD2	3.075
6G9B	B_LYS_510	NZ	A_GLU_292	OE1	3.414
6G9B	B_HIS_516	NE2	B_GLU_545	OE1	2.666
6G9B	B_ARG_559	NH1	A_GLU_103	OE1	2.574
6G9B	B_ARG_559	NH1	A_GLU_103	OE2	3.760
6G9B	B_ARG_559	NH2	A_GLU_103	OE1	3.199
6G9B	B_ARG_559	NH2	A_GLU_103	OE2	2.870
6G9B	B_LYS_588	NZ	A_ASP_47	OD1	3.317
6G9B	B_LYS_588	NZ	A_ASP_47	OD2	2.892
6G9B	B_LYS_617	NZ	B_ASP_614	OD2	3.817
6G9B	B_HIS_628	NE2	B_ASP_629	OD1	3.701
6G9B	B_HIS_628	NE2	B_ASP_629	OD2	3.971

Table 31: 6G9B-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G9I	A_HIS_39	NE2	A_ASP_55	OD1	3.027
6G9I	A_HIS_39	NE2	A_ASP_55	OD2	2.861
6G9I	A_ARG_85	NH1	A_GLU_178	OE1	3.616
6G9I	A_ARG_85	NH1	A_GLU_178	OE2	2.527
6G9I	A_LYS_114	NZ	A_GLU_120	OE2	3.647
6G9I	A_ARG_130	NH2	A_ASP_163	OD1	3.039
6G9I	A_HIS_154	NE2	A_GLU_178	OE1	2.656
6G9I	A_ARG_164	NH1	A_ASP_163	OD1	3.026
6G9I	A_ARG_164	NH1	A_ASP_163	OD2	3.451
6G9I	A_ARG_266	NH2	A_ASP_237	OD2	3.464
6G9I	B_HIS_516	NE2	B_GLU_545	OE1	2.739
6G9I	B_ARG_559	NH1	A_GLU_103	OE1	2.689
6G9I	B_ARG_559	NH1	A_GLU_103	OE2	3.794
6G9I	B_ARG_559	NH2	A_GLU_103	OE1	3.340
6G9I	B_ARG_559	NH2	A_GLU_103	OE2	2.940
6G9I	B_LYS_622	NZ	B_ASP_621	OD1	2.501
6G9I	B_LYS_622	NZ	B_ASP_621	OD2	3.672

Table 32: 6G9I-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6HRO	A_ARG_85	NH1	A_GLU_178	OE1	3.459
6HRO	A_ARG_85	NH1	A_GLU_178	OE2	2.606
6HRO	A_LYS_114	NZ	A_GLU_120	OE2	3.759
6HRO	A_ARG_130	NH2	A_ASP_163	OD1	2.957
6HRO	A_HIS_154	NE2	A_GLU_178	OE1	3.012
6HRO	A_ARG_164	NH1	A_ASP_163	OD1	3.206
6HRO	A_ARG_164	NH1	A_ASP_163	OD2	3.548
6HRO	A_ARG_266	NH2	A_ASP_237	OD2	3.585
6HRO	B_LYS_510	NZ	A_GLU_292	OE1	3.852
6HRO	B_HIS_516	NE2	B_GLU_545	OE1	2.827
6HRO	B_ARG_559	NH1	A_GLU_103	OE1	2.817
6HRO	B_ARG_559	NH1	A_GLU_103	OE2	3.911
6HRO	B_ARG_559	NH2	A_GLU_103	OE1	3.514
6HRO	B_ARG_559	NH2	A_GLU_103	OE2	3.164
6HRO	B_LYS_588	NZ	A_ASP_47	OD1	3.207
6HRO	B_LYS_588	NZ	A_ASP_47	OD2	2.778

Table 33: 6HRO-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6HS4	A_HIS_39	NE2	A_ASP_55	OD1	3.180
6HS4	A_HIS_39	NE2	A_ASP_55	OD2	2.847
6HS4	A_ARG_85	NH1	A_GLU_178	OE1	3.429
6HS4	A_ARG_85	NH1	A_GLU_178	OE2	2.535
6HS4	A_LYS_114	NZ	A_GLU_120	OE2	3.578
6HS4	A_ARG_130	NH2	A_ASP_163	OD1	3.064
6HS4	A_HIS_154	NE2	A_GLU_178	OE1	2.801
6HS4	A_ARG_164	NH1	A_ASP_163	OD1	3.114
6HS4	A_ARG_164	NH1	A_ASP_163	OD2	3.585
6HS4	A_ARG_266	NH2	A_ASP_237	OD2	3.211
6HS4	B_HIS_516	NE2	B_GLU_545	OE1	2.734
6HS4	B_ARG_559	NH1	A_GLU_103	OE1	2.624
6HS4	B_ARG_559	NH1	A_GLU_103	OE2	3.811
6HS4	B_ARG_559	NH2	A_GLU_103	OE1	3.176
6HS4	B_ARG_559	NH2	A_GLU_103	OE2	2.846
6HS4	B_LYS_588	NZ	A_ASP_47	OD1	3.053
6HS4	B_LYS_588	NZ	A_ASP_47	OD2	2.954

Table 34: 6HS4-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MAM	A_ARG_38	NH1	A_ASP_92	OD1	3.032
6MAM	A_ARG_38	NH2	A_GLU_46	OE1	3.455
6MAM	A_ARG_38	NH2	A_GLU_46	OE2	3.429
6MAM	A_ARG_50	NH1	A_ASP_61	OD2	2.812
6MAM	A_ARG_50	NH2	A_GLU_116	OE2	2.918
6MAM	A_ARG_69	NH1	A_ASP_92	OD2	2.800
6MAM	A_ARG_69	NH2	A_ASP_92	OD1	3.038
6MAM	A_ARG_69	NH2	A_ASP_92	OD2	2.756
6MAM	A_ARG_74	NH2	A_ASP_76	OD1	3.398
6MAM	A_LYS_78	NZ	A_ASP_75	OD2	3.612
6MAM	A_ARG_106	NH1	A_ASP_56	OD2	3.214
6MAM	A_ARG_106	NH2	A_ASP_56	OD1	3.431
6MAM	A_ARG_106	NH2	A_ASP_56	OD2	2.235
6MAM	A_LYS_161	NZ	A_ASP_162	OD1	2.861
6MAM	A_LYS_227	NZ	B_GLU_125	OE1	3.431
6MAM	A_LYS_228	NZ	A_GLU_230	OE1	2.933
6MAM	A_LYS_228	NZ	A_GLU_230	OE2	2.500
6MAM	B_ARG_3	NH1	B_ASP_1	OD1	3.296
6MAM	B_ARG_3	NH2	B_ASP_1	OD1	3.656
6MAM	B_ARG_24	NH2	B_ASP_70	OD1	3.387
6MAM	B_ARG_24	NH2	B_ASP_70	OD2	3.517
6MAM	B_ARG_61	NH2	B_GLU_81	OE2	3.262
6MAM	B_ARG_61	NH2	B_ASP_82	OD1	3.695
6MAM	B_LYS_105	NZ	B_GLU_167	OE1	2.898
6MAM	B_LYS_105	NZ	B_GLU_167	OE2	3.314
6MAM	B_LYS_151	NZ	B_GLU_197	OE1	2.860
6MAM	C_ARG_38	NH1	C_ASP_92	OD1	2.663
6MAM	C_ARG_38	NH2	C_GLU_46	OE1	3.453
6MAM	C_ARG_38	NH2	C_GLU_46	OE2	3.332
6MAM	C_ARG_38	NH2	C_ASP_92	OD1	3.874
6MAM	C_ARG_50	NH1	C_ASP_61	OD2	3.061
6MAM	C_ARG_69	NH1	C_ASP_92	OD2	2.947
6MAM	C_ARG_69	NH2	C_ASP_92	OD1	3.364
6MAM	C_ARG_69	NH2	C_ASP_92	OD2	2.722
6MAM	C_ARG_74	NH2	C_ASP_76	OD1	3.320
6MAM	C_LYS_78	NZ	C_ASP_75	OD2	3.377
6MAM	C_LYS_89	NZ	C_GLU_91	OE2	3.915
6MAM	C_ARG_106	NH2	C_ASP_56	OD1	3.976
6MAM	C_ARG_106	NH2	C_ASP_56	OD2	2.463
6MAM	C_LYS_161	NZ	C_ASP_162	OD1	2.840
6MAM	C_LYS_161	NZ	C_ASP_162	OD2	3.813
6MAM	C_HIS_182	NE2	D_ASP_169	OD2	3.087
6MAM	C_LYS_227	NZ	D_GLU_125	OE1	3.951
6MAM	D_ARG_3	NH1	D_ASP_1	OD1	3.278
6MAM	D_ARG_3	NH1	D_ASP_1	OD2	3.738
6MAM	D_ARG_3	NH2	D_ASP_1	OD1	2.805
6MAM	D_ARG_3	NH2	D_ASP_1	OD2	3.711
6MAM	D_ARG_61	NH2	D_GLU_81	OE2	3.528
6MAM	D_ARG_61	NH2	D_ASP_82	OD1	2.930
6MAM	D_ARG_61	NH2	D_ASP_82	OD2	3.239
6MAM	D_LYS_105	NZ	D_GLU_167	OE1	2.533
6MAM	D_LYS_105	NZ	D_GLU_167	OE2	3.413
6MAM	D_LYS_151	NZ	D_GLU_197	OE1	2.852
6MAM	D_HIS_191	ND1	D_ASP_153	OD2	2.884
6MAM	E_ARG_38	NH1	E_ASP_92	OD1	2.865
6MAM	E_ARG_38	NH2	E_GLU_46	OE1	3.478
6MAM	E_ARG_38	NH2	E_GLU_46	OE2	3.114

6MAM	E_ARG_38	NH2	E_ASP_92	OD1	3.571
6MAM	E_ARG_50	NH2	E_ASP_61	OD2	2.222
6MAM	E_ARG_69	NH1	E_ASP_92	OD2	3.919
6MAM	E_ARG_74	NH2	E_ASP_76	OD1	3.361
6MAM	E_LYS_78	NZ	E_ASP_75	OD2	3.911
6MAM	E_ARG_106	NH1	E_ASP_56	OD1	3.912
6MAM	E_ARG_106	NH1	E_ASP_56	OD2	2.681
6MAM	E_ARG_106	NH2	E_ASP_56	OD2	2.658
6MAM	E_LYS_161	NZ	E_ASP_162	OD1	2.972
6MAM	F_ARG_24	NH2	F_ASP_70	OD1	3.490
6MAM	F_ARG_24	NH2	F_ASP_70	OD2	3.587
6MAM	F_ARG_61	NH2	F_GLU_81	OE2	3.395
6MAM	F_ARG_61	NH2	F_ASP_82	OD1	2.777
6MAM	F_ARG_61	NH2	F_ASP_82	OD2	3.559
6MAM	F_LYS_105	NZ	F_GLU_167	OE1	3.155
6MAM	F_LYS_105	NZ	F_GLU_167	OE2	3.321
6MAM	F_LYS_128	NZ	F_GLU_125	OE1	3.556
6MAM	F_LYS_128	NZ	F_GLU_125	OE2	3.637
6MAM	F_LYS_151	NZ	F_GLU_197	OE1	2.889
6MAM	F_LYS_190	NZ	F_ASP_187	OD1	3.330
6MAM	G_ARG_85	NH1	G_GLU_178	OE1	3.649
6MAM	G_ARG_85	NH1	G_GLU_178	OE2	2.952
6MAM	G_LYS_114	NZ	G_GLU_120	OE2	3.654
6MAM	G_ARG_130	NH2	G_ASP_163	OD2	3.414
6MAM	G_HIS_154	NE2	G_GLU_178	OE1	2.787
6MAM	G_ARG_164	NH1	G_ASP_163	OD1	2.973
6MAM	G_ARG_164	NH1	G_ASP_163	OD2	3.775
6MAM	G_ARG_164	NH2	G_ASP_163	OD1	3.075
6MAM	G_ARG_164	NH2	G_ASP_163	OD2	2.437
6MAM	G_ARG_172	NH1	G_GLU_120	OE2	3.996
6MAM	H_HIS_516	NE2	H_GLU_545	OE1	2.716
6MAM	H_ARG_559	NH1	G_GLU_103	OE1	2.237
6MAM	H_ARG_559	NH1	G_GLU_103	OE2	3.123
6MAM	H_ARG_559	NH2	G_GLU_103	OE1	3.565
6MAM	H_ARG_559	NH2	G_GLU_103	OE2	2.826
6MAM	I_ARG_85	NH1	I_GLU_178	OE1	3.469
6MAM	I_ARG_85	NH1	I_GLU_178	OE2	2.648
6MAM	I_LYS_114	NZ	I_GLU_120	OE1	3.810
6MAM	I_LYS_114	NZ	I_GLU_120	OE2	3.218
6MAM	I_ARG_130	NH2	I_ASP_163	OD2	3.267
6MAM	I_HIS_154	NE2	I_GLU_178	OE1	2.764
6MAM	I_ARG_164	NH1	I_ASP_163	OD1	3.601
6MAM	I_ARG_164	NH1	I_ASP_163	OD2	2.921
6MAM	I_ARG_172	NH1	I_GLU_120	OE2	3.984
6MAM	J_HIS_516	NE2	J_GLU_545	OE1	2.735
6MAM	J_ARG_559	NH1	I_GLU_103	OE1	2.281
6MAM	J_ARG_559	NH1	I_GLU_103	OE2	3.223
6MAM	J_ARG_559	NH2	I_GLU_103	OE1	3.504
6MAM	J_ARG_559	NH2	I_GLU_103	OE2	2.826
6MAM	K_ARG_85	NH1	K_GLU_178	OE1	3.549
6MAM	K_ARG_85	NH1	K_GLU_178	OE2	2.788
6MAM	K_LYS_114	NZ	K_GLU_120	OE1	3.898
6MAM	K_LYS_114	NZ	K_GLU_120	OE2	3.320
6MAM	K_ARG_130	NH2	K_ASP_163	OD2	3.275
6MAM	K_HIS_154	NE2	K_GLU_178	OE1	3.032
6MAM	K_ARG_164	NH1	K_ASP_163	OD1	3.574
6MAM	K_ARG_164	NH1	K_ASP_163	OD2	2.908
6MAM	K_ARG_172	NH1	K_GLU_120	OE2	3.957

6MAM	L_HIS_516	NE2	L_GLU_545	OE1	2.681
6MAM	L_ARG_559	NH1	K_GLU_103	OE1	2.658
6MAM	L_ARG_559	NH1	K_GLU_103	OE2	3.420
6MAM	L_ARG_559	NH2	K_GLU_103	OE1	3.722
6MAM	L_ARG_559	NH2	K_GLU_103	OE2	2.995

Table 35: 6MAM-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NAE	A_HIS_39	NE2	A_ASP_55	OD1	2.745
6NAE	A_HIS_39	NE2	A_ASP_55	OD2	3.133
6NAE	A_ARG_85	NH1	A_GLU_178	OE1	3.501
6NAE	A_ARG_85	NH1	A_GLU_178	OE2	2.362
6NAE	A_ARG_130	NH2	A_ASP_163	OD2	3.231
6NAE	A_HIS_154	NE2	A_GLU_178	OE1	2.851
6NAE	A_ARG_164	NH1	A_ASP_163	OD1	3.478
6NAE	A_ARG_164	NH1	A_ASP_163	OD2	2.808
6NAE	A_ARG_172	NH1	A_GLU_120	OE2	3.850
6NAE	A_ARG_266	NH2	A_ASP_237	OD2	3.596
6NAE	B_LYS_510	NZ	A_GLU_292	OE1	2.350
6NAE	B_LYS_510	NZ	A_GLU_292	OE2	3.768
6NAE	B_HIS_516	NE2	B_GLU_545	OE1	2.507
6NAE	B_ARG_559	NH1	A_GLU_103	OE1	2.669
6NAE	B_ARG_559	NH1	A_GLU_103	OE2	3.739
6NAE	B_ARG_559	NH2	A_GLU_103	OE1	3.488
6NAE	B_ARG_559	NH2	A_GLU_103	OE2	3.068

Table 36: 6NAE-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6QD7	L_ARG_45	NH1	L_GLU_81	OE2	3.933
6QD7	L_ARG_61	NH1	L_GLU_79	OE1	3.350
6QD7	L_ARG_61	NH1	L_GLU_79	OE2	2.563
6QD7	L_ARG_61	NH2	L_GLU_79	OE1	3.628
6QD7	L_ARG_61	NH2	L_GLU_79	OE2	3.965
6QD7	L_ARG_61	NH2	L_GLU_81	OE1	3.504
6QD7	L_ARG_91	NH1	D_GLU_502	OE1	3.607
6QD7	L_ARG_91	NH2	L_GLU_50	OE1	3.410
6QD7	H_ARG_38	NH1	H_ASP_87	OD1	2.843
6QD7	H_LYS_65	NZ	D_ASP_552	OD1	3.151
6QD7	H_LYS_65	NZ	D_ASP_552	OD2	3.487
6QD7	H_ARG_67	NH1	H_ASP_87	OD1	3.877
6QD7	H_ARG_67	NH1	H_ASP_87	OD2	2.749
6QD7	H_ARG_67	NH2	H_ASP_87	OD1	3.605
6QD7	H_ARG_67	NH2	H_ASP_87	OD2	3.759
6QD7	H_LYS_95	NZ	H_ASP_106	OD1	2.959
6QD7	H_LYS_95	NZ	H_ASP_106	OD2	3.089
6QD7	H_ARG_101	NH1	D_GLU_564	OE1	3.838
6QD7	H_ARG_101	NH1	D_GLU_564	OE2	2.869
6QD7	H_ARG_101	NH2	D_GLU_502	OE1	3.497
6QD7	H_ARG_101	NH2	D_GLU_502	OE2	3.635
6QD7	H_ARG_101	NH2	D_GLU_564	OE1	3.061
6QD7	H_ARG_101	NH2	D_GLU_564	OE2	3.438
6QD7	A_ARG_64	NH2	A_ASP_192	OD1	3.858
6QD7	A_ARG_85	NH1	A_GLU_178	OE1	3.413
6QD7	A_ARG_85	NH1	A_GLU_178	OE2	3.024
6QD7	A_LYS_114	NZ	A_GLU_120	OE1	3.280
6QD7	A_ARG_130	NH2	A_ASP_163	OD1	3.286
6QD7	A_ARG_134	NH1	B_GLU_545	OE2	3.138
6QD7	A_HIS_154	ND1	A_GLU_156	OE1	3.400
6QD7	A_HIS_154	NE2	A_GLU_178	OE1	2.937
6QD7	A_ARG_164	NH1	A_ASP_163	OD1	3.712
6QD7	A_ARG_164	NH1	A_ASP_163	OD2	3.939
6QD7	B_ARG_559	NH1	A_GLU_103	OE1	2.604
6QD7	B_ARG_559	NH1	A_GLU_103	OE2	3.895
6QD7	B_ARG_559	NH2	A_GLU_103	OE1	3.220
6QD7	B_ARG_559	NH2	A_GLU_103	OE2	3.089
6QD7	B_ARG_587	NH2	B_GLU_578	OE2	3.922
6QD7	B_LYS_588	NZ	A_ASP_47	OD2	3.517
6QD7	B_HIS_602	ND1	F_GLU_611	OE2	2.318
6QD7	B_HIS_628	ND1	B_ASP_624	OD1	3.831
6QD7	B_HIS_628	NE2	B_ASP_624	OD1	2.455
6QD7	C_ARG_64	NH2	C_ASP_192	OD1	3.858
6QD7	C_ARG_85	NH1	C_GLU_178	OE1	3.413
6QD7	C_ARG_85	NH1	C_GLU_178	OE2	3.024
6QD7	C_LYS_114	NZ	C_GLU_120	OE1	3.281
6QD7	C_ARG_130	NH2	C_ASP_163	OD1	3.286
6QD7	C_ARG_134	NH1	D_GLU_545	OE2	3.066
6QD7	C_HIS_154	ND1	C_GLU_156	OE1	3.400
6QD7	C_HIS_154	NE2	C_GLU_178	OE1	2.937
6QD7	C_ARG_164	NH1	C_ASP_163	OD1	3.711
6QD7	C_ARG_164	NH1	C_ASP_163	OD2	3.938
6QD7	E_ARG_64	NH2	E_ASP_192	OD1	3.857
6QD7	E_ARG_85	NH1	E_GLU_178	OE1	3.413
6QD7	E_ARG_85	NH1	E_GLU_178	OE2	3.024
6QD7	E_LYS_114	NZ	E_GLU_120	OE1	3.279
6QD7	E_ARG_130	NH2	E_ASP_163	OD1	3.285

6QD7	E_ARG_134	NH1	F_GLU_545	OE2	2.931
6QD7	E_HIS_154	ND1	E_GLU_156	OE1	3.400
6QD7	E_HIS_154	NE2	E_GLU_178	OE1	2.937
6QD7	E_ARG_164	NH1	E_ASP_163	OD1	3.712
6QD7	E_ARG_164	NH1	E_ASP_163	OD2	3.939
6QD7	D_ARG_559	NH1	C_GLU_103	OE1	2.624
6QD7	D_ARG_559	NH1	C_GLU_103	OE2	3.858
6QD7	D_ARG_559	NH2	C_GLU_103	OE1	3.320
6QD7	D_ARG_559	NH2	C_GLU_103	OE2	3.132
6QD7	D_ARG_587	NH2	D_GLU_578	OE2	3.922
6QD7	D_LYS_588	NZ	C_ASP_47	OD2	3.598
6QD7	D_HIS_602	ND1	B_GLU_611	OE2	2.828
6QD7	D_HIS_628	ND1	D_ASP_624	OD1	3.831
6QD7	D_HIS_628	NE2	D_ASP_624	OD1	2.456
6QD7	F_ARG_559	NH1	E_GLU_103	OE1	2.462
6QD7	F_ARG_559	NH1	E_GLU_103	OE2	3.800
6QD7	F_ARG_559	NH2	E_GLU_103	OE1	3.090
6QD7	F_ARG_559	NH2	E_GLU_103	OE2	2.951
6QD7	F_ARG_587	NH2	F_GLU_578	OE2	3.922
6QD7	F_LYS_588	NZ	E_ASP_47	OD2	3.686
6QD7	F_HIS_602	ND1	D_GLU_611	OE2	2.771
6QD7	F_HIS_628	ND1	F_ASP_624	OD1	3.831
6QD7	F_HIS_628	NE2	F_ASP_624	OD1	2.455
6QD7	X_ARG_38	NH1	X_ASP_87	OD1	2.843
6QD7	X_LYS_65	NZ	F_ASP_552	OD1	3.082
6QD7	X_LYS_65	NZ	F_ASP_552	OD2	3.701
6QD7	X_ARG_67	NH1	X_ASP_87	OD1	3.876
6QD7	X_ARG_67	NH1	X_ASP_87	OD2	2.748
6QD7	X_ARG_67	NH2	X_ASP_87	OD1	3.604
6QD7	X_ARG_67	NH2	X_ASP_87	OD2	3.759
6QD7	X_LYS_95	NZ	X_ASP_106	OD1	2.959
6QD7	X_LYS_95	NZ	X_ASP_106	OD2	3.089
6QD7	X_ARG_101	NH1	F_GLU_564	OE1	3.893
6QD7	X_ARG_101	NH1	F_GLU_564	OE2	2.816
6QD7	X_ARG_101	NH2	F_GLU_502	OE1	3.631
6QD7	X_ARG_101	NH2	F_GLU_502	OE2	3.812
6QD7	X_ARG_101	NH2	F_GLU_564	OE1	3.108
6QD7	X_ARG_101	NH2	F_GLU_564	OE2	3.371
6QD7	U_ARG_38	NH1	U_ASP_87	OD1	2.842
6QD7	U_LYS_65	NZ	B_ASP_552	OD1	2.927
6QD7	U_LYS_65	NZ	B_ASP_552	OD2	3.579
6QD7	U_ARG_67	NH1	U_ASP_87	OD1	3.877
6QD7	U_ARG_67	NH1	U_ASP_87	OD2	2.749
6QD7	U_ARG_67	NH2	U_ASP_87	OD1	3.604
6QD7	U_ARG_67	NH2	U_ASP_87	OD2	3.760
6QD7	U_LYS_95	NZ	U_ASP_106	OD1	2.959
6QD7	U_LYS_95	NZ	U_ASP_106	OD2	3.089
6QD7	U_ARG_101	NH1	B_GLU_564	OE1	3.771
6QD7	U_ARG_101	NH1	B_GLU_564	OE2	2.902
6QD7	U_ARG_101	NH2	B_GLU_502	OE1	3.404
6QD7	U_ARG_101	NH2	B_GLU_502	OE2	3.473
6QD7	U_ARG_101	NH2	B_GLU_564	OE1	3.146
6QD7	U_ARG_101	NH2	B_GLU_564	OE2	3.609
6QD7	Z_ARG_45	NH1	Z_GLU_81	OE2	3.706
6QD7	Z_ARG_45	NH2	Z_GLU_81	OE2	3.775
6QD7	Z_ARG_61	NH1	Z_GLU_79	OE1	3.427
6QD7	Z_ARG_61	NH1	Z_GLU_79	OE2	2.720
6QD7	Z_ARG_61	NH2	Z_GLU_79	OE1	3.521

6QD7	Z_ARG_61	NH2	Z_GLU_81	OE1	3.408
6QD7	Z_ARG_61	NH2	Z_ASP_82	OD1	3.494
6QD7	Z_ARG_61	NH2	Z_ASP_82	OD2	2.754
6QD7	Z_ARG_91	NH1	F_GLU_502	OE1	3.548
6QD7	Z_ARG_91	NH2	Z_GLU_50	OE1	3.368
6QD7	P_ARG_45	NH1	P_GLU_81	OE2	3.704
6QD7	P_ARG_45	NH2	P_GLU_81	OE2	3.711
6QD7	P_ARG_61	NH1	P_GLU_79	OE1	3.312
6QD7	P_ARG_61	NH1	P_GLU_79	OE2	2.568
6QD7	P_ARG_61	NH2	P_GLU_79	OE1	3.625
6QD7	P_ARG_61	NH2	P_GLU_79	OE2	3.928
6QD7	P_ARG_61	NH2	P_GLU_81	OE1	3.239
6QD7	P_ARG_61	NH2	P_ASP_82	OD1	2.611
6QD7	P_ARG_61	NH2	P_ASP_82	OD2	3.516
6QD7	P_ARG_91	NH1	B_GLU_502	OE1	3.467
6QD7	P_ARG_91	NH2	P_GLU_50	OE1	3.343

Table 37: 6QD7-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6QD8	Z_LYS_39	NZ	Z_GLU_81	OE2	3.248
6QD8	Z_ARG_61	NH2	Z_ASP_82	OD1	2.630
6QD8	Z_ARG_61	NH2	Z_ASP_82	OD2	3.110
6QD8	Z_ARG_96	NH1	W_GLU_51	OE1	3.187
6QD8	Z_ARG_96	NH1	W_GLU_51	OE2	3.722
6QD8	A_ARG_64	NH2	B_ASP_522	OD2	3.626
6QD8	A_ARG_85	NH1	A_GLU_178	OE1	3.877
6QD8	A_ARG_85	NH1	A_GLU_178	OE2	3.145
6QD8	A_LYS_114	NZ	A_GLU_112	OE2	2.626
6QD8	A_LYS_114	NZ	A_GLU_120	OE2	3.220
6QD8	A_ARG_130	NH2	A_ASP_163	OD1	3.061
6QD8	A_ARG_134	NH1	B_GLU_545	OE2	3.117
6QD8	A_HIS_154	NE2	A_GLU_178	OE1	2.431
6QD8	A_ARG_266	NH2	A_ASP_237	OD2	3.394
6QD8	Y_LYS_39	NZ	Y_GLU_81	OE2	3.248
6QD8	Y_ARG_61	NH2	Y_ASP_82	OD1	2.630
6QD8	Y_ARG_61	NH2	Y_ASP_82	OD2	3.109
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE1	3.080
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE2	3.529
6QD8	B_ARG_559	NH1	A_GLU_103	OE1	3.695
6QD8	B_ARG_559	NH1	A_GLU_103	OE2	2.598
6QD8	B_ARG_559	NH2	A_GLU_103	OE1	3.315
6QD8	B_ARG_559	NH2	A_GLU_103	OE2	3.288
6QD8	B_HIS_602	ND1	F_GLU_611	OE2	3.837
6QD8	B_HIS_613	NE2	B_ASP_614	OD2	3.771
6QD8	L_LYS_39	NZ	L_GLU_81	OE2	3.248
6QD8	L_ARG_61	NH2	L_ASP_82	OD1	2.630
6QD8	L_ARG_61	NH2	L_ASP_82	OD2	3.110
6QD8	L_ARG_96	NH1	H_GLU_51	OE1	3.060
6QD8	L_ARG_96	NH1	H_GLU_51	OE2	3.554
6QD8	H_ARG_44	NH2	H_GLU_47	OE1	3.870
6QD8	H_ARG_55	NH1	B_GLU_564	OE1	2.303
6QD8	H_ARG_55	NH1	B_GLU_564	OE2	3.666
6QD8	H_LYS_76	NZ	H_ASP_73	OD2	2.834
6QD8	C_ARG_64	NH2	D_ASP_522	OD2	3.747
6QD8	C_ARG_85	NH1	C_GLU_178	OE1	3.878
6QD8	C_ARG_85	NH1	C_GLU_178	OE2	3.144
6QD8	C_LYS_114	NZ	C_GLU_112	OE2	2.626
6QD8	C_LYS_114	NZ	C_GLU_120	OE2	3.220
6QD8	C_ARG_130	NH2	C_ASP_163	OD1	3.061
6QD8	C_ARG_134	NH1	D_GLU_545	OE2	2.972
6QD8	C_HIS_154	NE2	C_GLU_178	OE1	2.430
6QD8	C_ARG_266	NH2	C_ASP_237	OD2	3.393
6QD8	E_ARG_64	NH2	F_ASP_522	OD2	3.901
6QD8	E_ARG_85	NH1	E_GLU_178	OE1	3.877
6QD8	E_ARG_85	NH1	E_GLU_178	OE2	3.145
6QD8	E_LYS_114	NZ	E_GLU_112	OE2	2.626
6QD8	E_LYS_114	NZ	E_GLU_120	OE2	3.220
6QD8	E_ARG_130	NH2	E_ASP_163	OD1	3.061
6QD8	E_ARG_134	NH1	F_GLU_545	OE2	2.891
6QD8	E_HIS_154	NE2	E_GLU_178	OE1	2.431
6QD8	E_ARG_266	NH2	E_ASP_237	OD2	3.393
6QD8	F_ARG_559	NH1	E_GLU_103	OE1	3.653
6QD8	F_ARG_559	NH1	E_GLU_103	OE2	2.383
6QD8	F_ARG_559	NH2	E_GLU_103	OE1	3.116
6QD8	F_ARG_559	NH2	E_GLU_103	OE2	2.960
6QD8	F_HIS_602	ND1	D_GLU_611	OE2	3.980

6QD8	F_HIS_613	NE2	F_ASP_614	OD2	3.772
6QD8	D_ARG_559	NH1	C_GLU_103	OE1	3.634
6QD8	D_ARG_559	NH1	C_GLU_103	OE2	2.515
6QD8	D_ARG_559	NH2	C_GLU_103	OE1	3.283
6QD8	D_ARG_559	NH2	C_GLU_103	OE2	3.254
6QD8	D_HIS_602	ND1	B_GLU_611	OE2	3.920
6QD8	D_HIS_613	NE2	D_ASP_614	OD2	3.772
6QD8	W_ARG_44	NH2	W_GLU_47	OE1	3.870
6QD8	W_ARG_55	NH1	F_GLU_564	OE1	2.296
6QD8	W_ARG_55	NH1	F_GLU_564	OE2	3.607
6QD8	W_LYS_76	NZ	W_ASP_73	OD2	2.835
6QD8	Q_ARG_44	NH2	Q_GLU_47	OE1	3.871
6QD8	Q_ARG_55	NH1	D_GLU_564	OE1	2.265
6QD8	Q_ARG_55	NH1	D_GLU_564	OE2	3.539
6QD8	Q_LYS_76	NZ	Q_ASP_73	OD2	2.836

Table 38: 6QD8-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8D	L_LYS_109	NZ	L_ASP_88	OD1	3.182
6S8D	H_ARG_30	NH2	P_ASP_104	OD2	3.844
6S8D	H_ARG_38	NH1	H_ASP_92	OD1	2.379
6S8D	H_LYS_78	NZ	H_ASP_75	OD1	3.645
6S8D	H_LYS_78	NZ	H_ASP_75	OD2	2.608
6S8D	A_ARG_85	NH1	A_GLU_178	OE1	3.862
6S8D	A_ARG_85	NH1	A_GLU_178	OE2	3.009
6S8D	A_ARG_130	NH2	A_ASP_163	OD2	3.703
6S8D	A_ARG_136	NH1	A_GLU_106	OE2	3.841
6S8D	A_HIS_154	NE2	A_GLU_178	OE1	2.356
6S8D	A_ARG_164	NH1	A_ASP_163	OD2	3.715
6S8D	B_ARG_559	NH1	A_GLU_103	OE1	3.375
6S8D	B_ARG_559	NH1	A_GLU_103	OE2	3.357
6S8D	B_ARG_559	NH2	A_GLU_103	OE1	3.329
6S8D	B_ARG_587	NH2	B_GLU_578	OE1	3.148
6S8D	B_ARG_596	NH2	A_ASP_55	OD2	3.730
6S8D	D_ARG_559	NH1	C_GLU_103	OE1	3.344
6S8D	D_ARG_559	NH1	C_GLU_103	OE2	3.304
6S8D	D_ARG_559	NH2	C_GLU_103	OE1	3.261
6S8D	D_ARG_559	NH2	C_GLU_103	OE2	3.986
6S8D	D_ARG_587	NH2	D_GLU_578	OE1	3.148
6S8D	D_ARG_596	NH2	C_ASP_55	OD2	3.794
6S8D	F_ARG_559	NH1	E_GLU_103	OE1	3.445
6S8D	F_ARG_559	NH1	E_GLU_103	OE2	3.366
6S8D	F_ARG_559	NH2	E_GLU_103	OE1	3.372
6S8D	F_ARG_587	NH2	F_GLU_578	OE1	3.148
6S8D	F_ARG_596	NH2	E_ASP_55	OD2	3.605
6S8D	O_LYS_109	NZ	O_ASP_88	OD1	3.182
6S8D	U_LYS_109	NZ	U_ASP_88	OD1	3.181
6S8D	C_ARG_85	NH1	C_GLU_178	OE1	3.862
6S8D	C_ARG_85	NH1	C_GLU_178	OE2	3.008
6S8D	C_ARG_130	NH2	C_ASP_163	OD2	3.703
6S8D	C_ARG_136	NH1	C_GLU_106	OE2	3.842
6S8D	C_HIS_154	NE2	C_GLU_178	OE1	2.356
6S8D	C_ARG_164	NH1	C_ASP_163	OD2	3.715
6S8D	E_ARG_85	NH1	E_GLU_178	OE1	3.862
6S8D	E_ARG_85	NH1	E_GLU_178	OE2	3.008
6S8D	E_LYS_114	NZ	Y_ASP_56	OD2	3.842
6S8D	E_ARG_130	NH2	E_ASP_163	OD2	3.703
6S8D	E_ARG_136	NH1	E_GLU_106	OE2	3.841
6S8D	E_HIS_154	NE2	E_GLU_178	OE1	2.357
6S8D	E_ARG_164	NH1	E_ASP_163	OD2	3.715
6S8D	P_ARG_30	NH2	Y_ASP_104	OD2	3.808
6S8D	P_ARG_38	NH1	P_ASP_92	OD1	2.379
6S8D	P_LYS_78	NZ	P_ASP_75	OD1	3.644
6S8D	P_LYS_78	NZ	P_ASP_75	OD2	2.608
6S8D	Y_ARG_30	NH2	H_ASP_104	OD2	3.626
6S8D	Y_ARG_38	NH1	Y_ASP_92	OD1	2.379
6S8D	Y_LYS_78	NZ	Y_ASP_75	OD1	3.645
6S8D	Y_LYS_78	NZ	Y_ASP_75	OD2	2.608

Table 39: 6S8D-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8I	L_ARG_57	NH1	L_ASP_63	OD1	3.936
6S8I	L_ARG_57	NH2	L_ASP_63	OD2	3.681
6S8I	L_ARG_64	NH2	L_ASP_85	OD1	3.247
6S8I	L_LYS_109	NZ	L_ASP_88	OD1	3.092
6S8I	L_LYS_109	NZ	L_ASP_88	OD2	3.761
6S8I	H_ARG_38	NH1	H_ASP_92	OD1	3.736
6S8I	H_ARG_50	NH2	H_GLU_61	OE1	3.922
6S8I	H_ARG_67	NH2	H_GLU_61	OE2	3.135
6S8I	H_ARG_69	NH2	H_ASP_92	OD1	2.684
6S8I	H_ARG_78	NH1	H_ASP_75	OD2	3.325
6S8I	H_ARG_105	NH1	L_GLU_102	OE1	3.601
6S8I	H_ARG_105	NH1	L_GLU_102	OE2	3.239
6S8I	H_ARG_105	NH2	L_GLU_102	OE2	2.950
6S8I	A_ARG_85	NH1	A_GLU_178	OE1	3.349
6S8I	A_ARG_85	NH1	A_GLU_178	OE2	2.593
6S8I	A_LYS_114	NZ	H_ASP_56	OD1	2.454
6S8I	A_LYS_114	NZ	H_ASP_56	OD2	2.783
6S8I	A_LYS_114	NZ	A_GLU_120	OE2	3.868
6S8I	A_ARG_134	NH1	B_GLU_545	OE2	3.078
6S8I	A_ARG_136	NH1	A_GLU_106	OE2	3.794
6S8I	A_LYS_140	NZ	A_GLU_112	OE2	3.972
6S8I	A_HIS_154	NE2	A_GLU_178	OE1	2.780
6S8I	A_ARG_164	NH1	A_ASP_163	OD1	3.922
6S8I	A_ARG_164	NH1	A_ASP_163	OD2	3.313
6S8I	B_ARG_559	NH1	A_GLU_103	OE1	3.895
6S8I	B_ARG_559	NH1	A_GLU_103	OE2	3.783
6S8I	B_ARG_559	NH2	A_GLU_103	OE1	3.282
6S8I	B_ARG_559	NH2	A_GLU_103	OE2	3.928
6S8I	B_ARG_596	NH2	A_ASP_55	OD1	3.671
6S8I	D_ARG_559	NH1	C_GLU_103	OE1	3.877
6S8I	D_ARG_559	NH1	C_GLU_103	OE2	3.822
6S8I	D_ARG_559	NH2	C_GLU_103	OE1	3.248
6S8I	D_ARG_559	NH2	C_GLU_103	OE2	3.953
6S8I	D_ARG_596	NH2	C_ASP_55	OD1	3.743
6S8I	F_ARG_559	NH1	E_GLU_103	OE1	3.975
6S8I	F_ARG_559	NH1	E_GLU_103	OE2	3.796
6S8I	F_ARG_559	NH2	E_GLU_103	OE1	3.335
6S8I	F_ARG_559	NH2	E_GLU_103	OE2	3.908
6S8I	F_ARG_596	NH2	E_ASP_55	OD1	3.553
6S8I	C_ARG_85	NH1	C_GLU_178	OE1	3.349
6S8I	C_ARG_85	NH1	C_GLU_178	OE2	2.593
6S8I	C_LYS_114	NZ	C_GLU_120	OE2	3.868
6S8I	C_LYS_114	NZ	P_ASP_56	OD1	2.515
6S8I	C_LYS_114	NZ	P_ASP_56	OD2	2.783
6S8I	C_ARG_134	NH1	D_GLU_545	OE2	3.135
6S8I	C_ARG_136	NH1	C_GLU_106	OE2	3.793
6S8I	C_LYS_140	NZ	C_GLU_112	OE2	3.972
6S8I	C_HIS_154	NE2	C_GLU_178	OE1	2.781
6S8I	C_ARG_164	NH1	C_ASP_163	OD1	3.921
6S8I	C_ARG_164	NH1	C_ASP_163	OD2	3.312
6S8I	E_ARG_85	NH1	E_GLU_178	OE1	3.349
6S8I	E_ARG_85	NH1	E_GLU_178	OE2	2.594
6S8I	E_LYS_114	NZ	E_GLU_120	OE2	3.868
6S8I	E_LYS_114	NZ	Y_ASP_56	OD1	2.476
6S8I	E_LYS_114	NZ	Y_ASP_56	OD2	2.735
6S8I	E_ARG_134	NH1	F_GLU_545	OE2	3.154
6S8I	E_ARG_136	NH1	E_GLU_106	OE2	3.794

6S8I	E_LYS_140	NZ	E_GLU_112	OE2	3.972
6S8I	E_HIS_154	NE2	E_GLU_178	OE1	2.779
6S8I	E_ARG_164	NH1	E_ASP_163	OD1	3.921
6S8I	E_ARG_164	NH1	E_ASP_163	OD2	3.313
6S8I	O_ARG_57	NH1	O_ASP_63	OD1	3.936
6S8I	O_ARG_57	NH2	O_ASP_63	OD2	3.681
6S8I	O_ARG_64	NH2	O_ASP_85	OD1	3.246
6S8I	O_LYS_109	NZ	O_ASP_88	OD1	3.092
6S8I	O_LYS_109	NZ	O_ASP_88	OD2	3.761
6S8I	U_ARG_57	NH1	U_ASP_63	OD1	3.937
6S8I	U_ARG_57	NH2	U_ASP_63	OD2	3.681
6S8I	U_ARG_64	NH2	U_ASP_85	OD1	3.247
6S8I	U_LYS_109	NZ	U_ASP_88	OD1	3.092
6S8I	U_LYS_109	NZ	U_ASP_88	OD2	3.761
6S8I	P_ARG_38	NH1	P_ASP_92	OD1	3.736
6S8I	P_ARG_50	NH2	P_GLU_61	OE1	3.922
6S8I	P_ARG_67	NH2	P_GLU_61	OE2	3.135
6S8I	P_ARG_69	NH2	P_ASP_92	OD1	2.683
6S8I	P_ARG_78	NH1	P_ASP_75	OD2	3.324
6S8I	P_ARG_105	NH1	O_GLU_102	OE1	3.789
6S8I	P_ARG_105	NH1	O_GLU_102	OE2	3.289
6S8I	P_ARG_105	NH2	O_GLU_102	OE2	3.143
6S8I	Y_ARG_38	NH1	Y_ASP_92	OD1	3.736
6S8I	Y_ARG_50	NH2	Y_GLU_61	OE1	3.922
6S8I	Y_ARG_67	NH2	Y_GLU_61	OE2	3.135
6S8I	Y_ARG_69	NH2	Y_ASP_92	OD1	2.683
6S8I	Y_ARG_78	NH1	Y_ASP_75	OD2	3.325
6S8I	Y_ARG_105	NH1	U_GLU_102	OE1	3.606
6S8I	Y_ARG_105	NH1	U_GLU_102	OE2	3.273
6S8I	Y_ARG_105	NH2	U_GLU_102	OE2	2.978

Table 40: 6S8I-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8J	L_ARG_57	NH1	L_ASP_63	OD1	3.597
6S8J	L_ARG_57	NH2	L_ASP_63	OD2	3.474
6S8J	L_ARG_64	NH2	L_ASP_85	OD1	3.929
6S8J	L_LYS_109	NZ	L_ASP_88	OD1	2.806
6S8J	L_LYS_109	NZ	L_ASP_88	OD2	3.179
6S8J	H_ARG_38	NH2	H_GLU_46	OE1	3.358
6S8J	H_ARG_69	NH1	H_ASP_92	OD1	3.693
6S8J	H_ARG_69	NH2	H_ASP_92	OD1	3.149
6S8J	H_ARG_69	NH2	H_ASP_92	OD2	3.494
6S8J	H_ARG_74	NH1	H_ASP_76	OD1	3.838
6S8J	H_ARG_74	NH1	H_ASP_76	OD2	3.202
6S8J	A_ARG_85	NH1	A_GLU_178	OE1	3.872
6S8J	A_ARG_85	NH1	A_GLU_178	OE2	2.923
6S8J	A_LYS_114	NZ	H_ASP_56	OD1	3.168
6S8J	A_LYS_114	NZ	H_ASP_56	OD2	2.312
6S8J	A_LYS_114	NZ	A_GLU_120	OE2	3.844
6S8J	A_ARG_134	NH1	B_GLU_545	OE2	2.814
6S8J	A_ARG_136	NH1	A_GLU_106	OE2	3.658
6S8J	A_HIS_154	NE2	A_GLU_178	OE1	2.462
6S8J	A_ARG_164	NH1	A_ASP_163	OD2	3.447
6S8J	B_ARG_559	NH1	A_GLU_103	OE1	3.955
6S8J	B_ARG_559	NH1	A_GLU_103	OE2	3.604
6S8J	B_ARG_559	NH2	A_GLU_103	OE1	3.443
6S8J	B_ARG_559	NH2	A_GLU_103	OE2	3.830
6S8J	B_ARG_596	NH2	A_ASP_55	OD1	2.986
6S8J	B_ARG_596	NH2	A_ASP_55	OD2	3.529
6S8J	O_ARG_57	NH1	O_ASP_63	OD1	3.597
6S8J	O_ARG_57	NH2	O_ASP_63	OD2	3.473
6S8J	O_ARG_64	NH2	O_ASP_85	OD1	3.931
6S8J	O_LYS_109	NZ	O_ASP_88	OD1	2.805
6S8J	O_LYS_109	NZ	O_ASP_88	OD2	3.179
6S8J	U_ARG_57	NH1	U_ASP_63	OD1	3.597
6S8J	U_ARG_57	NH2	U_ASP_63	OD2	3.473
6S8J	U_ARG_64	NH2	U_ASP_85	OD1	3.930
6S8J	U_LYS_109	NZ	U_ASP_88	OD1	2.806
6S8J	U_LYS_109	NZ	U_ASP_88	OD2	3.179
6S8J	D_ARG_559	NH1	C_GLU_103	OE1	3.872
6S8J	D_ARG_559	NH1	C_GLU_103	OE2	3.635
6S8J	D_ARG_559	NH2	C_GLU_103	OE1	3.272
6S8J	D_ARG_559	NH2	C_GLU_103	OE2	3.792
6S8J	D_ARG_596	NH2	C_ASP_55	OD1	2.928
6S8J	D_ARG_596	NH2	C_ASP_55	OD2	3.762
6S8J	D_HIS_602	ND1	B_GLU_611	OE1	3.866
6S8J	D_HIS_602	NE2	B_GLU_611	OE1	3.805
6S8J	D_HIS_602	NE2	B_GLU_611	OE2	3.737
6S8J	F_ARG_559	NH1	E_GLU_103	OE1	3.993
6S8J	F_ARG_559	NH1	E_GLU_103	OE2	3.748
6S8J	F_ARG_559	NH2	E_GLU_103	OE1	3.468
6S8J	F_ARG_559	NH2	E_GLU_103	OE2	3.952
6S8J	F_ARG_596	NH2	E_ASP_55	OD1	2.985
6S8J	F_ARG_596	NH2	E_ASP_55	OD2	3.707
6S8J	F_HIS_602	ND1	D_GLU_611	OE1	3.880
6S8J	F_HIS_602	NE2	D_GLU_611	OE2	3.765
6S8J	C_ARG_85	NH1	C_GLU_178	OE1	3.872
6S8J	C_ARG_85	NH1	C_GLU_178	OE2	2.922
6S8J	C_LYS_114	NZ	C_GLU_120	OE2	3.844
6S8J	C_LYS_114	NZ	P_ASP_56	OD1	3.173

6S8J	C_LYS_114	NZ	P_ASP_56	OD2	2.252
6S8J	C_ARG_134	NH1	D_GLU_545	OE2	2.837
6S8J	C_ARG_136	NH1	C_GLU_106	OE2	3.658
6S8J	C_HIS_154	NE2	C_GLU_178	OE1	2.463
6S8J	C_ARG_164	NH1	C_ASP_163	OD2	3.447
6S8J	E_ARG_85	NH1	E_GLU_178	OE1	3.872
6S8J	E_ARG_85	NH1	E_GLU_178	OE2	2.923
6S8J	E_LYS_114	NZ	E_GLU_120	OE2	3.844
6S8J	E_LYS_114	NZ	Y_ASP_56	OD1	3.177
6S8J	E_LYS_114	NZ	Y_ASP_56	OD2	2.185
6S8J	E_ARG_134	NH1	F_GLU_545	OE2	2.997
6S8J	E_ARG_136	NH1	E_GLU_106	OE2	3.659
6S8J	E_HIS_154	NE2	E_GLU_178	OE1	2.462
6S8J	E_ARG_164	NH1	E_ASP_163	OD2	3.447
6S8J	P_ARG_38	NH2	P_GLU_46	OE1	3.357
6S8J	P_ARG_69	NH1	P_ASP_92	OD1	3.693
6S8J	P_ARG_69	NH2	P_ASP_92	OD1	3.150
6S8J	P_ARG_69	NH2	P_ASP_92	OD2	3.494
6S8J	P_ARG_74	NH1	P_ASP_76	OD1	3.838
6S8J	P_ARG_74	NH1	P_ASP_76	OD2	3.202
6S8J	Y_ARG_38	NH2	Y_GLU_46	OE1	3.357
6S8J	Y_ARG_69	NH1	Y_ASP_92	OD1	3.693
6S8J	Y_ARG_69	NH2	Y_ASP_92	OD1	3.150
6S8J	Y_ARG_69	NH2	Y_ASP_92	OD2	3.494
6S8J	Y_ARG_74	NH1	Y_ASP_76	OD1	3.838
6S8J	Y_ARG_74	NH1	Y_ASP_76	OD2	3.202

Table 41: 6S8J-specific salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EBO	A_LYS_87	NZ	C_ASP_106	OD2	3.887
1EBO	A_HIS_112	ND1	B_GLU_77	OE1	3.658
1EBO	A_HIS_112	ND1	B_GLU_77	OE2	3.104
1EBO	B_HIS_112	ND1	C_GLU_77	OE1	3.068
1EBO	B_HIS_112	ND1	C_GLU_77	OE2	2.658
1EBO	C_LYS_7	NZ	B_GLU_9	OE1	3.472
1EBO	C_LYS_26	NZ	A_GLU_21	OE1	2.847
1EBO	C_LYS_26	NZ	A_GLU_21	OE2	3.880
1EBO	C_LYS_87	NZ	B_ASP_106	OD2	3.920
1EBO	D_HIS_112	ND1	E_GLU_77	OE1	3.490
1EBO	D_HIS_112	ND1	E_GLU_77	OE2	2.696
1EBO	E_LYS_26	NZ	F_GLU_21	OE2	3.162
1EBO	E_LYS_87	NZ	D_ASP_106	OD2	3.925
1EBO	F_LYS_26	NZ	D_GLU_21	OE1	3.927
1EBO	F_LYS_87	NZ	E_ASP_106	OD2	3.651
1EBO	F_HIS_112	ND1	D_GLU_77	OE2	3.188

Table 42: 1EBO-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2EBO	A_HIS_613	ND1	B_GLU_578	OE1	3.396
2EBO	A_HIS_613	ND1	B_GLU_578	OE2	3.211
2EBO	B_HIS_613	ND1	C_GLU_578	OE1	3.346
2EBO	B_HIS_613	ND1	C_GLU_578	OE2	2.789

Table 43: 2EBO-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QHR	H_LYS_143	NZ	L_GLU_125	OE2	2.743
2QHR	H_HIS_164	ND1	L_GLU_168	OE1	3.446
2QHR	H_HIS_164	ND1	L_GLU_168	OE2	2.691
2QHR	H_LYS_208	NZ	L_GLU_124	OE1	3.025
2QHR	H_LYS_208	NZ	L_GLU_124	OE2	3.278
2QHR	L_LYS_204	NZ	H_ASP_130	OD1	2.837
2QHR	L_LYS_204	NZ	H_ASP_130	OD2	3.813
2QHR	P_HIS_407	ND1	L_ASP_92	OD1	3.553
2QHR	P_ARG_409	NH1	H_ASP_33	OD2	2.967

Table 44: 2QHR-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y6S	C_ARG_100	NH1	D_GLU_50	OE1	2.758
2Y6S	D_LYS_208	NZ	C_GLU_127	OE1	3.225
2Y6S	H_LYS_208	NZ	L_GLU_127	OE1	3.152
2Y6S	L_ARG_100	NH1	H_GLU_50	OE1	2.759
2Y6S	L_ARG_100	NH2	H_GLU_50	OE1	3.945

Table 45: 2Y6S-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CSY	A_LYS_221	NZ	B_GLU_123	OE1	3.090
3CSY	A_LYS_221	NZ	B_GLU_123	OE2	3.307
3CSY	C_HIS_172	NE2	D_ASP_167	OD2	3.885
3CSY	C_LYS_221	NZ	D_GLU_123	OE1	3.258
3CSY	C_LYS_221	NZ	D_GLU_123	OE2	3.282
3CSY	E_LYS_221	NZ	F_GLU_123	OE1	3.238
3CSY	E_LYS_221	NZ	F_GLU_123	OE2	3.205
3CSY	G_HIS_172	NE2	H_ASP_167	OD2	3.733
3CSY	G_LYS_221	NZ	H_GLU_123	OE1	3.440
3CSY	G_LYS_221	NZ	H_GLU_123	OE2	3.445
3CSY	I_ARG_134	NH1	J_GLU_545	OE2	3.043
3CSY	J_ARG_559	NH2	I_GLU_103	OE1	3.261
3CSY	J_ARG_559	NH2	I_GLU_103	OE2	3.005
3CSY	K_ARG_134	NH1	L_GLU_545	OE2	3.181
3CSY	L_ARG_559	NH2	K_GLU_103	OE1	3.317
3CSY	L_ARG_559	NH2	K_GLU_103	OE2	3.156
3CSY	M_ARG_134	NH1	N_GLU_545	OE2	2.894
3CSY	N_ARG_559	NH2	M_GLU_103	OE1	2.925
3CSY	N_ARG_559	NH2	M_GLU_103	OE2	3.048
3CSY	O_ARG_134	NH1	P_GLU_545	OE2	3.026
3CSY	P_ARG_559	NH2	O_GLU_103	OE1	3.054
3CSY	P_ARG_559	NH2	O_GLU_103	OE2	2.808

Table 46: 3CSY-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3VE0	J_ARG_559	NH1	I_GLU_103	OE1	3.852
3VE0	J_ARG_559	NH1	I_GLU_103	OE2	3.848
3VE0	J_ARG_559	NH2	I_GLU_103	OE1	2.444
3VE0	J_ARG_559	NH2	I_GLU_103	OE2	2.766
3VE0	J_ARG_595	NH2	I_ASP_49	OD2	3.842
3VE0	J_ARG_596	NH1	I_ASP_55	OD1	3.003
3VE0	A_ARG_98	NH2	I_GLU_44	OE1	3.137
3VE0	A_ARG_98	NH2	I_GLU_44	OE2	3.008
3VE0	A_LYS_214	NZ	B_GLU_123	OE1	3.666
3VE0	A_LYS_214	NZ	B_GLU_123	OE2	2.624

Table 47: 3VE0-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5F1B	A_ARG_134	NH1	B_GLU_545	OE2	3.659
5F1B	B_ARG_559	NH1	A_GLU_103	OE1	3.219
5F1B	B_ARG_559	NH1	A_GLU_103	OE2	3.449
5F1B	B_ARG_559	NH2	A_GLU_103	OE1	3.928
5F1B	B_ARG_559	NH2	A_GLU_103	OE2	2.697
5F1B	B_LYS_588	NZ	A_ASP_47	OD1	3.551
5F1B	B_LYS_588	NZ	A_ASP_47	OD2	3.521

Table 48: 5F1B-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5FHC	J_ARG_559	NH2	K_GLU_103	OE1	3.531
5FHC	J_ARG_559	NH2	K_GLU_103	OE2	3.399
5FHC	K_ARG_134	NH1	J_GLU_545	OE2	2.861
5FHC	A_LYS_143	NZ	B_GLU_124	OE2	2.678
5FHC	A_LYS_209	NZ	B_GLU_123	OE1	2.702
5FHC	A_LYS_209	NZ	B_GLU_123	OE2	3.358
5FHC	H_LYS_209	NZ	L_GLU_123	OE1	3.238
5FHC	H_LYS_209	NZ	L_GLU_123	OE2	3.173

Table 49: 5FHC-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HJ3	D_LYS_510	NZ	J_GLU_55	OE1	3.743
5HJ3	D_LYS_510	NZ	J_GLU_55	OE2	3.493
5HJ3	D_ARG_559	NH2	C_GLU_103	OE1	2.496
5HJ3	D_ARG_559	NH2	C_GLU_103	OE2	2.573
5HJ3	E_LYS_221	NZ	F_GLU_123	OE2	3.658
5HJ3	H_LYS_510	NZ	F_GLU_55	OE2	3.815
5HJ3	H_ARG_559	NH2	G_GLU_103	OE1	2.521
5HJ3	H_ARG_559	NH2	G_GLU_103	OE2	2.719
5HJ3	I_HIS_172	NE2	J_ASP_167	OD2	3.705
5HJ3	I_LYS_221	NZ	J_GLU_123	OE1	3.253
5HJ3	I_LYS_221	NZ	J_GLU_123	OE2	2.800
5HJ3	L_ARG_559	NH2	K_GLU_103	OE1	2.680
5HJ3	L_ARG_559	NH2	K_GLU_103	OE2	2.484
5HJ3	L_HIS_602	ND1	H_GLU_611	OE1	3.679
5HJ3	L_HIS_602	NE2	H_GLU_611	OE1	3.945
5HJ3	M_LYS_221	NZ	N_GLU_123	OE1	3.397
5HJ3	M_LYS_221	NZ	N_GLU_123	OE2	3.011
5HJ3	P_LYS_510	NZ	B_GLU_55	OE1	3.843
5HJ3	P_LYS_510	NZ	B_GLU_55	OE2	3.553
5HJ3	P_ARG_559	NH2	O_GLU_103	OE1	2.547
5HJ3	P_ARG_559	NH2	O_GLU_103	OE2	2.625
5HJ3	P_HIS_602	NE2	L_GLU_611	OE1	3.277
5HJ3	A_LYS_221	NZ	B_GLU_123	OE1	3.583
5HJ3	A_LYS_221	NZ	B_GLU_123	OE2	3.404

Table 50: 5HJ3-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JNX	C_ARG_134	NH1	D_GLU_545	OE2	3.659
5JNX	D_ARG_559	NH1	C_GLU_103	OE1	3.220
5JNX	D_ARG_559	NH1	C_GLU_103	OE2	3.450
5JNX	D_ARG_559	NH2	C_GLU_103	OE1	3.927
5JNX	D_ARG_559	NH2	C_GLU_103	OE2	2.697
5JNX	D_LYS_588	NZ	C_ASP_47	OD1	3.551
5JNX	D_LYS_588	NZ	C_ASP_47	OD2	3.521
5JNX	E_ARG_134	NH1	F_GLU_545	OE2	3.660
5JNX	E_LYS_155	NZ	A_ASP_502	OD2	3.701
5JNX	F_ARG_559	NH1	E_GLU_103	OE1	3.219
5JNX	F_ARG_559	NH1	E_GLU_103	OE2	3.448
5JNX	F_ARG_559	NH2	E_GLU_103	OE1	3.927
5JNX	F_ARG_559	NH2	E_GLU_103	OE2	2.697
5JNX	F_LYS_588	NZ	E_ASP_47	OD1	3.552
5JNX	F_LYS_588	NZ	E_ASP_47	OD2	3.520
5JNX	G_ARG_134	NH1	H_GLU_545	OE2	3.659
5JNX	H_ARG_559	NH1	G_GLU_103	OE1	3.221
5JNX	H_ARG_559	NH1	G_GLU_103	OE2	3.449
5JNX	H_ARG_559	NH2	G_GLU_103	OE1	3.928
5JNX	H_ARG_559	NH2	G_GLU_103	OE2	2.697
5JNX	H_LYS_588	NZ	G_ASP_47	OD1	3.552
5JNX	H_LYS_588	NZ	G_ASP_47	OD2	3.522

Table 51: 5JNX-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQ3	B_ARG_559	NH1	A_GLU_103	OE1	2.754
5JQ3	B_ARG_559	NH1	A_GLU_103	OE2	3.830
5JQ3	B_ARG_559	NH2	A_GLU_103	OE1	3.362
5JQ3	B_ARG_559	NH2	A_GLU_103	OE2	2.945

Table 52: 5JQ3-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQ7	B_LYS_510	NZ	A_GLU_292	OE1	3.131
5JQ7	B_ARG_559	NH1	A_GLU_103	OE1	2.800
5JQ7	B_ARG_559	NH1	A_GLU_103	OE2	3.720
5JQ7	B_ARG_559	NH2	A_GLU_103	OE1	3.375
5JQ7	B_ARG_559	NH2	A_GLU_103	OE2	2.748

Table 53: 5JQ7-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JQB	B_LYS_510	NZ	A_GLU_292	OE1	2.746
5JQB	B_LYS_510	NZ	A_GLU_292	OE2	3.918
5JQB	B_ARG_559	NH1	A_GLU_103	OE1	2.703
5JQB	B_ARG_559	NH1	A_GLU_103	OE2	3.788
5JQB	B_ARG_559	NH2	A_GLU_103	OE1	3.188
5JQB	B_ARG_559	NH2	A_GLU_103	OE2	2.857
5JQB	B_LYS_588	NZ	A_ASP_47	OD1	3.558
5JQB	B_LYS_588	NZ	A_ASP_47	OD2	3.148

Table 54: 5JQB-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEL	A_ARG_130	NH1	B_GLU_540	OE2	3.053
5KEL	A_LYS_272	NZ	C_ASP_54	OD2	3.464
5KEL	A_LYS_272	NZ	C_ASP_56	OD2	2.595
5KEL	B_ARG_559	NH1	A_GLU_103	OE2	3.831
5KEL	B_ARG_559	NH2	A_GLU_103	OE1	3.279
5KEL	B_ARG_559	NH2	A_GLU_103	OE2	3.801
5KEL	E_ARG_130	NH1	G_GLU_540	OE2	3.054
5KEL	E_LYS_272	NZ	J_ASP_54	OD2	3.464
5KEL	E_LYS_272	NZ	J_ASP_56	OD2	2.596
5KEL	G_ARG_559	NH1	E_GLU_103	OE2	3.832
5KEL	G_ARG_559	NH2	E_GLU_103	OE1	3.279
5KEL	G_ARG_559	NH2	E_GLU_103	OE2	3.802
5KEL	F_ARG_130	NH1	I_GLU_540	OE2	3.053
5KEL	F_LYS_272	NZ	M_ASP_54	OD2	3.463
5KEL	F_LYS_272	NZ	M_ASP_56	OD2	2.596
5KEL	I_ARG_559	NH1	F_GLU_103	OE2	3.831
5KEL	I_ARG_559	NH2	F_GLU_103	OE1	3.279
5KEL	I_ARG_559	NH2	F_GLU_103	OE2	3.801

Table 55: 5KEL-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEM	A_LYS_272	NZ	D_ASP_54	OD1	2.876
5KEM	A_LYS_272	NZ	D_ASP_54	OD2	3.185
5KEM	F_LYS_272	NZ	I_ASP_54	OD1	2.876
5KEM	F_LYS_272	NZ	I_ASP_54	OD2	3.185

Table 56: 5KEM-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KEN	A_ARG_134	NH2	B_GLU_545	OE1	2.859
5KEN	B_LYS_510	NZ	D_GLU_56	OE1	3.639
5KEN	B_LYS_510	NZ	D_GLU_56	OE2	2.773
5KEN	B_HIS_549	NE2	C_ASP_52	OD1	3.874
5KEN	B_ARG_559	NH1	A_GLU_103	OE1	3.709
5KEN	B_ARG_559	NH1	A_GLU_103	OE2	2.818
5KEN	B_ARG_559	NH2	A_GLU_103	OE1	3.114
5KEN	B_ARG_559	NH2	A_GLU_103	OE2	3.662
5KEN	E_LYS_272	NZ	J_ASP_54	OD2	3.722
5KEN	E_LYS_272	NZ	J_ASP_56	OD1	3.736
5KEN	E_LYS_272	NZ	J_ASP_56	OD2	2.765
5KEN	F_LYS_510	NZ	H_GLU_56	OE2	2.720
5KEN	F_HIS_549	NE2	G_ASP_52	OD1	3.491
5KEN	F_ARG_559	NH1	E_GLU_103	OE1	3.868
5KEN	F_ARG_559	NH1	E_GLU_103	OE2	2.947
5KEN	F_ARG_559	NH2	E_GLU_103	OE1	3.043
5KEN	F_ARG_559	NH2	E_GLU_103	OE2	3.542
5KEN	G_LYS_62	NZ	H_ASP_1	OD2	2.735
5KEN	K_LYS_272	NZ	Q_ASP_54	OD2	3.814
5KEN	K_LYS_272	NZ	Q_ASP_56	OD1	3.710
5KEN	K_LYS_272	NZ	Q_ASP_56	OD2	2.769
5KEN	M_LYS_510	NZ	O_GLU_56	OE2	2.667
5KEN	M_ARG_559	NH1	K_GLU_103	OE1	3.708
5KEN	M_ARG_559	NH1	K_GLU_103	OE2	2.824
5KEN	M_ARG_559	NH2	K_GLU_103	OE1	3.090
5KEN	M_ARG_559	NH2	K_GLU_103	OE2	3.645
5KEN	N_LYS_62	NZ	O_ASP_1	OD2	2.793

Table 57: 5KEN-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DZL	G_HIS_96	ND1	J_GLU_55	OE2	3.342
6DZL	G_HIS_96	NE2	J_GLU_55	OE1	3.570
6DZL	G_HIS_96	NE2	J_GLU_55	OE2	3.728
6DZL	H_HIS_96	ND1	K_GLU_55	OE2	3.341
6DZL	H_HIS_96	NE2	K_GLU_55	OE1	3.571
6DZL	H_HIS_96	NE2	K_GLU_55	OE2	3.727
6DZL	I_HIS_96	ND1	L_GLU_55	OE2	3.341
6DZL	I_HIS_96	NE2	L_GLU_55	OE1	3.571
6DZL	I_HIS_96	NE2	L_GLU_55	OE2	3.727

Table 58: 6DZL-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EA7	B_ARG_559	NH1	A_GLU_103	OE1	2.641
6EA7	B_ARG_559	NH1	A_GLU_103	OE2	3.432
6EA7	B_ARG_559	NH2	A_GLU_103	OE2	3.686
6EA7	B_HIS_602	ND1	F_GLU_611	OE1	3.135
6EA7	D_ARG_559	NH1	C_GLU_103	OE1	2.573
6EA7	D_ARG_559	NH1	C_GLU_103	OE2	3.488
6EA7	D_ARG_559	NH2	C_GLU_103	OE1	3.832
6EA7	D_ARG_559	NH2	C_GLU_103	OE2	3.318
6EA7	D_HIS_602	ND1	B_GLU_611	OE1	3.062
6EA7	F_ARG_559	NH1	E_GLU_103	OE1	2.812
6EA7	F_ARG_559	NH1	E_GLU_103	OE2	3.584
6EA7	F_ARG_559	NH2	E_GLU_103	OE2	3.608
6EA7	F_ARG_596	NH2	E_ASP_55	OD1	2.483
6EA7	F_ARG_596	NH2	E_ASP_55	OD2	3.342
6EA7	F_HIS_602	ND1	D_GLU_611	OE1	3.253
6EA7	H_HIS_100	ND1	L_GLU_55	OE1	3.325
6EA7	H_HIS_100	NE2	L_GLU_55	OE1	3.655
6EA7	H_HIS_108	NE2	L_ASP_50	OD1	2.912
6EA7	H_HIS_173	ND1	L_ASP_166	OD1	3.947
6EA7	H_HIS_173	ND1	L_ASP_166	OD2	3.590
6EA7	H_LYS_218	NZ	L_GLU_122	OE1	2.826
6EA7	M_HIS_100	ND1	N_GLU_55	OE1	3.446
6EA7	M_HIS_100	ND1	N_GLU_55	OE2	3.681
6EA7	M_HIS_108	ND1	N_ASP_50	OD1	3.757
6EA7	M_HIS_108	NE2	N_ASP_50	OD1	3.718
6EA7	M_HIS_173	ND1	N_ASP_166	OD2	3.701
6EA7	Q_HIS_108	NE2	R_ASP_50	OD1	3.227
6EA7	Q_HIS_173	ND1	R_ASP_166	OD1	3.817
6EA7	Q_HIS_173	ND1	R_ASP_166	OD2	3.600

Table 59: 6EA7-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F5U	B_LYS_510	NZ	A_GLU_292	OE1	3.345
6F5U	B_ARG_559	NH1	A_GLU_103	OE1	2.631
6F5U	B_ARG_559	NH1	A_GLU_103	OE2	3.833
6F5U	B_ARG_559	NH2	A_GLU_103	OE1	3.290
6F5U	B_ARG_559	NH2	A_GLU_103	OE2	2.992

Table 60: 6F5U-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6I	B_LYS_510	NZ	A_GLU_292	OE1	3.377
6F6I	B_ARG_559	NH1	A_GLU_103	OE1	3.800
6F6I	B_ARG_559	NH1	A_GLU_103	OE2	2.815
6F6I	B_ARG_559	NH2	A_GLU_103	OE1	3.096
6F6I	B_ARG_559	NH2	A_GLU_103	OE2	3.529

Table 61: 6F6I-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6N	B_LYS_510	NZ	A_GLU_292	OE1	2.639
6F6N	B_ARG_559	NH1	A_GLU_103	OE1	2.593
6F6N	B_ARG_559	NH1	A_GLU_103	OE2	3.789
6F6N	B_ARG_559	NH2	A_GLU_103	OE1	3.215
6F6N	B_ARG_559	NH2	A_GLU_103	OE2	2.904
6F6N	B_LYS_588	NZ	A_ASP_47	OD1	3.696
6F6N	B_LYS_588	NZ	A_ASP_47	OD2	2.975

Table 62: 6F6N-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6F6S	B_LYS_510	NZ	A_GLU_292	OE1	2.331
6F6S	B_LYS_510	NZ	A_GLU_292	OE2	3.397
6F6S	B_ARG_559	NH1	A_GLU_103	OE1	2.656
6F6S	B_ARG_559	NH1	A_GLU_103	OE2	3.920
6F6S	B_ARG_559	NH2	A_GLU_103	OE1	3.146
6F6S	B_ARG_559	NH2	A_GLU_103	OE2	2.951
6F6S	B_LYS_588	NZ	A_ASP_47	OD1	2.944
6F6S	B_LYS_588	NZ	A_ASP_47	OD2	2.772

Table 63: 6F6S-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G95	B_ARG_559	NH1	A_GLU_103	OE1	2.683
6G95	B_ARG_559	NH1	A_GLU_103	OE2	3.879
6G95	B_ARG_559	NH2	A_GLU_103	OE1	3.249
6G95	B_ARG_559	NH2	A_GLU_103	OE2	2.973

Table 64: 6G95-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G9B	B_LYS_510	NZ	A_GLU_292	OE1	3.414
6G9B	B_ARG_559	NH1	A_GLU_103	OE1	2.574
6G9B	B_ARG_559	NH1	A_GLU_103	OE2	3.760
6G9B	B_ARG_559	NH2	A_GLU_103	OE1	3.199
6G9B	B_ARG_559	NH2	A_GLU_103	OE2	2.870
6G9B	B_LYS_588	NZ	A_ASP_47	OD1	3.317
6G9B	B_LYS_588	NZ	A_ASP_47	OD2	2.892

Table 65: 6G9B-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6G9I	B_ARG_559	NH1	A_GLU_103	OE1	2.689
6G9I	B_ARG_559	NH1	A_GLU_103	OE2	3.794
6G9I	B_ARG_559	NH2	A_GLU_103	OE1	3.340
6G9I	B_ARG_559	NH2	A_GLU_103	OE2	2.940

Table 66: 6G9I-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6HRO	B_LYS_510	NZ	A_GLU_292	OE1	3.852
6HRO	B_ARG_559	NH1	A_GLU_103	OE1	2.817
6HRO	B_ARG_559	NH1	A_GLU_103	OE2	3.911
6HRO	B_ARG_559	NH2	A_GLU_103	OE1	3.514
6HRO	B_ARG_559	NH2	A_GLU_103	OE2	3.164
6HRO	B_LYS_588	NZ	A_ASP_47	OD1	3.207
6HRO	B_LYS_588	NZ	A_ASP_47	OD2	2.778

Table 67: 6HRO-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6HS4	B_ARG_559	NH1	A_GLU_103	OE1	2.624
6HS4	B_ARG_559	NH1	A_GLU_103	OE2	3.811
6HS4	B_ARG_559	NH2	A_GLU_103	OE1	3.176
6HS4	B_ARG_559	NH2	A_GLU_103	OE2	2.846
6HS4	B_LYS_588	NZ	A_ASP_47	OD1	3.053
6HS4	B_LYS_588	NZ	A_ASP_47	OD2	2.954

Table 68: 6HS4-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MAM	A_LYS_227	NZ	B_GLU_125	OE1	3.431
6MAM	C_HIS_182	NE2	D_ASP_169	OD2	3.087
6MAM	C_LYS_227	NZ	D_GLU_125	OE1	3.951
6MAM	H_ARG_559	NH1	G_GLU_103	OE1	2.237
6MAM	H_ARG_559	NH1	G_GLU_103	OE2	3.123
6MAM	H_ARG_559	NH2	G_GLU_103	OE1	3.565
6MAM	H_ARG_559	NH2	G_GLU_103	OE2	2.826
6MAM	J_ARG_559	NH1	I_GLU_103	OE1	2.281
6MAM	J_ARG_559	NH1	I_GLU_103	OE2	3.223
6MAM	J_ARG_559	NH2	I_GLU_103	OE1	3.504
6MAM	J_ARG_559	NH2	I_GLU_103	OE2	2.826
6MAM	L_ARG_559	NH1	K_GLU_103	OE1	2.658
6MAM	L_ARG_559	NH1	K_GLU_103	OE2	3.420
6MAM	L_ARG_559	NH2	K_GLU_103	OE1	3.722
6MAM	L_ARG_559	NH2	K_GLU_103	OE2	2.995

Table 69: 6MAM-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NAE	B_LYS_510	NZ	A_GLU_292	OE1	2.350
6NAE	B_LYS_510	NZ	A_GLU_292	OE2	3.768
6NAE	B_ARG_559	NH1	A_GLU_103	OE1	2.669
6NAE	B_ARG_559	NH1	A_GLU_103	OE2	3.739
6NAE	B_ARG_559	NH2	A_GLU_103	OE1	3.488
6NAE	B_ARG_559	NH2	A_GLU_103	OE2	3.068

Table 70: 6NAE-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6QD7	L_ARG_91	NH1	D_GLU_502	OE1	3.607
6QD7	H_LYS_65	NZ	D_ASP_552	OD1	3.151
6QD7	H_LYS_65	NZ	D_ASP_552	OD2	3.487
6QD7	H_ARG_101	NH1	D_GLU_564	OE1	3.838
6QD7	H_ARG_101	NH1	D_GLU_564	OE2	2.869
6QD7	H_ARG_101	NH2	D_GLU_502	OE1	3.497
6QD7	H_ARG_101	NH2	D_GLU_502	OE2	3.635
6QD7	H_ARG_101	NH2	D_GLU_564	OE1	3.061
6QD7	H_ARG_101	NH2	D_GLU_564	OE2	3.438
6QD7	A_ARG_134	NH1	B_GLU_545	OE2	3.138
6QD7	B_ARG_559	NH1	A_GLU_103	OE1	2.604
6QD7	B_ARG_559	NH1	A_GLU_103	OE2	3.895
6QD7	B_ARG_559	NH2	A_GLU_103	OE1	3.220
6QD7	B_ARG_559	NH2	A_GLU_103	OE2	3.089
6QD7	B_LYS_588	NZ	A_ASP_47	OD2	3.517
6QD7	B_HIS_602	ND1	F_GLU_611	OE2	2.318
6QD7	C_ARG_134	NH1	D_GLU_545	OE2	3.066
6QD7	E_ARG_134	NH1	F_GLU_545	OE2	2.931
6QD7	D_ARG_559	NH1	C_GLU_103	OE1	2.624
6QD7	D_ARG_559	NH1	C_GLU_103	OE2	3.858
6QD7	D_ARG_559	NH2	C_GLU_103	OE1	3.320
6QD7	D_ARG_559	NH2	C_GLU_103	OE2	3.132
6QD7	D_LYS_588	NZ	C_ASP_47	OD2	3.598
6QD7	D_HIS_602	ND1	B_GLU_611	OE2	2.828
6QD7	F_ARG_559	NH1	E_GLU_103	OE1	2.462
6QD7	F_ARG_559	NH1	E_GLU_103	OE2	3.800
6QD7	F_ARG_559	NH2	E_GLU_103	OE1	3.090
6QD7	F_ARG_559	NH2	E_GLU_103	OE2	2.951
6QD7	F_LYS_588	NZ	E_ASP_47	OD2	3.686
6QD7	F_HIS_602	ND1	D_GLU_611	OE2	2.771
6QD7	X_LYS_65	NZ	F_ASP_552	OD1	3.082
6QD7	X_LYS_65	NZ	F_ASP_552	OD2	3.701
6QD7	X_ARG_101	NH1	F_GLU_564	OE1	3.893
6QD7	X_ARG_101	NH1	F_GLU_564	OE2	2.816
6QD7	X_ARG_101	NH2	F_GLU_502	OE1	3.631
6QD7	X_ARG_101	NH2	F_GLU_502	OE2	3.812
6QD7	X_ARG_101	NH2	F_GLU_564	OE1	3.108
6QD7	X_ARG_101	NH2	F_GLU_564	OE2	3.371
6QD7	U_LYS_65	NZ	B_ASP_552	OD1	2.927
6QD7	U_LYS_65	NZ	B_ASP_552	OD2	3.579
6QD7	U_ARG_101	NH1	B_GLU_564	OE1	3.771
6QD7	U_ARG_101	NH1	B_GLU_564	OE2	2.902
6QD7	U_ARG_101	NH2	B_GLU_502	OE1	3.404
6QD7	U_ARG_101	NH2	B_GLU_502	OE2	3.473
6QD7	U_ARG_101	NH2	B_GLU_564	OE1	3.146
6QD7	U_ARG_101	NH2	B_GLU_564	OE2	3.609
6QD7	Z_ARG_91	NH1	F_GLU_502	OE1	3.548
6QD7	P_ARG_91	NH1	B_GLU_502	OE1	3.467

Table 71: 6QD7-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6QD8	Z_ARG_96	NH1	W_GLU_51	OE1	3.187
6QD8	Z_ARG_96	NH1	W_GLU_51	OE2	3.722
6QD8	A_ARG_64	NH2	B_ASP_522	OD2	3.626
6QD8	A_ARG_134	NH1	B_GLU_545	OE2	3.117
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE1	3.080
6QD8	Y_ARG_96	NH1	Q_GLU_51	OE2	3.529
6QD8	B_ARG_559	NH1	A_GLU_103	OE1	3.695
6QD8	B_ARG_559	NH1	A_GLU_103	OE2	2.598
6QD8	B_ARG_559	NH2	A_GLU_103	OE1	3.315
6QD8	B_ARG_559	NH2	A_GLU_103	OE2	3.288
6QD8	B_HIS_602	ND1	F_GLU_611	OE2	3.837
6QD8	L_ARG_96	NH1	H_GLU_51	OE1	3.060
6QD8	L_ARG_96	NH1	H_GLU_51	OE2	3.554
6QD8	H_ARG_55	NH1	B_GLU_564	OE1	2.303
6QD8	H_ARG_55	NH1	B_GLU_564	OE2	3.666
6QD8	C_ARG_64	NH2	D_ASP_522	OD2	3.747
6QD8	C_ARG_134	NH1	D_GLU_545	OE2	2.972
6QD8	E_ARG_64	NH2	F_ASP_522	OD2	3.901
6QD8	E_ARG_134	NH1	F_GLU_545	OE2	2.891
6QD8	F_ARG_559	NH1	E_GLU_103	OE1	3.653
6QD8	F_ARG_559	NH1	E_GLU_103	OE2	2.383
6QD8	F_ARG_559	NH2	E_GLU_103	OE1	3.116
6QD8	F_ARG_559	NH2	E_GLU_103	OE2	2.960
6QD8	F_HIS_602	ND1	D_GLU_611	OE2	3.980
6QD8	D_ARG_559	NH1	C_GLU_103	OE1	3.634
6QD8	D_ARG_559	NH1	C_GLU_103	OE2	2.515
6QD8	D_ARG_559	NH2	C_GLU_103	OE1	3.283
6QD8	D_ARG_559	NH2	C_GLU_103	OE2	3.254
6QD8	D_HIS_602	ND1	B_GLU_611	OE2	3.920
6QD8	W_ARG_55	NH1	F_GLU_564	OE1	2.296
6QD8	W_ARG_55	NH1	F_GLU_564	OE2	3.607
6QD8	Q_ARG_55	NH1	D_GLU_564	OE1	2.265
6QD8	Q_ARG_55	NH1	D_GLU_564	OE2	3.539

Table 72: 6QD8-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8D	H_ARG_30	NH2	P_ASP_104	OD2	3.844
6S8D	B_ARG_559	NH1	A_GLU_103	OE1	3.375
6S8D	B_ARG_559	NH1	A_GLU_103	OE2	3.357
6S8D	B_ARG_559	NH2	A_GLU_103	OE1	3.329
6S8D	B_ARG_596	NH2	A_ASP_55	OD2	3.730
6S8D	D_ARG_559	NH1	C_GLU_103	OE1	3.344
6S8D	D_ARG_559	NH1	C_GLU_103	OE2	3.304
6S8D	D_ARG_559	NH2	C_GLU_103	OE1	3.261
6S8D	D_ARG_559	NH2	C_GLU_103	OE2	3.986
6S8D	D_ARG_596	NH2	C_ASP_55	OD2	3.794
6S8D	F_ARG_559	NH1	E_GLU_103	OE1	3.445
6S8D	F_ARG_559	NH1	E_GLU_103	OE2	3.366
6S8D	F_ARG_559	NH2	E_GLU_103	OE1	3.372
6S8D	F_ARG_596	NH2	E_ASP_55	OD2	3.605
6S8D	E_LYS_114	NZ	Y_ASP_56	OD2	3.842
6S8D	P_ARG_30	NH2	Y_ASP_104	OD2	3.808
6S8D	Y_ARG_30	NH2	H_ASP_104	OD2	3.626

Table 73: 6S8D-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8I	H_ARG_105	NH1	L_GLU_102	OE1	3.601
6S8I	H_ARG_105	NH1	L_GLU_102	OE2	3.239
6S8I	H_ARG_105	NH2	L_GLU_102	OE2	2.950
6S8I	A_LYS_114	NZ	H_ASP_56	OD1	2.454
6S8I	A_LYS_114	NZ	H_ASP_56	OD2	2.783
6S8I	A_ARG_134	NH1	B_GLU_545	OE2	3.078
6S8I	B_ARG_559	NH1	A_GLU_103	OE1	3.895
6S8I	B_ARG_559	NH1	A_GLU_103	OE2	3.783
6S8I	B_ARG_559	NH2	A_GLU_103	OE1	3.282
6S8I	B_ARG_559	NH2	A_GLU_103	OE2	3.928
6S8I	B_ARG_596	NH2	A_ASP_55	OD1	3.671
6S8I	D_ARG_559	NH1	C_GLU_103	OE1	3.877
6S8I	D_ARG_559	NH1	C_GLU_103	OE2	3.822
6S8I	D_ARG_559	NH2	C_GLU_103	OE1	3.248
6S8I	D_ARG_559	NH2	C_GLU_103	OE2	3.953
6S8I	D_ARG_596	NH2	C_ASP_55	OD1	3.743
6S8I	F_ARG_559	NH1	E_GLU_103	OE1	3.975
6S8I	F_ARG_559	NH1	E_GLU_103	OE2	3.796
6S8I	F_ARG_559	NH2	E_GLU_103	OE1	3.335
6S8I	F_ARG_559	NH2	E_GLU_103	OE2	3.908
6S8I	F_ARG_596	NH2	E_ASP_55	OD1	3.553
6S8I	C_LYS_114	NZ	P_ASP_56	OD1	2.515
6S8I	C_LYS_114	NZ	P_ASP_56	OD2	2.783
6S8I	C_ARG_134	NH1	D_GLU_545	OE2	3.135
6S8I	E_LYS_114	NZ	Y_ASP_56	OD1	2.476
6S8I	E_LYS_114	NZ	Y_ASP_56	OD2	2.735
6S8I	E_ARG_134	NH1	F_GLU_545	OE2	3.154
6S8I	P_ARG_105	NH1	O_GLU_102	OE1	3.789
6S8I	P_ARG_105	NH1	O_GLU_102	OE2	3.289
6S8I	P_ARG_105	NH2	O_GLU_102	OE2	3.143
6S8I	Y_ARG_105	NH1	U_GLU_102	OE1	3.606
6S8I	Y_ARG_105	NH1	U_GLU_102	OE2	3.273
6S8I	Y_ARG_105	NH2	U_GLU_102	OE2	2.978

Table 74: 6S8I-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S8J	A_LYS_114	NZ	H_ASP_56	OD1	3.168
6S8J	A_LYS_114	NZ	H_ASP_56	OD2	2.312
6S8J	A_ARG_134	NH1	B_GLU_545	OE2	2.814
6S8J	B_ARG_559	NH1	A_GLU_103	OE1	3.955
6S8J	B_ARG_559	NH1	A_GLU_103	OE2	3.604
6S8J	B_ARG_559	NH2	A_GLU_103	OE1	3.443
6S8J	B_ARG_559	NH2	A_GLU_103	OE2	3.830
6S8J	B_ARG_596	NH2	A_ASP_55	OD1	2.986
6S8J	B_ARG_596	NH2	A_ASP_55	OD2	3.529
6S8J	D_ARG_559	NH1	C_GLU_103	OE1	3.872
6S8J	D_ARG_559	NH1	C_GLU_103	OE2	3.635
6S8J	D_ARG_559	NH2	C_GLU_103	OE1	3.272
6S8J	D_ARG_559	NH2	C_GLU_103	OE2	3.792
6S8J	D_ARG_596	NH2	C_ASP_55	OD1	2.928
6S8J	D_ARG_596	NH2	C_ASP_55	OD2	3.762
6S8J	D_HIS_602	ND1	B_GLU_611	OE1	3.866
6S8J	D_HIS_602	NE2	B_GLU_611	OE1	3.805
6S8J	D_HIS_602	NE2	B_GLU_611	OE2	3.737
6S8J	F_ARG_559	NH1	E_GLU_103	OE1	3.993
6S8J	F_ARG_559	NH1	E_GLU_103	OE2	3.748
6S8J	F_ARG_559	NH2	E_GLU_103	OE1	3.468
6S8J	F_ARG_559	NH2	E_GLU_103	OE2	3.952
6S8J	F_ARG_596	NH2	E_ASP_55	OD1	2.985
6S8J	F_ARG_596	NH2	E_ASP_55	OD2	3.707
6S8J	F_HIS_602	ND1	D_GLU_611	OE1	3.880
6S8J	F_HIS_602	NE2	D_GLU_611	OE2	3.765
6S8J	C_LYS_114	NZ	P_ASP_56	OD1	3.173
6S8J	C_LYS_114	NZ	P_ASP_56	OD2	2.252
6S8J	C_ARG_134	NH1	D_GLU_545	OE2	2.837
6S8J	E_LYS_114	NZ	Y_ASP_56	OD1	3.177
6S8J	E_LYS_114	NZ	Y_ASP_56	OD2	2.185
6S8J	E_ARG_134	NH1	F_GLU_545	OE2	2.997

Table 75: 6S8J-specific interfacial salt bridging network analysis. In this table, the residue naming scheme is **Chain ID_residue name_residue number**

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-1.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.51	1.63	20.85
2RLJ-11.PDB	O, A_TRP_8	N, A_TYR_11	H, A_TYR_11	2.98	2.09	19.25
2RLJ-11.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.62	1.69	14.63
2RLJ-12.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.59	1.69	19.30
2RLJ-13.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.63	1.78	24.81
2RLJ-14.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.62	8.91
2RLJ-15.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.69	20.08
2RLJ-16.PDB	O, A_ILE_9	N, A_GLY_13	H, A_GLY_13	2.99	2.03	10.52
2RLJ-19.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.73	1.89	26.29

Table 76: 2RLJ-1-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
2RLJ-11.PDB	O, A_TRP_8	N, A_TYR_11	H, A_TYR_11	2.98	2.09	19.25
2RLJ-11.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.62	1.69	14.63

Table 77: 2RLJ-11-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-12.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.59	1.69	19.30

Table 78: 2RLJ-12-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-13.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.63	1.78	24.81

Table 79: 2RLJ-13-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-14.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.62	8.91

Table 80: 2RLJ-14-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-15.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.69	20.08

Table 81: 2RLJ-15-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
2RLJ-16.PDB	O, A_ILE_9	N, A_GLY_13	H, A_GLY_13	2.99	2.03	10.52

Table 82: 2RLJ-16-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-19.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.73	1.89	26.29

Table 83: 2RLJ-19-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-2.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.58	1.69	19.33

Table 84: 2RLJ-2-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-3.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.54	1.66	20.38

Table 85: 2RLJ-3-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
2RLJ-4.PDB	O, A_TRP_8	N, A_TYR_11	H, A_TYR_11	2.94	2.08	23.85

Table 86: 2RLJ-4-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-5.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.60	1.76	25.80
2RLJ-5.PDB	O, A_PRO_10	N, A_GLY_13	H, A_GLY_13	2.75	1.88	22.12

Table 87: 2RLJ-5-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-6.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.54	1.66	20.70

Table 88: 2RLJ-6-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-7.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.71	1.84	22.67

Table 89: 2RLJ-7-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
2RLJ-9.PDB	O, A_ILE_9	N, A_PHE_12	H, A_PHE_12	2.57	1.64	13.83

Table 90: 2RLJ-9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5HJ3.PDB	O, C_ALA_166	N, C_VAL_97	H, C_VAL_97	2.93	2.10	12.03
5HJ3.PDB	O, C_VAL_97	N, C_ALA_166	H, C_ALA_166	2.88	2.11	22.07
5HJ3.PDB	O, C_LEU_68	N, C_VAL_180	H, C_VAL_180	2.78	1.98	17.26
5HJ3.PDB	O, C_VAL_66	N, C_ALA_182	H, C_ALA_182	2.79	1.96	12.90
5HJ3.PDB	OE1, J_GLN_89	OH, J_TYR_36	HH, J_TYR_36	2.57	1.82	22.55
5HJ3.PDB	O, A_SER_49	N, A_TRP_36	H, A_TRP_36	2.98	2.17	16.41
5HJ3.PDB	O, A_TYR_91	N, A_VAL_37	H, A_VAL_37	2.94	2.09	8.77
5HJ3.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.97	2.16	16.17
5HJ3.PDB	O, A_VAL_37	N, A_TYR_91	H, A_TYR_91	2.58	1.73	5.25
5HJ3.PDB	O, A_ASN_35	N, A_VAL_93	H, A_VAL_93	3.00	2.19	17.25

Table 91: 5HJ3-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
5T42-1.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.93	1.95	0.17
5T42-1.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.78	19.27
5T42-1.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.87	1.99	20.76
5T42-1.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.56	18.05
5T42-1.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.60	1.70	18.73
5T42-1.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.66	14.81
5T42-10.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.99	2.02	8.43
5T42-10.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.93	2.13	29.57
5T42-10.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.94	2.13	28.24
5T42-10.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.79
5T42-10.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	3.00	2.20	29.07
5T42-10.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.01	29.53
5T42-10.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.58	17.30
5T42-10.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	15.97
5T42-10.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.64	15.53
5T42-11.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.81	1.85	11.13
5T42-11.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.82	1.97	23.92
5T42-11.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.70	1.78	16.16
5T42-11.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	20.64
5T42-11.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.83
5T42-11.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.62	15.58
5T42-12.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.97	2.01	7.30
5T42-12.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.85	1.89	9.61
5T42-12.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.71	1.80	16.55
5T42-12.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.92	2.10	27.43
5T42-12.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.85
5T42-12.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.74	18.61
5T42-12.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.65	23.17
5T42-13.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.59	1.66	14.08
5T42-13.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.78	19.44
5T42-13.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.94	2.05	20.83
5T42-13.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.45	1.56	19.27
5T42-13.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.98
5T42-13.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.62	12.60
5T42-14.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.95	1.98	4.18
5T42-14.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.91	1.94	7.26
5T42-14.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.68	1.76	16.51
5T42-14.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.08	29.84
5T42-14.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.90
5T42-14.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.74	18.08
5T42-14.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.44
5T42-15.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.70	1.74	9.57
5T42-15.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.66	1.78	20.70
5T42-15.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.88	2.00	21.01
5T42-15.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	19.25
5T42-15.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.62	1.73	20.10
5T42-15.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.64	13.08
5T42-16.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.96	2.14	27.44
5T42-16.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.75	1.84	17.63
5T42-16.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.15	27.18
5T42-16.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.86	2.06	29.61
5T42-16.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	20.21
5T42-16.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.73	16.77
5T42-16.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.52	1.56	10.87
5T42-17.PDB	O, A_ASN_641	N, A_TRP_644	H, A_TRP_644	2.88	1.91	6.60
5T42-17.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.78	1.97	27.65
5T42-17.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.63	1.72	16.57

5T42-17.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.02	29.77
5T42-17.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.62	21.02
5T42-17.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.72	18.50
5T42-17.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.66	24.43
5T42-18.PDB	O, A_TRP_644	NH1, A_ARG_649	HH11, A_ARG_649	2.95	2.14	29.60
5T42-18.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.77	1.80	7.61
5T42-18.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.78	1.94	24.62
5T42-18.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.76	1.84	15.74
5T42-18.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.59	19.69
5T42-18.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.18
5T42-18.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.61	13.20
5T42-19.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.79	1.82	5.18
5T42-19.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.49
5T42-19.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.06	28.72
5T42-19.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.50
5T42-19.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.70	15.62
5T42-19.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.60	14.03

Table 92: 5T42-1-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-10.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.99	2.02	8.43
5T42-10.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.93	2.13	29.57
5T42-10.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.94	2.13	28.24
5T42-10.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.79
5T42-10.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	3.00	2.20	29.07
5T42-10.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.01	29.53
5T42-10.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.58	17.30
5T42-10.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	15.97
5T42-10.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.64	15.53

Table 93: 5T42-10-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
5T42-11.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.81	1.85	11.13
5T42-11.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.82	1.97	23.92
5T42-11.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.70	1.78	16.16
5T42-11.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	20.64
5T42-11.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.83
5T42-11.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.62	15.58

Table 94: 5T42-11-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-12.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.97	2.01	7.30
5T42-12.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.85	1.89	9.61
5T42-12.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.71	1.80	16.55
5T42-12.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.92	2.10	27.43
5T42-12.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.85
5T42-12.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.74	18.61
5T42-12.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.65	23.17

Table 95: 5T42-12-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-13.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.59	1.66	14.08
5T42-13.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.78	19.44
5T42-13.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.94	2.05	20.83
5T42-13.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.45	1.56	19.27
5T42-13.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.98
5T42-13.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.62	12.60

Table 96: 5T42-13-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-14.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.95	1.98	4.18
5T42-14.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.91	1.94	7.26
5T42-14.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.68	1.76	16.51
5T42-14.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.08	29.84
5T42-14.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.90
5T42-14.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.74	18.08
5T42-14.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.44

Table 97: 5T42-14-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
5T42-15.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.70	1.74	9.57
5T42-15.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.66	1.78	20.70
5T42-15.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.88	2.00	21.01
5T42-15.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	19.25
5T42-15.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.62	1.73	20.10
5T42-15.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.64	13.08

Table 98: 5T42-15-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-16.PDB	O, A_GLY_657	N, A_VAL_661	H, A_VAL_661	2.96	2.14	27.44
5T42-16.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.75	1.84	17.63
5T42-16.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.15	27.18
5T42-16.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.86	2.06	29.61
5T42-16.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	20.21
5T42-16.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.65	1.73	16.77
5T42-16.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.52	1.56	10.87

Table 99: 5T42-16-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-17.PDB	O, A_ASN_641	N, A_TRP_644	H, A_TRP_644	2.88	1.91	6.60
5T42-17.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.78	1.97	27.65
5T42-17.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.63	1.72	16.57
5T42-17.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.81	2.02	29.77
5T42-17.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.62	21.02
5T42-17.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.72	18.50
5T42-17.PDB	O, A_ALA_672	N, A_PHE_676	H, A_PHE_676	2.50	1.66	24.43

Table 100: 5T42-17-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-18.PDB	O, A_TRP_644	NH1, A_ARG_649	HH11, A_ARG_649	2.95	2.14	29.60
5T42-18.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.77	1.80	7.61
5T42-18.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.78	1.94	24.62
5T42-18.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.76	1.84	15.74
5T42-18.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.59	19.69
5T42-18.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.69	16.18
5T42-18.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.61	13.20

Table 101: 5T42-18-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-19.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.79	1.82	5.18
5T42-19.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.69	1.77	16.49
5T42-19.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.87	2.06	28.72
5T42-19.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.61	19.50
5T42-19.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.63	1.70	15.62
5T42-19.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.54	1.60	14.03

Table 102: 5T42-19-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-2.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.85	1.99	23.63
5T42-2.PDB	O, A_GLN_650	N, A_VAL_658	H, A_VAL_658	2.89	2.05	24.99
5T42-2.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.80	1.82	2.37
5T42-2.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.67	1.75	16.21
5T42-2.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.88	2.06	27.64
5T42-2.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.59	19.13
5T42-2.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.72	16.09
5T42-2.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.86
5T42-20.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.93	1.95	4.32
5T42-20.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.94	2.14	29.59
5T42-20.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.80	1.85	12.29
5T42-20.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.73	1.85	21.16
5T42-20.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.83	1.95	21.15
5T42-20.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	18.76
5T42-20.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.40
5T42-20.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.55	1.62	15.71

Table 103: 5T42-2-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-20.PDB	O, A_ASP_642	N, A_TRP_645	H, A_TRP_645	2.93	1.95	4.32
5T42-20.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.94	2.14	29.59
5T42-20.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.80	1.85	12.29
5T42-20.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.73	1.85	21.16
5T42-20.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.83	1.95	21.15
5T42-20.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.58	18.76
5T42-20.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.40
5T42-20.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.55	1.62	15.71

Table 104: 5T42-20-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-3.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.55	1.77	29.97
5T42-3.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.73	1.82	17.54
5T42-3.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.99	2.18	28.74
5T42-3.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.79	1.98	28.05
5T42-3.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.71
5T42-3.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.66	1.74	16.19
5T42-3.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	14.42

Table 105: 5T42-3-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-4.PDB	O, A_GLY_647	N, A_TRP_651	H, A_TRP_651	2.59	1.68	16.69
5T42-4.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.57	1.78	28.87
5T42-4.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.61	1.73	20.44
5T42-4.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.87	1.99	21.34
5T42-4.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.47	1.57	17.87
5T42-4.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.61	1.72	19.23
5T42-4.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.63	13.71

Table 106: 5T42-4-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-5.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.85	1.98	22.54
5T42-5.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.92	1.95	7.59
5T42-5.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.70	1.79	17.07
5T42-5.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.14	26.58
5T42-5.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.96	2.16	29.30
5T42-5.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	20.58
5T42-5.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.66	1.76	19.47
5T42-5.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.57	1.64	14.61

Table 107: 5T42-5-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-6.PDB	O, A_ASP_642	N, A_THR_646	H, A_THR_646	2.82	1.99	26.68
5T42-6.PDB	O, A_GLY_657	N, A_VAL_662	H, A_VAL_662	2.76	1.79	8.30
5T42-6.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.76	1.89	21.67
5T42-6.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.85	1.95	19.14
5T42-6.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.61	21.67
5T42-6.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.75	19.95
5T42-6.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.63	1.70	15.13

Table 108: 5T42-6-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-7.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.74	1.91	26.39
5T42-7.PDB	O, A_GLY_655	N, A_THR_659	H, A_THR_659	2.58	1.78	28.20
5T42-7.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.65	1.77	20.26
5T42-7.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.84	1.96	20.50
5T42-7.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.58	18.36
5T42-7.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.60	1.68	15.41
5T42-7.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.63	14.62

Table 109: 5T42-7-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-8.PDB	O, A_GLY_647	N, A_GLN_650	H, A_GLN_650	2.71	1.91	28.69
5T42-8.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.71	1.80	17.39
5T42-8.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.15	26.89
5T42-8.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.86	2.06	28.83
5T42-8.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.49	1.58	18.05
5T42-8.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.73	17.27
5T42-8.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.59	1.65	13.58

Table 110: 5T42-8-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-9.PDB	OG1, A_THR_634	NZ, A_LYS_633	HZ2, A_LYS_633	2.68	1.67	11.19
5T42-9.PDB	O, A_VAL_661	N, A_VAL_665	H, A_VAL_665	2.72	1.81	17.22
5T42-9.PDB	O, A_VAL_662	N, A_ILE_666	H, A_ILE_666	2.97	2.16	28.57
5T42-9.PDB	O, A_ILE_663	N, A_ALA_667	H, A_ALA_667	2.80	2.00	29.42
5T42-9.PDB	O, A_ILE_666	N, A_ALA_670	H, A_ALA_670	2.48	1.60	19.55
5T42-9.PDB	O, A_LEU_668	N, A_ILE_671	H, A_ILE_671	2.64	1.73	16.82
5T42-9.PDB	O, A_ILE_671	N, A_VAL_675	H, A_VAL_675	2.56	1.62	13.44

Table 111: 5T42-9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
5HJ3.PDB	OE1, J_GLN_89	OH, J_TYR_36	HH, J_TYR_36	2.57	1.82	22.55

Table 112: 5HJ3-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
5T42-9.PDB	OG1, A_THR_634	NZ, A_LYS_633	HZ2, A_LYS_633	2.68	1.67	11.19

Table 113: 5T42-9-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).