

Datos suplementarios (2)

Estudio y caracterización de la dinámica celular
y morfogénesis de una estructura epitelial
primitiva en *Dictyostelium discoideum*

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Los alineamientos que se describen a continuación fueron obtenidos mediante el programa Clustal Omega (múltiples). Relacionado con las secciones 3.2.3 y 3.3.4

Parte 1: Alineamientos múltiples de secuencias de las proteínas de adhesión celular en Metazoos y sus homólogos en *D. discoideum* (Pág 3-36)

Parte 2: Alineamientos múltiples de secuencias de las proteínas de polaridad celular en Metazoos y sus homólogos en *D. discoideum* (Pág 37-53)

Moléculas de Adhesión Celular

- 1) Dd α -Actinina 1/Hs α -Actinina 2
- 2) DdCortexilina 1/Hs α -Actinina 4
- 3) DdAardvark/Hs β -Catenina
- 4) DdCoronina 7/HsCoronina 7
- 5) DdAbp120/HsFilamina
- 6) DdMiosina 7/HsMiosina 7
- 7) DdPaxilina/HsPaxilina
- 8) DdTM9 Proteína A/HsTM9SF4
- 9) DdRacI/HsRAC2
- 10) DdRacJ/HsRAC2
- 11) DdRacL/HsRAC1
- 12) DdFrmA/HsTalina 1
- 13) DdTalina A/HsTalina 2
- 14) Dd α -Catenina/HsVinculina

Moléculas de Polaridad Celular

- 15) Dd14-3-3/Hs14-3-3
- 16) DdRac1A/HsCdc42
- 17) DdRacB/HsCdc42
- 18) DDB_G0295485/HsCrb1
- 19) DdMarj-A/HsMark2
- 20) DdPakB/HsPak1
- 21) DdPakC/HsPak1
- 22) DdlrrA/HsScrib

DDB0191133	DDB_G0268632	MSEEP---TPVSGNDKQLLNKAWITQKKFTTAWCNSHLRKLKAGSSIE	44
sp Q3ZC55 ACTN2_BOVIN		MNQIEPGVQYNYVYDEDEYMIQEEEWDRDLLLDPAWEKQQRKTFTAWCNSHLRKAGTQIE	60
sp P35609 ACTN2_HUMAN		MNQIEPGVQYNYVYDEDEYMIQEEEWDRDLLLDPAWEKQQRKTFTAWCNSHLRKAGTQIE	60
sp Q9JI91 ACTN2_MOUSE		MNQIEPGVQYNYVYDEDEYMIQEEEWDRDLLLDPAWEKQQRKTFTAWCNSHLRKAGTQIE	60
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DDB0191133	DDB_G0268632	QIDTDFDGIKLAQLLEVISNDPVFKVNTPKLRIHNIQNVGLCLKHIESHGVLKLVGIGA	104
sp Q3ZC55 ACTN2_BOVIN		NIEEDFRNGLKLMLLLEVISGERLPKP-DRGKMRFHKIANVNKALDYASKGVKLVSIGA	119
sp P35609 ACTN2_HUMAN		NIEEDFRNGLKLMLLLEVISGERLPKP-DRGKMRFHKIANVNKALDYASKGVKLVSIGA	119
sp Q9JI91 ACTN2_MOUSE		NIEEDFRNGLKLMLLLEVISGERLPKP-DRGKMRFHKIANVNKALDYASKGVKLVSIGA	119
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DDB0191133	DDB_G0268632	EELVDKNLKMTLGMiWTIILRFaiQDISIEELSAKEALLLWCQRKTEGYDRVKVGNFHTS	164
sp Q3ZC55 ACTN2_BOVIN		EEIVDGNVKMTLGMiWTIILRFaiQDISVEETSACEGLLLWCQRKTAPYRNVNIQNFHTS	179
sp P35609 ACTN2_HUMAN		EEIVDGNVKMTLGMiWTIILRFaiQDISVEETSACEGLLLWCQRKTAPYRNVNIQNFHTS	179
sp Q9JI91 ACTN2_MOUSE		EEIVDGNVKMTLGMiWTIILRFaiQDISVEETSACEGLLLWCQRKTAPYRNVNIQNFHTS	179
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DDB0191133	DDB_G0268632	FQDGLAFCALIHKHRPDLINFDSLNKDDKAGNLQLAFDIAEKELDIPKMLDVSDMLDVVR	224
sp Q3ZC55 ACTN2_BOVIN		WKDGLGLCALIHHRPDLIDYSKLNKDDPIGNINLAMEIAEKHLDIPKMLDAEDIVNTPK	239
sp P35609 ACTN2_HUMAN		WKDGLGLCALIHHRPDLIDYSKLNKDDPIGNINLAMEIAEKHLDIPKMLDAEDIVNTPK	239
sp Q9JI91 ACTN2_MOUSE		WKDGLGLCALIHHRPDLIDYSKLNKDDPIGNINLAMEIAEKHLDIPKMLDAEDIVNTPK	239
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DDB0191133	DDB_G0268632	PDERSVMTYVAQYHHFSASRKAEAGKQVGVLDTFMLLEQTKSDYLKRANELVQWIND	284
sp Q3ZC55 ACTN2_BOVIN		PDERAIMTYVSCFYHAFAGAEQAETAANRICKVLAVNQENERLMEEYERLASELLEWIRR	299
sp P35609 ACTN2_HUMAN		PDERAIMTYVSCFYHAFAGAEQAETAANRICKVLAVNQENERLMEEYERLASELLEWIRR	299
sp Q9JI91 ACTN2_MOUSE		PDERAIMTYVSCFYHAFAGAEQAETAANRICKVLAVNQENERLMEEYERLASELLEWIRR	299
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DDB0191133	DDB_G0268632	KQASLESRDFGDSIESVQSFMAHKEYKTEKPPKGQEVSELEAIYNSLQTKLRLIKREP	344
sp Q3ZC55 ACTN2_BOVIN		TIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQEKQCLEINFNTLQTKLRISNRPA	359
sp P35609 ACTN2_HUMAN		TIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQEKQCLEINFNTLQTKLRISNRPA	359
sp Q9JI91 ACTN2_MOUSE		TIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQEKQCLEINFNTLQTKLRISNRPA	359
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DDB0191133	DDB_G0268632	FVAPAGLTPNEIDSTWSALEKAEQEHAEALRIELKRQKKIAVLLQKYNRIKLKLENWATT	404
sp Q3ZC55 ACTN2_BOVIN		FMPSEGKMVSDIAGAWQRLQAEKGYEELLNEIRRLERVEHLAEKFRQKASTHETWAYG	419
sp P35609 ACTN2_HUMAN		FMPSEGKMVSDIAGAWQRLQAEKGYEELLNEIRRLERVEHLAEKFRQKASTHETWAYG	419
sp Q9JI91 ACTN2_MOUSE		FMPSEGKMVSDIAGAWQRLQAEKGYEELLNEIRRLERVEHLAEKFRQKASTHETWAYG	419
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DDB0191133	DDB_G0268632	KSVYLG-SNETGDSITAVQAKLNLEAFDGCQSLEGGQNSDLLSILAQLTELNYNGVPE	463
sp Q3ZC55 ACTN2_BOVIN		KEQILLQKDYESSLTLEVRALLRKHEAFESDLAAHQD-RVEQIAAIAQELNELDYHDAVN	478
sp P35609 ACTN2_HUMAN		KEQILLQKDYESSLTLEVRALLRKHEAFESDLAAHQD-RVEQIAAIAQELNELDYHDAVN	478
sp Q9JI91 ACTN2_MOUSE		KEQILLQKDYESSLTLEVRALLRKHEAFESDLAAHQD-RVEQIAAIAQELNELDYHDAVN	478
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DDB0191133	DDB_G0268632	LTERKDTFFAQQTGVKSSAETYNKTLLEALERLQKIEDSLVEFAKRAAQLNVWIEAADD	523
sp Q3ZC55 ACTN2_BOVIN		VNDRQC-KICDQWDRGLTLTQKRREALERTEKLLTIDQLHLEFAKRAAPFNNWMEGAME	537
sp P35609 ACTN2_HUMAN		VNDRQC-KICDQWDRGLTLTQKRREALERTEKLLTIDQLHLEFAKRAAPFNNWMEGAME	537
sp Q9JI91 ACTN2_MOUSE		VNDRQC-KICDQWDRGLTLTQKRREALERTEKLLTIDQLHLEFAKRAAPFNNWMEGAME	537
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DDB0191133	DDB_G0268632	HVFDPINVDVSGVQVEIQE---KFDAFLHDQSQQFAEL---EALAALTQQRLRELGRSEN	576
sp Q3ZC55 ACTN2_BOVIN		DLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSILAIQNEVEKVIQSYSIRISSN	597
sp P35609 ACTN2_HUMAN		DLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSN	597
sp Q9JI91 ACTN2_MOUSE		DLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSILAIQNEVEKVIQSYSIRISSN	597
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DDB0191133	DDB_G0268632	DYSVISYDELSAKWNLLAGIEERKVLANELTTQTNDVLQCSFSVKANEISDYVRVTL	636
sp Q3ZC55 ACTN2_BOVIN		PYSTVTVDIEIRSKWDVKVQLVPIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNM	657
sp P35609 ACTN2_HUMAN		PYSTVTMDLRTKWDVKVQLVPIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNM	657
sp Q9JI91 ACTN2_MOUSE		PYSTVTMDLRNKKWDVKVQLVPIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNM	657
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DDB0191133	DDB_G0268632	DAISQNTSS---DPQEQLNNIRAIITAHAEKKPELDELYIASQLEEAQVVDNKHTQHS	693
sp Q3ZC55 ACTN2_BOVIN		EEIARSSIQITGALEDQMNQLQYEHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTM	717
sp P35609 ACTN2_HUMAN		EEIARSSIQITGALEDQMNQLQYEHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTM	717
sp Q9JI91 ACTN2_MOUSE		EEIARSSIQITGALEDQMNQLQYEHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTM	717
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DDB0191133	DDB_G0268632	ESIKLKWDLNTLAKKNEQVVEGEILAKQLTGVTAEEELSEFKACFSHFDDKNDNKNLRLE	753
sp	Q3ZC55	ACTN2_BOVIN	777
sp	P35609	ACTN2_HUMAN	777
sp	Q9JI91	ACTN2_MOUSE	777
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DDB0191133	DDB_G0268632	FSSCLKSIGDELTEEQLNQVISKIDTDGNGTISFEEFIDYMVSSRKGTDSVESTKAAFKV	813
sp	Q3ZC55	ACTN2_BOVIN	837
sp	P35609	ACTN2_HUMAN	837
sp	Q9JI91	ACTN2_MOUSE	837
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DDB0191133	DDB_G0268632	MAEDKDFITEAQIRAAISDSKQIDYLLASMPA-----VEGGFDYNSFAEKLYQ----	861
sp	Q3ZC55	ACTN2_BOVIN	894
sp	P35609	ACTN2_HUMAN	894
sp	Q9JI91	ACTN2_MOUSE	894
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0191103 DDB_G0289483	-----MAGKDWEIVQEKAFTAW	17
sp 043707 ACTN4_HUMAN	MVDYHAANQSYQYGPSA-GNGAGGGGSGMDYMAQEDDWRDLLLLPAWEKQQRKTTFTAW	59
sp P57780 ACTN4_MOUSE	MVDYHAANQAYQYGPNSGGGNGAGGGGSGMDYMAQEDDWRDLLLLPAWEKQQRKTTFTAW	60
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DDB0191103 DDB_G0289483	VNSVLDKRGEEKISDVGKDLSDGVKLIFFLLEISSKKFNKKYDFEPKARINMIQNVALALK	77
sp 043707 ACTN4_HUMAN	CNSHLRKAGTQIENIDEDFRDGLKMLLLEVISGERLPKPE--RGKMRVHKINNPNKALD	117
sp P57780 ACTN4_MOUSE	CNSHLRKAGTQIENIDEDFRDGLKMLLLEVISGERLPKPE--RGKMRVHKINNPNKALD	118
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DDB0191103 DDB_G0289483	FLDEELKIKVQGISSEDFVNNKKMILGFLWTLYRKYRIAVISSEGDSSSEGLLLWCCKNT	137
sp 043707 ACTN4_HUMAN	FIAS-KGKLVSIGAEIIVDGNAKMTLGMWITILRFQIDISVEETSAKEGLLLWCQRK	176
sp P57780 ACTN4_MOUSE	FIAS-KGKLVSIGAEIIVDGNAKMTLGMWITILRFQIDISVEETSAKEGLLLWCQRK	177
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DDB0191103 DDB_G0289483	TTGYDGVNITSFTKSF RDGLAFLALSHKFEPESFKFQFEAMDPIARLNAAFDFAEKG LG	197
sp 043707 ACTN4_HUMAN	TAPYKNVNVQNFHISWKDGLAFNALIHRHRELIEYDKLRKDDPVTNLNNAFEVAEKYLD	236
sp P57780 ACTN4_MOUSE	TAPYKNVNVQNFHISWKDGLAFNALIHRHRELIEYDKLRKDDPVTNLNNAFEVAEKYLD	237
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DDB0191103 DDB_G0289483	VPKLLAEVVMRG-TTDERSLVLYTSLFFHAYRAKEEKARLESSKNEMANRLAGLENSLE	256
sp 043707 ACTN4_HUMAN	IPKMLDAEDIVNTARPDEKAIMTYVSSFYHAFSGAQKAETAA--NRICKVLAVN---QE	290
sp P57780 ACTN4_MOUSE	IPKMLDAEDIVNTARPDEKAIMTYVSSFYHAFSGAQKAETAA--NRICKVLAVN---QE	291
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DDB0191103 DDB_G0289483	SEKVSREQLIKQKQDQNSLLAS-LES-----EGAEREKRLRELEAKLDET LKNLELEKLA	310
sp 043707 ACTN4_HUMAN	-----NEHLMEDYEKLASDLEWIRRTIPWLED RVPQKTIQEMQQKLEDFRDYRRVHKPP	345
sp P57780 ACTN4_MOUSE	-----NEHLMEDYERLASDLEWIRRTIPWLED RVPQKTIQEMQQKLEDFRDYRRVHKPP	346
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DDB0191103 DDB_G0289483	RMELEARLAKTEKDRAILELKLAEAIDEKSKLEQQIEATRIRGAEEAQGLGLLRKNLDTH	370
sp 043707 ACTN4_HUMAN	KVQ-----EKQCLEINFNT-LQTKLRLSNRPAF-----MPSEGMVSDI---	383
sp P57780 ACTN4_MOUSE	KVQ-----EKQCLEINFNT-LQTKLRLSNRPAF-----MPSEGRMVSDI---	384
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DDB0191103 DDB_G0289483	VHDLWKQKLT MNSSSSSIDDQIIVEVSGLPFGEQVKHLATKLEA-----	416
sp 043707 ACTN4_HUMAN	---NNGWQHLEQAEKG---YEELLNEIRR---LERLDHLAEKFRQKASIEAWTDGKEA	434
sp P57780 ACTN4_MOUSE	---NNGWQHLEQAEKG---YEELLNEIRR---LERLDHLAEKFRQKASIEAWTDGKEA	435
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DDB0191103 DDB_G0289483	-----ENLAIMKLLNQKE---DDL-----K	433
sp 043707 ACTN4_HUMAN	MLKHRDYETATLSDIKALIRKHEAFESDLAAHQDRVEQIAAIAQELNELDYD SHNVNTR	494
sp P57780 ACTN4_MOUSE	MLKQRDYETATLSDIKALIRKHEAFESDLAAHQDRVEQIAAIAQELNELDYD SHNVNTR	495
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DDB0191103 DDB_G0289483	AQKLKS-----SK-----SKK*-----	444
sp 043707 ACTN4_HUMAN	CQKICDQWDALGSLTHSRREALEKTEKQLEAIDQLHLEYAKRAAPFNNWMESAMEDLQDM	554
sp P57780 ACTN4_MOUSE	CQKICDQWDNLGSLTHSRREALEKTEKQLEITDQLHLEYAKRAAPFNNWMESAMEDLQDM	555
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DDB0191103 DDB_G0289483	-----FIVHTIEEIEGLISAHDQFKSTLPADREREAAILHKEAQRIAESNHIKLSGSPYTTV	444
sp 043707 ACTN4_HUMAN	FIVHTIEEIEGLISAHDQFKSTLPADREREAAILHKEAQRIAESNHIKLSGSPYTTV	614
sp P57780 ACTN4_MOUSE	FIVHTIEEIEGLISAHDQFKSTLPADREREAAILHKEAQRIAESNHIKLSGSPYTTV	615
DDB0191103 DDB_G0289483	-----TPQIINSKWEKVQQLVPKRDHALL EEQSKQSQSNEHLRRQFASQANVVGPIQTKMEEIGR	444
sp 043707 ACTN4_HUMAN	TPQIINSKWEKVQQLVPKRDHALL EEQSKQSQSNEHLRRQFASQANVVGPIQTKMEEIGR	674
sp P57780 ACTN4_MOUSE	TPQIINSKWEKVQQLVPKRDHALL EEQSKQSQSNEHLRRQFASQANMVGPWIQTKMEEIGR	675
DDB0191103 DDB_G0289483	-----ISIEMNGTLEDQLSHLKQYERSIVDYKPNLDLLEQQHQLIQEALIFDNKHTNYTMEHIRV	444
sp 043707 ACTN4_HUMAN	ISIEMNGTLEDQLSHLKQYERSIVDYKPNLDLLEQQHQLIQEALIFDNKHTNYTMEHIRV	734
sp P57780 ACTN4_MOUSE	ISIEMNGTLEDQLSHLKQYERSIVDYKPSLDLLEQQHQLIQEALIFDNKHTNYTMEHIRV	735
DDB0191103 DDB_G0289483	-----	444

sp 043707 ACTN4_HUMAN	GWEQLLTTIARTINEVENQILTRDAKGISQEQMQEFRASFNFDDKHGGALGPPEEFKACL	794
sp P57780 ACTN4_MOUSE	GWEQLLTTIARTINEVENQILTRDAKGISQEQMQEFRASFNFDDKHGGALGPPEEFKACL	795
DDB0191103 DDB_G0289483	-----	444
sp 043707 ACTN4_HUMAN	ISLGYDVENDRQGEAEFNRIIMSLVDPNHSGLVTFQAFIDFMSRETTDDTADQVIASFVKV	854
sp P57780 ACTN4_MOUSE	ISLGYDVENDRQGDAEFNRIIMSVVDPNHSGLVTFQAFIDFMSRETTDDTADQVIASFVKV	855
DDB0191103 DDB_G0289483	-----	444
sp 043707 ACTN4_HUMAN	LAGDKNFITAEELRRELPPDQAEYCIARMAPYQGPDAVPGALDYKSFSTALYGESDL	911
sp P57780 ACTN4_MOUSE	LAGDKNFITAEELRRELPPDQAEYCIARMAPYQGPDAAPGALDYKSFSTALYGESDL	912

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0191132 DDB_G0288877	MNDCGSLFNKKLFKMNLLFKHLKLQQHLKLQQKPLNNSSINNNINNNNNNNNNNSNND	60
sp Q18825 BAR1_CAEEEL	-----MDLD-----PNLVINHDDT--NLSE-----A----	19
sp P35222 CTNB1_HUMAN	-----M-----ATQ-----	4
sp Q02248 CTNB1_MOUSE	-----M-----ATQ-----	4
sp P18824 ARM_DROME	-----MSYM-----PAQ-----	7
DDB0191132 DDB_G0288877	SNNTNTNIFNNSFLNSDLIERLIIKFTIGYLNKNITEDIYIEQILLENQNNFIKSTTTSNY	120
sp Q18825 BAR1_CAEEEL	--SFTMEQHTSSYSDIHMGSTP-----CTGHRKVDWNRNHN--DSGFQTM	61
sp P35222 CTNB1_HUMAN	---A-----DLMELDMAMEP-----DRKAAVSHWQQQSYL--DSGIHSG	38
sp Q02248 CTNB1_MOUSE	---A-----DLMELDMAMEP-----DRKAAVSHWQQQSYL--DSGIHSG	38
sp P18824 ARM_DROME	---NRTMSHNNQYNPPDLPPMV-----SAKEQTLMWQQNSYLGDSGIHSG	49
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DDB0191132 DDB_G0288877	ILENNSSS	160
sp Q18825 BAR1_CAEEEL	NHSEAPS-----IISSL	73
sp P35222 CTNB1_HUMAN	ATTTAPSLSGKGNPEEEDVDTSQVLYEWEQGFSSQFTQEQQVADIDGQYAMTRAQVRRAAM	98
sp Q02248 CTNB1_MOUSE	ATTTAPSLSGKGNPEEEDVDTSQVLYEWEQGFSSQFTQEQQVADIDGQYAMTRAQVRRAAM	98
sp P18824 ARM_DROME	AVTVQVPSLSGKED---EEMEGDPLMFDLDTGFPQNFQDQVDDMNQQLSQTRSQRVRAAM	106
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DDB0191132 DDB_G0288877	SSSSI-----LSKFNKLEEDNELELQKKQKQQLQQEELF-----NQFNFLGIEDQ	208
sp Q18825 BAR1_CAEEEL	HPSSHLSGMSSM-ADYEP--TL----SDQKQKFDGITQNGADGQYNTVRAIPEL	123
sp P35222 CTNB1_HUMAN	FPETLDEGMQIPSTQFDDAAHPTNVQRLAE-PSQMLKHAVVNLI-NYQDDAELATRAIPEL	156
sp Q02248 CTNB1_MOUSE	FPETLDEGMQIPSTQFDDAAHPTNVQRLAE-PSQMLKHAVVNLI-NYQDDAELATRAIPEL	156
sp P18824 ARM_DROME	FPETLEEGIEIPSTQFDPQPTAVQRLSE-PSQMLKHAVVNLI-NYQDDAELATRAIPEL	164
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DDB0191132 DDB_G0288877	NDFLSEQET--IQKIK ---FLIKMTAKSMSNYSSPNTLIPSVSKTYISPFGLSSNGSTN	262
sp Q18825 BAR1_CAEEEL	TMLMKDQDNEVVHKAVILMQNIAKMECDPMRRQNEARIVDPRVIFTLRDLLRDKVE----	179
sp P35222 CTNB1_HUMAN	TKLLNDEQVVVNKAAMVMVHQLSKKEASRHAIMR-----SPQMVAIVRTMQN-TN----	206
sp Q02248 CTNB1_MOUSE	TKLLNDEQVVVNKAAMVMVHQLSKKEASRHAIMR-----SPQMVAIVRTMQN-TN----	206
sp P18824 ARM_DROME	IKLLNDEQVVVSQAAMVMVHQLSKKEASRHAIMN-----SPQMVAALVRAISN-SN----	214
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DDB0191132 DDB_G0288877	NHNNNNNNHHHSHSNGNLISSNNVNNQLNVSNNNNNSNHYDENNQFDIFLIPTMLV	322
sp Q18825 BAR1_CAEEEL	-----FPNIIRCTLGTFFHICNRQEGIDLVTIAIE-----QPD--IIPN-LIR	220
sp P35222 CTNB1_HUMAN	-----DVETARCTAGTLHNLSHHREGLLAIF-----KSG--GIPA-LVK	242
sp Q02248 CTNB1_MOUSE	-----DVETARCTAGTLHNLSHHREGLLAIF-----KSG--GIPA-LVK	242
sp P18824 ARM_DROME	-----DLESTKAAVGTLHNLSHHRQGLLAIF-----KSG--GIPA-LVK	250
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DDB0191132 DDB_G0288877	HLLSFLSANDLWRLSLTCKRIWYIVDVFKWELLFEQTCPRIYYAMQFNSRWSNPTSFQS	382
sp Q18825 BAR1_CAEEEL	HIGTYPSSI-----YKY--AILTMHSILSDKQGGQSVII-----	253
sp P35222 CTNB1_HUMAN	MLGSPVDSV-----LFY--AITTLHNLHLHQEGAKMAVRL-----	275
sp Q02248 CTNB1_MOUSE	MLGSPVDSV-----LFY--AITTLHNLHLHQEGAKMAVRL-----	275
sp P18824 ARM_DROME	LLSSPVESV-----LFY--AITTLHNLHLHQDGSKMAVRL-----	283
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DDB0191132 DDB_G0288877	KMILCYIDRLPTDNYKNFDKSDESGQIKKIIG-VMNENLHNPMLIRETCYILKRLSYRQR	441
sp Q18825 BAR1_CAEEEL	-----ARQQDAITHVTPWLEAEK--SEKLLPVIQDLIRVLCE---	288
sp P35222 CTNB1_HUMAN	-----AGG--LQKMVA-LLNKT--NVKFLAITTDCLQILAY---	306
sp Q02248 CTNB1_MOUSE	-----AGG--LQKMVA-LLNKT--NVKFLAITTDCLQILAY---	306
sp P18824 ARM_DROME	-----AGG--LQKMVT-LLQRN--NVKFLAIVTDCLQILAY---	314
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DDB0191132 DDB_G0288877	KEDEHESLIARYGGISLILQAMKNHPYDAGVQEDACGALGNLTCDSPNNMGLYSN--DNY	499
sp Q18825 BAR1_CAEEEL	KNTEQKIKFVKMGGPQKLLMLLQHRVYENLLWRT-----TQLLKTFSN--FDA	334
sp P35222 CTNB1_HUMAN	GNQESKLIILASGGPQALVNMRTTYTYEKLWTT-----SRVLKVLVSVCSNPK	354
sp Q02248 CTNB1_MOUSE	GNQESKLIILASGGPQALVNMRTTYTYEKLWTT-----SRVLKVLVSVCSNPK	354
sp P18824 ARM_DROME	GNQESKLIILASGGPNELVRIMRSDYDEKLWTT-----SRVLKVLVSVCSNPK	362
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DDB0191132 DDB_G0288877	LSVVEQGGIQLILQAMKNHMPGVQYNTSFVLRNLARNDVESRVAIEGGIQSIATAMK	559
sp Q18825 BAR1_CAEEEL	PNLVAFGGRQILANLL--SHGSPRLVQSTLETLRNISDVPS--KIKE-DLLKSLLELV-	388
sp P35222 CTNB1_HUMAN	PAIVEAGGMQALGLHL--TDPQRLVQNCWLTLRNLSDAAT--KQEGMEGLGLTLVQLL-	409

sp Q02248 CTNB1_MOUSE	PAIVEAGGMQALGLHL--TDP SQR LVQNCLWTLRNLSDAAT--KQEGMEGLLGLTVQLL-	409
sp P18824 ARM_DROME	PAIVDAGGMQALAMHL--GNMSPRLVQNCLWTLRNLSDAAT--KVEGLEALLQSLVQVL-	417
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DDB0191132 DDB_G0288877	NHPNHIGIQTGCGALRNLGCNDS-NKVL SAK EGG IGLILRAMR SFSH-----	607
sp Q18825 BAR1_CAEE L	-NSRNTTIRLYSAQIMSNLVANNRHNKEFCGNNGVVILVRALT IATKEMGDLRDKEAQQ	447
sp P35222 CTNB1_HUMAN	-GSDDIN VVTC AAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLR A-----GD	456
sp Q02248 CTNB1_MOUSE	-GSDDIN VVTC AAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLR A-----GD	456
sp P18824 ARM_DROME	-GSTDVNVVTC AAGILSNLTCNNQRNKATVCQVGGVDALVRTIINA-----GD	464
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DDB0191132 DDB_G0288877	-PDLQLNGCGALRNLARNEDN---KNMIS RQNGIQLVLGAMSNHPDDPDVQDEGCAALI	662
sp Q18825 BAR1_CAEE L	MEDYIESLIC TLRHLCVGH PMSDKVQAFVFRDPALFL-HKLLT---MRPVLLKHTLSLLL	503
sp P35222 CTNB1_HUMAN	REDITEPAICALRH LTSRHQEAEMAQNAVRLHYGLPVVVKLLH-PPSHWPLIKATVGLIR	515
sp Q02248 CTNB1_MOUSE	REDITEPAICALRH LTSRHQEAEMAQNAVRLHYGLPVVVKLLH-PPSHWPLIKATVGLIR	515
sp P18824 ARM_DROME	REEITEPAICALRH LTSRHVDS ELAQNAVRLNYGLSVIVKLLH-PPSRWPLIKAVIGLIR	523
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DDB0191132 DDB_G0288877	NLA---YQDEANEETIAREGGINLILKAMR-----NHPFHSGVQ	698
sp Q18825 BAR1_CAEE L	KVVSQHALLAPFRSCRIGDKGFVEQLIHILRVACTQ-----LNVQESIEGVR	550
sp P35222 CTNB1_HUMAN	N---LALCPANHAPLR EQGAIPRLVQLLVRAHQDTQRRTSMG-----GTQQQFVEGVR	565
sp Q02248 CTNB1_MOUSE	N---LALCPANHAPLR EQGAIPRLVQLLVRAHQDTQRRTSMG-----GTQQQFVEGVR	565
sp P18824 ARM_DROME	N---LALCPANHAPLR EHGAIHHLVRLLMRAFDTERQRSSIATTGSQQPSAYADGVR	578
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DDB0191132 DDB_G0288877	MQG.....	701
sp Q18825 BAR1_CAEE L	VKDIHLCIQILRWITRDQDILNEVVFLLQTPENSRMGDGH TLPIFVLQKANVEENTKSS	610
sp P35222 CTNB1_HUMAN	MEEIVEGCTGALHILARDVHNR-----IVIRGLNTIPLFVQLLYSPIENIQRV	613
sp Q02248 CTNB1_MOUSE	MEEIVEGCTGALHILARDVHNR-----IVIRGLNTIPLFVQLLYSPIENIQRV	613
sp P18824 ARM_DROME	MEEIVEGTVGALHILARESHNR-----ALIRQQSVIPIFVRLLFNIEINIQRV	626
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DDB0191132 DDB_G0288877	-RGALKNLSCNPKNKLT IARSGGIE---LMNIAMQNHPNFAN-----	739
sp Q18825 BAR1_CAEE L	ALALIYNLMHHEQMANVLD RDDL VKMLQNVQM QSQTHPELASLANNILKMMYEKR-EKT	669
sp P35222 CTNB1_HUMAN	AAGVLC ELAQDKEAAEAIEAEGATAPLTLLH---SRNEGVATYAAAVLFRMS EDKPDQY	670
sp Q02248 CTNB1_MOUSE	AAGVLC ELAQDKEAAEAIEAEGATAPLTLLH---SRNEGVATYAAAVLFRMS EDKPDQY	670
sp P18824 ARM_DROME	AAGVLC ELAADKEGAIEIEQEGATGPLTDLH---SRNEGVATYAAAVLFRMS EDKPDQY	683
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DDB0191132 DDB_G0288877	-RFLELSRILQVALEDGNI*------	757
sp Q18825 BAR1_CAEE L	RN--TLPRYNSYLES-----QFGHMSMTTPRSEALNS-----SGE	702
sp P35222 CTNB1_HUMAN	KKRLSVELTSSLF RTEPMAWNETADLG LDIGA-----QGEPLG-YRQDDPSY-----R	717
sp Q02248 CTNB1_MOUSE	KKRLSVELTSSLF RTEPMAWNETADLG LDIGA-----QGEALG-YRQDDPSY-----R	717
sp P18824 ARM_DROME	KKRLSIELTNSLLREDNNIWANA-DLGMGPDLQDMLGPEEAYEGLYGQGPSVHSSHGGR	742
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DDB0191132 DDB_G0288877	757
sp Q18825 BAR1_CAEE L	VCEGAGEQWSTPLTDDTMMDSYCN S---SGRDSSKPYNSPMYHSP PAMYPEYSIGPPE TY	759
sp P35222 CTNB1_HUMAN	SFHSGGY-GQDALGMDPMMEHEM---GG---HHPGAD-----	747
sp Q02248 CTNB1_MOUSE	SFHSGGY-GQDALGMDPMMEHEM---GG---HHPGAD-----	747
sp P18824 ARM_DROME	AFHQQGY-DT--LPIDSMQGLEISSPVGGGGAGGAPGNNGGAVGGA-----	784
DDB0191132 DDB_G0288877	757
sp Q18825 BAR1_CAEE L	LDPHATASCYPRPTPPQ---YNSYD----RS--PPVYNDLP SNPGPSSHSSDYYP SRNS	809
sp P35222 CTNB1_HUMAN	-----YPVDGLPD-----LGHAQDLMDGLPPGDSNQLAWFDTDL-	781
sp Q02248 CTNB1_MOUSE	-----YPVDGLPD-----LGHAQDLMDGLPPGDSNQLAWFDTDL-	781
sp P18824 ARM_DROME	SGGGGNGI AIPPSGAP TSPYSMDMDVGEIDAGALNF DLDAMPTPPNDNNNLAAWYD TDC-	843
DDB0191132 DDB_G0288877	-- 757	
sp Q18825 BAR1_CAEE L	RF 811	
sp P35222 CTNB1_HUMAN	-- 781	
sp Q02248 CTNB1_MOUSE	-- 781	
sp P18824 ARM_DROME	-- 843	

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DDB0232260 DDB_G0269388	--MFKVSKYRHTVGKIDKRELWYPDVNTTGNSSASTFIKANSKWVALNWQSN	TGTIGLIP	58
sp P57737 COR07_HUMAN	MNRFRVSKFRHTEARPPRRESWISDIRAGTAPSCRNHKSSCSLIAFNS-DRP	GV	59
sp Q9D2V7 COR07_MOUSE	MSRFKVS	KFRHMEARPSRREAWISDIRAVTPTCGNHKSSCSLIAFNS-DRP	59
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DDB0232260 DDB_G0269388	LKSF	GKRG	118
sp P57737 COR07_HUMAN	LQGG	EDKRRVAHLGCHSDLV	116
sp Q9D2V7 COR07_MOUSE	LEGHEENKRV	VTYLGCHSDLV	116
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DDB0232260 DDB_G0269388	SASIVCSGHSKSV	ECIAFPVANNILASCSADKTLKI	178
sp P57737 COR07_HUMAN	APGV	VLGPEDLPVEVLQFHPTSDGILVS-AAGTTVKVWDAKQQPLTELA	175
sp Q9D2V7 COR07_MOUSE	VPGV	VLGPPELPVEVLQFHPTVDGVLVS-TAGTKVKVWDVAKQQPLTELA	175
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DDB0232260 DDB_G0269388	WNYDGS	LLVATGKDLKNRIIDARTGESI-QVGDGNQGVKASRVVWLGNL	237
sp P57737 COR07_HUMAN	WSRD	GALVGTACKDKQLRIFDPRTKPRASQSTQAHENS	235
sp Q9D2V7 COR07_MOUSE	WSRD	GAIVGTACKDKQLRIFDPRTQASQSTQAHENNRDIRLAWTGI	235
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DDB0232260 DDB_G0269388	RERQLVLWSSQDLSKPIKSITLDSSTGIISPIYDQDAQLLFISGSGDSSRVVFD	MNTQFT	297
sp P57737 COR07_HUMAN	RERE	VKLWDRFFSSALASLTLD	293
sp Q9D2V7 COR07_MOUSE	RERE	AKLWDRFLSSALASVTLDTSPGLIPLLPD	293
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DDB0232260 DDB_G0269388	KDPAFTE	LSPVPSDTPSKGICALPKRALD	357
sp P57737 COR07_HUMAN	-QPALSPVTQCVLES	VLRGAA	351
sp Q9D2V7 COR07_MOUSE	-QPALSPVTQCI	LENVLRGAALVPRRALAVMSCEVLQVLQ	351
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DDB0232260 DDB_G0269388	FADDLFPNTASTKPSLSSIDWLSGENKQPI	LVSLNPSDNQINNDL	417
sp P57737 COR07_HUMAN	FHEDLFPD	TAGCVPATDPHSWAGDNQVQKVSLNPACRPHPSFTSCL-VPPAE	410
sp Q9D2V7 COR07_MOUSE	FHEDLFPD	TAGSVPASDAHMMWAGDNQVQKVSLNPARRPHPCFTSSL-VPTME	410
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DDB0232260 DDB_G0269388	F--FID	NTNDSNVVEQSKSEPEQQQEEKISSSSSSSPTNSSSNVIN	475
sp P57737 COR07_HUMAN	QPAV	METPV-GDADASEGFSPPSSL-----TSPSTPSSLGPSLSSTSGIGTSPS-----	459
sp Q9D2V7 COR07_MOUSE	QPAEM--PR-AD	TLSEGFSSP-SSL-----MSPSTPSSLGPSLSSTSGIGTSPS-----	456
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DDB0232260 DDB_G0269388	DNIQRTGIVPKVVRSSKYRHI	SGSAHQSKQFYTNLKIN--GSTNTCIAVNS	532
sp P57737 COR07_HUMAN	---	LQSLGPSSKFRHAQGTVLHRD	515
sp Q9D2V7 COR07_MOUSE	---	LQSLGPSSKFRHTQGSLLHRD	512
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DDB0232260 DDB_G0269388	VGIGG	PLAVIPLADKGRQI--QVPCIEIGSQLCDYDLSQHNTSLVATGSEDSHV	590
sp P57737 COR07_HUMAN	LSSGGQ	VAVLELRKPGRLPD	575
sp Q9D2V7 COR07_MOUSE	LSSGGQ	VAVLELQKPGRLPD	572
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DDB0232260 DDB_G0269388	TGGIPKTTANKSN	NYTTTEADFVGHNRKVISVNFHPTAENVLITSGGDMVVKLWDL	650
sp P57737 COR07_HUMAN	AEGLEEV	-----LTPPETVL	628
sp Q9D2V7 COR07_MOUSE	PGGLENV	-----LTPPETVL	625
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DDB0232260 DDB_G0269388	AGEKLSFANVHTDMITSVDV	VNWTGDKILTSSKDKKMRI	710
sp P57737 COR07_HUMAN	DR	LKLQ---GHQDQIFSLAWSPDGQLATVCKDGRVRYRPRSGPEPLQE-GP	684
sp Q9D2V7 COR07_MOUSE	ERLKLQ---GHQDQIFSLAWSPDGQLATVCKDGHVRVYEPRSSPLPLQE-GP		681
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DDB0232260 DDB_G0269388	GKAVWL	GTGNIFSVGFNKSSE	770
sp P57737 COR07_HUMAN	ARIVW	CDGRCLLVSGFDSQSERQLLLYEAEALAGG-PLAVLGLDVAPSTLLPSYDPD	743
sp Q9D2V7 COR07_MOUSE	ARIVW	CDGGCLLVSGFDSRERQLQLYIADALAQG-PSALLGLDVAPSTLLPSYDPD	740
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DDB0232260 DDB_G0269388	VIYLAGK	GDSSIRMF	830

sp P57737 COR07_HUMAN	LVLLTGKGDTRVFLYELLPESPFFLECNSTSPDPHKGLVLL-PKTECDVREVELMRCLR	802
sp Q9D2V7 COR07_MOUSE	LVLLTGKGDTRVFLYEVLP EAPFFLECNSTSPDPHKGFVLL-PKTECDIQDVEFARCLR	799
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DDB0232260 DDB_G0269388	STDSTIEPLSMTVPRNQEFFQDDIYPDTRQTCTPVMTSEEWFDGCIREPEFVSMKPSDM	890
sp P57737 COR07_HUMAN	LRQSSLEPVAFR LPRVRKEFFQDDVFPDTAVIWEPVLSAEAWLQGANGQPWLLSLQPPDM	862
sp Q9D2V7 COR07_MOUSE	LRQTSLEPVAFR LPRVRKEFFQDDVFPDTAVTWEPALSAKAWFEGANGQPRLLSLQPPGM	859
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DDB0232260 DDB_G0269388	INLSDAPPPPKKEDKFVVSQE---VDNTPSRDQVTNSLLSRVSNQNASSNWEQIEKLKHN	947
sp P57737 COR07_HUMAN	SPVSQAPREAPARRAPSSAQYLEEKSDQQKKEELLNAMVAKLGNREDPL-----	911
sp Q9D2V7 COR07_MOUSE	TPVSQAPREVPAARRAPSSAQYLEEKSDQQKKEELLNAMVAKLGNREDPL-----	908
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DDB0232260 DDB_G0269388	FTDYDNGDISDSEWD*	962
sp P57737 COR07_HUMAN	-PQDSFEGVDEDEWD-	925
sp Q9D2V7 COR07_MOUSE	-PQDSFEGVDEDEWD-	922
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0201554 DDB_G0269100	-----MAAAPSGKTWIDVQKKTFTGWANNYLKER	29
sp Q9VEN1 FLNA_DROME	-----MEAERDLAEDAQWKKIQQNTFTRWANEHLKTI	32
sp P21333 FLNA_HUMAN	MSSSHSRAGQSAAGAAPGGGVDTDAEMPATEKDLAEDAPWKKIQQNTFTRWCNEHLKCV	60
sp Q8BTM8 FLNA_MOUSE	MSSSHSRGQSAAVASPGGSIDSRDAEMPATEKDLAEDAPWKKIQQNTFTRWCNEHLKCV	60
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DDB0201554 DDB_G0269100	ILKIEDLATSLDGLLLINLLEIISKKIL-KYNKAPKIRMQKIENNMAVNFIKSEGLK	88
sp Q9VEN1 FLNA_DROME	DRSINNLETDLSDGLRLIALIEVLSQKRMP-KYNKRPTFRSQKLENVSVALKFLQDEGIK	91
sp P21333 FLNA_HUMAN	SKRIANLQTDLSGLRLIALLEVLSQKKMHRKHNRPTFRQMQLENVSVALEFLDRESIK	120
sp Q8BTM8 FLNA_MOUSE	SKRIANLQTDLSGLRLIALLEVLSQKKMHRKHNRPTFRQMQLENVSVALEFLDRESIK	120
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DDB0201554 DDB_G0269100	LVGIGAEDIVDSQLKLILGLIWTLLILRYQIQMSE-----SDNSPKAALLEWVRK	137
sp Q9VEN1 FLNA_DROME	IVNIDSSDIVDCKLKLILGLIWTLLILHYSISMPMWDGEDDKQLNGSGHTPKQRLLNWIHA	151
sp P21333 FLNA_HUMAN	LVSIDSKAIVDGNLKLILGLIWTLLILHYSISMPMWDEEEDDEA--KKQTPKQRLLGWIQN	178
sp Q8BTM8 FLNA_MOUSE	LVSIDSKAIVDGNLKLILGLIWTLLILHYSISMPMWDEEEDDEA--KKQTPKQRLLGWIQN	178
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DDB0201554 DDB_G0269100	QVAPYKVVVNNFTSWCDGRVLSALTDSLKPGVREMSTL--TGDAVQDIDRSMIDIALEEY	195
sp Q9VEN1 FLNA_DROME	KIPD--LPINNFTNDWTTGKAVGALVDACAPGLCPDWELWDPKDAVQNASAMGLADDWL	209
sp P21333 FLNA_HUMAN	KLPQ--LPITNFSRDWQSGRALGALVDSCAPGLCPDWSWDASKPVTNAREAMQQADDWL	236
sp Q8BTM8 FLNA_MOUSE	KLPQ--LPITNFSRDWQSGRALGALVDSCAPGLCPDWSWDASKPVNNAREAMQQADDWL	236
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DDB0201554 DDB_G0269100	EIPKIMDAND-MNSLPDELSVITYVSYFRDYALNKEKRDADALAALKRRETSDASKVE	254
sp Q9VEN1 FLNA_DROME	NVRQLIKPEELVNPVDEQSMMTYLSQYPNSKLKTGA-----PLRPKTNPNVRV	258
sp P21333 FLNA_HUMAN	GIPQVITPEEIVDPNVDEHSVMTYLSQFPKAKLKPGA-----PLRPKLNPKKAR	285
sp Q8BTM8 FLNA_MOUSE	GIPQVITPEEIVDPNVDEHSVMTYLSQFPKAKLKPGA-----PLRPKLNPKKAR	285
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DDB0201554 DDB_G0269100	VYGPGEV--GGFVNKSADFHIKAVNYYGEPLANGGEGFTVSVVGADGVE--VPCKLVNDK	310
sp Q9VEN1 FLNA_DROME	AYGPGIEPIGPVVGAPANFTVETF-----SAGKGSVDVIQGPNGEIEKADVRFNNDK	311
sp P21333 FLNA_HUMAN	AYGPGIEPTGNMVKKRAEFTVETR-----SAGQGEVLVYVEDPAGHQEEAKVTANNDK	338
sp Q8BTM8 FLNA_MOUSE	AYGPGIEPTGNMVKKRAEFTVETR-----SAGQGEVLVYVEDPAGHQEEAKVTANNDK	338
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DDB0201554 DDB_G0269100	NGIYDASYTATVPQDYTVVVQLDDVHCKDSPYNVKIDGSDAQ--HSNAYGPGLEGGKV--	366
sp Q9VEN1 FLNA_DROME	NLYTYSYIPKSEGSCHKVAVKFSGRDIPKSPFPVKVEGHAGDASKVKVTGPGIQPNGVTI	371
sp P21333 FLNA_HUMAN	NRTFSVWYVPEVTGTHKVTVLFAGQHIKASPFEVYVDKSQGDASKVTAQGGPLEPSGNIA	398
sp Q8BTM8 FLNA_MOUSE	NRTFSVWYVPEVTGTHKVTVLFAGQHIKASPFEVYVDKSQGDASKVTAQGGPLEPSGNIA	398
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DDB0201554 DDB_G0269100	GVPAAFKIQGRNKDGETVTQGGDDFTVKVQ--SPEGPVDAQIKDNGDGSYDVEYKPTKG	423
sp Q9VEN1 FLNA_DROME	KKPTFFDILAKDA-----GRGVPEVIIIDPANHKTSVAAKVRQLENDTWRCEYVTALQ	424
sp P21333 FLNA_HUMAN	NKTTYFEIFTAGA-----GTGEVEVVIQDPMGQKGTVEPQLEARGDSTYRCSYQPTME	451
sp Q8BTM8 FLNA_MOUSE	NKTTYFEIFTAGA-----GMGEVEVVIQDPTGQKGTVEPQLEARGDSTYRCSYQPTME	451
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DDB0201554 DDB_G0269100	GDHTVEVFLRGEPLAQGPTEVKILNSDSQNSYCD--GPGFEK--AQAKRPTFTIHSVGA	479
sp Q9VEN1 FLNA_DROME	GLHSVNVFYAGTPIPNSPFPVKVAPLSD-ARKVRASGRGLQATGVRVGDDADFKIYTEG-	482
sp P21333 FLNA_HUMAN	GVHTVHVTFAGVPPIRSPYTVTVGQACN-PSACRAVGRGLQPKGVRVKETADFKVYTKG-	509
sp Q8BTM8 FLNA_MOUSE	GVHTVHVTFAGVPPIRSPYTVTVGQACN-PAACRAIGRGLQPKGVRVKETADFKVYTKG-	509
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DDB0201554 DDB_G0269100	DNKPCAAGGDPFQVSIISGHPV--NVGITDNDGTYTVAYTPEQPGDYEIQVTLNDEAIK	537
sp Q9VEN1 FLNA_DROME	-----AGEGEPEVRVIGPGGMNQNVMSKVDGNTYECHYPTKEGRYVIMVTFAGQVEVA	536
sp P21333 FLNA_HUMAN	-----AGSGELKVTVKGPKEER-VKQKDLGDGVYGFEEYPMVPGTYIVTITWGGQNIG	562
sp Q8BTM8 FLNA_MOUSE	-----AGSGELKVTVKGPKEER-VKQKDLGDGVYGFEEYPTIPGTYTVTITWGGQNIG	562
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DDB0201554 DDB_G0269100	DIPKSIHIKPAADPEKSYAEGPLDGGECFQPSKFKIHAVDPDGVHRTDGGDGFVVTIEG	597
sp Q9VEN1 FLNA_DROME	KSPFEVKVGPKKE--SSIVAYGPGLSGVIYGPAAFFVETNG-E-----TG--ALGFTVAG	587
sp P21333 FLNA_HUMAN	RSPFEVKVGTECGNQKVRWGPGLGEGVVGKSADFVVEAIGDD-----VG--TLGFSVEG	615
sp Q8BTM8 FLNA_MOUSE	RSPFEVKVGTECGNQKVRWGPGLGEGIVGKSADFVVEAIGDD-----VG--TLGFSVEG	615
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DDB0201554 DDB_G0269100	PAPVDPVMVDNGDGTVDVEFEPKEAGDYVINLTLDGDNVNGFPKTVTVPAPSAEHS---	654
sp Q9VEN1 FLNA_DROME	PSQAEIECHDNGDGSALVKYHPTAVGEYAVHILCDNEDIPKSPFIAQILP-RTDFHPELV	646
sp P21333 FLNA_HUMAN	PSQAKIECDDKGDGSCDVRYPQEAGEYAVHVLCNSEDIRLSPFMADIRDAPQDFHPDRV	675
sp Q8BTM8 FLNA_MOUSE	PSQAKIECDDKGDGSCDVRYPQEAGEYAVHVLCNSEDIRLSPFMADIREAPQDFHPDRV	675
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DDB0201554 DDB_G0269100	YAEGLV--KVFDNAPAEFTTFAVDTKGVARTDGGDPFEVAINGPDGLVVDKVTDNND	712
sp Q9VEN1 FLNA_DROME	KASGPGLEKNGVTINQPTSFTVDP ----- SKAGNAPLDVVVQDVFGTKLPVELKNNPD	699
sp P21333 FLNA_HUMAN	KARGPGLEKTVAVNKPAEFTVDA ----- KHGGKAPLRVQVQDNEGCPVEALVKDNGN	728
sp Q8BTM8 FLNA_MOUSE	KARGPGLEKTVAVNKPAEFTVDA ----- KHAGKAPLRVQVQDNEGCSVEATVKDNGN	728
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DDB0201554 DDB_G0269100	GTGTVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCI EGANGED--SSFGSF-----	761
sp Q9VEN1 FLNA_DROME	GTKKVTYPTPTSGVPHTVEVNYGGVSTPNSPHRVYVGPVDAAKVQAFGPWLQ-PGVRPNA	758
sp P21333 FLNA_HUMAN	GTYSCSYVPRKPVKHTAMVSWGGVSIIPNSPFRVNVGAGSHPNKVKVYGPVAKTGLKAHE	788
sp Q8BTM8 FLNA_MOUSE	GTYSCSYVPRKPVKHTAMVSWGGVSIIPNSPFRVNVGAGSHPNKVKVYGPVAKTGLKAHE	788
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DDB0201554 DDB_G0269100	--TFTVAAKN-KKGEV-----	774
sp Q9VEN1 FLNA_DROME	ATHFNVDAREAGDAELK-----	775
sp P21333 FLNA_HUMAN	PTYFTVDCAEAGQGDVSIIGKCAPGVVGPAAEADIDFDIIRNDNTFTVKYTPRGAGSYTI	848
sp Q8BTM8 FLNA_MOUSE	PTYFTVDCTEAGQGDVSIIGKCAPGVVGPTEADIDFDIIRNDNTFTVKYTPCGAGSYTI	848
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DDB0201554 DDB_G0269100	-----KTYGGDKFE	783
sp Q9VEN1 FLNA_DROME	-----	775
sp P21333 FLNA_HUMAN	MVLFADQATPTSPIRVKVEPSHDASKVKAEGPGLSRTGVELGKPTHFTVNAKAAGKGKLD	908
sp Q8BTM8 FLNA_MOUSE	MVLFADQATPTSPIRVKVEPSHDASKVKAEGPGLNRTGVELGKPTHFTVNAKTAGKGKLD	908
DDB0201554 DDB_G0269100	VSITG---PAEEITLDAIDNQDGYTAAYSLVGNRSTGVKLNKGHIEGSPFKQVLGNP	840
sp Q9VEN1 FLNA_DROME	VKIIHE-ETKIEVPCRIIDNEDNTYSVEVIPPCKGAYTTMTYGGQRVPLGEK-VVVEQT	833
sp P21333 FLNA_HUMAN	VQFSGLTKGDAVRVDIIDHHDNTYTVKYTPVQQGPVGVNVTYGGDIPKSPFSVAVSPS	968
sp Q8BTM8 FLNA_MOUSE	VQFSGLAKGDAVRVDIIDHHDNTYTVKYIPVQQGPVGVNVTYGGDHIPKSPFSVGVS	968
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DDB0201554 DDB_G0269100	GKKN-PEVK-----SFTTTRTAN*------	857
sp Q9VEN1 FLNA_DROME	VDVSKIKVDGLEPSVIMNAATDF-----	856
sp P21333 FLNA_HUMAN	LDLSKIKVSGLGKVDVGKDQEFVTKSKGAGGQGVASKIVGPSGAAPCKVEPGLGADN	1028
sp Q8BTM8 FLNA_MOUSE	LDLSKIKVSGLGKVDVGKDQEFVTKSKGAGGQGVASKIVSPSGAAPCKVEPGLGADN	1028
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DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	-----	856
sp P21333 FLNA_HUMAN	SVVRFVLPREEGPYEVVTDYGVVPVGPSPFPLEAVAPTKPSKVKAFFGGLQGGAGSPARF	1088
sp Q8BTM8 FLNA_MOUSE	SVVRFVLPREEGPYEVVTDYGVVPVGPSPFPLEAVAPTKPSKVKAFFGGLQGGNAGSPARF	1088
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	-----	856
sp P21333 FLNA_HUMAN	TIDTKGAGTGGLGLTVEGPCEAQLECLDNGDGTCSVSYVPTPEGDYINILFADTHIPGS	1148
sp Q8BTM8 FLNA_MOUSE	TIDTKGAGTGGLGLTVEGPCEAQLECLDNGDGTCSVSYVPTPEGDYINILFADTHIPGS	1148
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	-----MVDMSKVGSN-----	866
sp P21333 FLNA_HUMAN	PFKAHVVPFCFASKVKCSGPGLERATAGEVGQFQVDCSSAGSAELTIEICSEAGLPAEVY	1208
sp Q8BTM8 FLNA_MOUSE	PFKAHVAPCFDASKVKCSGPGLERATAGEVGQFQVDCSSAGSAELTIEICSEAGLPAEVY	1208
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	-----IDSGKLSC-----	874
sp P21333 FLNA_HUMAN	IQDHGDGHTITYIPLCPGAYTVTIKYGQGPVPNFPKSLQVEPAVDTSGVQCYPGPIEGQ	1268
sp Q8BTM8 FLNA_MOUSE	IQDHGDGHTITYIPLCPGAYTVTIKYGQGPVPNFPKSLQVEPAVDTSGVQCYPGPIEGQ	1268
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	-----AIFDPMGHVLPISKIVQGPTDDIFRIMYTPFEAG	907
sp P21333 FLNA_HUMAN	GVFREATTTFESVDARALTQTGGPHVKARVANPSG-NLTETVYQDRGDGMKYVEYTPYEEG	1327
sp Q8BTM8 FLNA_MOUSE	GVFREATTTFESVDARALTQTGGPHVKARVANPSG-NLDTYVQDCGDGTYSKYVEYTPYEEG	1327

DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	RHTIELMYDNIPVPGSPFVNVKSGCDPARCKAYGPGLEKGLTNQKNKFTVETKGAGNGG	967
sp P21333 FLNA_HUMAN	LHSVDTVYDGSPVPSSPFQVPVTEGCDPSRVRVHGPGIQSGTTNKPKNKFTVETRGAGTGG	1387
sp Q8BTM8 FLNA_MOUSE	VHSVDTVYDGSPVPSSPFQVPVTEGCDPSRVRVHGPGIQSGTTNKPKNKFTVETRGAGTGG	1387
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	LSLAIEGPGSEAKMCTDNRDGSCVDYLATDPGEYDITIRFADKHIPGSPFRVLVEETVD	1027
sp P21333 FLNA_HUMAN	LGLAVEGPGSEAKMSCMDNKDGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFKVPVHDVTD	1447
sp Q8BTM8 FLNA_MOUSE	LGLAVEGPGSEAKMSCMDNKDGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFKVPVHDVTD	1447
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	PSKVKVYGPGLIEHGQVRESVPTFFNVDVGEAGPGRIAVKLTNSGIPVDNLRVEDKGNCI	1087
sp P21333 FLNA_HUMAN	ASKVKCSGPGLSPGMVRANLPQSFQVDTSKAGVAPLQVKVQGPVKGLV-EPVDVVDNADGT	1506
sp Q8BTM8 FLNA_MOUSE	ASKVKCSGPGLSPGMVRANLPQSFQVDTSKAGVAPLQVKVQGPVKGLV-EPVDVVDNADGT	1506
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	YAVHYVPPKAGSVLTCQVKFSEVEVPCSPFVMTVFPKSEPTKVVKVGVNE-KKKTPASLP	1146
sp P21333 FLNA_HUMAN	QTVNYVPSREGPY-SISVLVGDEEVPSPFKVKVLPTHDASKVKASGPGLNTTGVPASLP	1565
sp Q8BTM8 FLNA_MOUSE	QTVNYVPSREGSY-SISVLVGEEVPSPFVKVLPTHDASKVKASGPGLNTTGVPASLP	1565
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	AEFEIDTKQAGQADINVAIKNPKGKAMQPRLEEVSTGTYVVSFVPDECGTYQCSIKYGDK	1206
sp P21333 FLNA_HUMAN	VEFTIDAKDAGEGLLAVQITDPEGKPKKTHIQDNHDGTYTVAYVPDVTGRYTILIKYGGD	1625
sp Q8BTM8 FLNA_MOUSE	VEFTIDAKDAGEGLLAVQITDPEGKPKKTHIQDNHDGTYTVAYVPDVPGRYTILIKYGGD	1625
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	EIEGSPFKLEAFPTGEAKKCKLVEQAPK ----- IQTSGSQSHLKVDAREAGDGAVT	1257
sp P21333 FLNA_HUMAN	EIPFSPYRVRAVPTGDASKCTVTVSIGGHGLGAGIGPTIQIGEETVITVDTKAAGKGKVT	1685
sp Q8BTM8 FLNA_MOUSE	EIPFSPYRVRAVPTGDASKCTVTVSIGGHGLGAGIGPTIQIGEETVITVDTKAAGKGKVT	1685
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	CKITNKAGSEIVDIDVIEKDGFDDILYALNDPGDYDINVKFGGKDIPNGSFSIKAVESIE	1317
sp P21333 FLNA_HUMAN	CTVCTPDGSEVDVDVVENEDGTFDIFYTAPQPGKYVICVRFGGEHVPNSPFQVTALAGDQ	1745
sp Q8BTM8 FLNA_MOUSE	CTVCTPDGSEVDVDVVENEDGTFDIFYTAPQPGKYVICVRFGGEHVPNSPFQVTALAGDQ	1745
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	QYSHSEYIEEHHTKV--VQQTQ ---- S--ELVNGKSEITYRSVAFKLPPTTGGNV	1367
sp P21333 FLNA_HUMAN	PSVQPPLRSQQLAPQYTYAQQGQQTWAPERPLVGVNGLDVTSLRP-FDLVIPFTIKKGEI	1804
sp Q8BTM8 FLNA_MOUSE	PTVQTPLRSQQLAPQYNYPQGSQQTWIPERPMVGVNGLDVTSLRP-FDLVIPFTIKKGEI	1804
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	TAEVRMPSGKVDPVIQDNRDGTVSVKYDPREEGSHLELVVKYNGEPVQGSPPKFHVDSIT	1427
sp P21333 FLNA_HUMAN	TGEVRMPSGKVAQPTITDNKDGTVTVRYAPSEAGLHEMDIRYDNMHIPGSPLQFYVDYVN	1864
sp Q8BTM8 FLNA_MOUSE	TGEVRMPSGKVAQPSITDNKDGTVTVRYSPSEAGLHEMDIRYDNMHIPGSPLQFYVDYVN	1864
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	SGYVTAYGPGLTHGVTGEPANFTISTKGASAGGLTMAVEGPSKADINYHDNKDGTVSQY	1487
sp P21333 FLNA_HUMAN	CGHVTAYGPGLTHGVVNKPATFTVNTKDAGEGGLSLAIEGPSKAEISCTDNQDGTCSVSY	1924
sp Q8BTM8 FLNA_MOUSE	CGHITAYGPGLTHGVVNKPATFTVNTKDAGEGGLSLAIEGPSKAEISCTDNQDGTCSVSY	1924
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	LPTAPGEYQVSVRFGDKHIKGSPLYFAKITGEGRKRN-QISVGSCEVTMPGDIITDDDLRA	1546
sp P21333 FLNA_HUMAN	LPVLPGDYSILVKYNEQHVPGPSPTARVTGDDSMRMSHLKVGs--AADIPINISETDLSL	1982
sp Q8BTM8 FLNA_MOUSE	LPVLPGDYSILVKYNDQHIPGPSPTARVTGDDSMRMSHLKVGs--AADIPINISETDLSL	1982
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	LNASIQAPSGLEPCFLKRMPTGNIGISFTPREIGEHLVSVKRLGKHINNSPFKVTVCER	1606
sp P21333 FLNA_HUMAN	LTATVPPPSGREPECLLKRLRNGHVGISFVPKETGEHLVHVKNKGQHVASSPIPVIISQS	2042
sp Q8BTM8 FLNA_MOUSE	LTATVPPPSGREPECLLKRLRNGHVGISFVPKETGEHLVHVKNKGQHVASSPIPVIISQS	2042

DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	EVGD AKK VSGTGLKEGQTHADNIFSV D TRNAGFGGLSVSIEG PSK AEIQCTDKDDGTL	1666
sp P21333 FLNA_HUMAN	EIGDASRV RV SGQGLHEGHTFEPAEFIIDTRDAGYGGLSLSIEG PSK VDINTEDLEDGTC	2102
sp Q8BTM8 FLNA_MOUSE	EIGDASRV RV SGQGLHEGHTFEPAEFIIDTRDAGYGGLSLSIEG PSK VDINTEDLEDGTC	2102
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	NISYK PTE PGYYIVNLKFADHHV EG SPFTVKVAG ES NRKREKIQ RER DAVPITEIGSQC	1726
sp P21333 FLNA_HUMAN	RVTYC PTE PGNYIINIKFADQHVP GS PF SVK VTGEGR--VKESITRRRRAPS VAN VGSHC	2160
sp Q8BTM8 FLNA_MOUSE	RVTYC PTE PGNYIINIKFADQHVP GS PF SVK VTGEGR--VKESITRRRRAPS VAN IGSHC	2160
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	KLTFKMPGITSFDLAACVTS PS SNVTEDAEIQEVEDGLYAVH FV PKELGVHTVSVRYSEM H	1786
sp P21333 FLNA_HUMAN	DL SL KIPEISIQDMTAQVTS PS SGKTHEAEIVEGENHTYCIRFVPAEMGHTHTVSVKYKGQH	2220
sp Q8BTM8 FLNA_MOUSE	DL SL KIPEISIQDMTAQVTS PS SGKTHEAEIVEGENHTYCIRFVPAEMGMHTVSVKYKGQH	2220
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	IPGSPFQFTVGPLRDSGSHLVKAGGSGLERGVVGEAAEFNVWTR EAG GGSLAISVEG PSK	1846
sp P21333 FLNA_HUMAN	VP GS PFQFTVGPLGEGGAHKVRAGGPGLERAEAGVPAEF SIW TR EAG AGGLAIAVEG PSK	2280
sp Q8BTM8 FLNA_MOUSE	VP GS PFQFTVGPLGEGGAHKVRAGGPGLERAEVGP AE F GIW TR EAG AGGLAIAVEG PSK	2280
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	ADIEF KDR KDGS CD VS YK VT EP GEYRVGLKFNDRHIPDS PF KVYVSPDAGDAHKLE VQ QF	1906
sp P21333 FLNA_HUMAN	AEIS FED RKDGSCGVAYV VQ EPGDYEVSVKFNEEHIPDS PF VVPV AS PSGDARRLTVSS L	2340
sp Q8BTM8 FLNA_MOUSE	AEIS FED RKDGSCGVAYV VQ EPGDYEVSVKFNEEHIPDS PF VVPV AS PSGDARRLTVSS L	2340
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	PQGNIQADAPYQFMV RK NGAKGELDAKIVAPSGTDDDCFIQVIDGEMYSVRFYPRENGI H	1966
sp P21333 FLNA_HUMAN	QESGLKVNQ PAS FAVSLNGAKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGVY	2400
sp Q8BTM8 FLNA_MOUSE	QESGLKVNQ PAS FAVSLNGAKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGIY	2400
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	AIHVKFNGVHIPDS PF RIKVGKD--VADPAAVHASGNGLDEVKTGHKADFIINTCNAGVG	2024
sp P21333 FLNA_HUMAN	LIDVKFNGTHIPGS PF KIRVGE PG HGGDPLVSAYGAGLEGGVTGNPAEFV VNT SNAGAG	2460
sp Q8BTM8 FLNA_MOUSE	LIDVKFNGTHIPGS PF KIRVGE PG HGGDPLVSAYGAGLEGGVTGSPA EF IV VNT SNAGAG	2460
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	T LAV SIDG PS KVAMDC TE VEEGYKVRYP LL PGEHYITVKYNN-MHIVGSPFKV NAT GDK	2083
sp P21333 FLNA_HUMAN	ALSV TID G PS KVKMDCQCEP EG YRV TYT PMAPGSYLISIKYGGPYHIGGS PF KAKVTGPR	2520
sp Q8BTM8 FLNA_MOUSE	ALSV TID G PS KVKMDCQCEP EG YRV TYT PMAPGSYLISIKYGGPYHIGGS PF KAKVTGPR	2520
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	LADEG-AQETSTVIVETVQKVAKGGKNTGVHLPTFKSDASKV VSK GMGLKKAYIGKQ Q QF	2142
sp P21333 FLNA_HUMAN	LVS NH SLHETSSVFVDSLT KAT CAP-QHGAP-GPGPADASKV VAK GLGLSKAYVGQK SS F	2578
sp Q8BTM8 FLNA_MOUSE	LVS NH SLHETSSVFVDSLT KVAT VP-QHATS-GPGPADVSKV VAK GLGLSKAYVGQK SN F	2578
DDB0201554 DDB_G0269100	-----	857
sp Q9VEN1 FLNA_DROME	SISATDAGNNILYVGMYPKGPCEEFHVKHAGHNNYNVQYLVRDRGQYVLLIKWGE EH IP	2202
sp P21333 FLNA_HUMAN	TVD CS KAGN M LLVG VH GPRT PC EEILVKHMGSR LY SVSYLLKDKGEYTLVVKW GDE HIP	2638
sp Q8BTM8 FLNA_MOUSE	TVD CS KAGN M LLVG VH GPRT PC EEILVKHMGSR LY SVSYLLKDKGEYTLVVKW GDE HIP	2638
DDB0201554 DDB_G0269100	----- 857	
sp Q9VEN1 FLNA_DROME	GS PF QIDV- 2210	
sp P21333 FLNA_HUMAN	GS PY RVVVP 2647	
sp Q8BTM8 FLNA_MOUSE	GS PY RI M VP 2647	

sp P12883 MYH7_HUMAN	MGDSEMAVFGAAAPYLRKSEKERLEAQT	60
DDB0185049 DDB_G0274455	-----	0
sp Q9V3Z6 MYO7A_DROME	-----MV-IVTRGDIWIE-----PASGREFD-----VAIGARVVSAGERRIQ	37
sp P12883 MYH7_HUMAN	AET EY G K T V T V - K E D Q V M Q Q N P P K F D K I E D M A M L T F L H E P A V L Y N L K D R Y G S W M I Y T Y S G	119
DDB0185049 DDB_G0274455	-----MEDDDTLNGEYFQPVEDMITLPILTEESLLLLNLMRYKKKEIYTYTG	47
sp Q9V3Z6 MYO7A_DROME	VRDDGDGEVWLAPERRIKAMHASSVQGVEDMISLGDLHEAGILRNLLIRYKENLIYTYTG	97
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sp P12883 MYH7_HUMAN	LFCVTVPYKWLVPYTPVVAAYRGKKRSEAPPHIFSIDNAYQYMLTDRENQSILITGE	179
DDB0185049 DDB_G0274455	SILVAVNPYEILPIYTADIVKSYFAKSRNLMPLHIFAVSDAAFTNMIEEGKNQSIISGE	10
sp Q9V3Z6 MYO7A_DROME	SILVAVNPYQILPIYTGDIKLYKERKIGELPPHIFAIGDNAYAHMKRYRQDQCIVISGE	157
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sp P12883 MYH7_HUMAN	SGAGKT VNTKRVIQYFAVIAAIGDRSKKDQSPGKGTLEDQIIQANPALEAFGNAKTVRND	239
DDB0185049 DDB_G0274455	SGAGKTESTKLIQYLAARTN-----RHSQVEQMIVESSPILEAFGNAKTIRNN	156
sp Q9V3Z6 MYO7A_DROME	SGAGKTESTKLILQYLAISG-----KHSWIEQQILEANPILEAFGNAKTIRND	206
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sp P12883 MYH7_HUMAN	NSSRFGKFIRIHFGATGKLASADIETYLLEKSRVIFQLKAERDYHIFYQLSNKKPELLD	299
DDB0185049 DDB_G0274455	NSSRFGKFIEIQFNREGHISGARINYLLEKSRISHQASSERNYHIFYQLLAGASDELKE	216
sp Q9V3Z6 MYO7A_DROME	NSSRFGKYIDIHFSANGVIEGAKIEQYLLKSRIVSQNHSEERNYHVFCYILAGLSADEKS	266
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sp P12883 MYH7_HUMAN	MLLITNPNPYDAFISQGE--TTVASIDDAEELMATDNADFVLGFTSEEKNSMYKLTGAIMH	358
DDB0185049 DDB_G0274455	KL-KLGEPEDYHYLSQSGCIRIENINDVEDFEHVKYAMNVGLPEDKQFTIFSIVSAVLH	275
sp Q9V3Z6 MYO7A_DROME	RL-DLGMADYKYL TGGNSITCEGRDDAAEFSDIRSAMKVLFLSDQEIWEIILKLAALLH	325
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sp P12883 MYH7_HUMAN	FGNMKFKLKQREEQAPDGT EAD--KSA YLMGLNSADLLKGLCHPRVKVGN EYVTKGQ	415
DDB0185049 DDB_G0274455	IGNLKFEKSEKTQGAEGSEVSNKDTLKIIAQLLSVDPVKLETCLTIRHVLIRGQNFVIPL	335
sp Q9V3Z6 MYO7A_DROME	CGNIKYKATVVD-NLDAT EIP EHNVERVAGLLGLPIQPLIDALT RRTLFAHGETV VSTL	384
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sp P12883 MYH7_HUMAN	NVQQVIYATGALAKAVYERMFNWMVTRINATLETQKPR-QYF IGVLDIAGFEIFDFNSFE	474
DDB0185049 DDB_G0274455	KVNEAEDTRDSLAKALYGNVFNWLVFINSKIHKPQKN-STF IGVLDFGFENFKKNSFE	394
sp Q9V3Z6 MYO7A_DROME	SRDQSVDRDAFVKGIYGRMFVHVRKINTAIFKPRGTSRNAIGVLDFGFENFDQNSFE	444
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sp P12883 MYH7_HUMAN	QLCINFNT EKLQQFFNHMFVLEQE EYKKEGIEWTFIDFGMDLQACIDLIE-KPMGIMSI	533
DDB0185049 DDB_G0274455	QFCINFANEKLQQHFNQHF KLEQE EYKEKINWSKIVYN-DNQ ECLDLEIKRPLGILSL	453
sp Q9V3Z6 MYO7A_DROME	QFCINYANENLQQFFVQHIFKLEQE EYNHEAINWQHIEFV-DNQDALDLIAIKQLNIMAL	503
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sp P12883 MYH7_HUMAN	LEE ECFPKATDMTFKAKLFDNHLGKSANFQKPRNIKGP EAHFSLIH YAGIVDYNII GW	593
DDB0185049 DDB_G0274455	LDEESRF PQATDLYLDKLHTNHE-KHPY YEKPRRSK----NTFVVKHYAGEVHYDTQGF	508
sp Q9V3Z6 MYO7A_DROME	IDEEARFPKGTDTMLAKLHKTHG-SHKNYLKP KSDI---NTS FGLNHFAGVVFYDTRGF	559
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sp P12883 MYH7_HUMAN	LQKNKDPLNETVVG L YQKSS LKLLSTLFANYAGADAPIEKGKGAKKGSS FQTVSALHRE	653
DDB0185049 DDB_G0274455	LDKNKDTVSDLLSSLLQGS KSKFIELFPPREGDDSDKGREKKK-----TTAGQTFKT	563
sp Q9V3Z6 MYO7A_DROME	LDKNRDTFSPDLLHLVSQSTNKFRLQIFAQDIEMGAETRK---RT-----PTLSTQFRK	610
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sp P12883 MYH7_HUMAN	NLNKMLTNLRSTH P HVRCIIPNETKSPGVMDNPLVMHQLRCNGVLEGRICRKGFPNRI	713
DDB0185049 DDB_G0274455	QLQSLINILSSQPHYVRCIKPNTTKEPAVYDRELIQAQLRYAGMMETIRIRKLGYPIRH	623
sp Q9V3Z6 MYO7A_DROME	SLDALMKT LSSCQ PFFIRCIKP NELKKPMMFDRGLCCRQLRYS GMMETIRIRRAGYPIRH	670
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sp P12883 MYH7_HUMAN	LYGDFRQRYRILNPAAIPEGQFIDSRKGA EKLLSSLDIDHNQYKFGHTKVFFKAGLLGLL	773
DDB0185049 DDB_G0274455	THKEFRDRYLILDYRARSTDHKQTCAGLINLLSGTGGLERDEWQLGNTKVFIRDHQYKLK	683
sp Q9V3Z6 MYO7A_DROME	GFREFVERYRFLIPGVP-PAHRTDCQAATS RIC-AVVLGKSDYQLGHTKVFLKDAHDLFL	728
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sp P12883 MYH7_HUMAN	EEMRDERLSRIITRIQAQSGV LARMEYKLLERRDSLLVIQWNIRAFMGVKNWPWMKLY	833

DDB0185049 DDB_G0274455	EELRKLLKLLKVVTLIQ ----- SVWRMYRCKKRYQQIRAS	717
sp Q9V3Z6 MY07A_DROME	EQERDRLTRKILILQRSIRGWVYRRFLRLRA---AAITVQRFWKGYAQRKRYRNMVRVG	785
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sp P12883 MYH7_HUMAN	FKI-KPLLKSAEREKEMASMKEEFTRLKEALEKSEARRK ----- ELEEKMVSLLEQEKND	886
DDB0185049 DDB_G0274455	AKILGAAMLSH-----SSRRDFEQRQAVQ----RIKGFFKMLTYQKQ-FKIIQ----	761
sp Q9V3Z6 MY07A_DROME	YMLRLQALIRSR-----VLSHRFRLRGHIVGLQAHARGYLVRREYGHKMWAVI-----	833
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sp P12883 MYH7_HUMAN	LQLQVQAEQDNLA----DAEERCDQLIKNKIQLEAKVKEMNERLEDEEEMNAEL-----	936
DDB0185049 DDB_G0274455	--INLRIVQNNIRSFIAARRHSRNAVLLKRDRL--NARMLEI-QREKDEEERNRQEKKEERDR	816
sp Q9V3Z6 MY07A_DROME	-----KIQSHVRRMIAMRRYRKLRLL-EHKQ--FAEVLQL-RKLEEQELLHRGNKHAREI	883
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sp P12883 MYH7_HUMAN	-----TAKKRKLEDECSELKRDID--DLELTAKVEKEKHATENKVKNLTEEMAG	984
DDB0185049 DDB_G0274455	QEKEDKE-KETADRRQLQEEQKRREEELRAKREEEELKKLEEKKSQ--LKELNQIDELSS	873
sp Q9V3Z6 MY07A_DROME	AEQHYRDLRHLERREIQEQ-----LENRRRV--EVNMIINDA--	920
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sp P12883 MYH7_HUMAN	LDEIIAKLTKEKKALQEAHQALDDLQAEEDKVNTLTAKVKLEQQVDDLEGSLEQEKKV	1044
DDB0185049 DDB_G0274455	LERMLKEQ-----QDKNINELDD ----FVNSLEA--FSFEGGVDDSQPYSF-NHKM	917
sp Q9V3Z6 MY07A_DROME	-----ARKQEEPVDGK ---LVEAMFD--FLPDSSSDAPTPHGGRETSTV	959
	: : : ** *: : . : *	
sp P12883 MYH7_HUMAN	RMDLERAKRK-----LEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNA ----- RI-	1094
DDB0185049 DDB_G0274455	YEMSPEALDKISITDLLQGLKQTVRSVTKFEVDE ----- SKFELPPGIENVLKRAP	968
sp Q9V3Z6 MY07A_DROME	FNDLPHAQ-NVNQDDIIAPTH-----ISEDEEDL-----SEFKF-----	992
	.* : : : : . * * ..* : :	
sp P12883 MYH7_HUMAN	-----EDEQALGSQQLKKLKLQARIEELEEELEAERTAKAVEKL ----- RSDLSR--	1141
DDB0185049 DDB_G0274455	GIKRQASSFLPGQPIPDVYSSPQYPVDEADDDDSNNNYINSNNGDLPLPTSQSSDFSLPP	1028
sp Q9V3Z6 MY07A_DROME	--QKFAATYFQGN-----VNHQYAKKALKH-----	1015
	*	
sp P12883 MYH7_HUMAN	-----ELEEISERLEEAGGATSVQIE-----M ----- NKKREAEFQKMRRDLEEA	1181
DDB0185049 DDB_G0274455	PPSSSSMDFGLPP-PPSSSSSGGTYSLPPMPVDFGMIDPILGAPPPPPS-TSDSTSP--	1084
sp Q9V3Z6 MY07A_DROME	-----P-LLPLHTQGDQLAAQAL ---WITILRFTGDMPEPKYHTMDRMDTTS	1058
	*. : . .	
sp P12883 MYH7_HUMAN	TLQHEATAAALRKKHADSV ----- AELGEQIDNL-QRVKQKLEKEK-SEFKL-ELDD	1230
DDB0185049 DDB_G0274455	-----SATATGNNTPNSSASASQSTNQVNPQPTVSVVELPQILNDEEISLYSFYDYAN	1138
sp Q9V3Z6 MY07A_DROME	VMSK--VTATLGRNFIRSKF---FQEAQLMGLDPDAFLKQKPRSIRHKLVSLE-----	1105
	: : : . * : : . : : : *	
sp P12883 MYH7_HUMAN	VTSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAETQRSVN-----DLTSQRA----	1278
DDB0185049 DDB_G0274455	KNFNIEK-LKQKDDIFSQKSHIKSSLL-VHSDAEQTKVAVEIFSKVLHYMNSNPLVSKK	1196
sp Q9V3Z6 MY07A_DROME	-----T-LKRKNKL-----GED--VRRRLQDDEYTA -----DSYQSWLQS	1137
	: * * . : . : : : : *	
sp P12883 MYH7_HUMAN	-----KLQTENGELSRLQD----- EKEALISQLTRGKLTYT	1309
DDB0185049 DDB_G0274455	DPADFYSVPVKFILTKGLAIESLRDEIYCQLIKQSTSNPIQDLNIRVWELIHFTCSTFPPT	1256
sp Q9V3Z6 MY07A_DROME	RPTSNLEKLHFIIGHGILRAELRDEIYCQICKQLTNNPLKSSHARGWILLSLCVGCFAFS	1197
	: : : * . *	
sp P12883 MYH7_HUMAN	QQLEDLKRQLEEEVKAKNALAHALQSAHDCDLLREQYEEETEAKAELQRVL-SKANSEV	1368
DDB0185049 DDB_G0274455	RKLIKYFAAYLKTIIQQSDVSKSVKDSAQSYF ----- ILQRFTLNGARKQV	1303
sp Q9V3Z6 MY07A_DROME	EKFVNYLRAFIREGPPGYA-----PYCEE ----- RLKRTFNNGTRNQP	1235
	: : . . *.* . : : :	
sp P12883 MYH7_HUMAN	AQWRTKYETDAIQRTLEEAKK--KLAQRLQEAEEAVEA -----VNAKCSSLEKTK	1418
DDB0185049 DDB_G0274455	PSVTE ----- LESIKENRPIFVRITATDGSCLKGLHIDSATTCQESSNDLSQRS	1351
sp Q9V3Z6 MY07A_DROME	PSWLE ----- LQATKSKKPIMLPITFMDGNTKTL LADSATTARELCNQLSDKI	1283
	. *: * . : : : : *	
sp P12883 MYH7_HUMAN	-HRL--QN--EIEDLMVDVERSNA-----AAAL--DKKQRNF ----- D	1450
DDB0185049 DDB_G0274455	RMRVNSKENGFTIIE-SFNGIERDIAPTDKLCDVLSKVENLQATL-SSKIQVNFKFVFKK	1409
sp Q9V3Z6 MY07A_DROME	SLKD---QFGFSLYIALFDKVVSSLGSGGDHVMDAISQCEQYAKEQGAQERNAPWRLFFRK	1340
	: : : : : : : .	
sp P12883 MYH7_HUMAN	KILAEWKQKYEESQSELESSQKEARSLSTELFK ----- LKNAYEESLEHLETFKRE	1501
DDB0185049 DDB_G0274455	KLFFDNITNNVPTTS-----INVENEFYHQLFNDL-FNSNYCKDQDYQISIGSLKL----	1460
sp Q9V3Z6 MY07A_DROME	EIFAPWHE--PT-H ---DQVATNLIYQQVVRGVKFGFYRCDKKEEDLAMIAAQQYFIEY	1392


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sp|P12883|MYH7_HUMAN      NKN ---- LQEEISDLTEQLGSSGKTIHELEKVRKQLEAEKMLQSALEAEAS-LEHEE      1555
DDB0185049|DDB_G0274455 -----QFESSDYTD -----EIRAWLPNGNR      1480
sp|Q9V3Z6|MYO7A_DROME    STDMSMERLFTLLPNFIPDFCLSGVDK-----AIERWAALV--      1428
                               :: * .

sp|P12883|MYH7_HUMAN      GKILRAQLFNFQIKAEIERKLAEKDEEMEQAKR-----      1588
DDB0185049|DDB_G0274455 GKYFTTDIEKNRDFDFINKYKSHKGLSPEDAKQMVQLLE-KHPLANCSLVVCCHQSESL      1539
sp|Q9V3Z6|MYO7A_DROME    -----LQAYKKSYYVKDKIAPLKIKEDIVSYAKYKWPLLFSEFYEAARN-SGP      1475
                               :. : .. . * .

sp|P12883|MYH7_HUMAN      -----NHLRVVDSLQTSL-DAETRSRNEALRV--KKKMEGDLNEMEIQLSHA      1632
DDB0185049|DDB_G0274455 PYP-KNFVLALNVNGINIYDPATSKMLESVKYSNQ -----SQQNLKSDDKSVSIILENK      1592
sp|Q9V3Z6|MYO7A_DROME    NLPKNDVIAVNWTVGVVVDQEQVLELE-SFPEITAVSSQKTNKVFTQTFSLSTVRGEE      1534
                               . : : * : : . . : : : . : .

sp|P12883|MYH7_HUMAN      NRMAAEAKQKVKSLSQSLKDTQIQLDDAVRANDDLKENIAIVERRNLLQAELEELRAVV      1692
DDB0185049|DDB_G0274455 STLQA-FTGDVQKLVS LIKEYSLYLRNNA-----KYARALKDYNVS-      1632
sp|Q9V3Z6|MYO7A_DROME    FTFQS---PNAEDIRDLVVYFLDGLKKRS-----KYVIALQDYRAP-      1572
                               : : : : : * : * . * : : .

sp|P12883|MYH7_HUMAN      EQTERSRKLAQEELIETSERVQLLHSONTSLINQKKMDADLSQLQTEVEEAVQECRNAE      1752
DDB0185049|DDB_G0274455 -----DTSLLPFKRNDIITITFK -----DQENKWFMGQLNG--      1663
sp|Q9V3Z6|MYO7A_DROME    -----SDGTSFLSFFKGLIILEDESCG--ESVLNNGWCIGRCDRSQ      1612
                               ..:* . : * : : : .

sp|P12883|MYH7_HUMAN      EKAKKAITDAAMMAEELKKEQDTSAPHLERMKKNMEQTIKDLQHRLD -----EAE-      1801
DDB0185049|DDB_G0274455 KEGSFPVDHVEILLSDVPPPPQVHP-VATLSPPMSPITIPNITNTPPPPPSISDSMSPPPQ      1722
sp|Q9V3Z6|MYO7A_DROME    ERGDFPAETVYVLPITLSKPPQDILA-LFNIE-----      1642
                               :... . : : * : : .

sp|P12883|MYH7_HUMAN      -----      1801
DDB0185049|DDB_G0274455 VGMLPPPPPPSVMGSTKPIEIPSLGIPPPPPSSSNSSVPNSPIGSPMMGIPPPPTISVH      1782
sp|Q9V3Z6|MYO7A_DROME    -----      1642

sp|P12883|MYH7_HUMAN      -----QIALKGKK-----      1810
DDB0185049|DDB_G0274455 SLNSNGNSTPPPLPSLSTPPTLSTPPPISSPPNFRSSLRVSMNLSNDGGDN-SSDDPS      1841
sp|Q9V3Z6|MYO7A_DROME    -----EAHHGRRLSMASNGGAVEPRDRPH      1666
                               . : .**

sp|P12883|MYH7_HUMAN      -----QLQKL-EARVRELENELEAEQKRNAESVKGMRKSERRIKELTY-QTE      1855
DDB0185049|DDB_G0274455 KRLTVSPAIGTDSQLAQWASTFRFSFKRASTL ----NQQQATLKRKAPVDNPTAFYFNKD      1897
sp|Q9V3Z6|MYO7A_DROME    -----TLMEYALDHFRLPKRTMS---K--TLTL---SSKRSEELWRYSRD      1704
                               * : :.* . : . : : . :

sp|P12883|MYH7_HUMAN      EDRKNLLRLQDLVDKLQLKVKAYKRRQAEAEQANTNLKFRKVQHELDEAEERADIAES      1915
DDB0185049|DDB_G0274455 PIKESL-----IE--MEAKL-----SKKAIKNFSEIMMWGDYPIP--KGQTASL      1938
sp|Q9V3Z6|MYO7A_DROME    PIKAPL-----LRKLQSKKEF-----AEEACFAFAAILKYMGLDPSK--RPRMGNE      1748
                               : * : : : : * : : : : .

sp|P12883|MYH7_HUMAN      QVNKLRAKSRDIGTKGLNEE-----      1935
DDB0185049|DDB_G0274455 VIQ--SIISRGIEHNLRLDEIYCQAYRQTNKPKVESAKKGFELIYFLSITFSPDSLQ      1996
sp|Q9V3Z6|MYO7A_DROME    ITD--HIFDGLPKHEILRLDEIYCLMKQLTDNRNRMSSEERGWELMWLATGLFACSQGLLK      1806
                               : . : . * . : *

sp|P12883|MYH7_HUMAN      -----      1935
DDB0185049|DDB_G0274455 PFMEQLMSRNIAIQSSSP-QLASLIAVCIKLESHPIPSYQQRKMGPSATEIQSFRSNLE      2055
sp|Q9V3Z6|MYO7A_DROME    ELLLF LRTRRHPISQDSMHR LQKTIR -----HGQRKYPPHQVEVAIQHKT      1853

sp|P12883|MYH7_HUMAN      -----      1935
DDB0185049|DDB_G0274455 NGDISTCKIRFIDQSTKLAKINTYTTIREITD TVCRQYGISQQSIKMFGISAVNETAGIS      2115
sp|Q9V3Z6|MYO7A_DROME    ---QIFHKVYFPDDTDEAFVDSSTRAKD---FCNNISQRL -----SLRTSEGF      1897

sp|P12883|MYH7_HUMAN      -----      1935
DDB0185049|DDB_G0274455 KVVSETDMIYDLARWEQSEEKGEFYFQVRRRFF--LDDV -----NKILDQEH      2161
sp|Q9V3Z6|MYO7A_DROME    LFV -----KIADKVISVPEGDFFDVVRHLTDWIKKARPIRDGANPQFTYQVFFMKK      1949

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sp P12883 MYH7_HUMAN	-----	1935
DDB0185049 DDB_G0274455	LWTD-- ICFELTYCQIRDEWMKGLYTNVNEKDSSIIAAILIQLLY-PNQSKLVL	2214
sp Q9V3Z6 MYO7A_DROME	LWTNTVPGKDRNADLIFHYHQELPKLLRGYHKCSR-EAAKLAALVFRVRFGENKQELQA	2008
sp P12883 MYH7_HUMAN	-----	1935
DDB0185049 DDB_G0274455	TKEVVRQVLPDQILNSQNIKVWISMIESQIFELVSQTPEYKLMFINLIGKSPLFGCTL	2274
sp Q9V3Z6 MYO7A_DROME	IPQMLRELIPSDIMKIQSTSEWKRISIVASYNQDGGMTSEDAKVAFLKI-VYRWPTFGSAF	2067
sp P12883 MYH7_HUMAN	-----	1935
DDB0185049 DDB_G0274455	FNIQQKENP--PKAWLAINKKGVSIFDPHTKESKNFWTFQISNVAFTDDTFCIMTGNL	2331
sp Q9V3Z6 MYO7A_DROME	FEVKQTTEPNYPEMLLIAINKHGVSLIHPVTKDILVTHPFTRISNWSSGNTYFHMTIGNL	2127
sp P12883 MYH7_HUMAN	-----	1935
DDB0185049 DDB_G0274455	MKPIKQFTTDEHSSIASVYQFYSSQ* -----	2357
sp Q9V3Z6 MYO7A_DROME	VRGSKLLCETSLGYKMDDLTSYISLMLTNMKNRTIRAN	2167

DDB0185208	DDB_G0274109	MATKGLNMDLLDLLLADLGRPKSSIKVTATVQTATPSS-----GKNFDNSD-----	47
sp Q09476 PXL1_CAEEEL		-----	0
tr Q2PDT4 Q2PDT4_DROME		-----MDRT--MYGKID-----PGARQPYRTARSKGILPGYALLAD-----	34
sp P49023 PAXI_HUMAN		-----MDDL DALLADLESTTSHISKRPVFLSEETPSYSPTGNHTYQEI AVPPPPVPPPP	53
sp Q8VI36 PAXI_MOUSE		-----MDDL DALLADLESTTSHISKRPVFLSEEPYSYPTGNHTYQEI AVPPPPVPPPP	53
DDB0185208	DDB_G0274109	IQNEIQSII-EEL-----DQQP-----QTVQTI STPA	73
sp Q09476 PXL1_CAEEEL		-----	0
tr Q2PDT4 Q2PDT4_DROME		LQNSVPGQPQQPQPQYGTVPKHHQALQQQQFVDNTPGYGSLRGKAQPPQVYQEHYSVETRSL	94
sp P49023 PAXI_HUMAN		SSEALNGTILDPLDQ---WQPSSSRFIHQQPQSSSPVYGS SAKTSSVSNPQ--DSVGSPC	108
sp Q8VI36 PAXI_MOUSE		SSEALNGTVL DPLDQ---WQPSGSRYAHQQPPSPLPVYSSSAKNSSASNTQ--DVGSLC	108
DDB0185208	DDB_G0274109	PK---NHNTTTTASFSVSSQ-PAPQPP-QQSQQIDGLDDLDELMESLNTSISTALKAVP	128
sp Q09476 PXL1_CAEEEL		-----	0
tr Q2PDT4 Q2PDT4_DROME		PTAGHDFNGSSTTPGYANQ----GSLPRQAAGASTGLSELDSLQLDQKIDVP-----	143
sp P49023 PAXI_HUMAN		SRVGEEL---HVYSFPNKQKSAEPSPTVMSTSLGSLSELDRLLLELNAVQHN-----	158
sp Q8VI36 PAXI_MOUSE		SRAGEEL---HVYSFPNKQKSAEPSPTVMSSSLGSLSELDRLLLELNAVQHS-----	158
DDB0185208	DDB_G0274109	TTPEEHITHANSNSPP-P-----S	146
sp Q09476 PXL1_CAEEEL		-----MPSDDR FADAVKPA	14
tr Q2PDT4 Q2PDT4_DROME		---VNYS-----PVSK-----Y-----NTMNSYATVEERPS	167
sp P49023 PAXI_HUMAN		--PPGFPADEANSSPPLGALSPLYGVPTNSPLGGKAGPLTKEKPKRNGGRGLEDVRPS	216
sp Q8VI36 PAXI_MOUSE		--PPGFPADEAESPPPLGALSPLYGIPENNTPLGGKAGPLVKEKPKRNGGRGLEDVRPS	216
		:	
DDB0185208	DDB_G0274109	LHKNTSSTNSASSLSRPNNNPVVSTPQPKVTSTATITTKQPAL----SKATLET--	199
sp Q09476 PXL1_CAEEEL		LEALLSDLQHTTEVLRR-----HISDRRSQSRDDFEQSYDLQGNLNTQS	59
tr Q2PDT4 Q2PDT4_DROME		VDSLLKELDNAHIYAVPN--GSAHKSPTGRHVTITVRE-TKTEKLTGDPGPGVTVEEQI	224
sp P49023 PAXI_HUMAN		VESLLDELESSVPSP-----VPAIT	236
sp Q8VI36 PAXI_MOUSE		VESLLDELESSVPSP-----VPAIT	236
		:. . . :	:
DDB0185208	DDB_G0274109	TSGNNVYSS-----QPSQSPPQPYKVATNSQ--PSSDDLDELLKGLSPSTTTT	247
sp Q09476 PXL1_CAEEEL		VSNGNITTSPIKRRSSEKDYKSKQERIEYENESRLNPPVYSRPSVQSLLSQVEEPIRAS	119
tr Q2PDT4 Q2PDT4_DROME		VQQKDSYT-PNHAV--P---GQQVHQAYTSQAT-----KELDDLMA SLDFKVSNG	269
sp P49023 PAXI_HUMAN		VNQGE MSS-PQRVT--S---TQQQTRISASSAT-----RELDELMASLDFKIQGL	281
sp Q8VI36 PAXI_MOUSE		VNQGE MSS-PQRVT--S---SQQQTRISASSAT-----RELDELMASLDFKMQGL	281
		. . : : * : .
DDB0185208	DDB_G0274109	TVPPPVRQDQHQQHHQHQQHHHHNPNHNQTQT VTTQINIGRTN----TPNNNNNNNTNS	302
sp Q09476 PXL1_CAEEEL		-----SSRKS LGPPSQ----AQSYSDVR SNGR	142
tr Q2PDT4 Q2PDT4_DROME		TN----GIGNGSHPPQHS---STVQHQTVDYARPNGSQ--AHLTQT--I EETTI	315
sp P49023 PAXI_HUMAN		EQ----RAD-GERCWA A-----GWPRDGGRSSPGGQDEGGFMAQKGTGSSSPPG	325
sp Q8VI36 PAXI_MOUSE		EQ----RVD-GERPWAA-----GWPPSSRQSSPEGQDEGGFMAQKGTGSSSPPG	325
		: . . :	.
DDB0185208	DDB_G0274109	PKVVHGGDDL NLLNNLTSQVKDIDSTGPTSRGTCGGCRKPIFGETIQAMGKFYHPEHFCC	362
sp Q09476 PXL1_CAEEEL		SPSRDPLHSDSMIGTMNGELSSKHGVTIPKGDCAACGKPIIGQVVIALGKMWHP EHYTC	202
tr Q2PDT4 Q2PDT4_DROME		VEDSREDQLDSMLGNLQANM-SRQGVNTVQKCCNACEKPIVGQVITALGKTWHP EHFCTC	374
sp P49023 PAXI_HUMAN		GPPKPGSQLDSMLGSLQSDL-NKLG VATVAKGVC GACKKPIAGQVVTAMGKTWHP EHFVC	384
sp Q8VI36 PAXI_MOUSE		GLSKPGSQLDSMLGSLQSDL-NKLG VATVAKGVC GACKKPIAGQVVTAMGKTWHP EHFVC	384
		. * : . . . * * * * * : . : * * * * * :	
DDB0185208	DDB_G0274109	HNCQNPLGTKNYYEQESLPHCEKCYQELFCARCAHCD EISDR CITALGKKWHVHFVCT	422
sp Q09476 PXL1_CAEEEL		CECGAELGQRPFFERNGRAFC EEDYHNQFSPKQCGCHRAITDRCVSMKNFHI ECTCA	262
tr Q2PDT4 Q2PDT4_DROME		NHCSQELGTRNFFERDGFYCEPDYHNLFSPRCAYCNGAILDKCVTALDKTWHTEHFFCA	434
sp P49023 PAXI_HUMAN		THCQEEIGSRNFFERDGPYCEKDYHNLFSPRCYCNGPILDKVV TALDRTWHP EHFCCA	444
sp Q8VI36 PAXI_MOUSE		THCQEEIGSRNFFERDGPYCEKDYHLSFSPRCY CNGPILDKVV TALDRTWHP EHFCCA	444
		. * : : : * . . * * * . * : * * * * * :	
DDB0185208	DDB_G0274109	QCLKPFEGGNFFERDGRPYCEADFYSTFAVRCGGCNSPIRGECINALGTQWHP EHFVCQY	482
sp Q09476 PXL1_CAEEEL		ECNQPFGE DGFHEKNGQTYCKRDFRLLFAPKCNCSQPITSNFITALGTHWHPDCFVCQH	322
tr Q2PDT4 Q2PDT4_DROME		QCGQQFGEEGFHERDGKPYCRNDYFEMFAPKCNCGNRAIMENYISALNSQWHPDCFVC RD	494

sp P49023 PAXI_HUMAN	QCGAFFGPEGFHEKDGYKAYCRKDYFDMFAPKCGGCARAI LENYISALNTLWHPECFVCRE	504
sp Q8VI36 PAXI_MOUSE	QCGAFFGPEGFHEKDGYKAYCRKDYFDMFAPKCGGCARAI LENYISALNTLWHPECFVCRE	504
	: * * . * . * : : * : * * : * . * * * : * . * * . : * * : * * :	
DDB0185208 DDB_G0274109	CQKSFTNGQFFFFGGKPYCDVHYHQQAGSVCSGGKAVSGRCVDALDKKWHPEHFVCAFC	542
sp Q09476 PXL1_CAEEL	CGVSFNASFFFEHNGAPLCERHYHESRGSIC SQCRGAINGRCVAAMGRKFHPEHFRCSYC	382
tr Q2PDT4 Q2PDT4_DROME	CRQPFQGGSF FDHEGLPYCETHYHAKRGS LCAGCSKPITGRCITAMFKKFHPEHFVCAFC	554
sp P49023 PAXI_HUMAN	CFTPFVNGSF FFEHDGQPYCEVHYHERGSLCSGCQKPITGRCITAMAKKFHPEHFVCAFC	564
sp Q8VI36 PAXI_MOUSE	CFTPFVNGSF FFEHDGQPYCEVHYHERGSLCSGCQKPITGRCITAMAKKFHPEHFVCAFC	564
	* * . . . * * : . * * * : * * * * * : * : * : . * * : * : : * . * * * * * : . * *	
DDB0185208 DDB_G0274109	MNPLAGGSYTANNGKPYCKGCHNKLFA*---	569
sp Q09476 PXL1_CAEEL	NHQLTKGTFKEVDRRPFCHKCYNNTYALTPA	413
tr Q2PDT4 Q2PDT4_DROME	LKQLNKGT FKEQKDKPYCHTCFDKIFG----	581
sp P49023 PAXI_HUMAN	LKQLNKGT FKEQNDKPYCQNCFLKLFC----	591
sp Q8VI36 PAXI_MOUSE	LKQLNKGT FKEQNDKPYCQSCFVKLFC----	591
	: * * : : . . : * : * : * . : :	

CLUSTAL O(1.2.4) multiple sequence alignment

sp Q92544 TM9S4_HUMAN	MATAMDWLP-WSLLLFLSMCETSAFYVPGVAPINFHQNDPVEIKAVKLTSSRTQLPYEYY	59
sp Q8BH24 TM9S4_MOUSE	MAAAMIWWP-RFLLLCLCTCKGSTFYVPGVAPINFHQNDPVEIKAVKLTSSRTQLPYEYY	59
DDB0191123 DDB_G0267444	MKINKKQIVFFILFSIFLNHVNGIFYLPGMIPHDFAQGEEGAIVNKITSVHTQIPYKYY	60
	* : * . **:* : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	SLPF-CQPSK-ITYKAENLGEVLRGDRIVNTPFQVL-MNSEKKCEVLCSQSNKPVTLTVE	116
sp Q8BH24 TM9S4_MOUSE	SLPF-CQPIK-ITYKAENLGEVLRGDRIVNTPFQVL-MNSEKKCEVLCSQSNKPVTLTVE	116
DDB0191123 DDB_G0267444	QLPGVCQPKGEGIDDTENLGEILLGDRIDNSDYTFNFLTGGKCKVINSESCSPII-KKE	119
	.** *** : * .:*****:* ***** * : : . . . **:* : .* * : . *	
sp Q92544 TM9S4_HUMAN	QSRLLVAERITEDYYVHLIADNLPVATRLLELYS-NRDSDDKKKEKDVQFEHGYRLGFT---	172
sp Q8BH24 TM9S4_MOUSE	QSRLLVAERITEEYYVHLIADNLPVATRLLEYSSNRDSDDKKKEKDVQFEHGYRLGFT---	173
DDB0191123 DDB_G0267444	DLKVLDRIQNQYRVHWLLDGLPVRQTGRLAS -----DPGFDLGFMTLA	163
	: : : : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	-----DVNKIYLHNHLSFILYYHREDMEEDQEHTYRVVRFVIPQSIRLE---DLKADEK	224
sp Q8BH24 TM9S4_MOUSE	-----DVNKIYLHNHLSFILYYHREDMEEDQEHTYRVVRFVIPQSIRLE---DLKTGEK	225
DDB0191123 DDB_G0267444	EGQTVATAEKYLNHLEITIFYHSNPT----DNTSRIVGFEIFPTSRQYKVENWKDGTG	219
	. : **:* : : : : : : * * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	SSCTLPEGT-N--SSPQEIPTKENQLYFTYSVHWEESDIKWASRWDITYLTMSDVQIHWF	281
sp Q8BH24 TM9S4_MOUSE	SSCTLPEGA-N--SLPQEIPTKENQLYFTYSVHWEESDIKWASRWDITYLTMSDVQIHWF	282
DDB0191123 DDB_G0267444	DDCPQYGENFEQLSVSVKEGEDQERFVLWTYEVKYTPSPVLWNKRWDIYFESNDNSVHWF	279
	. * : * : . : * : : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	SIINSVVVVFLLSGILSMIIIRTLRKDIANYNKEDDIE--DTMEESGWLKHGDFVFRPPQ	339
sp Q8BH24 TM9S4_MOUSE	SIINSVVVVFLLSGILSMIIIRTLRKDIANYNKEDDIE--DTMEESGWLKHGDFVFRPPQ	340
DDB0191123 DDB_G0267444	SILNSLMIVFILVMVAMIIIRTLKKDIRRYSIDTSEDSDQEETGWKMIHGDVFRPPS	339
	**:* : : * : : : : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	YPMILSSLLSGSIQLFCMILIVIFVAMLGMLSPSSRGALMTTACFLFMFMGVFGGSFAGR	399
sp Q8BH24 TM9S4_MOUSE	YPMILSSLLSGSIQLFCMILIVIFVAMLGMLSPSSRGALMTTACFLFMFMGVFGGSFAGR	400
DDB0191123 DDB_G0267444	HPMLLSVCIGSGVQIFSMTLITMIFAVLGLSPANIGGLATALIVLVLAMFAGYFSTR	399
	: * : * : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	LYRTLKGHRWKKGAFCATLTPGVVFGICFVLNCFIWKGHSSGAVFPPTMVALLCMWFGI	459
sp Q8BH24 TM9S4_MOUSE	LYRTLKGHRWKKGAFCATLTPGVVFGICFVLNCFIWKGHSSGAVFPPTMVALLCMWFGI	460
DDB0191123 DDB_G0267444	VFTIFKGRNWKNTIYTALSMPIGIFGIFVNMFLRGAKSSAAMPFGTFASIAMWFGI	459
	: : * : * : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	SLPLVYLGYFGRKQPYDNPVRTNQIPRQIPQRYMNRVFGILMAGILPFGAMFIELF	519
sp Q8BH24 TM9S4_MOUSE	SLPLVYLGYFGRKQPYDNPVRTNQIPRQIPQRYMNRVFGILMAGILPFGAMFIELF	520
DDB0191123 DDB_G0267444	SVPLVFLGSYFASKKPVPEDPVRTNQIPRQVPDIWMNPYLSILMGGILPFGAVFIELH	519
	* : * : * : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	FIFSAIWENQFYLYFGFLFVLVFIILVVSCSQISIVMVYFQLCAEDYRWWRNFLVSGGSA	579
sp Q8BH24 TM9S4_MOUSE	FIFSAIWENQFYLYFGFLFVLVFIILVVSCSQISIVMVYFQLCAEDYRWWRNFLVSGGSA	580
DDB0191123 DDB_G0267444	FILTSLWDNQFYIFGFLFVLVFIILVTSAEISIVMCYFQLCAEDHWWRSFLTAGSSS	579
	** : : : * : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	FYVLVYAIIFYVKNKLDIVEFIPSLLYFGYTALMVLFWLLTGTIGFYAAYMFVRKIYAAV	639
sp Q8BH24 TM9S4_MOUSE	FYVLVYAIIFYVKNKLDIVEFIPSLLYFGYTALMVLFWLLTGTIGFYAAYMFVRKIYAAV	640
DDB0191123 DDB_G0267444	LYMFIYSVSFF-RYLGITKFISLLDFSYSFIMSLAFAALTGTIGFYSCYFLVRKIYSSI	638
	: * : : * : * : * : * : * : * : * : * : *	
sp Q92544 TM9S4_HUMAN	KID-	642
sp Q8BH24 TM9S4_MOUSE	KID-	643
DDB0191123 DDB_G0267444	HIN*	641
	: * :	

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0214826 DDB_G0277897	MQKSYIKLLVLGDSKGTGKTTMMMTYSTGSFPTGYVPSHVDATSLDIEYNKQVCHVGFWDS	60
sp P63000 RAC1_HUMAN	--MQAIKC VVVG DGAVGKTC LLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDT	58
sp P63001 RAC1_MOUSE	--MQAIKC VVVG DGAVGKTC LLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDT	58
sp P40792 RAC1_DROME	--MQAIKC VVVG DGAVGKTC LLISYTTNAFPGEYIPTVFDNYSANVMVDKPINLGLWDT	58
	. ** :*:*. .*** ::*:*.** *:*. . * * :: : : :*:**:	
DDB0214826 DDB_G0277897	SALAFDNTRPSTYPNTNVIILCFSIDSPTSFENVSKKWIPEIRQYAPSIHTPIILLGTK	120
sp P63000 RAC1_HUMAN	AGQEDYDRLRPLSYPTDVFLLICFSLVSPASFENVRAKWYPEVRHHCP--NTPIILVGTK	116
sp P63001 RAC1_MOUSE	AGQEDYDRLRPLSYPTDVFLLICFSLVSPASFENVRAKWYPEVRHHCP--NTPIILVGTK	116
sp P40792 RAC1_DROME	AGQEDYDRLRPLSYPTDVFLLICFSLVNPASFENVRAKWYPEVRHHCP--STPIILVGTK	116
	:. :*: . ** :*:*.** ::*:*. .*:***** ** *:*.** :. * *****:**	
DDB0214826 DDB_G0277897	CDLREDENTINLLKENNQMPPISYKQGLALSKEIKATMYLECSSLCNQGVNEIFKQVVR	180
sp P63000 RAC1_HUMAN	LDLRDDKDIEKLKEK-KLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRA	175
sp P63001 RAC1_MOUSE	LDLRDDKDIEKLKEK-KLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRA	175
sp P40792 RAC1_DROME	LDLRDDKNTIEKLKDK-KLAPITYPQGLAMAKEIGAVKYLECSALTQKGLKTVFDEAIRS	175
	:*.** :*: : : **:* **:*** * , *****: * ::*: :*.:.**.	
DDB0214826 DDB_G0277897	HL YCKDGV LNDPTTTTNTSKIIQ	205
sp P63000 RAC1_HUMAN	VLC-P-----PPVKRKRKC LLL	192
sp P63001 RAC1_MOUSE	VLC-P-----PPVKRKRKC LLL	192
sp P40792 RAC1_DROME	VLC-P-----VLQPKSKRKCALL	192
	* . . ** :	

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0201669 DDB_G0292560	MERNFNNFLVKIFCLGDDGVGKSCVMNSYSSGGPLTSLFQGS	ELTWDTYTVSVTHNQKPL	60			
sp Q94124 RAC2_CAEEEL	-----MQAIKCVVVG	DGAVGKTCLLLSYTTNAFPGEYI---	LTVFD	TYSTNVMDGRPI	51	
sp P48554 RAC2_DROME	-----MQAIKCVVVG	DGAVGKTCLLLSYTTNAFPGEYI---	PTVFD	NYSANVMVDAKPI	51	
sp P15153 RAC2_HUMAN	-----MQAIKCVVVG	DGAVGKTCLLLSYTTNAFPGEYI---	PTVFD	NYSANVMVDSKPV	51	
sp Q05144 RAC2_MOUSE	-----MQAIKCVVVG	DGAVGKTCLLLSYTTNAFPGEYI---	PTVFD	NYSANVMVDSKPV	51	
	: * . : * * . * * : * : * : . : . : * : . * : : * :					
DDB0201669 DDB_G0292560	KLRLVI-GDQNELRRIKQ--	IEFNDVFLICFSVDSKASYDNI-EKWNT	TEIRKILPTPNII		116	
sp Q94124 RAC2_CAEEEL	NLSLWDTAGQDDYDQFRHLSFPQT	DVFLVCFALNNPASFENVRAKWPEVSHHC	PNTPII		111	
sp P48554 RAC2_DROME	NLGLWDTAGQEDYDRLRPLSYPQT	DVFLICFSLVNPASFENVRAKWFPEVRHHC	PSVPII		111	
sp P15153 RAC2_HUMAN	NLGLWDTAGQEDYDRLRPLSYPQT	DVFLICFSLVSPASYENVRAKWFPEVRHHC	PSPTII		111	
sp Q05144 RAC2_MOUSE	NLGLWDTAGQEDYDRLRPLSYPQT	DVFLICFSLVSPASYENVRAKWFPEVRHHC	PSPTII		111	
	: * * ..*:: ::: .*****:*:: . *::*: * * * : * . **					
DDB0201669 DDB_G0292560	LVG	TKIDLRKEGGELKK-----SIVTQEMGIEKAKEINAIKYM	ECSTATYEGVKEVFDE		170	
sp Q94124 RAC2_CAEEEL	LVG	TKADLRREDRTIERLRERRLQPV	SHTQGYVMAKEIKAVKYLECSALTQIGLKQVFDE		171	
sp P48554 RAC2_DROME	LVG	TKLDLRDDKQTEIKLKD	KKLTPI	TPQGLAMAKEIAAVKYLECSALTQKGLKTVFDE	171	
sp P15153 RAC2_HUMAN	LVG	TKLDLRDDKQTEIKLKEKKL	APITYPQGLALAKEIDSVKYLECSALTQKGLKTVFDE		171	
sp Q05144 RAC2_MOUSE	LVG	TKLDLRDDKQTEIKLKEKKL	APITYPQGLALAKIDSVKYLECSALTQKGLKTVFDE		171	
	***** **.*: ::: ::: * **:* :*:**:* * *:* *****					
DDB0201669 DDB_G0292560	SINIYMTKKLYIQDLR	KKSF	FLIPKKN	TNKK	SCKTQ	205
sp Q94124 RAC2_CAEEEL	AIR	TGLTPPQTPQTRA-----	KKS	NCTVL		195
sp P48554 RAC2_DROME	AIR	SVLCPVVRGP-----	KRHK	CALL		192
sp P15153 RAC2_HUMAN	AIR	AVLCPQPTRQ-----	QKR	ACSL		192
sp Q05144 RAC2_MOUSE	AIR	AVLCPQPTRQ-----	QKR	PCSL		192
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0201660 DDB_G0292816	MQYIKMVICGDGAVGKTSLLIAFASGEFPRDYQPTVFDNFSTLYMFQNKAYNLGLFDTAG	60
sp P63000 RAC1_HUMAN	MQAIKCVVVG DGAVGKTCLLSYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAG	60
sp P63001 RAC1_MOUSE	MQAIKCVVVG DGAVGKTCLLSYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAG	60
sp P40792 RAC1_DROME	MQAIKCVVVG DGAVGKTCLLSYTTNAFPGEYIPTVFDNYSANVMVDAKPINLGLWDTAG	60
	** ** *: *****,*:::. ** :* *****,*: *.: * *****:***	
DDB0201660 DDB_G0292816	QEDFDRRLPLGYNDTLFLICYSVINPPSYANVYDKWYSEIKLYTGSEIPLILVGTQNDL	120
sp P63000 RAC1_HUMAN	QEDYDRRLPLSYPTDVF LICFSLVSPASFENVRAKWYPEVRHH-CPNTPIILVGTKLDL	119
sp P63001 RAC1_MOUSE	QEDYDRRLPLSYPTDVF LICFSLVSPASFENVRAKWYPEVRHH-CPNTPIILVGTKLDL	119
sp P40792 RAC1_DROME	QEDYDRRLPLSYPTDVF LICFSLVNPASFENVRAKWYPEVRHH-CPSTPIILVGTKLDL	119
	:**.* :*:*****:*::.* *: ** ***:*: : . *:*****: **	
DDB0201660 DDB_G0292816	RHDKATRETLALKQQAPISYEEGMMMRKRI GAKAFTECSVVS GKNVKQVFEEAIKVYQDR	180
sp P63000 RAC1_HUMAN	RDDKDTIEKLKEKKLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCP	179
sp P63001 RAC1_MOUSE	RDDKDTIEKLKEKKLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCP	179
sp P40792 RAC1_DROME	RDDKNTIEKL RDKKLAPITYPQGLAMAKEIGAVKYLECSALTQKGLKTVFDEAIRSVLCP	179
	. * *. * *: :*: * :*: * *.*** : ***.:: :.:* ***:***:	
DDB0201660 DDB_G0292816	QIEISKSEKNNC IIL	196
sp P63000 RAC1_HUMAN	---PPVKRKRKCLLL	192
sp P63001 RAC1_MOUSE	---PPVKRKRKCLLL	192
sp P40792 RAC1_DROME	---VLQPKSKRKCALL	192
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0233517 DDB_G0291303	MAVLSLVELCFISIMERMEYNNQALQKIPPQLIERLINFMVYKLPNNHLSLQTISKPIRI	60
tr G5EGK1 G5EGK1_CAEEEL	-----MGVLS-----LTV	8
sp P26039 TLN1_MOUSE	-----MVA-----LSL	6
sp Q9Y490 TLN1_HUMAN	-----MVA-----LSL	6
	: : : :	
DDB0233517 DDB_G0291303	KLVRQNRVITMRFSIYNTIDKIIHQIYERIINEEKMEQNEKQKNSSNNNLLSLTLNNNN	120
tr G5EGK1 G5EGK1_CAEEEL	SSAEKGIKKTMQFEP-----	23
sp P26039 TLN1_MOUSE	KISIGNVVKTMQFEP-----	21
sp Q9Y490 TLN1_HUMAN	KISIGNVVKTMQFEP-----	21
	. . **:*	
DDB0233517 DDB_G0291303	QNNNSSIITTTTTTNNNNNSNCGSSSSSSSSKQILWGSINIYGLFQQSGSFRNARWLQL	180
tr G5EGK1 G5EGK1_CAEEEL	---STLIY-----DAAKL--IREKFAMH-DVNANEYGFRLDENPSKSLWMDN	65
sp P26039 TLN1_MOUSE	---STMVY-----DACRM--IRERIPEALAGPPNDFGLFLSDDDPKKGIWLEA	64
sp Q9Y490 TLN1_HUMAN	---STMVY-----DACRI--IRERIPEAPAGPPSDFGLFLSDDDPKKGIWLEA	64
	::: . . . :: * . . : *	
DDB0233517 DDB_G0291303	DKTLAYYEIDSNETLEFKTCKSVLKIRFFGPWERVVHPLHQSTMDETIKTFVFDESKTV	240
tr G5EGK1 G5EGK1_CAEEEL	GRTFEHYLVRNKDEIEYKRKIRLLKVR-----MLDGAVKTSVDESQPV	109
sp P26039 TLN1_MOUSE	GKALDYYMLRNGDTMEYRKKQRPLKIR-----MLDGTVKTIMVDDSKTV	108
sp Q9Y490 TLN1_HUMAN	GKALDYYMLRNGDTMEYRKKQRPLKIR-----MLDGTVKTIMVDDSKTV	108
	::: * : . : *:: **:* *** :*: *:*: *	
DDB0233517 DDB_G0291303	SEISMELAKKLQKYPEELSCLKVQCEE-----	267
tr G5EGK1 G5EGK1_CAEEEL	SQLMMTVCNKIGISNYEYSLVRRDILMQNGGGGGGGQNGGSTWNLKEKESRSKSSDR	169
sp P26039 TLN1_MOUSE	TDMLMTICARIGITNHDEYSLVRELMEEKKDEGTGL-----	145
sp Q9Y490 TLN1_HUMAN	TDMLMTICARIGITNHDEYSLVRELMEEKKEEITGTL-----	145
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DDB0233517 DDB_G0291303	-----EDDGRGIWLSADLTLPSEQGIDPLYTIFLLKRQFFFC	303
tr G5EGK1 G5EGK1_CAEEEL	GGGGIYGTMRKKNEQKLEELRKKLHTDEELPWL DHTKTLREQGITEEETLI-LRRKYFFS	228
sp P26039 TLN1_MOUSE	---RKDKTLLRDEKKMEKLKQKLHTDDELNWL DHGRTLREQGVEEHETLL-LRRKFFYS	200
sp Q9Y490 TLN1_HUMAN	---RKDKTLLRDEKKMEKLKQKLHTDDELNWL DHGRTLREQGVEEHETLL-LRRKFFYS	200
	. * . ** . ** ***: *: *:*:*::	
DDB0233517 DDB_G0291303	KDIIIDFSMDAEMLHFVFCQCLDAIIDTSHPCSPTESILFAALQCQICFGDYVHGSKEID	363
tr G5EGK1 G5EGK1_CAEEEL	DSNV--DSRDPVQLNLLYVQCRDGI LRGLHPVEKETAFQLAALQSHIQYGFYDYPKPK-F	285
sp P26039 TLN1_MOUSE	DQNV--DSRDPVQLNLLYVQARDDILNGSHPVSFDKACEFAGFQCQIQFGPHNEQKHKAG	258
sp Q9Y490 TLN1_HUMAN	DQNV--DSRDPVQLNLLYVQARDDILNGSHPVSFDKACEFAGFQCQIQFGPHNEQKHKAG	258
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DDB0233517 DDB_G0291303	QIRQRDFLPMEFINQKNILKEILIQYRLIGMSEQAKLNYIQLAKSLKTYGYTFFKVTN	423
tr G5EGK1 G5EGK1_CAEEEL	HLDGRDVLPEKYAKNKENEKKVAMYKELSGTSELDAKSKYVHLCRGLKTYGVTFVVK	345
sp P26039 TLN1_MOUSE	FLDLKDFLPKEYVKQKGE-RKIFQAHKNCGQMSEIAKVRVVKLARSLKTYGVSFVLVKE	317
sp Q9Y490 TLN1_HUMAN	FLDLKDFLPKEYVKQKGE-RKIFQAHKNCGQMSEIAKVRVVKLARSLKTYGVSFVLVKE	317
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DDB0233517 DDB_G0291303	RQTSIVNNNLSSSGGSGNGSGSGNGSSSSSSNSSSGNNNNHHHHNHQQLFGISSAVLTL	483
tr G5EGK1 G5EGK1_CAEEEL	KLPG-----KNKLVPRLLGVNKE SVMRV	368
sp P26039 TLN1_MOUSE	KMKG-----KNKLVPRLLGITKECVMRV	340
sp Q9Y490 TLN1_HUMAN	KMKG-----KNKLVPRLLGITKECVMRV	340
	: . :*:*:*:*:*: :	
DDB0233517 DDB_G0291303	DPMTNNTISLYSLNIRKWHVLNNVFTIEYNDRKDTFISME---AEAISHLVSSYIHHNL	540
tr G5EGK1 G5EGK1_CAEEEL	DENSKQILKEWPLEQVRRWVPSAKCFSLDFGDYQDGYYSVQTTEGEKIAQLIQGYVDIIL	428
sp P26039 TLN1_MOUSE	DEKTKEVIQEWLNTIKRWAASPKSFTLDFGDYQDGYYSVQTTEGEQIAQLIAGYIDIIL	400
sp Q9Y490 TLN1_HUMAN	DEKTKEVIQEWLNTIKRWAASPKSFTLDFGDYQDGYYSVQTTEGEQIAQLIAGYIDIIL	400
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DDB0233517 DDB_G0291303	RETPSIQKQWDQNYLSVSGRNSLT-----NGRKRLST-----C-	573
tr G5EGK1 G5EGK1_CAEEEL	KKKRTQDH-----QGIEGDEGSTMLEDMVAPAKATLVAHGQIGSGQHATDGLVAVRGVL	482
sp P26039 TLN1_MOUSE	KKKKSKDH-----FGLEGDEESTMLEDSVSPKSTVLQQQYNRVGK-VEHGSVALPAIM	453
sp Q9Y490 TLN1_HUMAN	KKKKSKDH-----FGLEGDEESTMLEDSVSPKSTVLQQQYNRVGK-VEHGSVALPAIM	453
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DDB0233517 DDB_G0291303	-----SNCSSDSMEFDSKSN TKDKDWKYQYGLVIKKCALYIEPKKLYINPLSTQITG	626
tr G5EGK1 G5EGK1_CAEEEL	RTPQGQ--GYGNGAQYGA VSGEITSQE--LARAQRLRYQDMYQHPQRALIGTIEA----	535
sp P26039 TLN1_MOUSE	RS GASGPENFQV GSM--PPAQQQITSGQ--MHRGH----MPPLTSAQQALTGTINS----	501
sp Q9Y490 TLN1_HUMAN	RS GASGPENFQV GSM--PPAQQQITSGQ--MHRGH----MPPLTSAQQALTGTINS----	501
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DDB0233517 DDB_G0291303	SMVNKELNKD TKVTKVLKVLTDLSSKMILSFSKSSPAKEREIVVKFSDKKVKS FVVDQEK	686
tr G5EGK1 G5EGK1_CAEEEL	TIRAVEDAE-----IELEAEP-----QIDIPRFND DYSQNRWMEEQQ	572
sp P26039 TLN1_MOUSE	SMQAVQAAQ-----ATLDD-----FETLPPLGQDAASKAWRK NKM	536
sp Q9Y490 TLN1_HUMAN	SMQAVQAAQ-----ATLDD-----FDTLPPLGQDAASKAWRK NKM	536
	: : : * : : : . . : :	
DDB0233517 DDB_G0291303	TVSEITQEIGLKLGIKNPEE-FSLQLIVNNKNNNNNNNSNN-----SSTSSSSSSSVNNS	740
tr G5EGK1 G5EGK1_CAEEEL	AVNK--ENVNERLAAMGAATAQV VQWTAVE---EYDDRVTGTAIATIGSNLPDVS RNV RDL	627
sp P26039 TLN1_MOUSE	DESK--HEIHSQVDAITAGTASV VNLTAGDPAETDYTAVGCAVTTISSNLT EMSRGVKLL	594
sp Q9Y490 TLN1_HUMAN	DESK--HEIHSQVDAITAGTASV VNLTAGDPAETDYTAVGCAVTTISSNLT EMSRGVKLL	594
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DDB0233517 DDB_G0291303	GIFDGLNNSNVN VFYNSYIVNSSISNNSNSNSNINLNSNDEQSTSTSTSSSLGG---	797
tr G5EGK1 G5EGK1_CAEEEL	GAFM-----EHRE--RGDLLDATKKLCGAFG	651
sp P26039 TLN1_MOUSE	AALL-----EDEGGNGRPLLQAAKGLAGAVS	620
sp Q9Y490 TLN1_HUMAN	AALL-----EDEGGSGRPLLQAAKGLAGAVS	620
	. : : : : * *	
DDB0233517 DDB_G0291303	IWLKPYQPLSEQSISPDSKLLFKKK-----FYTSDIGAADD CNDPVYFNLLFFQSKD	850
tr G5EGK1 G5EGK1_CAEEEL	KFLNTVNPETEA---RRNEVFRTAGHVGETSQHLINVMEAPN--EGQKFDER-LVQSAK	705
sp P26039 TLN1_MOUSE	ELLRSAQPASAE---PRQNLLQAAGNVGQASGELLQQIGES---DTPHFQDV-LMQLAK	673
sp Q9Y490 TLN1_HUMAN	ELLRSAQPASAE---PRQNLLQAAGNVGQASGELLQQIGES---DTPHFQDA-LMQLAK	673
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DDB0233517 DDB_G0291303	AI-----ISNT-----YTCSKEEAIQLAATLFQ	873
tr G5EGK1 G5EGK1_CAEEEL	NVATSTAQLVLCAKTISAECDPEQVQVERVIQSATKCAFATSQLVACARVVAPTIDNNACQ	765
sp P26039 TLN1_MOUSE	AVASAAAALVLKAKSVAQRTEDSGLQTQVIAAATQCALSTSQLVACTKVVAPTISSPVCQ	733
sp Q9Y490 TLN1_HUMAN	AVASAAAALVLKAKSVAQRTEDSGLQTQVIAAATQCALSTSQLVACTKVVAPTISSPVCQ	733
	: * : : * : *	
DDB0233517 DDB_G0291303	INFGDHNPNIHKPGFLKSQDLKFFLPNLSLEWLGSFQKIEKSIYKEHQNL RGIKEVYAK	933
tr G5EGK1 G5EGK1_CAEEEL	QQLS-----TAATEVTQSVNLLHDA-----EH-AVYQSSLTDIHEAARQ	805
sp P26039 TLN1_MOUSE	EQLV-----EAGRLVAKAVEGCVSAS-----QA-ATEDGQLLRGVGAAATA	773
sp Q9Y490 TLN1_HUMAN	EQLV-----EAGRLVAKAVEGCVSAS-----QA-ATEDGQLLRGVGAAATA	773
	: : . : : : : : . * . :	
DDB0233517 DDB_G0291303	-----YRYVQLCRSLK-----TFGAI-----FFSVR	954
tr G5EGK1 G5EGK1_CAEEEL	VT SALD S LLEHAKCSPKQTTRREEEEMYN EVLRR TNRMVVHQGPS EDLTREARKVVRHS	865
sp P26039 TLN1_MOUSE	VTQALNELLQHVKAHATGAGPAGRYDQATDTILTVTENIFSSMGDAGEMVRQARILAQAT	833
sp Q9Y490 TLN1_HUMAN	VTQALNELLQHVKAHATGAGPAGRYDQATDTILTVTENIFSSMGDAGEMVRQARILAQAT	833
	. : : : :	
DDB0233517 DDB_G0291303	QLLPNKTN GSSSSSSNNNGNSNNGINGNGII-----TGGNGSGGGGSGIGGNGSG	1006
tr G5EGK1 G5EGK1_CAEEEL	QLLTEQFQH--EAH--QRPEHRERLLDAAAKVAHATSEMILATEQAESQPRQ--VET EYA	919
sp P26039 TLN1_MOUSE	SDLVNAIKADAEGE--SDLENSRKLLSAAKILADATAKMVEAAKGAAHPDS--EEQQQR	889
sp Q9Y490 TLN1_HUMAN	SDLVNAIKADAEGE--SDLENSRKLLSAAKILADATAKMVEAAKGAAHPDS--EEQQQR	889
	. * : : . . : : : : : . : . . .	
DDB0233517 DDB_G0291303	INTGGN-----	1012
tr G5EGK1 G5EGK1_CAEEEL	LRTAAERLGQVTNETTQEQQEQHIMQRLQAAKQTAYDATQTISAANS AKDVIESRSYKE	979
sp P26039 TLN1_MOUSE	LREAAEGLRMATNAAAQNAIKKKLVQRLEHAAKQAAASATQTIAAAQHAASAPKASAGPQ	949
sp Q9Y490 TLN1_HUMAN	LREAAEGLRMATNAAAQNAIKKKLVQRLEHAAKQAAASATQTIAAAQHAASAPKASAGPQ	949
	: . . :	
DDB0233517 DDB_G0291303	-----GFGGSQQIPINQPLV----LGFSRK-----CILFMTAK	1041
tr G5EGK1 G5EGK1_CAEEEL	-NLVYESTQTAGHLPNLITSIRESQKVDNTGPEKFKAQSR LIRD SYKVL ETSVR LFETAR	1038
sp P26039 TLN1_MOUSE	PLL VQSC KAVAEQIPLL VQGV RGSQAQPDSPSA-----QLALIAASQSFLQPGGKMVA AAK	1005
sp Q9Y490 TLN1_HUMAN	PLL VQSC KAVAEQIPLL VQGV RGSQAQPDSPSA-----QLALIAASQSFLQPGGKMVA AAK	1005
	. . ** . : : : *	
DDB0233517 DDB_G0291303	TKKFL-----VEYPLTHLRWAYHKDTQC LTLD FGDYEMGRIVLQTTES	1085
tr G5EGK1 G5EGK1_CAEEEL	TAVPMVSDSHLASSLDQSANRLGTS LADLR TSVNDAQQLNFSQQLL-----YS	1086
sp P26039 TLN1_MOUSE	ASVPTIQDQASAMQLSQCAKNLGTALAE LR TAAQKAQEACGPLEMD-----SA	1053
sp Q9Y490 TLN1_HUMAN	ASVPTIQDQASAMQLSQCAKNLGTALAE LR TAAQKAQEACGPLEMD-----SA	1053
	: : * : * . . : : :	

DDB0233517 DDB_G0291303	EEISSYLSDYIDYIQTK-----LVGSQSF--RSIFNSDNNSSSFFSNSFCN-----N	1131
tr G5EGK1 G5EGK1_CAEEEL	EELIKELDDQLVNTQKRAIARELPPIQNATSFVSSKLMATTSNVGSQVAQLITAAATSN	1146
sp P26039 TLN1_MOUSE	LSVVQNLEKDLQEIKAAARDGKCLKPLPGETMEKCTQDLGNSTKAVSSAIAKLLGE-IAQG	1112
sp Q9Y490 TLN1_HUMAN	LSVVQNLEKDLQEVKAAARDGKCLKPLPGETMEKCTQDLGNSTKAVSSAIAQLLGE-VAQG	1112
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DDB0233517 DDB_G0291303	TT-----TTTTTTTTTTTTTTTTTNNV*-----	1154
tr G5EGK1 G5EGK1_CAEEEL	DDKYVGTSAVELAQGLRDFDTAITEIVTVRTDIQLDKLIVSARSV-----VHESGRV	1198
sp P26039 TLN1_MOUSE	NENYAGIAARDVAGGLRSLAQAAAGVAALSDPAVQAIVLDTASDVLDKASSLIEEAKKA	1172
sp Q9Y490 TLN1_HUMAN	NENYAGIAARDVAGGLRSLAQAAAGVAALSDPAVQAIVLDTASDVLDKASSLIEEAKKA	1172
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DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	FDRVREKSAPTVLTDAAENVSTSLKQVISCLPDTKHIEKAIHEIQTHTSANIRPMEVRQ	1258
sp P26039 TLN1_MOUSE	SGHPGDPESSQRLAQVAKAVTQALNRCVSLPGQRVDNALRAVGDAKRLLSLSD--SLPP	1230
sp Q9Y490 TLN1_HUMAN	AGHPGDPESSQRLAQVAKAVTQALNRCVSLPGQRVDNALRAVGDAKRLLSLSD--SLPP	1230
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	AANKFIEATSQLV-----VTIGSPDSR-----EAVDIFVRAYCDLHG	1295
sp P26039 TLN1_MOUSE	STGTFQEASRLNEAAAGLNQAATELVQASRGTPQDLARASGRFGQDFSTFLEAGVEMAG	1290
sp Q9Y490 TLN1_HUMAN	STGTFQEASRLNEAAAGLNQAATELVQASRGTPQDLARASGRFGQDFSTFLEAGVEMAG	1290
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	SVVAQLQRQSNMNVKTAIIDRLEEQRGSI-GVLETLRQAGNPSDHTLSQQFTSKTREEL	1354
sp P26039 TLN1_MOUSE	QAPSQEDRAQVVSNLKG-----ISMSSSKLLAALKALSTDPASPNLKSQLA AAAARAV	1342
sp Q9Y490 TLN1_HUMAN	QAPSQEDRAQVVSNLKG-----ISMSSSKLLAALKALSTDPAAPNLKSQLA AAAARAV	1342
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	ATTVNQLVELSGMDGGESRWQRECDAAALRRIQAVYHVTHANVPLNDNGYFASLQSVSDG	1414
sp P26039 TLN1_MOUSE	TDSINQLITM---CTQQAPGQKECDNALRQLETVRELLLENPVQPINDMSYFGCLDSVMEN	1399
sp Q9Y490 TLN1_HUMAN	TDSINQLITM---CTQQAPGQKECDNALRELETVRELLLENPVQPINDMSYFGCLDSVMEN	1399
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	SRRLGEAMTGMARHAKGNDTEGCTSVRDSADALCSLAESASHSAYLVGISHPASSPGRRA	1474
sp P26039 TLN1_MOUSE	SKVLGEAMTGISQNAKNGNLPEFGDAIATASKALCGFTEAAQAAYLVGVSDPN SQAGQQ	1459
sp Q9Y490 TLN1_HUMAN	SKVLGEAMTGISQNAKNGNLPEFGDAISTASKALCGFTEAAQAAYLVGVSDPN SQAGQQ	1459
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	ALIDSSSEVARSVESINASCQRVESRQLNREELMSDISSITKQSSSLAQLCRIASEKTQNP	1534
sp P26039 TLN1_MOUSE	GLVEPTQFARANQAIQMACQSLGEPGCTQAQVLSAATIVAKHTSALCNSCRLASARTANP	1519
sp Q9Y490 TLN1_HUMAN	GLVEPTQFARANQAIQMACQSLGEPGCTQAQVLSAATIVAKHTSALCNSCRLASARTTNP	1519
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	NVKKHLVGCAMGVASKTSSLVTAFKDLDRMP--DAESRCTSSASELRQVALQLLHFADKP	1592
sp P26039 TLN1_MOUSE	TAKRQFVQSAKEVANSTANLVKTIKALDGFTEENRAQCRAATAPLLEAVDNLSAFASNP	1579
sp Q9Y490 TLN1_HUMAN	TAKRQFVQSAKEVANSTANLVKTIKALDGAFTENRAQCRAATAPLLEAVDNLSAFASNP	1579
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	DFAAIQGSISTEGHSAQQPILQSSREMLDSSAQMIQTAKSWASAPQDEATWQRMVNSRQ	1652
sp P26039 TLN1_MOUSE	EFSSVPAQISPEGRAAMEPIVISAKTMLESAAGGLIQTARALAVNPRDPPRWSVLAGHSRT	1639
sp Q9Y490 TLN1_HUMAN	EFSSIPAQISPEGRAAMEPIVISAKTMLESAAGGLIQTARALAVNPRDPPSWSVLAGHSRT	1639
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	VSDSIMRLVNAIHEAAPGQMELEAAIGRLSALSGQIERSAMD CYASGNVQKHGANA---E	1709
sp P26039 TLN1_MOUSE	VSDSIKKLITSMRDKAPGQLECETAIAALNSCLRDLQASLAAVSQQLAPREGISQEALH	1699
sp Q9Y490 TLN1_HUMAN	VSDSIKKLITSMRDKAPGQLECETAIAALNSCLRDLQASLAAVSQQLAPREGISQEALH	1699
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	RQLLQQVQHIASQLEDKVDLHNAAVEHGERLPKVVQLHCQMVEDLADAACCAAGMTVDS	1769
sp P26039 TLN1_MOUSE	TQMLTAVQEISHLIE---PLASAARAEASQLGHKVSQMAQYFEPLTLAAVGAASKTLSH	1755
sp Q9Y490 TLN1_HUMAN	TQMLTAVQEISHLIE---PLANAARAEASQLGHKVSQMAQYFEPLTLAAVGAASKTLSH	1755

DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	NQQT <small>EL</small> FDK <small>CKT</small> VVEAEELAMMVAS <small>RES</small> GGNPN <small>AVH</small> -AHANVKDAAGQLKHAIGDMRQT <small>IA</small>	1828
sp P26039 TLN1_MOUSE	PQQ <small>MALL</small> DQTKT <small>LA</small> ESALQLLYTAKEAGGNPKQAAHTQEAL <small>EE</small> AVQMMTEAVEDLTTT <small>LN</small>	1815
sp Q9Y490 TLN1_HUMAN	PQQ <small>MALL</small> DQTKT <small>LA</small> ESALQLLYTAKEAGGNPKQAAHTQEAL <small>EE</small> AVQMMTEAVEDLTTT <small>LN</small>	1815
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	KVSS <small>EQ</small> GA <small>VQ</small> GMVD <small>TI</small> SSSIAHTDVAVSSAHPGSSFADAQTRMTAYLEDIRRTAIEMPT-	1887
sp P26039 TLN1_MOUSE	EAA <small>SA</small> AGVVGGMVD <small>SIT</small> QAINQLDEGPM-GD <small>PE</small> GSFVDYQTTMVRTAKAIAVTVQEMVTK	1874
sp Q9Y490 TLN1_HUMAN	EAA <small>SA</small> AGVVGGMVD <small>SIT</small> QAINQLDEGPM-GE <small>PE</small> GSFVDYQTTMVRTAKAIAVTVQEMVTK	1874
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	--LNTTDLGAASLNLSEKYRLVAGDV <small>Q</small> AAAGMLPEADIGRLKLAVQKLGTSC <small>IE</small> TVTVA	1945
sp P26039 TLN1_MOUSE	SNTSP <small>EE</small> LGPLANQLTSDYGR <small>LA</small> SQAKPAAVAAE <small>NEE</small> IGAHIKHRVQELGHGCSALVTKA	1934
sp Q9Y490 TLN1_HUMAN	SNTSP <small>EE</small> LGPLANQLTSDYGR <small>LA</small> SEAKPAAVAAE <small>NEE</small> IGSHIKHRVQELGHGCAALVTKA	1934
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	GGKRAHP <small>ED</small> ER <small>IQ</small> RLSSQAGTVV <small>ER</small> VEQVLAALHSASRG <small>TQ</small> ACINAANTVSGIIGD <small>LD</small> LT	2005
sp P26039 TLN1_MOUSE	GALQCSPSDVYTKK <small>EL</small> IECARRVSEKVS <small>HV</small> LAALQAGNRGTQACITAA <small>SA</small> VS <small>SG</small> IAD <small>LD</small> LT	1994
sp Q9Y490 TLN1_HUMAN	GALQCSPSDAYTKK <small>EL</small> IECARRVSEKVS <small>HV</small> LAALQAGNRGTQACITAA <small>SA</small> VS <small>SG</small> IAD <small>LD</small> LT	1994
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	T <small>IM</small> FATSGSLNSSDDRKFP <small>SH</small> KEAIVKTAKALVEDTKALVAGAA <small>SN</small> QEQ <small>L</small> AVAAQN <small>AV</small> RT	2065
sp P26039 TLN1_MOUSE	T <small>IM</small> FATAGTLN <small>RE</small> GAETFADH <small>RE</small> GILKTAKVLVEDTKVLVQ <small>NA</small> AGSQEK <small>LA</small> QAAQSSVAT	2054
sp Q9Y490 TLN1_HUMAN	T <small>IM</small> FATAGTLN <small>RE</small> GTETFADH <small>RE</small> GILKTAKVLVEDTKVLVQ <small>NA</small> AGSQEK <small>LA</small> QAAQSSVAT	2054
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	IVNLSDAVKTGAVSLSS <small>EN</small> SETQVLVIHAVRDVAAALTS <small>LI</small> QATKNASGLSLQHPAMGHL	2125
sp P26039 TLN1_MOUSE	ITRLADVVKLGAASLGAEDPETQVVLINAVKDVAKALGDLISATKAAAGKVGD <small>DP</small> PAVWQL	2114
sp Q9Y490 TLN1_HUMAN	ITRLADVVKLGAASLGAEDPETQVVLINAVKDVAKALGDLISATKAAAGKVGD <small>DP</small> PAVWQL	2114
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	KDAAKVMVSNVARLLKT <small>VAT</small> VEEK <small>NQ</small> QGT <small>RA</small> VEAAVDAIGFEMKQF <small>EH</small> DLNE-GAAIP <small>TD</small>	2184
sp P26039 TLN1_MOUSE	KNSAKVMVTNVTSL <small>LKT</small> VKAVEDEATKGTRALEATTEHIRQ <small>EL</small> AVFCSP <small>EP</small> PAKTSTPED	2174
sp Q9Y490 TLN1_HUMAN	KNSAKVMVTNVTSL <small>LKT</small> VKAVEDEATKGTRALEATTEHIRQ <small>EL</small> AVFCSP <small>EP</small> PAKTSTPED	2174
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	FRPEHLQQT <small>AE</small> HVS <small>EIT</small> KRVMQGA <small>DAP</small> QSE <small>EEE</small> IIGVANLS <small>RS</small> AVR <small>SL</small> LAVVRTISNDADT	2244
sp P26039 TLN1_MOUSE	FI ---- RMTKGITMATAKA-VAAGNSCRQ <small>ED</small> VIATANLSRR <small>AI</small> ADMLRACK <small>EA</small> AFHP <small>EV</small>	2228
sp Q9Y490 TLN1_HUMAN	FI ---- RMTKGITMATAKA-VAAGNSCRQ <small>ED</small> VIATANLSRR <small>AI</small> ADMLRACK <small>EA</small> AYHP <small>EV</small>	2228
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	AP-QRYAVLD <small>SG</small> RDVANNVKSLLVSLHTQMVRNPGQ <small>EE</small> SRRL <small>LE</small> ASKGVSSALSHLVGL	2303
sp P26039 TLN1_MOUSE	APD <small>VR</small> LRLALHYG <small>RE</small> CANGYLELLDHVLLTL-QKPN <small>PD</small> -LKQQLTGHSKRVAGSV <small>TE</small> LIQA	2286
sp Q9Y490 TLN1_HUMAN	APD <small>VR</small> LRLALHYG <small>RE</small> CANGYLELLDHVLLTL-QKPS <small>PE</small> -LKQQLTGHSKRVAGSV <small>TE</small> LIQA	2286
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	CNEMTGLPHNH <small>ME</small> SAAQA <small>EN</small> ELLGAASS <small>IE</small> AASAKLAELRP <small>RQ</small> IVQ <small>ENT</small> QEIVET <small>EF</small> D	2363
sp P26039 TLN1_MOUSE	AEAMKGTEWV-DPEDPTVIA <small>EN</small> ELLGAAAA <small>IE</small> AAAKKLEQLKP <small>RA</small> KPK <small>EA</small> DE---SLN <small>FE</small>	2342
sp Q9Y490 TLN1_HUMAN	AEAMKGTEWV-DPEDPTVIA <small>EN</small> ELLGAAAA <small>IE</small> AAAKKLEQLKP <small>RA</small> KPK <small>EA</small> DE---SLN <small>FE</small>	2342
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	DNIIISAKGILHAVHTLMRSASNAQ <small>RE</small> LAMQGR <small>AA</small> ---AGGTGT <small>YQ</small> W <small>SE</small> GLISAARVVVA	2420
sp P26039 TLN1_MOUSE	EQILEAAKSIAAATSALVKAA <small>SA</small> AQ <small>RE</small> LVAQGKVGAI <small>PAN</small> ALDDGQ <small>WS</small> QGLISAARMVAA	2402
sp Q9Y490 TLN1_HUMAN	EQILEAAKSIAAATSALVKAA <small>SA</small> AQ <small>RE</small> LVAQGKVGAI <small>PAN</small> ALDDGQ <small>WS</small> QGLISAARMVAA	2402
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEEEL	SVHKL <small>CD</small> AANTLMKGQT <small>TE</small> ERLISAAKQVSSSTAQLLVACNV <small>RAD</small> PSQANRRLLQAAGQA	2480
sp P26039 TLN1_MOUSE	ATNNLCEAANA <small>AV</small> QGHASQ <small>EK</small> LISSAKQVAASTAQLLVACVKADQ <small>DS</small> EAMKRLQAAGNA	2462
sp Q9Y490 TLN1_HUMAN	ATNNLCEAANA <small>AV</small> QGHASQ <small>EK</small> LISSAKQVAASTAQLLVACVKADQ <small>DS</small> EAMKRLQAAGNA	2462

DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEL	VRNAAERLVQSAQQEMIAR--DDRNIATSDRLVNGIAQVMDAQEEVLRKERELGEARHKL	2538
sp P26039 TLN1_MOUSE	VKRASDNLVKAAQKAAAFEDQENETVVVKEKMGVGGIAQIIAAQEEMLRKERELEEARKKL	2522
sp Q9Y490 TLN1_HUMAN	VKRASDNLVKAAQKAAAFEEQENETVVVKEKMGVGGIAQIIAAQEEMLRKERELEEARKKL	2522
DDB0233517 DDB_G0291303	-----	1154
tr G5EGK1 G5EGK1_CAEL	AHLNKARYERDGEFA----	2553
sp P26039 TLN1_MOUSE	AQIRQQQYKFLPSELRDEH	2541
sp Q9Y490 TLN1_HUMAN	AQIRQQQYKFLPSELRDEH	2541

[illegible]

sp Q9Y4G6 TLN2_HUMAN	QLIEAGKLVDRSVENCVRACQAATDSSELLKQVSAASVVSQALHDLQHVRRQFASRGEF	797
sp Q71LX4 TLN2_MOUSE	QLIEAGKLVDRSVENCVRACQAATDSSELLKQVSAASVVSQALHDLQHVRRQFASRGEF	798
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DDB0305711 DDB_G0290481	EQDYNLLNARVSDIIESVNLINYAMDCSREYKISITSNGVEVGEGEILAGTNLTEEFAT	751
sp Q9Y4G6 TLN2_HUMAN	IGRYDQATD-----TIMCVTESIFSSMGDAGEMVRQARVLA ----- Q	834
sp Q71LX4 TLN2_MOUSE	IGRYDQATD-----TIMCVTESIFSSMGDAGEMVRQARVLA ----- Q	835
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DDB0305711 DDB_G0290481	VANDLTNAIMTMRSN ----- LKNPDTVMESYKMOVAGHANRLITCTKAVASRADTQSQQR	805
sp Q9Y4G6 TLN2_HUMAN	ATSDLVN---AMRSDAEAEIDMENSKKLLAAAKLLADSTARMVEAAKG-----	879
sp Q71LX4 TLN2_MOUSE	ATSDLVN---AMRSDAEAEIDMENSKKLLAAAKLLADSTARMVEAAKG-----	880
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DDB0305711 DDB_G0290481	LFNSTNAVFESVANLSNHCRSYIKNPQEAAHTFQIVETAGHLQFLTQNMSTDAGKIACIT	865
sp Q9Y4G6 TLN2_HUMAN	-----AAANPENEDQQRLREAAEGLRVATNAAQNAIKKKIVN	918
sp Q71LX4 TLN2_MOUSE	-----AAANPENEDQQRLREAAEGLRVATNAAQNAIKKKIVN	919
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DDB0305711 DDB_G0290481	SLRDYSKEMIAQVSSLISTSRTS-SQYLPDANGITLLKGAKDVSDALSKLMVGIKKVVD	924
sp Q9Y4G6 TLN2_HUMAN	RLEVAAKQAAAAATQTIAASQNAAVSNKNPAAQQQLVQSCKAVADHIPQLVQGVGRGSAQ	978
sp Q71LX4 TLN2_MOUSE	RLEVAAKQAAAAATQTIAASQNAAISNKNPSAQQLVQSCKAVADHIPQLVQGVGRGSAQ	979
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DDB0305711 DDB_G0290481	PKSEATQMELLTLAQKQSLPPMNLVSTCKRFAPKISDPNQKQRLIFSSDAAQSVQKLMK	984
sp Q9Y4G6 TLN2_HUMAN	AEDLSAQLALIISSQNFLQPGSKMVSSAKAAVPTVSDQAAAMQLSQCAKNLATSLAELRT	1038
sp Q71LX4 TLN2_MOUSE	AEDLSAQLALIISSQNFLQPGSKMVSSAKAAVPTVSDQAAAMQLSQCAKNLATSLAELRT	1039
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DDB0305711 DDB_G0290481	AGEAYKRICGHIIEEAEVFDSTIADLETTEIAIAGGFLDAVSGTTRGAAELLMVAIK	1044
sp Q9Y4G6 TLN2_HUMAN	ASQKAHEACGPMEIDSALNTVQTLKNELDQAKMAAVESQLKPLPGETLEKCAQDLGSTSK	1098
sp Q71LX4 TLN2_MOUSE	ASQKAHEACGPMEIDSALNTVQTLKNELDQAKMAAVESQLKPLPGETLEKCAQDLGSTSK	1099
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DDB0305711 DDB_G0290481	DLNKVNNELVTDIRV-NPARLGDLVKSATESASSVAISAKTLICATTGKQVQKKLMGITK	1103
sp Q9Y4G6 TLN2_HUMAN	AVGSSMAQLLTCAAQGNHEHTGVAARETAQALKTLQAARGVAASTDPAAAHAMLD SAR	1158
sp Q71LX4 TLN2_MOUSE	GVGSSMAQLLTCAAQGNHEHTGVAARETAQALKTLQAARGVAASTNDPEAAHAMLD SAR	1159
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DDB0305711 DDB_G0290481	QLMIDMEQLIRASRSVASNPNDAASELLDASNDVSISTA ---- ALVGST-ANVDCK--	1156
sp Q9Y4G6 TLN2_HUMAN	DVMEGSAMLIQEAKQALIAPGDAERQORLAQVAKAVSHSLNNCVNCVLPQKQDV DVALKSI	1218
sp Q71LX4 TLN2_MOUSE	DVMEGSAMLIQEAKQALIAPGDTESQORLAQVAKAVSHSLNNCVNCVLPQKQDV DVALKSI	1219
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DDB0305711 DDB_G0290481	-----ELDEASADIS----- NLLSLKMGSLESILSQPTE	1185
sp Q9Y4G6 TLN2_HUMAN	GESSKKLLVDSLPPSTKPFQEAQSELNQAAADLNQSAGEVHATRGQSGELAAASGKFSD	1278
sp Q71LX4 TLN2_MOUSE	GEASKLLVDSLPPSTKPFQEAQSELNQAAADLNQSAGEVHATRGQSGELAAASGKFSD	1279
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DDB0305711 DDB_G0290481	EFAFYVEE-----	1193
sp Q9Y4G6 TLN2_HUMAN	DFDEF LDAGIEMAGQAQTKEDQIQVIGNLKNISMASSKLLLAAKSLSVDPGAPNAKNLLA	1338
sp Q71LX4 TLN2_MOUSE	DFDEF LDAGIEMAGQAQTKEDQMQVIGNLKNISMASSKLLLAAKSLSVDPGAPNAKNLLA	1339
	: * : : :	
DDB0305711 DDB_G0290481	-----I	1194
sp Q9Y4G6 TLN2_HUMAN	AAARAVTESINQLITLCTQQAPGQKECDNALRELETVKGMLDNPNEPVSDLSYFDCIESV	1398
sp Q71LX4 TLN2_MOUSE	AAARAVTESINQLIMLCTQQAPGQKECDNALRELETVKGMLDNPNEPVSDLSYFDCIESV	1399
	:	
DDB0305711 DDB_G0290481	ASSTKALNAASQQVVAMARNKNLKG LGASAKITASALSTLVSHAQNAIVLTENEATKNAI	1254
sp Q9Y4G6 TLN2_HUMAN	MENSKVLGESMAGISQNAKTGDLPAFGCECVGIASKALCGLTEAAQAAYLVGIS-----	1452
sp Q71LX4 TLN2_MOUSE	MENSKVLGESMAGISQNAKTGDLPAFGCECVGIASKALCGLTEAAQAAYLVGIS-----	1453
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DDB0305711 DDB_G0290481	LASTVALG-GQIIIGLLDFSKARIANY*-----	1279
sp Q9Y4G6 TLN2_HUMAN	-DPNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAATIVAKHTSALCNAC	1511
sp Q71LX4 TLN2_MOUSE	-DPNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAATIVAKHTSALCNAC	1512
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DDB0305711 DDB_G0290481	-----	1279
sp Q9Y4G6 TLN2_HUMAN	RIASSKTANPVAKRHFVQSAKEVANSTANLVKTIKALDGD FSEDNRNKCRIATAPLIEAV	1571
sp Q71LX4 TLN2_MOUSE	RIASSKTANPVAKRHFVQSAKEVANSTANLVKTIKALDGD FSEDNRNKCRIATTPLIEAV	1572

DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	ENLTAFASNP EFVSIPAQISS EGSQAQEPILVSAKTMLESSSYLIRTARSLAINPKDPPT	1631
sp Q71LX4 TLN2_MOUSE	ENLTAFASNP EFASIPAQISS EGSQAQEPILVSAKTMLESSSYLIRTARSLAINPKDPPT	1632
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	WSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRCIRDIEQASLAAVSQSLAT	1691
sp Q71LX4 TLN2_MOUSE	WSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRCIRDIEQASLAAVSQSLAT	1692
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	RDDISVEALQEQLTSVVQEIGHLIDPIATAARGEAAQLGHKVTQLASYFEPLILAAVGVA	1751
sp Q71LX4 TLN2_MOUSE	RDDISVEALQEQLTSVVQEIGHLIDPIATAARGEAAQLGHKVTQLASYFEPLILAAVGVA	1752
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	SKILDHQQQMTVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMKEAVDDI	1811
sp Q71LX4 TLN2_MOUSE	SKMLDHQQQMTVLDQTKTLAESALQMLYAAKEGGGNPKAVH-----	1793
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	MVTLNAAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKGTFVDYQTTVVKYSKAIAVTAQE	1871
sp Q71LX4 TLN2_MOUSE	-----TAPEPKGTFVDYQTTVVKYSKAIAVTAQE	1822
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	MMTKSVTNPEELGGLASQMTSDYGH LAFQGQMAAAATAPEEIGFQIRTRVQDLGHGCIFL	1931
sp Q71LX4 TLN2_MOUSE	-----MIGFQIRTRVQDLGHGCIFL	1842
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	VQKAGALQVCPTDSYTKRELIECARAVTEKVS LVL SALQAGNKG TQACITAA TAVSGIIA	1991
sp Q71LX4 TLN2_MOUSE	VQKAGALQVCPTDSYTKRELIECARSVTEKVS LVL SALQAGNKG TQACITAA TAVSGIIA	1902
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	DLDTTIMFATAGT LNAENSETFADHRENILK TAKALVEDTKLLVSGAASTPDKLAQAAQS	2051
sp Q71LX4 TLN2_MOUSE	DLDTTIMFATAGT LNAENGETFADHRENILK TAKALVEDTKLLVSGAASTPDKLAQAAQS	1962
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	SAATITQLAEVVKLGAASLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPS	2111
sp Q71LX4 TLN2_MOUSE	SAATITQLAEVVKLGAASLGSDNPE TQVVLINAIKDVAKALSDLIGATKGAASKPADDPS	2022
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	MYQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQELTVFQSKDVPEKTS	2171
sp Q71LX4 TLN2_MOUSE	MYQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIEYIKQELTVFQSKDIPEKTS	2082
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	SPEESIRMTKGITMATAKAVAAGNSCRQEDVIATANLSRKAVSDMLTACKQASFHPDVSD	2231
sp Q71LX4 TLN2_MOUSE	SPEESIRMTKGITMATAKAVAAGNSCRQEDVIATANLSRKAVSDMLTACKQASFYPDVSE	2142
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	EVRTRALRFGT ECTLG YLDLLEHVLVILQKPTPEFKQQLAAFSKRVAGAVTELIQA AEAM	2291
sp Q71LX4 TLN2_MOUSE	EVRTRALRYGT ECTLG YLDLLEHVLVILQKPTPELKHQLAAFSKRVAGAVTELIQA AEAM	2202
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	KGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAKPKQADETLDFEEQILEAAK	2351
sp Q71LX4 TLN2_MOUSE	KGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAKPKQADETLDFEEQILEAAK	2262
DDB0305711 DDB_G0290481		1279
sp Q9Y4G6 TLN2_HUMAN	SIAAATSALVKASAAQRELV AQGKVGSIPANAADDGQWSQGLISAARMVAAATSSLC EA	2411
sp Q71LX4 TLN2_MOUSE	SIAAATSALVKASAAQRELV AQGKVGSIPANAADDGQWSQGLISAARMVAAATSSLC EA	2322

DDB0305711 DDB_G0290481	-----	1279
sp Q9Y4G6 TLN2_HUMAN	ANASVQGHASEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAVKRASDNL	2471
sp Q71LX4 TLN2_MOUSE	ANASVQGHASEEKLISSAKQVAASTAQLLVACKVKADQDSEAMKRLQAAGNAV-----	2375
DDB0305711 DDB_G0290481	-----	1279
sp Q9Y4G6 TLN2_HUMAN	VRAAQKAAFGKADDDVVVKTKFVGGIAGIIAAQEMLKKERLEEARKKLAQIRQQQYK	2531
sp Q71LX4 TLN2_MOUSE	-----	2375
DDB0305711 DDB_G0290481	-----	1279
sp Q9Y4G6 TLN2_HUMAN	FLPTELREDEG	2542
sp Q71LX4 TLN2_MOUSE	-----	2375

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0232320 DDB_G0285939	MDEVL	5
sp P19826 VINC_CAEEEL	MPVFHTKTIENILEPVAQQLHYVLAMAEKNATSVDEVRLGTSMPNLDRFASRSALALS	60
sp O46037 VINC_DROME	MPVFHTKTIESI LDPVAQQV-----	20
sp P18206 VINC_HUMAN	MPVFHTRTIESILEPVAQQI-----	20
sp Q64727 VINC_MOUSE	MPVFHTRTIESILEPVAQQI-----	20
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DDB0232320 DDB_G0285939	-----EMIADAVSSLVVAITDSEEKNTLFGDM	32
sp P19826 VINC_CAEEEL	ASSRRSIP EYITPDTVRHVVNDDDCPVCLMMPRGKGCVSRLVILHEEAN-DGNAMPDL	119
sp O46037 VINC_DROME	-----SRLVILHEEAE-DGNAMPDL	39
sp P18206 VINC_HUMAN	-----SHLVIMHEEGEVDGKAIPDL	40
sp Q64727 VINC_MOUSE	-----SHLVIMHEEGEVDGKAIPDL	40
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DDB0232320 DDB_G0285939	VPGVVELIQQAVNGMAEAAEETVSLIDEEFIGQLE-STSKQLKNSAGQLYVHAVRAREDPW	91
sp P19826 VINC_CAEEEL	TGVPVGMVSRVAGNLIQVGYDTCDHSDDRILQQDMPPALQRVEGSSKLL EESSYSLKHPY	179
sp O46037 VINC_DROME	SRPVQVVSAAVANLVKVGRTINSSDDKILRQDMP SALHRV EGA S Q L L E A S D M L R S D P Y	99
sp P18206 VINC_HUMAN	TAPVAAVQA AVSNLVRVGKETVQTTE D Q I L K R D M P P A F I K V E N A C T K L V Q A A Q M L Q S D P Y	100
sp Q64727 VINC_MOUSE	TAPVAAVQA AVSNLVRVGKETVQTTE D Q I L K R D M P P A F I K V E N A C T K L V Q A A Q M L Q S D P Y	100
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DDB0232320 DDB_G0285939	NRVPQKDAIKAAKQILQNVVLLVLIEEQSNIKVLVNIAKKAAEGVRRIDEIENIKQLDVM	151
sp P19826 VINC_CAEEEL	SVPARKKILIDGARGILQGT SALLLCFDESEVRKII R V C R K A N D Y V A V S E V I E S M A D L Q Q F	239
sp O46037 VINC_DROME	SGPARKKILIEGSRGILQGTSSLLLCFDESEVRKIIQECKRVL DY L A V A E V I N T M E Q L V Q F	159
sp P18206 VINC_HUMAN	SVPARDYLIDGSRGILSGTSDLLLTFDEAEVRKII R V C K G I L E Y L T V A E V V E T M E D L V T Y	160
sp Q64727 VINC_MOUSE	SVPARDYLIDGSRGILSGTSDLLLTFDEAEVRKII R V C K G I L E Y L T V A E V V E T M E D L V T Y	160
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DDB0232320 DDB_G0285939	IGDVNQ LQNE----LVKRSQRRSEGSHP E L R S K L E D I A T M V N I L S E Q H Q A S A R D V C --R	205
sp P19826 VINC_CAEEEL	VKDISPVLHDVTNDVNLRQQELTHQVHREILIRCMDSIKVIAPILICSMKTSIELGTPHP	299
sp O46037 VINC_DROME	LKDLSPCLSKVHREVGAREKELTHQVHSEILVRCL EQVKT LAPILICSMKVYIHIVE-QQ	218
sp P18206 VINC_HUMAN	TKNLGPGMTKMAKMIDERQQELTHQEH R V M L V N S M N T V K E L L P V L I S A M K I F V T T K N - S K	219
sp Q64727 VINC_MOUSE	TKNLGPGMTKMAKMIDERQQELTHQEH R V M L V N S M N T V K E L L P V L I S A M K I F V T T K N - S K	219
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DDB0232320 DDB_G0285939	NPREETLRSKRSELSSKLLSAIDDLIYTIKLIFENN -----TKFVDL	247
sp P19826 VINC_CAEEEL	RQGHAEAIANRNFM SQRMT EEMNEIIRVLQLTTYDEDEWDADNVTVMRKALSAAKSLLTA	359
sp O46037 VINC_DROME	GRGAEEAAENRNLYLAARMSDELQE IIRVLQLTTYDEDTSELDNLTVLKKLSNAISNKMEQ	278
sp P18206 VINC_HUMAN	NQGIEEALKNRNFTVEKMSAEINEIIRVLQLTSWDEDAWASKDTEAMKRALASIDSKLNQ	279
sp Q64727 VINC_MOUSE	NQGIEEALKNRNFTVEKMSAEINEIIRVLQLTSWDEDAWASKDTEAMKRALASIDSKLNQ	279
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DDB0232320 DDB_G0285939	AFKWKPVRTMAEDEVTRASAVLIDNLR L T L P K S I E A G N G P A A A R E I V N A A N L -----	298
sp P19826 VINC_CAEEEL	ALDWLAD-----PHARSGAVGEKAIRRIC EYADRISARALPED	397
sp O46037 VINC_DROME	ANEWLSN-----PYALRGGVGEKALRQVIDNATEISERCLPQD	316
sp P18206 VINC_HUMAN	AKGWLRD-----PSASPGDAGEQAIRQILDEAGKV GELCAGKE	317
sp Q64727 VINC_MOUSE	AKGWLRD-----PNASPGDAGEQAIRQILDEAGKV GELCAGKE	317
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DDB0232320 DDB_G0285939	-----	298
sp P19826 VINC_CAEEEL	AQSIKRSIFEITSFTDELCLNRNNGQPDRENLA AQT -----ARRLKD L	440
sp O46037 VINC_DROME	SYPIRKLAD E V T A M A N T L C E L R Q E G K G -----	343
sp P18206 VINC_HUMAN	RREILGTCKMLGQMTDQVADLRARGQGS SPVAMQKAQQVVSQGLDVL TAKVENAARKLEAM	377
sp Q64727 VINC_MOUSE	RREILGTCKMLGQMTDQVADLRARGQGS SPVAMQKAQQVVSQGLDVL TAKVENAARKLEAM	377
DDB0232320 DDB_G0285939	-----QISNAIIIVANRCQDPVK-----	315
sp P19826 VINC_CAEEEL	VG-----	442
sp O46037 VINC_DROME	-----	343
sp P18206 VINC_HUMAN	TNSKQSI AKKIDAAQNWLADPNGGPEGE EQIRGALAEARKIAELCDDPKERDDILRS LGE	437
sp Q64727 VINC_MOUSE	TNSKQSI AKKIDAAQNWLADPNGGPEGE EQIRGALAEARKIAELCDDPKERDDILRS LGE	437
DDB0232320 DDB_G0285939	-----	315
sp P19826 VINC_CAEEEL	-----SQNSSGLMGDALQNAQRHGGANPAHTAA	470
sp O46037 VINC_DROME	-----QSPQAESLVRGIRDRMGELKSLVHQAVLGV D K A G V Q Q T A H T I Q	386

sp P18206 VINC_HUMAN	ISALTSKGLADLRQGGKSDSPPEARALAKQVATALQNLTQKTNR---VANSRPAKAAVHLE	494
sp Q64727 VINC_MOUSE	IAALTSKGLDLRRQGGKSDSPPEARALAKQVATALQNLTQKTNR---VANSRPAKAAVHLE	494
DDB0232320 DDB_G0285939		315
sp P19826 VINC_CAEEEL	GRLEQALRWLDNPGLDGGGLGLQALRLLTADARKLADRLNPQDRNRLGLCSDIDRLAAQ	530
sp 046037 VINC_DROME	GRLEQAVKWLQHPEINDGGLGERAINLIVEEGRKVAEGCPGHQKAEIQQLCDEVERLKRQ	446
sp P18206 VINC_HUMAN	GKIEQAQRWIDNPTVDDRGVGQAIRGLVAEGHRLANVMMGPYRQDLLAKCDRVDQLTAQ	554
sp Q64727 VINC_MOUSE	GKIEQAQRWIDNPTVDDRGVGQAIRGLVAEGHRLANVMMGPYRQDLLAKCDRVDQLTAQ	554
DDB0232320 DDB_G0285939		315
sp P19826 VINC_CAEEEL	LADLERRGLGNSPEAHQIRNQLKNALRDLGDFMRRVLTDRVDDFADITTPLKQFVEAVH	590
sp 046037 VINC_DROME	-----AAGSGPAKQAAKQLTQKLYELKAAIQNALVNRIVQDFMDVSTPLKQFTEAVL	499
sp P18206 VINC_HUMAN	LADLAARGEESPPARALASQLQDSLKDLKARMQEAMTQEVSDVFSDTTTPIKLLAVAL	614
sp Q64727 VINC_MOUSE	LADLAARGEESPPARALASQLQDSLKDLKARMQEAMTQEVSDVFSDTTTPIKLLAVAL	614
DDB0232320 DDB_G0285939		331
sp P19826 VINC_CAEEEL	ADPYDPNREQNFVKSQRLTDHSQSMTTTARLVASCGPSKSKKTVEAILDTAEKVEQLTP	650
sp 046037 VINC_DROME	QPEGTPGREQNFNQSNLQAFSDRASKTSRMVAAGGACGNKKIAEILLSSAAQVDSLTP	559
sp P18206 VINC_HUMAN	APPDAPNREEVFDERAANFENHSGKLGATAEKAAAVGTAN-KSTVEGIQASVKTARELTP	673
sp Q64727 VINC_MOUSE	APPDAPNREEVFDERAANFENHSGRLGATAEKAAAVGTAN-KSTVEGIQASVKTARELTP	673
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DDB0232320 DDB_G0285939		389
sp P19826 VINC_CAEEEL	MLISAMKPVLENPNDEAQKHLESVIYSTQKASEALATAV--VSSPAEIVAASGVSLARD	707
sp 046037 VINC_DROME	QLVNAGRVRLHNPGE---QHFEIHKQYADALHRLRSHVDDAIDTGEFVRASETAMRRY	619
sp P18206 VINC_HUMAN	QLISAGRIRMNYPGSKAADEHLQNLKQYADTVLRMRTLCDQATDPADFIKTSSEHMVY	733
sp Q64727 VINC_MOUSE	QVVSAAIRILLRNPNGQAAYEHFETMKNQWIDNVEKMTGLVDEAIDTKSLLDASEEAIKDD	733
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DDB0232320 DDB_G0285939		449
sp P19826 VINC_CAEEEL	LDSLEEAIASGDKKRAQVILSHIPS AIDKHIELANALLEITDPGQRHQIKQSIERLQTL	767
sp 046037 VINC_DROME	TNHCEGAINGADAHGLVNSSQIARLGNRVLMTAQNEADNSEPSFVSRVRNAADQLHNA	679
sp P18206 VINC_HUMAN	AKLCEDAIHARQPQKMDVNTSNIARLINRVLLVAKQEADNSEDVPFTERLNAAANRLERS	793
sp Q64727 VINC_MOUSE	LDKCKVAMANIQQPMLVAGATSIARRANRILLVAKREVENSEDPKFRFAVKAASDELSKT	793
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DDB0232320 DDB_G0285939		509
sp P19826 VINC_CAEEEL	KPRIENANRAIANPNDEARKNLSSDIKEAKKAIGQISQPYEVVSALNTKIHNDLDSLI	799
sp 046037 VINC_DROME	IPPMVNNAKQIA-----QNPHDQYAAQNWRGTND-----HLL	711
sp P18206 VINC_HUMAN	LPAMVGDAKLVA-----TNIADPAAAAAWKNSFQ-----RLL	825
sp Q64727 VINC_MOUSE	ISPMVMDAKAVA-----GNISDPGLQKSFLD SGY-----RIL	825
	ISPMVMDAKAVA-----GNISDPGLQKSFLD SGY-----RIL	
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DDB0232320 DDB_G0285939		569
sp P19826 VINC_CAEEEL	KCIDEGGPDMQVKGQVYAKDIANSIKKQIEAAEAYAQTITDPDRKKQVLDSIEQLKKLTP	853
sp 046037 VINC_DROME	NSVRAVGDAI--TGVPMSNGRHSSYQESISRASPY----NPPPPSSQVIRSVNASPTAP	740
sp P18206 VINC_HUMAN	GDVREVRDAI--APPQ-----PPPLPTSL--PPPIPEL-----	849
sp Q64727 VINC_MOUSE	GAVAKVREAF--QPQE-----P----DF--PPPPDL-----	849
	GAVAKVREAF--QPQE-----P----DF--PPPPDL-----	
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DDB0232320 DDB_G0285939		629
sp P19826 VINC_CAEEEL	QLLEAIRACLANPDDKEARKRLDDVVRVKEASSNLSQVIQPTADELKEEKRKRNEEIAR	896
sp 046037 VINC_DROME	I----IHNMKIREDIPAPPRPP-----PPVELSPPPRPPPPPEYDEEEETR-----	782
sp P18206 VINC_HUMAN	-----SALHLSNQNAERAPPRPP-----LPREGLAPVRPPPPETDDEDEGVF-----	888
sp Q64727 VINC_MOUSE	-----EQLRLT--DELAPPKPP-----LPEGEVPPPRPPPPPEEKDEEFPEQ-----	888
	-----EQLRLT--DELAPPKPP-----LPEGEVPPPRPPPPPEEKDEEFPEQ-----	
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DDB0232320 DDB_G0285939		675
sp P19826 VINC_CAEEEL	IEAEKAKARALLKAAELARIEAEE--EK-----KRLAIEEEKKR-----L-AAEEEE	900
sp 046037 VINC_DROME	-AF-----WE-----	782
sp P18206 VINC_HUMAN	-----KAGEVINQPMMAARQLHD-EARKWSSKPGIPAAEVGIGVVAEADAADAAGFPVPPDME	946
sp Q64727 VINC_MOUSE	-----KAGEVINQPMMAARQLHD-EARK-----	911
DDB0232320 DDB_G0285939		731
sp P19826 VINC_CAEEEL	RKRAPKL-V-VPEGPVNKAVFGAAADVAQALESKVRDGTPLGILVQLSDEIAQQMALI--	949
sp 046037 VINC_DROME	-----RYPLPQASHQPMIAAAHNLHNE LKQWSSQEND---IVAAAKRMAILMARLSQ	829
sp P18206 VINC_HUMAN	-----RTMPHANQPILIAARGLHQEVQRWSSKDNE---IIAAAKRMAILMARLSE	1003
sp Q64727 VINC_MOUSE	DDYEPPELLMPSNQPVNQPIIAAQSLHREATKWSSKGND---IIAAAKRMALLMAEMSR	935
	-----WSSKGND---IIAAAKRMALLMAEMSR	

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DDB0232320 DDB_G0285939	-ASFAMNGDVKGMITAARKIADTIKQVQTQAKHIADNCTDPRLKQNVLTTCDCGGNFSTQ	790	
sp P19826 VINC_CAEEEL	LVR-GEGGTKKDLINCSKAIAADSS EEVTRLAVQLARLCTDIKMR TALLQVSERIPTIATQ	1008	
sp 046037 VINC_DROME	LVLSDSRGSKRELIA TAKKIAEASEDVTRLAKE LARQCTDRRI RTNLLQVCERIPTIGTQ	889	
sp P18206 VINC_HUMAN	LVR-GGSGTKRALIQCAKDI AKASDEVTRLAKEVAKQCTDKRIR TNLLQVCERIPTISTQ	1062	
sp Q64727 VINC_MOUSE	LVR-GGSGTKRALIQCAKDI AKASDEVTRLAKEVAKQCTDKRIR TNLLQVCERIPTISTQ	994	
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DDB0232320 DDB_G0285939	LKILCAVKSNDNF -----DPTAEEQLVTCAKGLSGAVINLVKSSEAAS	833	
sp P19826 VINC_CAEEEL	LKVLSTVKATMLGSANVIGPYGQPV EGSEEDDEAMQQLVHNAQNLMQSVKDVVRAAEAAS	1068	
sp 046037 VINC_DROME	LKILSTVKATMLGAQGS -----DEDREATEMLVGNAQNLMQSVKETVRAAEGAS	938	
sp P18206 VINC_HUMAN	LKILSTVKATMLGR TNIS -----DEESEQATEMLVHNAQNLMQSVKETVREAEAAS	1113	
sp Q64727 VINC_MOUSE	LKILSTVKATMLGR TNIS -----DEESEQATEMLVHNAQNLMQSVKETVREAEAAS	1045	
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DDB0232320 DDB_G0285939	IKQRKVPQQ*-----	842	
sp P19826 VINC_CAEEEL	IKIRTNIS-GLRLRWLRKPMWSNF	1090	
sp 046037 VINC_DROME	IKIRSDQTSNRLQWVRRQPWYQY	961	
sp P18206 VINC_HUMAN	IKIRTD A-GFTLRWVRKTPWYQ-	1134	
sp Q64727 VINC_MOUSE	IKIRTD A-GFTLRWVRKTPWYQ-	1066	
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DDB0232938 DDB_G0269138	---	MTREENVYMAKLAEQAERYDDEAMAMKVAELDVELTVEERNLLSVAYKNVIGARRA	57
sp P41932 14331_CAEEEL		-MSDTVEELVQRAKLAEQAERYDDMAAMKKVTEQGQELSNEERNLLSVAYKNVVGARRS	59
sp P29310 1433Z_DROME		MSTVDKEELVQKAKLAEQSERYDDMAQAMKSVTETGVELSNEERNLLSVAYKNVVGARRS	60
sp P63104 1433Z_HUMAN		---MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKNVVGARRS	57
sp P63101 1433Z_MOUSE		---MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKNVVGARRS	57
		: * * ***** : * * : * . * * : * * . * * : ***** : * * :	
DDB0232938 DDB_G0269138		SWRIISSIEQKEESKGNENHVKKIKEYCKVEKELTDICNDILEVLESHLIVSSASGESK	117
sp P41932 14331_CAEEEL		SWRVISSIEQKTEGS--EKKQQLAKEYRVKVEQELNDICQDVLKLLDEFLIVKAGAAESK	117
sp P29310 1433Z_DROME		SWRVISSIEQKTEAS--ARKQQLAKEYRERVEKELREICYEVLGLLDKYLPKASNPEK	118
sp P63104 1433Z_HUMAN		SWRVVSSIEQKTEGA--EKKQQMAREYREKIETELRDICNDVLSLLEKFLIPNASQAESK	115
sp P63101 1433Z_MOUSE		SWRVVSSIEQKTEGA--EKKQQMAREYREKIETELRDICNDVLSLLEKFLIPNASQPESK	115
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DDB0232938 DDB_G0269138		VFYYKMKGDYFRYLAEFATGNPRKTSAESSLIAAYKAASDIAVTELPPTHPIRLGLALNFS	177
sp P41932 14331_CAEEEL		VFYLMKMGDYYRYLAEVASE-DRAAVVEKSQKAYQEALDIKDKMQPTHPIRLGLALNFS	176
sp P29310 1433Z_DROME		VFYLMKMGDYYRYLAEVATGDARNTVVDSSQTAYQDAFDISKGMQPTHPIRLGLALNFS	178
sp P63104 1433Z_HUMAN		VFYLMKMGDYYRYLAEVAAGDDKKGIVDQSQAYQEAFAISKEMQPTHPIRLGLALNFS	175
sp P63101 1433Z_MOUSE		VFYLMKMGDYYRYLAEVAAGDDKKGIVDQSQAYQEAFAISKEMQPTHPIRLGLALNFS	175
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DDB0232938 DDB_G0269138		VFYYEILNSPDRACNLAKTAFDDAIAELDTLSEDSYKSDTLIMQLLRDNLTLWTSDVHNM	237
sp P41932 14331_CAEEEL		VFYYEILNTPEHACQLAKQAFDDAIAELDTLNEDSYKSDTLIMQLLRDNLTLWTSDVGA	236
sp P29310 1433Z_DROME		VFYYEILNSPDKACQLAKQAFDDAIAELDTLNEDSYKSDTLIMQLLRDNLTLWTSDTQGD	238
sp P63104 1433Z_HUMAN		VFYYEILNSPEKACSLAKTAFDEAIAELDTLSEESYKSDTLIMQLLRDNLTLWTSDTQGD	235
sp P63101 1433Z_MOUSE		VFYYEILNSPEKACSLAKTAFDEAIAELDTLSEESYKSDTLIMQLLRDNLTLWTSDTQGD	235
		***** : * * : * * * * * : * * : * * : * * : * * : * * : * * :	
DDB0232938 DDB_G0269138		EKNQDGGDDQNEPGM*	252
sp P41932 14331_CAEEEL		DQEQE-GNQEAGN---	248
sp P29310 1433Z_DROME		EAEPEEGGDN-----	248
sp P63104 1433Z_HUMAN		EAEAGEGGEN-----	245
sp P63101 1433Z_MOUSE		EAEAGEGGEN-----	245
		: : : . : :	

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0214822 DDB_G0277869	MQAIKCVVVG DGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPINLGLWDTAG	60
sp Q05062 CDC42_CAEEL	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P40793 CDC42_DROME	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P60953 CDC42_HUMAN	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P60766 CDC42_MOUSE	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
*:*****:..*:.*.*:***:***	
DDB0214822 DDB_G0277869	QEDYDRLRPLSYPQTDVFLICFSIISPSSFENVNGKWHPEICHHAPNVPIILVGTGLDMR	120
sp Q05062 CDC42_CAEEL	QEDYDRLRPLSYPQTDVFLVCFSVVAPASFENVREKWPVEISHHCKTPFLLVGTQVDLR	120
sp P40793 CDC42_DROME	QEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCQKTPFLLVGTQIDLR	120
sp P60953 CDC42_HUMAN	QEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCKTPFLLVGTQIDLR	120
sp P60766 CDC42_MOUSE	QEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCKTPFLLVGTQIDLR	120
	*****.*:.*:.*:*****.* * * * * *:.*:*****.*:*	
DDB0214822 DDB_G0277869	EDKETQDRLKEKKLYPISYEQGLAKMKEINAVKYLECSALTQKGLKTVFDEAIRAVINPP	180
sp Q05062 CDC42_CAEEL	DDPGMLEKLAKNKQKPVSTDVGEKLAKELKAVKYVECSALTQKGLKNVFDEAILAALDPP	180
sp P40793 CDC42_DROME	DENSTLEKLAKNKQKPITMEQGEKLAKELKAVKYVECSALTQKGLKNVFDEAILAALDPP	180
sp P60953 CDC42_HUMAN	DDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALDPP	180
sp P60766 CDC42_MOUSE	DDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALDPP	180
	:: :.* :.* *: : . : : :*****:*****.* * * * *:.*:*	
DDB0214822 DDB_G0277869	LSKKKKSSGGCNIL*	194
sp Q05062 CDC42_CAEEL	QQEKKK---KCNIL-	191
sp P40793 CDC42_DROME	EPTKKR---KCKFL-	191
sp P60953 CDC42_HUMAN	EPKKS---RCVLL-	191
sp P60766 CDC42_MOUSE	EPKKS---RCVLL-	191
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0214824 DDB_G0279605	MQSIKLVVVG DGAVGKTCLLISYTSNSFPTEYVPTVFDNYSANVMVDNKTVSLGLWDTAG	60
sp Q05062 CDC42_CAEEEL	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P40793 CDC42_DROME	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P60953 CDC42_HUMAN	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
sp P60766 CDC42_MOUSE	MQTIKCVVVG DGAVGKTCLLISYTTNKFPEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG	60
	**.* **	
DDB0214824 DDB_G0279605	QEDYDRLRPLSYPQTDVFLICFAIISQTSYTNVSKWVPEVTHHCPNCTIILVGTGKCDLR	120
sp Q05062 CDC42_CAEEEL	QEDYDRLRPLSYPQTDVFLVCFVVPASFENVREKWPVEISHHCSKTPFLLVGTQVDLR	120
sp P40793 CDC42_DROME	QEDYDRLRPLSYPQTDVFLVCFVVPSPSSFENVKEKWVPEITHHCQKTPFLLVGTQIDLR	120
sp P60953 CDC42_HUMAN	QEDYDRLRPLSYPQTDVFLVCFVVPSPSSFENVKEKWVPEITHHCQKTPFLLVGTQIDLR	120
sp P60766 CDC42_MOUSE	QEDYDRLRPLSYPQTDVFLVCFVVPSPSSFENVKEKWVPEITHHCQKTPFLLVGTQIDLR	120

DDB0214824 DDB_G0279605	EDKESLEKLRKHHQPLTFQGEQMAKEIKAFCEYMECSALTQKGLKVDFEAIKAVIFPD	180
sp Q05062 CDC42_CAEEEL	DDPGMLEKLAKNKQKPVSTDVGEKLAKELKAVKYVECSALTQKGLKNVDFEAILAALDPP	180
sp P40793 CDC42_DROME	DENSTLEKLAKNKQKPITMEQGEKLAKELKAVKYVECSALTQKGLKNVDFEAILAALDPP	180
sp P60953 CDC42_HUMAN	DDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVDFEAILAALDPP	180
sp P60766 CDC42_MOUSE	DDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVDFEAILAALDPP	180
	:: :*** ::*.*:: : .*::*::** .*.*****:***** *.: *	
DDB0214824 DDB_G0279605	RDKATNKKNSKCSIL*	195
sp Q05062 CDC42_CAEEEL	QQ --- EKKKKCNIL-	191
sp P40793 CDC42_DROME	EP --- TKKRKCKFL-	191
sp P60953 CDC42_HUMAN	EP --- KKSRRCVLL-	191
sp P60766 CDC42_MOUSE	EP --- KKSRRCVLL-	191
	. *.* :*	

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME MAKIANASLSQQQKQQAETATTTTTTVAASVETATTTARSRDRTKSAAQITSHLLKRAI
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 --MKS LFLNFI LLIFLGRV-FCQTCAGTTLANGACVKQVIT-----QITTATCRS
sp|P10040|CRB_DROME SVYSSPQWIPLFILIIYLATDVASVAVPTKEAYFNGSTYLRLLTTPMPIWDHSAISFRSCRG
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 GSKS-----DFYWLSGSANPCPSG----WSVEYVVRTAPITNNQLTWYWC
sp|P10040|CRB_DROME GEILAQYQYNKNSIVISVLNDFLQIS-LAGPAVHGPNRLDVKLPYQLL-----DNRWHTL
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 VDILDVGGFTTEVLV-SSVLNCGGYQAYTIGTITFSTTNRYLVVSFCSNQGMVSNKSP
sp|P10040|CRB_DROME QFKY EYGNLYLHVDRAASIFANSTYNSQFLTNQDIGYKDAILILG-NSFSGCLLDGPGLO
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 IT----SDATKNLCTKGKGTITDVRYLEIYSAVCPSGYTGTAPSCTDINECSTSNGGCA
sp|P10040|CRB_DROME FVNNSTVQNVVF GHCP LTPGPCSDHDLFTR---LPDNFCL-NDPCM GHG-----
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 HNCANTAGSFCTSCRAGYTLNSDKKSC--TDINECSTNNGGCNQVCTNSAGSFAC-----
sp|P10040|CRB_DROME -TCSSSP EGYECRTARYSGKNQCKDNGSPCAKNPCE-NGGSC---LENSRGDYQCFCDP
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 -----SCRAGYTLGTDKKTCVDINEC
sp|P10040|CRB_DROME NHSGQHCE TEVNIHPLCQTNPCLNNGACVVI GGSGALTCEPKGYAGARC----EVDTDEC
sp|P82279|CRUM1_HUMAN -----MALKNIN YLLIFY---LSFLLIYIKNSFC----NKNNTRC
sp|Q8VHS2|CRUM1_MOUSE -----MKLKRTAYLLFLY---LSSLLI CIKNSFC----NKNNTRC
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DDB0235380|DDB_G0295485 STNNGGCAHNCANTAGSFCTSCRA-GYTLNSDKKSC TDINECSTNNGGCNQVCTNSAGSF
sp|P10040|CRB_DROME ASQPCQNNGSCIDRINGFSCDCSGTGYT-GAF--CQTNVDECDKNPCLNGGRCFDYTGWY
sp|P82279|CRUM1_HUMAN LNSCQNNSTCKDFSKDNDCSCSDTANNLDKD--CDNMKDPCFSNQCQSATCVNTPG--
sp|Q8VHS2|CRUM1_MOUSE LSGPCQNNSTCKHFPQDNNC-CLDTANNLDKD--CEDLKDPCFSSPCQGIATCVKIPG--
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DDB0235380|DDB_G0295485 ACSNCAGYSLGTDKKTCTDINECSTNNGGCNQVCTNSAGSFACSCNSGYSLGTDKKT--C
sp|P10040|CRB_DROME TCQCLDGWGEICD RPMTCQTQQCLNGGTCLDKPIGFQCLCPPEYTGELCQIAPSC
sp|P82279|CRUM1_HUMAN ERSFL
sp|Q8VHS2|CRUM1_MOUSE EGNFL
* . *

DDB0235380|DDB_G0295485 -----ADINECSTNNGGCNQVCTNSAG
sp|P10040|CRB_DROME AQQCPIDSECVGGKCVCKPGSSGYNCQTSTGDGASALALTPINC NATNGKCLNGGTCSMN
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485 SFSCSCNSGYSLGTDQKTC--ADI-----NECSTNNGGCNQIC-
sp|P10040|CRB_DROME GTHCYCAVGYSGDRCEKAENCSP LNCQEP MVQVQNQCLPENKVCNQCATQPCQNGGECV
sp|P82279|CRUM1_HUMAN ---CKPPGYSGTICETTI-----GSCGKNSCQHGGICH
sp|Q8VHS2|CRUM1_MOUSE ---CQCPPGYSGLNCETAT-----NSCGGNLCQHGGTCR
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DDB0235380 | DDB_G0295485 TNSVGSFSCSCNSGYSLGTDKKTCTDINECSTNNGGC-NQVCTNSAGSFSCSCNQGYLLG
sp | P10040 | CRB_DROME DLPNGDYECKCTRGWTGRT---CGNDVDECTLHPKICGNGICKNEKGSYKCYCTPGFTGV
sp | P82279 | CRUM1_HUMAN QDPT-YPVICICPAGYAGRF---CEIDHDECASSPCQN-GAVCQDGDIDGYSCFCVPGYQGR
sp | Q8VHS2 | CRUM1_MOUSE KDPE-HPVICICPPGYAGRF---CETDHNECASSPCHN-GAMCQDGINGYSCFCVPGYQGR
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DDB0235380 | DDB_G0295485 TDQKTCADINECDQKIC-GTANCTNTVGSYQCSCPSGYSFTGSSCVDIDECESTNNGGCAQ
sp | P10040 | CRB_DROME H---CDSVDDECLSFPCLNGATCHNKINAYECVCQPGYEGEN-CEVDIDECGSNPPCSNGS
sp | P82279 | CRUM1_HUMAN H---CDLEVDECASDPCKNEATCLNEIGRYTCICPHNYSGVN-CELEIDECWSQPCLNGA
sp | Q8VHS2 | CRUM1_MOUSE H---CDLEVDECVS DPKNEAVCLNEIGRYTCVCPQEFSGVN-CELEIDECRSQPCLHGA
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DDB0235380 | DDB_G0295485 VCTNSAGGFSCSCNSGYILSTDKKNCNDINECSTNNGGCSQVCTNSAGSFSCSCNSGYLL
sp | P10040 | CRB_DROME TCIDRINNFTCNIPGMTGRICD---IDIDDCVGDPCNLGGQCIDQLGGFRCDCSGTGYE
sp | P82279 | CRUM1_HUMAN TCQDALGAYFCDCAQFLGDHCE---LNTDECASQPC LHGGLCVDGENRYSNCNCTGSGFT
sp | Q8VHS2 | CRUM1_MOUSE TCQDAPGGYSCDCAPGFLGEHCE---LSVNECESQPC LHGGLCVDGRNSYHCDCTGSGFT
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DDB0235380 | DDB_G0295485 STDKKTCTDKNECLTNNGGCTQVCTNSVGSFSCSCNSGFILNSNKLSCDDINECDQKICG
sp | P10040 | CRB_DROME GENC--ELNIDECLSNPCTNGAKCLDRVKDYFCDCHNGYKKG---NCEQDINECESNPCQ
sp | P82279 | CRUM1_HUMAN GTHC--ETLMLPCWSKPCHNNATCEDSVDNYTCHCWPYGTGA---QCEIDLNECNSNPCQ
sp | Q8VHS2 | CRUM1_MOUSE GMHC--ESLIPLCWSKPCNHNDATCEDTVDSYICHCRPGYTGA---LCETDINECNSNPCQ
. . * : : * : * . : * * * : . * : * : * :

DDB0235380 | DDB_G0295485 TA-NCTNIPGSYQCSCPSGYSFTGSGCIDIDECDQKICGTANCTNSPGSYQCSCPSGYSF
sp | P10040 | CRB_DROME YNGNCLERSN-----ITLYQMSRITDLPKVF----S-----
sp | P82279 | CRUM1_HUMAN SNGECVELSS-----EKQYG--RITGLP-----
sp | Q8VHS2 | CRUM1_MOUSE FWGECVELSS-----EGLYG--NTAGLP-----
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DDB0235380 | DDB_G0295485 TGSSCIDIDECSADNGGCSQICTNSVGSFSCSCNSGFTLNSNKLSCDDINECDQNICG-T
sp | P10040 | CRB_DROME -----QPFSEFENASGYECVCPGIIK --- NCEININECDSNPCSKH
sp | P82279 | CRUM1_HUMAN -----SSFYHEASGYVCICQPGFTGI --- HCEEDVNECSSNPCQNG
sp | Q8VHS2 | CRUM1_MOUSE -----SSFYVGASGYVCICQPGFTGI --- HCEEDVDECLHPCLNG
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DDB0235380 | DDB_G0295485 ANCANSPPGSYQCSCPNGYSFTGSGCIDIDECSTDNNGGCSQICTNSVGSFSCSCDSGYTLN
sp | P10040 | CRB_DROME GNCNDGIGTYTCECEPGFEGTH-CEINIDECDRYNPCQRGCTCYDQIDDYDCDCDANYGK
sp | P82279 | CRUM1_HUMAN GTCENLPGNYTCHCPF-----DNLSRTFYGGR
sp | Q8VHS2 | CRUM1_MOUSE GTCENLPGNYACHCPF-----DDTSRTFYGGE
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DDB0235380 | DDB_G0295485 VDN--KKSCDDIDECSNNGGCDQKCA-NIPGSFGCYCNSGFALNKNKTCDDIDECESTN
sp | P10040 | CRB_DROME NCSVLLKGCD-QNPCL-NGGACLPYLINEVTHLYNCTCENGFGDKCEKTTTL ----- SMV
sp | P82279 | CRUM1_HUMAN DCSDIILLGCT-HQQCL-NNGTCIPHFQD-GQHGFSCLCPSGYTGSLCEIATTL ----- SFE
sp | Q8VHS2 | CRUM1_MOUSE NCSEIILLGCT-HHQQCL-NNGKCIPIHFQN-GQHGFTQCQLSGYAGPLCETVTTL ----- SFG
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DDB0235380 | DDB_G0295485 NGDCGQICINQ--IG--SYQCSCNLGFTLNQNNK ----- NCDDIDECLTNNGDCQH
sp | P10040 | CRB_DROME --ATSLISVTTERE --- EGYDINLQFRITLPNGVLAFTTGKNEPVSYILELINGRLN
sp | P82279 | CRUM1_HUMAN --GDGFLWVKSGSVTTKGSVCNIALRFQTVQPMALLFRS ---- NRDVFVKLELLSGYIH
sp | Q8VHS2 | CRUM1_MOUSE --SNGFLWVTSGSHTGIGPECNISLRFHTVQPNALLIRG ---- NKDVSMKLELLNGCVH
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DDB0235380 | DDB_G0295485 VCKNLQGSFQCSCNSGYLLNQDNKKC--DDID--ECSTDNNGGCIQVCTNSVGS-----
sp | P10040 | CRB_DROME LHSSLLNKWEG-VFIGSKLNDSNWHKVFVAINTSHLVLSA --- NDEQAIFPVGSYETANN
sp | P82279 | CRUM1_HUMAN LSIQVNNQSKVLLFISHNTSDGEWHFVEVIFAEAVTLTLIDDSCKEKCIAPKAPPLESDQ
sp | Q8VHS2 | CRUM1_MOUSE LSEIVWNQKLVLLSISHNTSDGEWHFVEVTIAETLTALVGGSCKEKCTTKSSVPVENHQ
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DDB0235380 | DDB_G0295485 ---FSCSCNSGFTL NENKLS CDDIDECENGDNKCVGEFTSCQN-TDGSYSCICPSN---
sp | P10040 | CRB_DROME SQPSFPRTYLGGTIPNLK----SYLRH---- LTHQPSAFVGCMDIMVNGKWIIFPDEQDA
sp | P82279 | CRUM1_HUMAN SICAFQNSFLGGLPVGMTSNGVALLNFY---NMPSTPSFVGCLQDIKIDWNHITL ----- E
sp | Q8VHS2 | CRUM1_MOUSE SITCALQDSFLGGLPMGTANNSVSVLNIY---NVPSTPSFVGCLQDIRFDLNHITL ----- E
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DDB0235380 | DDB_G0295485 -----GFSNNSTYCEDINECLSNELNECSSNTICENRNGSVYQCNP SDYSHSSPFTCEP
sp | P10040 | CRB_DROME NISYTKLENVQSGCPRTEQC---KPNPCHSNGECTDLWHTFACHCPRPFFGHTC ----- QH
sp | P82279 | CRUM1_HUMAN NISSGSSLNWKAGCVRKDW---ESQPCQSRGRCINLWLSYQCDCHRPYEGPNC ----- LR
sp | Q8VHS2 | CRUM1_MOUSE NVSSGLSSNWKAGCLKDW---ESQPCQNRGRCINLWQGYQCECDRPTGSNC ----- LK
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
KPIITNFYQKPFRR-NIFVVQ-GINFVEFDTKVTIGEMICDYVTGNDTYECSSREGKEV
NMATAATFGHENTTHSAVIVETTDVARRAIRSILDISMF ----- IRTREP
EYVAGRFQDDSTGYVIFTLD-----ESYGDITSLSMF ----- VRTLQP
EYVAGRFQDDSTGYAAFSVN-----DNYGQNFSLSMF ----- VTRRQP
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
IGNVIVEANNILSDPFNFIGAPYIVSYSHNPPTIGND ----- LITITGRNLP TLGLVE
TGQVFYLGTDPRKAPTKNIGDSYVAAKLHGELLVKMQFSGTPEAYTVGGQKL-DNGYNH
SGLLLALENSTY-----QYIRVWLERGRLAM--LTPNSPKL--VVKFVL-NDGNVH
LGLLLALENSTY-----QYVSVWLEHGSLAL--QTPGSPKF--MVNFFL-SDGNVH
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
IIINSINCPVSIISNEQITCTIGQSGSYNYIRLYNESVTNTDTTYITYANPIIKSTSN
LIEVVRN-----QTLVQVKLNGTEYFRKTLSTTGLLDAQVLYLGGPAPTRESLLG
LISLKIK-----PYKIELYQSSQNLGFISASTWKIEKGDVIYIGGL-----
LISLRIK-----PNEIELYQSSQNLGFISVPTWTIRRGDVIFIGGL-----
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
VYSSGGILTVFGENFGLVTKSFATL - SVGN-KHC-SNVEIKS-HTELTCELESTSVIY
ATTEPGIIPVPGAGIPIEDTTPKEADDSRDYFKGIIQDVKVSNGSLNLIVEMYSLN--
-----PDKQETELNGGFFKGCIQDVRLNNQNL EFPNPNTNNA---
-----PDREKTEVYGGFFKGCVDVRLNSQTEFFPNSTNNA---
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
SQLIDLVDNLPVAN---DY-YFTYSTLEDTRCP-LDCSGKGQ ---- CTPSGCVCDIGFT
TDVQVNAKPLGAVTIDRASVLPGEVDDLCKRNKPLHNAECRNTWNDYTCCKPNGYK
-----SLNPV --LVNVITQGCAGDNSCKSNPCHNGGVCHSRWDDFSCSCPALTS
-----YDDPI --LVNVITQGCPGDNTCKSNPCHNGGVCHSLWDDFSCSCPNTA
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
GLSCNETRA-EIDPIPTVDVPSINVGSNNSE-----NGFGYKITI-IRIEELDINDQVEV
GKNCQEIEFCQHVTCPGQSLCQNLDDGYECVTNTTFTGQERSPLAFFYFQEQQSD--
GKACEEVQWCGFSPCPHGAQCQPVLGFFECIANAVFNGQSGQILFRS--N---GN---
GRACEQVQWQQLSPCPPTAECQLLPQGFECIANAVFSGLSREILFRS--N---GN---
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
SIDLLQSKWGRHSST--NQWTFNITLENQ--SYLEATFEYFKQSR--NITFA ---- SNSF
IVSEASPKSTLKPVIDIAFRTAGGTL--YIDNVDFGFFEIGVNGGRVTITWKL SALH
---ITR-----ELTNITFGFRTDANVILHAEKEPEFLNISIQDSRLFFQLSGNSF
---ITR-----ELTNITFAFRTHDTNVMILHAEKEPEFLNISIQDARLFFQLRSGNSF
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
VIPSESIKLSFKTQKWPFLRKLNLSLRIVVQTETLLLNDANQCSIDGPTVSTYNQHLWTT
FGESARFEKENTDGEWSRIY-----LRA-----HNS-KLEGGWKGWES
YMLSLSLTSQSVNDGTWHEVT-----LSM-----TDP-LS--QTSRWQM
YTLHLMGSQLVNDGTWHQVT-----FSM-----IDP-VA--QTSRWQM
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
TENPETGMITRFISYASV-----DGHVPV -----IAHIESLESPTSRTTSV
MVDPTPAFSTDIDQAQFSLIATSTQVYLGGMPESTRQARGSTLSAQGSQFKGCVGEARV
EVDNETPFVTSTIATGSLNLFKNDTDIYVGDRA-----IDNIKGLQGCLSTIEI
EVDNQTPFVISEVATGSLNLFKNDTDIYVGDQS-----VDNPKGLQGCLSTIEI
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
IGISVPYFKNESLIDPDFGMLLNVNKNPTGICEDDKTVDWKLATGVSIGGAAVAIAGI-
GDLLLLPYFSMAELYSR-----TNVSVQKQ---AQFRLNATRPEEGCI ----LCFQS
GGIYLSYFENVHGFIN-----KPQ---EE ---QFLKISTNSVVTGCLQLNVCNSN
GGIYLSYFENLHGFPG-----KPQ---EE ---QFLKVSTNMVLTGCLPSNACHSS
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
----GAF-----VFRDRKKKKQLNTMLNKK-INK-----
DCKNDGFCQSPSDEYACTCQPGFEGDDCGTDIDECLNTECLNNGTCINQVAFFCQCQPG
PCLHGGNCEDIYSSYHCSCPLGWSGKHCELNIDEFCFNPCHH-GNCSDRVAAYHCTCEPG
PCLHGGNCEDSYSSYRCACLSGWSGTHCEINIDEFCFSPCHH-GNCSGVAAYHCRCEPG
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DDB0235380 | DDB_G0295485
sp | P10040 | CRB_DROME
sp | P82279 | CRUM1_HUMAN
sp | Q8VHS2 | CRUM1_MOUSE
FEGQHCQNIDECADQPCHNGGCTDLIASYVCDPEDYMGPCDVLKQM--TCENEPGR
YTGVNCEVDIDNCQSHQCANGATCISHTNGYSCLCFGNFTGKFCRQSRPLPSTVCGNEK--
YTGVNCEVDVDNCKSHQCANGATCVPEAHGYSCLCFGNFTGRFCRHSRLPSTVCGNEK--

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME NGSTCQNGFNASTGNNFTCTCPVGFEGPLCDIPFCEITPCDNGGLCLTTGAVPMCKCSLG
sp|P82279|CRUM1_HUMAN -----TNLTCYNGGNCTEFQTELKCMCRPG
sp|Q8VHS2|CRUM1_MOUSE -----RNFTCYNGGSCSMFQEDWQCMCWPG

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME YTGRLCEQDINECESNPCQNGGQCKDLVGRYECDCQGTGFEGIRCENDIDECNMEGDYCG
sp|P82279|CRUM1_HUMAN FTGEWCEKIDECASDPCVNGGLCQDLLNKFQCLCD-VAFAGERCEVDLADDLISDIFT-
sp|Q8VHS2|CRUM1_MOUSE FTGEWCEEDINECASDPCINGGLCRDLVNRFLCICD-VAFAGERCELDLADDRLLGIFT-

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME GLGRCFNKPFSFQCICQKPYCGAYCNFTDPCNATDLCSNGGRCVESCgakPDYYCECPEG
sp|P82279|CRUM1_HUMAN
sp|Q8VHS2|CRUM1_MOUSE

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME FAGKNCTAPITAKEDGPSTTDIAIIVIPVVVLLLIAGALLGTFLVMARNKRATRGTYSP
sp|P82279|CRUM1_HUMAN -----TIGSVTV LLLILLLAIVASVVTSNKRATQGTYS
sp|Q8VHS2|CRUM1_MOUSE -----AVGSGTLA LFFILLLAGVASLIASNKRATQGTYS

DDB0235380|DDB_G0295485
sp|P10040|CRB_DROME SAQEYCNPRLEMDNVLKPPPEERLI
sp|P82279|CRUM1_HUMAN SRQEKEGSRVEMWNLMPPPPAMERLI
sp|Q8VHS2|CRUM1_MOUSE SGQEKAQPRVEMWIRMPPPALERLI

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0216369 DDB_G0292304	-----	0
tr Q963E6 Q963E6_DROME	MSTAMRTTLQSVPEALPADSVSNGTASNVAAPVSSATNAVPPPLAAVSSTTATYATNS	60
sp Q9P0L2 MARK1_HUMAN	-----	0
sp Q8VHJ5 MARK1_MOUSE	-----	0
sp Q9TW45 PAR1_CAEEEL	-----MSSAS-----VGKKPEH	12
DDB0216369 DDB_G0292304	-----METLKEEEQ-----	9
tr Q963E6 Q963E6_DROME	ISTSSHVKDQQQQQQQQHDSANANIVSLPPTTTPVANTNTMMPIVTSSNSATSNSTAA	120
sp Q9P0L2 MARK1_HUMAN	-----	0
sp Q8VHJ5 MARK1_MOUSE	-----	0
sp Q9TW45 PAR1_CAEEEL	VNTPP--GDNQKSSKENQKSNKDKQSSNQPPGQIPHST-----N-----	50
DDB0216369 DDB_G0292304	-----FRNFDTPLLNTPHHLKEETQIQKEREQQQQQQQLQQQLQLQN-----	53
tr Q963E6 Q963E6_DROME	TPTPASGAAATGGVGSVS---QGPATVSASANTNHSQHSQHHHHVANMMTTDGARLS	177
sp Q9P0L2 MARK1_HUMAN	-----MSARTP-----	6
sp Q8VHJ5 MARK1_MOUSE	-----MSARTP-----	6
sp Q9TW45 PAR1_CAEEEL	-----SGTRKSSGSLKTANLKHPARPSTES-----STSSSHRRPAQEMNGTSTATA	98
	:	
DDB0216369 DDB_G0292304	-----ERENRNHNITEELNKIPSSN-----NSSNSSSPNPLSIS--VSSS-----	91
tr Q963E6 Q963E6_DROME	SNNSAVVASSAINHHHHHTPGSGVAPTVMKNVLS-----THSAHPSAIKQRTSSAKGSPN	232
sp Q9P0L2 MARK1_HUMAN	-----LPTVNERDTENHTSVDGYTEPH-IQPTKSSSR--QN	39
sp Q8VHJ5 MARK1_MOUSE	-----LPTVNERDTENHTSVDGYTETH-IPPAKSSSR--QN	39
sp Q9TW45 PAR1_CAEEEL	TGG-----GGTSGATTTASSGAPAASSGGSSARYSSSGRSHPT-SGSSSSHARSTGQ	149
	*: . . *	
DDB0216369 DDB_G0292304	LG---SASSIHLTPQGTIGNYLVIKTIGRGQFGKVKLGYHKKIPNEKVAIKIINKGKLDP	148
tr Q963E6 Q963E6_DROME	MQMRSSAPMRWRATEEHIGKYKLIKTIKGNFAKVKLAKHL-PTGKEVAIKIIDKTQLNP	291
sp Q9P0L2 MARK1_HUMAN	IPRCRNSITSATDEQPHIGNYRLQKTIGKGNFAKVKLARHV-LTGREVAVKIIDKTQLNP	98
sp Q8VHJ5 MARK1_MOUSE	LPRCRNSITSATDEQPHIGNYRLQKTIGKGNFAKVKLARHV-LTGREVAVKIIDKTQLNP	98
sp Q9TW45 PAR1_CAEEEL	SGMSSRSAARNRDQDVHVGKYKLLKTIGKGNFAKVKLAKHV-ITGHEVAIKIIDKTALNP	208
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DDB0216369 DDB_G0292304	ETLKMVQREVIRIMKLLHHPNIIRLYEVIETSRALYLIMEYAGEGEVMDFMIAHGVLTESQ	208
tr Q963E6 Q963E6_DROME	GSLQKLFREVIRIMKLDHPNIVKLFQVIETKTLYLIMEYASGGEVFDYLVLHGRMKEKE	351
sp Q9P0L2 MARK1_HUMAN	TSLQKLFREVIRIMKILNHPNIVKLFQVIETKTLYLIMEYASGGEVFDYLVHGRMKEKE	158
sp Q8VHJ5 MARK1_MOUSE	TSLQKLFREVIRIMKILNHPNIVKLFQVIETKTLYLIMEYASGGEVFDYLVHGRMKEKE	158
sp Q9TW45 PAR1_CAEEEL	SSLQKLFREVKIMKQLDHPNIVKLYQVMEETEQLYLVLEYASGGEVFDYLVHGRMKEKE	268
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DDB0216369 DDB_G0292304	ARTFFTQIVSAINYCHSKRAVHRDLKPENLLDCNRQIKIIDFGLSNVFTPGSYLKTFCG	268
tr Q963E6 Q963E6_DROME	ARVKFRQIVSAVYQCHQKRIIHRDLKAENLLLDSELNIIKIADFGFSNEFTPGSKLDTFCG	411
sp Q9P0L2 MARK1_HUMAN	ARAKFRQIVSAVYQCHQKYIVHRDLKAENLLLDGMNIKIADFGFSNEFTVGNKLDTFCG	218
sp Q8VHJ5 MARK1_MOUSE	ARAKFRQIVSAVYQCHQKCIVHRDLKAENLLLDADMNIKIADFGFSNEFTVGNKLDTFCG	218
sp Q9TW45 PAR1_CAEEEL	ARAKFRQIVSAVQYLHKNIIHRDLKAENLLLDQDMNIKIADFGFSNTFSLGNKLDTFCG	328
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DDB0216369 DDB_G0292304	SPTYASPELILRKEYNGPSVDVWSMGVVLVLTGYLPFDGDNYVELFQKILAGNYTIPS	328
tr Q963E6 Q963E6_DROME	SPPYAAPELFGQKKYDGPEDVWSLGVILYTLVSGSLPFDGSTLRRLRERVLRGKYRIPF	471
sp Q9P0L2 MARK1_HUMAN	SPPYAAPELFGQKKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPF	278
sp Q8VHJ5 MARK1_MOUSE	SPPYAAPELFGQKKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPF	278
sp Q9TW45 PAR1_CAEEEL	SPPYAAPELFGSKKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPF	388
	** *:*:*: **:*:*:*:*:*:*:*:*: * *:*:*:*: *	
DDB0216369 DDB_G0292304	YLTHECKSLISRMLVDPDKRATMEEIINHPWLSSTKQIILSTMTDSLKNLNSCLEQQI	388
tr Q963E6 Q963E6_DROME	YMSTDCENLLRKFLVLNPAKRASLETIMGDKWMNGFEED-----ELKPY-----	516
sp Q9P0L2 MARK1_HUMAN	YMSTDCENLLKLLVLNPIKRGSLQIMKDRWMNVGHEE-----ELKPY-----	323
sp Q8VHJ5 MARK1_MOUSE	YMSTDCENLLKLLVLNPIKRGSLQIMKDRWMNVGHEE-----ELKPY-----	323
sp Q9TW45 PAR1_CAEEEL	YMSTDCENLLKFLVINPQRSSLDNIMKDRWMNVGYEDD-----ELKPF-----	433
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DDB0216369 DDB_G0292304	NVENLLNQSLNNSNNNNINNNINNTMATMNNNSNNNNNNNNNNNNNNNNNNNNNNNN	448
tr Q963E6 Q963E6_DROME	-----	516
sp Q9P0L2 MARK1_HUMAN	-----	323

sp Q8VHJ5 MARK1_MOUSE	-----	323
sp Q9TW45 PAR1_CAEEEL	-----	433
DDB0216369 DDB_G0292304	NNNNNNNNNNNNNNNTTTTNTATTTTITSPIQNRNNEELDQEIIEELVGLGFEREELC	508
tr Q963E6 Q963E6_DROME	-----IEPKAD-LADPKRIEAL---VAMGYNRSEIE	543
sp Q9P0L2 MARK1_HUMAN	-----TEPDPD-FNDTKRIDIM---VTMGFARDEIN	350
sp Q8VHJ5 MARK1_MOUSE	-----SEPELD-LSDAKRIDIM---VTMGFARDEIN	350
sp Q9TW45 PAR1_CAEEEL	-----IEPPKD-QIDEQRIEKLIQIFQLGFNKAAIL	463
	. * : : : : . : * : :	
DDB0216369 DDB_G0292304	NSIRQNKYNDAASTYFLLQGKKLRESQQNQTDNAKKLE -----KFYSEPLTIPAH	558
tr Q963E6 Q963E6_DROME	ASLSQVRYDDVFATYLLLGRKSTDPESDGSRSGSSLRLNISGNDAGANAGSASVQSPTH	603
sp Q9P0L2 MARK1_HUMAN	DALINQKYDEVMATYILLGRKPPEFEGGESLSSGNLCQRSRPS ----SDLNNSTLQSPA	406
sp Q8VHJ5 MARK1_MOUSE	DALVSQKYDEVMATYILLGRKPPEFEGGESLSSGNLCQRSRPS ----SDLNNSTLQSPA	406
sp Q9TW45 PAR1_CAEEEL	ESVEKEKFEDIHATYLLLGERKSDMDASEITMAQSLSSHSSI -----NVSSSLGQHPAG	517
	:: . : : : : * : * : : . . *	
DDB0216369 DDB_G0292304	VGENSPLI -----KYKRHHKRSNTVDSPKSTNTPQYRSSNTQQNNHHHQQQQQ	606
tr Q963E6 Q963E6_DROME	RGVHRISIAS-----STKPSRRASSGAETLRV-GPTNAAAT-VAA---A-----	642
sp Q9P0L2 MARK1_HUMAN	LKVQRSIS-----ANQKQRRFSD-----HA-GPSIPP-----AVSYTKRPQ---	441
sp Q8VHJ5 MARK1_MOUSE	LKVQRSIS-----ANQKQRRFSD-----HA-GPSIPP-----AVSYTKRPQ---	441
sp Q9TW45 PAR1_CAEEEL	VITREHVTSSSASGSSASPSRYSRSA--TAT-GASITAGSALAS---AANAQKHQSSA	571
	. : : : . . .	
DDB0216369 DDB_G0292304	QQQQQQQHHHTQQQNQQSQQQYNNNNHN-----	637
tr Q963E6 Q963E6_DROME	-----TGAVGAVNPSNNYNAA-GSAADRASVGSN -----FKRQNTIDSATI	682
sp Q9P0L2 MARK1_HUMAN	-----ANSVES-EQKEWDKDVARKLGSTTVGS-----KSEMT-----	473
sp Q8VHJ5 MARK1_MOUSE	-----ANSVES-EQKEWGKDTARRLGSTTVGS-----KSEVT-----	473
sp Q9TW45 PAR1_CAEEEL	A-----PSSGSSSS-RRSSQ-NDAAATAAGGTVVMGSTRHGGVQMRAQPTSRQATI	620
	: . . : .	
DDB0216369 DDB_G0292304	-----KPP-----TPTIVTTQASTTVNNHISINNNNNNNNNNNNNNSST	677
tr Q963E6 Q963E6_DROME	KENTARLAAQNQRPASATQKM-----LTTA-DTTLNSPAKPRT -----ATKYDPT	726
sp Q9P0L2 MARK1_HUMAN	-----ASP -----LVGP	480
sp Q8VHJ5 MARK1_MOUSE	-----ASP -----LVGP	480
sp Q9TW45 PAR1_CAEEEL	S----LLQPPSYKPSNNTTQIAQIPPLFNRN-STATSSAAQP -----STGI	661
	.	
DDB0216369 DDB_G0292304	PGSNTVSSTQSS-SINSSV-----NPSPLC-LSNAVPVS -----LRE	712
tr Q963E6 Q963E6_DROME	NGNRTVSGTSGIIPRRSTTLYEKTSSTEKT---NVIPA -----ETKMA	766
sp Q9P0L2 MARK1_HUMAN	ERK-----KSSTIPSNNVY-----SGGSM -----ARRNTYVCERTTDRYVA	516
sp Q8VHJ5 MARK1_MOUSE	DRK-----KSTASPSNNVY-----SGGSM -----ARRNTYVCERSTDRYAA	516
sp Q9TW45 PAR1_CAEEEL	TGTRKIADPKGRIPLNSTAVQGHRTATGAVAAANGGIPSHRDAQQQQYMNQLTSSTMMS	721
	
DDB0216369 DDB_G0292304	KLREKEATTTNTTTTTTTTTTTT-----TNTSSN -----NSS	744
tr Q963E6 Q963E6_DROME	S-----	767
sp Q9P0L2 MARK1_HUMAN	-----LQ-----NGKDSSL---TEMS	529
sp Q8VHJ5 MARK1_MOUSE	-----LQ-----NGRDSSL---TEMS	529
sp Q9TW45 PAR1_CAEEEL	KLINKTPAAGGTAATSSSSSSATSTAPLQKSGSQISHAPTEPVIREDDDENNSNQNGN	781
DDB0216369 DDB_G0292304	NQSISSISPPTS-----TSPNLQPF---	764
tr Q963E6 Q963E6_DROME	-----	767
sp Q9P0L2 MARK1_HUMAN	VSSISSAGSSVAS--AV-----PSARPRHQ-	552
sp Q8VHJ5 MARK1_MOUSE	ASSMSSAGSTVAS--AG-----PSARPRHQ-	552
sp Q9TW45 PAR1_CAEEEL	VPLIGGVGPQTSPAVQVPTEDATSSSDKEQQQKASSETPKESKPSMIHQSPMPSPQMM	841
DDB0216369 DDB_G0292304	-----SLAS-----TANNNNNNNNNNNNNNNNNNNNNN-	790
tr Q963E6 Q963E6_DROME	-----	767
sp Q9P0L2 MARK1_HUMAN	-----KSMSTSGHPKVTLPIT-	569
sp Q8VHJ5 MARK1_MOUSE	-----KSMSTSGHPKVTLPIT-	569
sp Q9TW45 PAR1_CAEEEL	TAMESLKLSESGQTGGPTVATGGPPQQRATSQQMSRSATTNSANMGASSGGAAAAASATNQ	901
DDB0216369 DDB_G0292304	-----NNN-----NNSLNSH-IQR---RATASSLQQQ-----	813
tr Q963E6 Q963E6_DROME	-----	767
sp Q9P0L2 MARK1_HUMAN	-----KDGSEAYRPGTTQRV---PAASPSAH-----SI-----	594
sp Q8VHJ5 MARK1_MOUSE	-----KDGSEAYRPGAAQRV---PAASPSAH-----SI-----	594
sp Q9TW45 PAR1_CAEEEL	LSGAPSSTGASSQQYHPKAPSSSSSSSTNPPHQHQLTHNASFSVTPSSYQIPTSTAVNVT	961

DDB0216369 DDB_G0292304	-QQMQQASNTRRLRSNSSSVADQSQRQESRKLEDDWVIFEDYSNDGHRDGPKNYHLQPS	872
tr Q963E6 Q963E6_DROME	-----AVKSSRHFPNRNVPSTFHSQTRARNNTAL-----EY--SGT-----SGAS	807
sp Q9P0L2 MARK1_HUMAN	---STATPDRTRFPRGSSSRSTFHGEQLRERRSVA-----Y--NGPPA-SPS-HETGAF	641
sp Q8VHJ5 MARK1_MOUSE	---SASTPDRTRFPRGSSSRSTFHGEQLRERRSAA-----Y--NGPPA-SPS-HETGAF	641
sp Q9TW45 PAR1_CAEEL	STGMP TSSSSSAFPRNTRNRQT FHGKTEKDKGGDD-----S--SDEIGETPGNVSIGAT	1013
	. : . . :	..
DDB0216369 DDB_G0292304	SLSSHKKQKSPVHSLSSFKNILKRSDDKSFNSSSSNNNTNNNTTTTSVS-TNNTPTLLE	931
tr Q963E6 Q963E6_DROME	GDSSHPG----RMSFFSKLSSRFSKRPNQ-----	832
sp Q9P0L2 MARK1_HUMAN	AHARRGT---STGIISKITSKFVRRDPS-----EGEASGRDTDSTRST-----	680
sp Q8VHJ5 MARK1_MOUSE	AHARRGT---STGIISKITSKFVRRDPS-----EGEASGRADTARGSG-----	680
sp Q9TW45 PAR1_CAEEL	GPSANNA----EATIWSK-LSKLTRRDHNR---ESMTQPVSGRAGTIGASQGGQTAAALA	1065
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DDB0216369 DDB_G0292304	VDHQNSNNNNQQATSSSPNVTSPPSSPQQQQQEPRIVRVFVGVNTTTMKDAPELMQQVLK	991
tr Q963E6 Q963E6_DROME	-----	832
sp Q9P0L2 MARK1_HUMAN	-----SGEPKERDKKEGKDSKPRSLRFTWSMKTTSSMDPNDMMREIRK	723
sp Q8VHJ5 MARK1_MOUSE	-----SGDPKERDKDEGKEAKPRSLRFTWSMKTTSSMDPNDMLREIRK	723
sp Q9TW45 PAR1_CAEEL	AI-----REQSGPIAPGAGQVAPSLPIHEGDKPRSLRFTWSMKTTSSLAPDDMMREIRK	1120
DDB0216369 DDB_G0292304	VVDTFICIPHTKKAPFLIECETE----GVRFSIEICRLPRLSVNGLKFKRIGGSSWRYK	1045
tr Q963E6 Q963E6_DROME	-----	832
sp Q9P0L2 MARK1_HUMAN	VLDANNCDYEQKERFLLFCVHGDAQDSLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFK	783
sp Q8VHJ5 MARK1_MOUSE	VLDANTCDYEQKERFLLFCVHGDAQDSLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFK	783
sp Q9TW45 PAR1_CAEEL	VLDANGCDYEQRERYMILCVHGDPNTDSLVQWEMEVCKLPRLSLNGVRFKRISGTSIGFK	1180
DDB0216369 DDB_G0292304	SICKDLLSQMKLNSH* 1060	
tr Q963E6 Q963E6_DROME	----- 832	
sp Q9P0L2 MARK1_HUMAN	NIASKIANELKL----- 795	
sp Q8VHJ5 MARK1_MOUSE	NIASKIANELKL----- 795	
sp Q9TW45 PAR1_CAEEL	NIASKIAQELNL----- 1192	

CLUSTAL O(1.2.4) multiple sequence alignment

DDB0191345 DDB_G0276459	MEQSKRVSMRMREKFEAQSN EA ESSPPPNRKPPPNKRVQNTGTSSLNSSGSSFVSPSPSP	60
sp Q17850 PK1_CAEEL	-----M-----	1
tr B7Z0W0 B7Z0W0_DROME	-----	0
sp Q13153 PAK1_HUMAN	-----MS-----	2
sp 088643 PAK1_MOUSE	-----MS-----	2
DDB0191345 DDB_G0276459	SPSPQQPVKRLPSPGV NK QAPPALPTQPRPQQQ Q PEIPVRPTTPTRTPPNLINSNGTSG	120
sp Q17850 PK1_CAEEL	-----	1
tr B7Z0W0 B7Z0W0_DROME	-----	0
sp Q13153 PAK1_HUMAN	-----	2
sp 088643 PAK1_MOUSE	-----	2
DDB0191345 DDB_G0276459	GSGFSSSSGNSGYSNNNNNSNSNSSINMNGNHSNGLNGGSSNPVPMRKVSSPINIANGT	180
sp Q17850 PK1_CAEEL	-----	1
tr B7Z0W0 B7Z0W0_DROME	-----	0
sp Q13153 PAK1_HUMAN	-----	2
sp 088643 PAK1_MOUSE	-----	2
DDB0191345 DDB_G0276459	TPPPPQPTPSQQPQQSPSSASHNNTQHNIPSPPLPN NK PKKLAPTAVPAGLGSIIGGP	240
sp Q17850 PK1_CAEEL	-----KAF-----	4
tr B7Z0W0 B7Z0W0_DROME	-----M-----	1
sp Q13153 PAK1_HUMAN	-----NNG-----	5
sp 088643 PAK1_MOUSE	-----NNG-----	5
DDB0191345 DDB_G0276459	KTPAISPGSTSPSLGSSNGNIPISTTTSTPITPTPPI SV PLATSPNNSHKDSISNSNSNN	300
sp Q17850 PK1_CAEEL	-----SSYDEKPPAPP IR FSSSATRE-----	25
tr B7Z0W0 B7Z0W0_DROME	-----SSEEDKPPAPPVRLTSNRGGNERSGGGVGVG-----	32
sp Q13153 PAK1_HUMAN	-----LDIQDKPPAPPMRNTSTMIGAG-----	27
sp 088643 PAK1_MOUSE	-----VDIQDKPPAPPMRNTSTMIGAG-----	27
	*.:**:	
DDB0191345 DDB_G0276459	NNNNNNNNNNSSNATTSPPSPVSNVGNKQDEEKKGFLSIFTNKKK-NKDKKKEFSVGSP	359
sp Q17850 PK1_CAEEL	-----NQVVGLKPLPKPEATKKKKTMPNPFMK-KNKDKKEASEKPVISRP	70
tr B7Z0W0 B7Z0W0_DROME	---GGGLGGGGMGDVPPDMRPLKPEDDSDRKKKTLKSKIKGSKPS--HTDSKPNISYP	86
sp Q13153 PAK1_HUMAN	-----SKDAGTLNHGSKPLPPNPEEKKKKDRFYRSILPGDKTNKKKEKERPEISLP	78
sp 088643 PAK1_MOUSE	-----SKDTGTLNHGSKPLPPNPEEKKKKDRFYRSILPGDKTNKKREKERPEISLP	78
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DDB0191345 DDB_G0276459	FNVKHNIHVNYHSVTG-FEGLPKEW EV ILQSSGITREDVVEHSEVVIDVLDFHMQQQQQQ	418
sp Q17850 PK1_CAEEL	SNFEHTIHVGYPKTGEFTGMPEAWARLLTDSQISKQEQQNPQAVLDALKYYTQGESSG	130
tr B7Z0W0 B7Z0W0_DROME	TNFEHTVHVGFDAVTGEFTGMPEAWARLLMNSNISKEQKKNPQAVLDVLKWF DNTTKQR	146
sp Q13153 PAK1_HUMAN	SDFEHTIHVGFD AVTGEFTGMPEQ WARLLQTSNITKSEQKKNPQAVLDVLEFYNSKKTS-	137
sp 088643 PAK1_MOUSE	SDFEHTIHVGFD AVTGEFTGMPEQ WARLLQTSNITKSEQKKNPQAVLDVLEFYNSKKTS-	137
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DDB0191345 DDB_G0276459	AQQEQQALMQKMQQSGIPAHMLNNPKP-----	446
sp Q17850 PK1_CAEEL	--QKWLQYDM--MFIDD-----APSRTPS-----YGLKPQPY S -----T	160
tr B7Z0W0 B7Z0W0_DROME	PSSKYMTNAI--TTHSGSSLSRVSSSSPSSPTDSELHGSNSGGNLIGVQLGSM T LGPN A	204
sp Q13153 PAK1_HUMAN	NSQK YMSFTD -KSAE-----DYNSS-NALNVK-----	162
sp 088643 PAK1_MOUSE	NSK KYMSFTD -KSAE-----DYNSS-NTLNVK-----	162
	.: .	
DDB0191345 DDB_G0276459	PTIPIRDANK----QP----HNQLQPTPHQ-----	468
sp Q17850 PK1_CAEEL	SSLPY----HG NKI QDPR----KMNPMTT-----STSSAGYNSKQGVPP--T--T	198
tr B7Z0W0 B7Z0W0_DROME	NNVAVAGQILGNHYQQQQQHLLQQQQPLLHQNHQHHMGISQSHSYNFVGHTVSSSTSQH	264
sp Q13153 PAK1_HUMAN	-----AVSETPA_V-PP	172
sp 088643 PAK1_MOUSE	-----TVSETPA_V-PP	172
DDB0191345 DDB_G0276459	-----PPQH HH QQQPPQ HH -----	484
sp Q17850 PK1_CAEEL	FSVNENRS--SMPPSYAPPVPHGETPADIVPPAIPDRPARTLSIYTKPK E -----	247
tr B7Z0W0 B7Z0W0_DROME	SSANEDDMLGPQHPPQQPP-----PPPVASRPERTKSIYTRPIEDLQPAIIPM	312

sp Q13153 PAK1_HUMAN	VSEDED-----DDDDATP-----PPVIAPRPEHTKSVYTRSVIE-----PL	209
sp 088643 PAK1_MOUSE	VSEDD-----DDDDATP-----PPVIAPRPEHTKSVYTRSVIE-----PL	209
	*	
DDB0191345 DDB_G0276459	-----QQ-----QQQQHNNNNNNNNNNNNNNNNNNNN-----QQSAQ--	512
sp Q17850 PK1_CAEEL		247
tr B7Z0W0 B7Z0W0_DROME	PVAPATTATPLQNHRTPGGISAPAAASPMHNNATTTLDKNKNNATPTSPTTTKTTAETE	372
sp Q13153 PAK1_HUMAN	PVTPTRDVAT.....	219
sp 088643 PAK1_MOUSE	PVTPTRDVAT.....	219
DDB0191345 DDB_G0276459	...QQ.....SAGILSQ.....	521
sp Q17850 PK1_CAEEL		247
tr B7Z0W0 B7Z0W0_DROME	GTDATSTLLSATNPSCSTTPTTDPAPAAPRGS�VETATAHATTAAATVATSTTTNHHSSA	432
sp Q13153 PAK1_HUMAN		219
sp 088643 PAK1_MOUSE		219
DDB0191345 DDB_G0276459QQEQQLLEEM.....	530
sp Q17850 PK1_CAEEL		252
tr B7Z0W0 B7Z0W0_DROME	SSFSSFPSSFHDDGTHHALPTIHCPTPTSSSNSTVSFPVAVPLPPIVTPASPTPASIES	492
sp Q13153 PAK1_HUMANSPISPTENNT..	229
sp 088643 PAK1_MOUSESPISPTENNT..	229
DDB0191345 DDB_G0276459	-----MCGGA-----YDDE-QYDLNNQPLP-DETNVS	555
sp Q17850 PK1_CAEEL	PDL-----S-----KGQFGVQARGQKAKKKMTDAEVLTK	281
tr B7Z0W0 B7Z0W0_DROME	PDLYTPEPTVAQVSAGGPSSQVAGNQIAVPQAAVAPAATPNTRAANAKKKKMSDEEILEK	552
sp Q13153 PAK1_HUMAN	-----TPPDALTRNTEKQKKPKMSDEEILEK	256
sp 088643 PAK1_MOUSE	-----TPPDALTRNTEKQKKPKMSDEEILEK	256
	: : : *	
DDB0191345 DDB_G0276459	LYDLVSQEDPTKLFEGGSTKIGEGAAGEVFVVTQLKTNNKVAIKKMPLNQQN-MKLIVTE	614
sp Q17850 PK1_CAEEL	LRTIVSIGNPDRKYR-KVDKIGSGASGSVYTAIEISTEAEVAIKQMNLDQPKKELINE	340
tr B7Z0W0 B7Z0W0_DROME	LRTIVSVGDPNRKYT-KMEKIGQGASGTVYTAIESSTGMEVAIKQMNLSQQPKKELINE	611
sp Q13153 PAK1_HUMAN	LRSIVSVGDPKKKYT-RFEKIGQGASGTVYTAMDVATGQEVAIKQMNLSQQPKKELINE	315
sp 088643 PAK1_MOUSE	LRSIVSVGDPKKKYT-PFEKIGQGASGTVYTAMDVATGQEVAIKQMNLSQQPKKELINE	315
	* : ** : * : : *** : ** : * : . : * : *** : * * : * : * : * : *	
DDB0191345 DDB_G0276459	IGIMKSCRHQNIIDYIDSYLVGDSLWVAMEFMGGCLTEILEQFNSVKLVQAQIAYVCAE	674
sp Q17850 PK1_CAEEL	ILVMRENKHANIVNYLDSYLVCDLWVMEYLAGGSLTDVVT---CQMEDGIIAAVCRE	397
tr B7Z0W0 B7Z0W0_DROME	ILVMRENKHNPVNYLDSYLVSEELWVMEYLPGGSLTDVVT---TCMDEGQIAAVCRE	668
sp Q13153 PAK1_HUMAN	ILVMRENKNPNIVNYLDSYLVGDELWVMEYLAGGSLTDVVT---TCMDEGQIAAVCRE	372
sp 088643 PAK1_MOUSE	ILVMRENKNPNIVNYLDSYLVGDELWVMEYLAGGSLTDVVT---TCMDEGQIAAVCRE	372
	* : * : : * : : * : * : * : * : * : * : * : * : * : * : * : *	
DDB0191345 DDB_G0276459	TLKGLAYIHSQHRHRIHRDIKSDNILLGSDGSVKLADFGYAAQLTKSKQKRVTVIGTPYWMA	734
sp Q17850 PK1_CAEEL	VLQALEFLHSRHVIHRDIKSDNILLGMDGSVKLTDGFGCAQLSPEQRKRTTMVGTPTYWMA	457
tr B7Z0W0 B7Z0W0_DROME	VLQALEFLHANQVIHRDIKSDNILLGLDGSVKLTDGFGCAQISPEQSKRTTMVGTPTYWMA	728
sp Q13153 PAK1_HUMAN	CLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLTDGFGCAQITPEQSKRSTMVGTPTYWMA	432
sp 088643 PAK1_MOUSE	CLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLTDGFGCAQITPEQSKRSTMVGTPTYWMA	432
	* : * : * : : * : * : * : * : * : * : * : * : * : * : * : *	
DDB0191345 DDB_G0276459	PELIRGQNYDRKVDIWSLIGIMAMEAESEPPYMSFPPLRALFLITTKGIPDLKDQNKWSD	794
sp Q17850 PK1_CAEEL	PEVVTRKQYGPVKVDVWSLIGMAIEMVEGEPYLNENPLRAIYLIATNGKPDFGRDSMTL	517
tr B7Z0W0 B7Z0W0_DROME	PEVVTRKQYGPVKVDLWSLIGMAIEMVEGEPYLNENPLKALYLIATNGKPEIKEKDKLSS	788
sp Q13153 PAK1_HUMAN	PEVVTRKAYGPVKVDIWSLIGMAIEMIEGEPYLNENPLRALYLIATNGTPELQNPEKLSA	492
sp 088643 PAK1_MOUSE	PEVVTRKAYGPVKVDIWSLIGMAIEMIEGEPYLNENPLRALYLIATNGTPELQNPEKLSA	492
	** : : : * : * : * : * : * : * : * : * : * : * : * : * : *	
DDB0191345 DDB_G0276459	DFKDFVKKCLDKDVENRPEAKVLLNHPFLKTACNSNGLVPAIMEAKKAKEAHSKFSIH*	852
sp Q17850 PK1_CAEEL	LFKDFVDSALEVQVENRWSASQLLTHPFLRCAKPLASLYYLIVAAKKSIAEASNS----	572
tr B7Z0W0 B7Z0W0_DROME	AFQDFLDQCLEVEVDRRASALDLLKHPFLKLARPLASLTPLIMAAKEATKGN-----	840
sp Q13153 PAK1_HUMAN	IFRDFLNRCLMDVEKRGSAKELLQHQLKIAKPLSSLTPLIAAAKEATKNNH-----	545
sp 088643 PAK1_MOUSE	IFRDFLQCCLMDVEKRGSAKELLQHQLKIAKPLSSLTPLMHAAKEATKNNH-----	545
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0267078 DDB_G0267450	-----	0
sp Q17850 PK1_CAEEL	-MKAFSSYDEKPPAPPPIRFSSSATRE-----NQVVGLKPLPKEPE	39
tr B7Z0W0 B7Z0W0_DROME	----MSSSEEDKPPAPPVRLTSNRGGNERSGGGVGVGGGGLGGGGMGDVPDMRPLPKEPD	56
sp Q13153 PAK1_HUMAN	MSNNGLDIQDKPPAPPMRNTSTMIGAG-----SKDAGTLNHGSKPLPPNPE	46
sp O88643 PAK1_MOUSE	MSNNGVDIQDKPPAPPMRNTSTMIGAG-----SKDTGTLNHGSKPLPPNPE	46
DDB0267078 DDB_G0267450	-----	0
sp Q17850 PK1_CAEEL	ATKKKKTMPNPFMK--KNKDKEASEKPVISRPSNFEHTIHVGYPKTGFTGMPEAWARL	98
tr B7Z0W0 B7Z0W0_DROME	DSDRKKKTLKSKIKGSKPS--HTDSKPNISYPTNFEHTVHVGFDVGTGFTGMPEAWARL	114
sp Q13153 PAK1_HUMAN	EKKKKDRFYRSILPGDKTNKKKEKERPEISLPSEFHTIHVGFDVGTGFTGMPEQWARL	106
sp O88643 PAK1_MOUSE	EKKKKDRFYRSILPGDKTNKKREKERPEISLPSEFHTIHVGFDVGTGFTGMPEQWARL	106
DDB0267078 DDB_G0267450	-----	0
sp Q17850 PK1_CAEEL	LTSQISKQEQQNPQAVLDALKYYTQGESG--QKWLQYDMMFIDD-----APSR	147
tr B7Z0W0 B7Z0W0_DROME	LMNSNISKQEKKNPQAVLDVLKWFNTTKQRPSSKYMTNAITTHSGSSLRVSSSSPSS	174
sp Q13153 PAK1_HUMAN	LQTSNITKSEQKKNPQAVLDVLEFYNSKTS-NSQKYSFTDKSAE-----	151
sp O88643 PAK1_MOUSE	LQTSNITKSEQKKNPQAVLDVLEFYNSKTS-NSKKYSFTDKSAE-----	151
DDB0267078 DDB_G0267450	-----MISLDLS-----PTLW	11
sp Q17850 PK1_CAEEL	TPS-----YGLKPQYS---TSSLPY---HGKIQDPR-----KMNPMTT	181
tr B7Z0W0 B7Z0W0_DROME	TPTDSELHGSSNGGNLIGVQLGSMTLGPNANNVAVAGQILGNHYQQQQHLLQQQQPLLH	234
sp Q13153 PAK1_HUMAN	-----DYNSS-NALNVK-----	162
sp O88643 PAK1_MOUSE	-----DYNSS-NTLNVK-----	162
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DDB0267078 DDB_G0267450	KSPDK-----EGELKKQGHVVKNWKKRKFII-QND-----	40
sp Q17850 PK1_CAEEL	-----STSSAGYNSKQGVPP--T--TFSVNEIRS--SMPPSYAPPVPHGETPADI	226
tr B7Z0W0 B7Z0W0_DROME	QNHNQHHMGISQSHSYNFVGHTVSSSTSQHSSANEDDMLGPQHPPQPP-----	283
sp Q13153 PAK1_HUMAN	-----AVSETPA--V-PPVSEDED-----DDDDDATP-----	186
sp O88643 PAK1_MOUSE	-----TVSETPA--V-PPVSEDE-----DDDDDATP-----	186
	.::	
DDB0267078 DDB_G0267450	-----MLFYFKDKEERPVGAVPLRMSRC-----	63
sp Q17850 PK1_CAEEL	VPPAIPDRPARTLSIYTKPKE-----	247
tr B7Z0W0 B7Z0W0_DROME	-PPPVASRPERTKSIYTRPIEDLQPAIIPMPVAPATTPATPLQNHRTPGGISAPAASPM	342
sp Q13153 PAK1_HUMAN	-PPVIAPRPEHTKS VYTRSVIE-----PLPVTPTRDVAT-----	219
sp O88643 PAK1_MOUSE	-PPVIAPRPEHTKS VYTRSVIE-----PLPVTPTRDVAT-----	219
	.* :	
DDB0267078 DDB_G0267450	-----YE-----NKSLGKPNCFELVS-----PRINK	84
sp Q17850 PK1_CAEEL	-----	247
tr B7Z0W0 B7Z0W0_DROME	HNNATTTLDKNKNNATPTSPTTTKTTAETEGTDATSTLLSATNPSCSTTPTDPAPAAPR	402
sp Q13153 PAK1_HUMAN	-----	219
sp O88643 PAK1_MOUSE	-----	219
DDB0267078 DDB_G0267450	TFFIQANTPD-----EM--ASWMKA-----VEKG	106
sp Q17850 PK1_CAEEL	-----	247
tr B7Z0W0 B7Z0W0_DROME	GLSVETATAHATTAATVATSTTTNHSSASSFSSFPSFHDDGTHHALPTIHCPTPTSS	462
sp Q13153 PAK1_HUMAN	-----	219
sp O88643 PAK1_MOUSE	-----	219
DDB0267078 DDB_G0267450	SEYSTVSQPFNLKHEVHVDNFNSAT-GFSGLPKEWEVILKSSNVSK---Q-----EVLDKP	157
sp Q17850 PK1_CAEEL	-----EEEEIPDL-----S-----	256
tr B7Z0W0 B7Z0W0_DROME	SRNSTVSFPVAVPLPPIVTPASPTPASIESPDLYTPEPTVAQVSAGGPSSQVAGNQIAVP	522
sp Q13153 PAK1_HUMAN	-----SPISPTENNT-----	229
sp O88643 PAK1_MOUSE	-----SPISPTENNT-----	229
DDB0267078 DDB_G0267450	SEWLSVLEFQAGRTMEKSNQNLALPDESNTLLSDLVTKEDPTKIYKNMTKIGEGAAGE	217
sp Q17850 PK1_CAEEL	-----KGQF--GVQ--ARGQAKKKMTDAEVLTKLRITVSIIGNPDRKYRKVDKIGSGASGS	308
tr B7Z0W0 B7Z0W0_DROME	QAAVAPAA--PNT--RAANAKKKKMSDEEILEKLRITVSVGDPNRKYTKMEKIGQGASGT	579

sp Q13153 PAK1_HUMAN	---TPPDAL--TRN-TEKQKKKPKMSDEEILEKLRSIVSVGDPKKKYTRFFEKIGQGASGT	283
sp 088643 PAK1_MOUSE	---TPPDAL--TRN-TEKQKKKPKMSDEEILEKLRSIVSVGDPKKKYTPFEKIGQGASGT	283
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DDB0267078 DDB_G0267450	VFVATSSKNNKRVAIKKIEINNDN-AKLLVTEIAIMKTSHHDNIVNYIDSYIVNDRELWV	276
sp Q17850 PK1_CAEL	VYTAIEISTEAEVAIKQMNLDQPKKELIINEILVMRENKHANIVNYLDSYLVCD-ELWV	367
tr B7Z0W0 B7Z0W0_DROME	VYTAIESSTGMEVAIKQMNLSQQPKKELIINEILVMRENKHPNVVNYLDSYLVSE-ELWV	638
sp Q13153 PAK1_HUMAN	VYTAMDVA TGQEVAIKQMNLDQPKKELIINEILVMRENKPNIVNYLDSYLVGD-ELWV	342
sp 088643 PAK1_MOUSE	VYTAMDVA TGQEVAIKQMNLDQPKKELIINEILVMRENKPNIVNYLDSYLVGD-ELWV	342
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DDB0267078 DDB_G0267450	AMEFMGGGCLTDILEAFDN IKMSEIQIAYVVKETLKALQYIHS LHR IHRDIKSDNILLGS	336
sp Q17850 PK1_CAEL	VMEYLAGGSLTDVVT--ECQMDEGQIAAVCREVLQALEFLHSRHVIHRDIKSDNILLGM	424
tr B7Z0W0 B7Z0W0_DROME	VMEYLPGGSLTDVVT--ETCMDEGQIAAVCREVLQALEFLHANQVIHRDIKSDNILLGL	695
sp Q13153 PAK1_HUMAN	VMEYLAGGSLTDVVT--ETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGM	399
sp 088643 PAK1_MOUSE	VMEYLAGGSLTDVVT--ETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGM	399
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DDB0267078 DDB_G0267450	EGSVK IADFGYAAQLTQKQK RNTVVGTPYWMAPELIRGH DYGVKVDIWSLGIMMEMAE	396
sp Q17850 PK1_CAEL	DGSVKLTD FGFCAQLSPEQRKRTTMVGTPYWMAPEVVTRKQYGPKV DVWSLGIMAIEMVE	484
tr B7Z0W0 B7Z0W0_DROME	DGSVKLTD FGFCAQISPEQSKRTTMVGTPYWMAPEVVTRKQYGPKV DLWSLGIMAIEMVE	755
sp Q13153 PAK1_HUMAN	DGSVKLTD FGFCAQITPEQSKRSTMVGTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMIE	459
sp 088643 PAK1_MOUSE	DGSVKLTD FGFCAQITPEQSKRSTMVGTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMIE	459
	: * * * : : * * : . * * : : * * * . * * * * * * * * : : * * * * * * * * : * * *	
DDB0267078 DDB_G0267450	GEPPYMDFPPLRALFLITTKGIPPLKETTKWSKTFQDFFSKCLDINVANRPDATDLLKHP	456
sp Q17850 PK1_CAEL	GEPPYL NENPLRAIYLIATNGKPD FPGRDSMTLLFKDFVDSALEVQVENRWSASQLLTHP	544
tr B7Z0W0 B7Z0W0_DROME	GEPPYL NENPLKALYLIATNGKPEIKEKDKLSSAFQDFLDQCLEVEVD RRASALDLLKHP	815
sp Q13153 PAK1_HUMAN	GEPPYL NENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLEMDVEKRGSAKELLQHQ	519
sp 088643 PAK1_MOUSE	GEPPYL NENPLRALYLIATNGTPELQNPEKLSAIFRDFLQCCEMDVEKRGSAKELLQHQ	519
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DDB0267078 DDB_G0267450	FMDLACDSSSEFKPLIQARNV*-----	477
sp Q17850 PK1_CAEL	FLRCAKPLASLYYLIVA AKKSIAEASNS	572
tr B7Z0W0 B7Z0W0_DROME	FLKLARPLASLTPLIMAAKEATKGN---	840
sp Q13153 PAK1_HUMAN	FLKIAKPLSSLTPLIAAAKEATKNNH--	545
sp 088643 PAK1_MOUSE	FLKIAKPLSSLTPLMHAAKEATKNNH--	545
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CLUSTAL O(1.2.4) multiple sequence alignment

DDB0215361 DDB_G0294094	MGGNLSSELKSTKYRKREIVDLRKMNDLKPPITIGAL--QCKELLLSENDLITIPPEEIGK	58
sp Q7KRY7 LAP4_DROME	MFK--CIPIFKGCNRQVEFVDKRHCSLQVPVEEILRYSRTLEELFLDANHIRDLKPNFFR	58
sp Q80U72 SCRIB_MOUSE	MLK--CIPLWR-CNRHVESVDKRHCSLQVVEEIIYRYSRSELELLLDANQLRELKPFPR	57
sp Q14160 SCRIB_HUMAN	MLK--CIPLWR-CNRHVESVDKRHCSLQAVPEEIIYRYSRSELELLLDANQLRELKPFPR	57
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DDB0215361 DDB_G0294094	LSKVEIIDFAKNRINYIPPEIGSLATLKQLFSLNNKLFYTPITPNIGALKNLTRLDLSSN	118
sp Q7KRY7 LAP4_DROME	LHRLRKLGLSDNEIGRL-----PPDIQNFENLVELDVSRN	93
sp Q80U72 SCRIB_MOUSE	LLNLRLKGLSDNEIQRL-----PPEVANFMQLVELDVSRN	92
sp Q14160 SCRIB_HUMAN	LLNLRLKGLSDNEIQRL-----PPEVANFMQLVELDVSRN	92
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DDB0215361 DDB_G0294094	QLDDLPEVISNCEALEYLDISDNQLQSFPLEFGKLYNLQVFNCSKNSKSLPSEISGWVK	178
sp Q7KRY7 LAP4_DROME	DIPDIPDDIKHLQSLQVADFSSNPPIKLPSGFSQKLNLTVLGLNDMSLTTLPADFGSLTQ	153
sp Q80U72 SCRIB_MOUSE	DIPDIPESIKFKCALEIADFSGNPLSRLPDGTQLRSLAHLALNDVSLQALPGDVGNLAN	152
sp Q14160 SCRIB_HUMAN	DIPDIPESIKFKCALEIADFSGNPLSRLPDGTQLRSLAHLALNDVSLQALPGDVGNLAN	152
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DDB0215361 DDB_G0294094	LEELNVSNNQLAFLPNQICLLGLLSTLNVGFNKLQQLPPEELSSMVSLTNLDLKVNPPLQY	238
sp Q7KRY7 LAP4_DROME	LESLELRNLLKHLPETISQLTKLKRDLGDNEIEDLPPYLGYPGLH-----	201
sp Q80U72 SCRIB_MOUSE	LVTLELRNLLKSLPASLSFLVKLEQLDLGGNDLEVLPTLGLALPNLR-----	200
sp Q14160 SCRIB_HUMAN	LVTLELRNLLKSLPASLSFLVKLEQLDLGGNDLEVLPTLGLALPNLR-----	200
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DDB0215361 DDB_G0294094	VPQLSNLRQLKILSIRNLQITHPLGLGLSELIELDIRDNPQLKIPYDIATLINLQKL	298
sp Q7KRY7 LAP4_DROME	-----ELWLDHNQLQRLPPELGLLTKLTYLDVSEN-RLEELPNEISGLVSLTDL	249
sp Q80U72 SCRIB_MOUSE	-----ELWLDNRNQLSALPPELGNLRRVLCVDVSEN-RLEELPVELGGLALLTDL	248
sp Q14160 SCRIB_HUMAN	-----ELWLDNRNQLSALPPELGNLRRVLCVDVSEN-RLEELPAELGGVLVLLTDL	248
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DDB0215361 DDB_G0294094	DLFGNNMRIVPREVGNLILNLTDLRQNKLTIDNIPSEIGKLVNLKLLLSNNLLIALPP	358
sp Q7KRY7 LAP4_DROME	DLAQNLLEALPDGIKLSRLTILKLDQNRQL--RLNDTLGNCENMQELILTENFLSELPA	307
sp Q80U72 SCRIB_MOUSE	LLSQNLQLRQLEIGQLKQLSILKVDQNRCL--EVTEAIGDCENLSELILTENLLTALPH	306
sp Q14160 SCRIB_HUMAN	LLSQNLRLRLPDGIGQLKQLSILKVDQNRCL--EVTEAIGDCENLSELILTENLLMALPR	306
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DDB0215361 DDB_G0294094	EIASMKALKEFEASNQLQAIPTEIGELSGLTKINLSGNKLTSPASFGNLSELQICDLK	418
sp Q7KRY7 LAP4_DROME	SIGQMTKLNLNVDNRNLEYLPLEIGQCANLGVLSLRDNKLLKLPPELGNCTVLHVLDVS	367
sp Q80U72 SCRIB_MOUSE	SLGKLTKLTLNVDNRNHEVLPPETGGCVALSVLRLDNRLAVLPPELAHTAELHVLDVA	366
sp Q14160 SCRIB_HUMAN	SLGKLTKLTLNVDNRNHEALPPEIGGCVALSVLSLRDNRLAVLPPELAHTTELHVLDVA	366
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DDB0215361 DDB_G0294094	SNEIAELPTTLDGLKSCTKIDL---SHNMLTELPWFGDLIGLTILDVGHNPLTIPPNPPI	475
sp Q7KRY7 LAP4_DROME	GNQLLYLPYSLVNLQLKAVWLSENQSPLLTFQP-DTDAETGEQVLSCYLLPQQ-EYQPI	425
sp Q80U72 SCRIB_MOUSE	GNRLRSLPFAALTHNLKALWLAENQAQPMRLRFQT-EDDAQTGEKVLTCYLLPQQ-PLPSL	424
sp Q14160 SCRIB_HUMAN	GNRLQSLPFAALTHNLKALWLAENQAQPMRLRFQT-EDDARTGEKVLTCYLLPQQ-PPPSL	424
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DDB0215361 DDB_G0294094	VMK-----GTESIIQLKKNEKEGR--KGKVSGLGIQQDNEK*-----	510
sp Q7KRY7 LAP4_DROME	TPARDLESDEPFEEERPSRTVV-KFSEET-----QEKETPFVRQNTPHPKDLKAK	476
sp Q80U72 SCRIB_MOUSE	EDAGQQSSPSESCSDAPLSRVSVIQFEDTLEGEEDAEEAAAEKRGQLRRATPHPSCLKVM	484
sp Q14160 SCRIB_HUMAN	EDAGQQGSLSETWSDAPPSRVSVIQFLEAPIGDEDAEEAAAEKRGQLRRATPHPSCLKVM	484
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DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	AQKLKVERSRNEEHANLVTLPPEENGTKLAEPTETRTIANNHQQQPHVPVQQPIVGVNSKQ	536
sp Q80U72 SCRIB_MOUSE	KRGIEERRN--EAF--VCKPDPS-----PSPSEEEK-RL-SAE	517
sp Q14160 SCRIB_HUMAN	KRSIEGRRS--EAC--PCQPDGSGS-----PLPAEEEEK-RL-SAE	517
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	PVVVGVVTPTT-----TTVAPTGVQGGSEGASSTANNVKAATAAVVAELAAATVGGSDDE	589
sp Q80U72 SCRIB_MOUSE	SALSGGSVPSASTASEGEPEILPAEVQGLGQHEAM-----P-AQ-EE	557
sp Q14160 SCRIB_HUMAN	SGLSEDSRPSASTVSEAEPEGPSAEAQGGSQQEAT-----TAGG-EE	558

DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	VQDDDEQE--DEFESDRR---VGFQVEGEDDDFYK--RPPKLHRRDTPHHLKNKRVQH	640
sp Q80U72 SCRIB_MOUSE	YTEDDYNEPTVHFAEDTLIPREDGESEEGQPEAAWPLPSGRQLIRKDTPHYKKHFKISK	617
sp Q14160 SCRIB_HUMAN	DAEEDYQEPVHFAEDALLPGDDREIEEGQPEAPWTLPGGRQLIRKDTPHYKKHFKISK	618
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	LTDKQASEILANALASQERNDTTPQHSLSGKVT--SPIE---EEEQL-----EVEQE	688
sp Q80U72 SCRIB_MOUSE	LPQPEAVVALLQGVQTDREGPT--AGWHNGPHTPWAPRAHEEEEEEEEN-----	665
sp Q14160 SCRIB_HUMAN	LPQPEAVVALLQGMQPDGEGPVAPGGWHNGPHAPWAPRAQKEEEEEEEGSPQEEEEEEEE	678
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	QQQQQQ--H---PFDSLSPTISAGKTAEASTDP--DNLDGVTELRLQEQYIHIERTAAGL	741
sp Q80U72 SCRIB_MOUSE	-RDEEEGEATTEEDDKEEAVASAPSVKGVSFQANNLLIEPARIEEEEELTLTIVRQTGGL	724
sp Q14160 SCRIB_HUMAN	ENRAEEEEASTEEDKEGAVVSAPSVKGVSFQANNLLIEPARIEEEEELTLTILRQTGGL	738
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	GLSIAGGKGSTPFKGGDDGIFISRVTEAGPADLAGLVGDKVIKVNIGIVVVDADHYQAVQ	801
sp Q80U72 SCRIB_MOUSE	GISIAGGKGSTPYKGDDEGIFISRVSEEGPAARAGVRVGDKLLEVNGVALQDAEHHEAVE	784
sp Q14160 SCRIB_HUMAN	GISIAGGKGSTPYKGDDEGIFISRVSEEGPAARAGVRVGDKLLEVNGVALQGAEHHEAVE	798
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	VLKACGAVLVLVQREVTRLIGHPVFSEDGSVSQISVETRPLVADAPPAASISHERYIPA	861
sp Q80U72 SCRIB_MOUSE	ALRGAGAAVQMRVWRERMVEPE-----N-----AVT-----	810
sp Q14160 SCRIB_HUMAN	ALRGAGTAVQMRVWRERMVEPE-----N-----AVT-----	824
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	PIEIVPQQQHLQQQQQQPIQQVAPTHSYSGNVFATPTAAQTVQPAVSAAPNGLLLNGREA	921
sp Q80U72 SCRIB_MOUSE	-----ITPLRPEDDYSPREWRGGGL-----RLPLLQPET	839
sp Q14160 SCRIB_HUMAN	-----ITPLRPEDDYSPRERRGGGL-----RLPLLPES	853
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	PLSYIQLHTTLIRDQIGQGLGFSIAGGKGSPPFKDDCDGIFISRITEGGLAYRDGKIMVG	981
sp Q80U72 SCRIB_MOUSE	PVSLRQRHAA-CLVRSEKGLGFSIAGGKGSTPYRAGDGGIFISRIAEGGAHRAGTLQVG	898
sp Q14160 SCRIB_HUMAN	PGPLRQRHVA-CLARSERGLGFSIAGGKGSTPYRAGDAGIFVSRIAEGGAHRAGTLQVG	912
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	DRVMAINGNDMTEAHHDAVAACLTQPFRVRLVLQREYRGPLEPPTSPRSPAVLNSLSPS	1041
sp Q80U72 SCRIB_MOUSE	DRVLSINGVDMTEARHDHAVSLTAASPTISLLLERETGGTYPPSPPPHSSPT-----	951
sp Q14160 SCRIB_HUMAN	DRVLSINGVDVTEARHDHAVSLTAASPTIALLLEREAGGPLPPSPLPHSSPP-----	965
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	GYLANRPANFRRSVVEVEQPYKYNTLATTTPTPKPTVPASISNNNNTLPSSKTNGFATAA	1101
sp Q80U72 SCRIB_MOUSE	-----PAATVAATV-----	960
sp Q14160 SCRIB_HUMAN	-----TAAVATTSI-----	974
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	AATIDSSTGQVPVPAPRRNTNSVPMGDDIGAGSTTSGDSGEAQPSLRLPLTSDDFQAMIPA	1161
sp Q80U72 SCRIB_MOUSE		960
sp Q14160 SCRIB_HUMAN		974
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	HFLSGGSQHQVHVARPNVEGVSAVTNVNKKQPDLPMPAAPTELGRVTETITKSTFTET	1221
sp Q80U72 SCRIB_MOUSE	-----STAVPGEPLLPRL-----	973
sp Q14160 SCRIB_HUMAN	-----TTATPGVPGLPSL-----	987
DDB0215361 DDB_G0294094		510
sp Q7KRY7 LAP4_DROME	VMTRITDNQLAEPLISEEVVLPKNQGS LGFSIIGGTDHSCVPFGTRPGIFISHIVPGGI	1281
sp Q80U72 SCRIB_MOUSE	-SPSLLATALEGPPVEEICLPRAAGPLGLSIVGGS DHSSHPFGVQDPGVFISKVLPRL	1032
sp Q14160 SCRIB_HUMAN	-APSLLAAALEGPPVEEIRLPRAAGPLGLSIVGGS DHSSHPFGVQEPGVFISKVLPRL	1046

DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	ASKCGKLRMGDRILKVNEADVSKATHQDAVLELLKPGDEIKLTIQHDLPPGFQEVLLSK	1341
sp Q80U72 SCRIB_MOUSE	AARCG-LRVGDRILAVNGQDVREATHQEAVSALLRPCLELCLLVRRDPPPPGMRELCTQK	1091
sp Q14160 SCRIB_HUMAN	AARSG-LRVGDRILAVNGQDVRDATHQEAVSALLRPCLELCLLVRRDPAPPGLRELCTQK	1105
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	AEGERLGMHIKGGNLNGQRGNPADPSDEGVFVSKINSVGAARRDGRLKVGMRLLLEVNGHSL	1401
sp Q80U72 SCRIB_MOUSE	APGKGLGISIRGGAKGHAGNPCDPTDEGIFISKVSPPTGAAGRDGRLRVGLRLLLEVNNQSSL	1151
sp Q14160 SCRIB_HUMAN	APGERLGISIRGGARGHAGNPRDPTDEGIFISKVSPPTGAAGRDGRLRVGLRLLLEVNNQSSL	1165
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	LGASHQDAVNVLNRAGNEIQLVVCKGYDKSNLIHSIGQAGGMSTGFNSSASCSGG-----S	1457
sp Q80U72 SCRIB_MOUSE	LGLTHAEAVQLLRVSGDTLTVLVCDGFDSTTTALEVSPGVIANPFAAGLGHRNSLESIS	1211
sp Q14160 SCRIB_HUMAN	LGLTHGAEVQLLRVSGDTLTVLVCDGFEASTDAALEVSPGVIANPFAAGIGHRNSLESIS	1225
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	RQGSRASET--GS-----ELSQSQSVSSLDHEEDERLRQDFDVFASQKPDAAQQPTGPS	1508
sp Q80U72 SCRIB_MOUSE	SIDRELSPEPGKEKELASQALPWESESAETTRNLEPLKLDYRALAALPSAGSLQRGPS	1271
sp Q14160 SCRIB_HUMAN	SIDRELSPEPGKEKELPGQTLHWGPATEAAGRGLQPLKLDYRALAAVPSAGSVQRVPS	1285
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	VLA AAA-----AMVHGASSPTPPAAT--SNIT-----PLPTAAAVASADLTAPDTPA	1553
sp Q80U72 SCRIB_MOUSE	ATTGGKTTIAPCSPGSGQP--PSPDELPANVKQAYRAFAAVPTVHPPEEN-SATQPPTPG	1327
sp Q14160 SCRIB_HUMAN	GAAAGGKMAESPCSPSGQPPSPSPDELPANVKQAYRAFAAVPTSHPPED-APAQPPTPG	1344
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	T--QTVALIHAEQQAHQQQQQTQLAP-LGQEKSTQEKVLEIVRAADFTTVPPKSPSEHH	1610
sp Q80U72 SCRIB_MOUSE	PAASPEQLSFRERQK----YFELEVRVPQAE-GPPKRVSLVGADD-LRKM-----QEE	1374
sp Q14160 SCRIB_HUMAN	PAASPEQLSFRERQK----YFELEVRVPQAE-GPPKRVSLVGADD-LRKM-----QEE	1391
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	EQDKIQKTTTIVVISKHTLDNTPTPTTAAAPLSIAGAE-----SANSAGAP	1656
sp Q80U72 SCRIB_MOUSE	EARKLQQKRAQMLREEAVTSGP-----DMGLASDRESDDQQEAEQPWAVP SHAGGS	1426
sp Q14160 SCRIB_HUMAN	EARKLQQKRAQMLREAAEAGAE-----ARLALDGETLGEEQEDEQPPWASPSPTSRQ	1444
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	SPAVPASTPGSAPVLPAAVAVQTQTQTSTTEKDEEESQLQST--PASRDGAEEQQEEVRA	1714
sp Q80U72 SCRIB_MOUSE	SPSSPPPLGGNAPVRTAKAER-----RHQERLRMQSPLEPAPER-----	1466
sp Q14160 SCRIB_HUMAN	SPASPPPLGGGAPVRTAKAER-----RHQERLRVQSPPEPAPER-----	1484
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	KPTPTKVPKSVSDKKRFFESAMEDQHKTQKTDKVFSLSKDEVEKLRQEERKIATLRR	1774
sp Q80U72 SCRIB_MOUSE	-LSPAERRALAEKRALWRAA-----RMKSLEQDALRAQMVLISK	1504
sp Q14160 SCRIB_HUMAN	-LSPAELRALAEKRALWRAA-----RMKSLEQDALRAQMVLISR	1522
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	DKN-----SRL LDAAND-----NIDKDAAQQRTKSNSSSS	1805
sp Q80U72 SCRIB_MOUSE	SQEGRGKRGPLERLAEAPSPAPTPSPTPLEDFGLQTSASGRLSPDFVEELRTL EASPS	1564
sp Q14160 SCRIB_HUMAN	SQEGRGTRGPLERLAEAPSPAPTPSPTPVEDLGPQTSTSPGRLSPDFAEELRSL EPS	1582
DDB0215361 DDB_G0294094	-----	510
sp Q7KRY7 LAP4_DROME	GDDNDDSDQEEGIARGDSVDNAALGHFDD---AEDM---RNPLDEIEAVFRS	1851
sp Q80U72 SCRIB_MOUSE	GSQEEDGEVAL-VLLGR-PSPGAVGPEDMTLCSSRRSVRPGRRGLGPVPS----	1612
sp Q14160 SCRIB_HUMAN	GPQEEDGEVAL-VLLGR-PSPGAVGPEDVALCSSRRSVRPGRRGLGPVPS----	1630