

Supplementary File 2: Amino acid sequence alignments of human and canine CNPase isoforms 2 showing the locations of the disease-related variants in the canine (green T42M) and blue (S82L)

CLUSTAL O(1.2.4) multiple sequence alignment

sp P09543 CN37_HUMAN	MNRGFSRKSHTFLPKIFFRKMSSSGAKDKPELQFPFLQDEDTVATLLECKTLFILRGLPG	60
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	MNRSFSRKSHAFLPKIFFRKMSSSGAKDKPELQFPFLQDEETVATLQECKTLFILRGLPG	60
	L	
sp P09543 CN37_HUMAN	SGKSTLARVIVDKYRDGTKMVSADAYKITPGARGAFSEEYKRLDEDLAAYCRRRDIRILV	120
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	SGKSTLARVIVDRYRDGTKMVSADAYKITPGARGDFSEEYKRLDEDLAAYCR-RDVRVLV	119
sp P09543 CN37_HUMAN	LDDTNHERERLEQLFEMADQYQYQVVLVEPKTAWRLDCAQLKEKNQWQLSADDLKKLKPG	180
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	LDDTNHERERLEQLFELADQYQYQVVLVEPKTAWRLDCAQLKEKNQWQLSADELKKLKPG	179
sp P09543 CN37_HUMAN	LEKDFLPLYFGWFLTKKSSETLRKAGQVFLEELGNHKAFKKELRQFVPGDEPREKMDLVT	240
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	LEKDFLPLYFGWFLTKKSSESLRKAGQAFLEELGNHKAFKKELRHFVSGDEPREKIELVT	239
sp P09543 CN37_HUMAN	YFGKRPPGVLHCTTKFCDYGKAPGAE EYAQQDVLKKSYSKAFTLTISALFVTPKTTGARV	300
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	YFGKRPPGVLHCTTKFCDYGKAAGADEYAQQDVVKKSYCKAFTLTITLALFVTPKTAGARV	299
sp P09543 CN37_HUMAN	ELSEQQLQLWPSDVKLSPTDNLPRGSRAHITLGCADVEAVQTGLDLLEILRQEKGGSR	360
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	ELSEQELPLWPNVDVKLSPSDSLPRGSRAHITLGCAGDVEPVQGTGIDLLEIVRQEKGGSR	359
sp P09543 CN37_HUMAN	GEEVGELSRGKLYSLGNGRWMLTLAKNMEVRAIFTGYYGKGKPVPTQGSRKGGALQSCTI	420
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	GEEVGELNRGKLYSLGNGRWLLSLAKKLEVRAIFTGYYGKGKPVPTHGSRKGGALQSCTI	419
sp P09543 CN37_HUMAN	I 421	
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	I 420	