

Supplementary File S2: 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 human (blue S82L)

CLUSTAL O(1.2.4) multiple sequence alignment

sp P09543 CN37_HUMAN	MNRGFSRKSHFLPKIFFRKMSSSGAKDKPELQFPFLQDEDTVATLLECKTLFILRGLPG	60
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	MNRSFSRKSHAFPLPKIFFRKMSSSGAKDKPELQFPFLQDEETVATLQECKTLFILRGLPG	60
		M
sp P09543 CN37_HUMAN	SGKSTLARVIVDKYRDGTMVLSADAYKITPGARGAFSEEYKRLDEDLAAYCRRRDIRILV	120
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	SGKSTLARVIVDRYRDGTMVLSADAYKITPGARGDFSEEYKRLDEDLAAYCR-RDVRVLV	119
		L
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	YFGKRPPGVLHCTTKFCDYGKAPGAEEYAQQDVLKKSYSKAFTLTISALFVTPKTTGARV	300
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	YFGKRPPGVLHCTTKFCDYGAAGADEYAQQDVVKKSYCKAFTLTITALFVTPKTAGARV	299
sp P09543 CN37_HUMAN	ELSEQQLQLWPSDVKLSPTDNLPRGSRAHITLGCADVEAVQTGLDLLEILRQEKGGSR	360
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	ELSEQELPLWPNDVDKLSPSDSLPRGSRAHITLGCAGDVEPVQTGIDLLEIVRQEKGGSR	359
sp P09543 CN37_HUMAN	GEEVGELSRGKLYSLGNRWMLTLAKNMEVRAIFTGYYGKGKPVPTQGSRKGGALQSCTI	420
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	GEEVGELNRGKLYSLGNRWLLSLAKKLEVRAIFTGYYGKGKPVPTHGSRKGGALQSCTI	419
sp P09543 CN37_HUMAN	I 421	
tr A0A8I3NGU6 A0A8I3NGU6_CANLF	I 420	