

gi | 6680828 | ref | NP_031610.1 | MGTGTLSS---LLLLLLLVIGDADMKGHFDPAKCRYALGMDRTIPDSDISASSWSWSDTAARHSRLESDDGGAWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 147
gi | 6978585 | ref | NP_037269.1 | MGTGTLSS---LLLLLLLVIGDADMKGHFDPAKCRYALGMDRTIPDSDISASSWSWSDTAARHSRLESDDGGAWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 147
gi | 83977450 | ref | NP_054699.2 | MGPEALSS---LLLLLLLVASGDADMKGHFDPAKCRYALGMDRTIPDSDISASSWSWSDTAARHSRLESDDGGAWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 146
gi | 114606277 | ref | XP_001150123.1 | MGPEALSS---LLLLLLLVASGDADMKGHFDPAKCRYALGMDRTIPDSDISASSWSWSDTAARHSRLESDDGGAWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 146
gi | 73972142 | ref | XP_532062.2 | MGPEALSSLLLLLLLLLVATGDADMKGHFDPAKCRYALGMDRTIPDSDISASSWSWSDTAARHSRLESDDGGAWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 150
gi | 292622258 | ref | XP_001345829.3 | MATQMVSLPALLIVLLASCTAAQDLDWHFETAKCRYALGMDRTIPDSDITASSAWSWSDTEAKHGRSLNNGEGDAGWCPAGVPFPKBEYYLQVLDLRRHLHLVALVGTQGRHAGGLGKEFSSRYRLRYSRDGRRWMDKDRWGQEVISGND 150



gi | 6680828 | ref | NP_031610.1 | PGGVVLKDLGPPMVARLVRFPYPRADRVMSVCLRVLYGCLWRDGLLSYAPVQGMQLSEVMVHLNDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 294
gi | 6978585 | ref | NP_037269.1 | PGGVVLKDLGPPMVARLVRFPYPRADRVMSVCLRVLYGCLWRDGLLSYAPVQGMQLSEVMVHLNDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 293
gi | 83977450 | ref | NP_054699.2 | PGGVVLKDLGPPMVARLVRFPYPRADRVMSVCLRVLYGCLWRDGLLSYAPVQGMQLSEVMVHLNDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 292
gi | 114606277 | ref | XP_001150123.1 | PGGVVLKDLGPPMVARLVRFPYPRADRVMSVCLRVLYGCLWRDGLLSYAPVQGMQLSEVMVHLNDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 292
gi | 73972142 | ref | XP_532062.2 | PGGVVLKDLGPPMVARLVRFPYPRADRVMSVCLRVLYGCLWRDGLLSYAPVQGMQLSEVMVHLNDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 299
gi | 292622258 | ref | XP_001345829.3 | TYDIVLKDLPPIIARVRFYPLADRVMSVCLRVLYGCVWKGDKLKYATAPLGHVMDLGSILVNFDSITYDGYAGGLQYGGGLGOLADGVGLDDFRSQBLRVWPGYDVVWGSNCFPPVGVVEMEFEDRLRFAQMOVHCNNMHT 297



gi | 6680828 | ref | NP_031610.1 | LGARLPGGVECRFRKGPAMAWEGEVRHALGGSGLDPPRARAVISVPLGGHVGRFLOCRFLFAGPWLLEISFISDVVNDSS---DTPPPAPWPPGPP---PTNFSSLELEPRGQC-----FVAKAEG 411
gi | 6978585 | ref | NP_037269.1 | LGARLPGGVECRFRKGPAMAWEGEVRHALGGSGLDPPRARAVISVPLGGHVGRFLOCRFLFAGPWLLEISFISDVVNDSS---DTPPPAPWPPGPP---PTNFSSLELEPRGQC-----FVAKAEG 410
gi | 83977450 | ref | NP_054699.2 | LGARLPGGVECRFRKGPAMAWEGEVRHALGGSGLDPPRARAVISVPLGGHVGRFLOCRFLFAGPWLLEISFISDVVNDSSPALGGTFPPAPWPPGPP---PTNFSSLELEPRGQC-----FVAKAEG 413
gi | 114606277 | ref | XP_001150123.1 | LGARLPGGVECRFRKGPAMAWEGEVRHALGGSGLDPPRARAVISVPLGGHVGRFLOCRFLFAGPWLLEISFISDVVNDSSPALGGTFPPAPWPPGPP---PTNFSSLELEPRGQC-----FVAKAEG 413
gi | 73972142 | ref | XP_532062.2 | LGARLPGGVECRFRKGPAMAWEGEVRHALGGSGLDPPRARAVISVPLGGHVGRFLOCRFLFAGPWLLEISFISDVVNDSSPALGGTFPPAPWPPGPP---PTNFSSLELEPRGQC-----FVAKAEG 420
gi | 292622258 | ref | XP_001345829.3 | QGVRFSEVVKCFKASLLSPWAEPELSQLQVS---DLHDLSESRITISLPLGGRPAQILRCHFAFADNLLIIEIFYSMPEDGS---VLPPIPSRRRLNATSYSPITANATSSPNTLLMTNSSLPLSPMPLEMSGILRVLGIVAKDDS 441



gi | 6680828 | ref | NP_031610.1 | SPTAILIGCLVAIITLLLLLIIALMLWRLHWRLLSKAERRVLEBEELVHLVSVPGDITLNNRPGPREPPPYOEPFRPRGTTPHSAFCVPPNGSALLS---NPAYRLLLATYARPPRGPPPTPAWAKPTINTQACSGDYMEPEKPGAPLL 556
gi | 6978585 | ref | NP_037269.1 | SPTAILIGCLVAIITLLLLLIIALMLWRLHWRLLSKAERRVLEBEELVHLVSVPGDITLNNRPGPREPPPYOEPFRPRGTTPHSAFCVPPNGSALLS---NPAYRLLLATYARPPRGPPPTPAWAKPTINTQACSGDYMEPEKPGAPLL 555
gi | 83977450 | ref | NP_054699.2 | SPTAILIGCLVAIITLLLLLIIALMLWRLHWRLLSKAERRVLEBEELVHLVSVPGDITLNNRPGPREPPPYOEPFRPRGTTPHSAFCVPPNGSALLS---NPAYRLLLATYARPPRGPPPTPAWAKPTINTQAYSGDYMEPEKPGAPLL 558
gi | 114606277 | ref | XP_001150123.1 | SPTAILIGCLVAIITLLLLLIIALMLWRLHWRLLSKAERRVLEBEELVHLVSVPGDITLNNRPGPREPPPYOEPFRPRGTTPHSAFCVPPNGSALLS---NPAYRLLLATYARPPRGPPPTPAWAKPTINTQAYSGDYMEPEKPGAPLL 558
gi | 73972142 | ref | XP_532062.2 | SPTAILIGCLVAIITLLLLLIIALMLWRLHWRLLSKAERRVLEBEELVHLVSVPGDITLNNRPGPREPPPYOEPFRPRGTTPHSAFCVPPNGSALLS---NPAYRLLLATYARPPRGPPPTPAWAKPTINTQACSGDYMEPEKPGAPLL 565
gi | 292622258 | ref | XP_001345829.3 | SPTAILIGCLVGIITLLLVAVIVILWQYWKLLGKAGSLSSDELRYVLSVPSDNNVINTNTITYSRYSRIHTFDDRDREGEYQEPSTVLRPRDRRSTACALDMVDKGLPIQEGPPYPGAPPPGLSGAHYG---EASGG--- 583



gi | 6680828 | ref | NP_031610.1 | PPPPQNSVPHYAEADIVTLQGVVGGNTYAVPALPPGAVGDPGRVDFPFRSRLRFKEKLGEGQFGEVHLCEVEDPQDLVSDFFPISVHKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVQDDPLCMIIDYMEGND 706
gi | 6978585 | ref | NP_037269.1 | PPPPQNSVPHYAEADIVTLQGVVGGNTYAVPALPPGAVGDPGRVDFPFRSRLRFKEKLGEGQFGEVHLCEVEDPQDLVSDFFPISVQKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVQDDPLCMIIDYMEGND 705
gi | 83977450 | ref | NP_054699.2 | PPPPQNSVPHYAEADIVTLQGVVGGNTYAVPALPPGAVGDPGRVDFPFRSRLRFKEKLGEGQFGEVHLCEVEDPQDLVSDFFPISVQKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVQDDPLCMIIDYMEGND 708
gi | 114606277 | ref | XP_001150123.1 | PPPPQNSVPHYAEADIVTLQGVVGGNTYAVPALPPGAVGDPGRVDFPFRSRLRFKEKLGEGQFGEVHLCEVEDPQDLVSDFFPISVQKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVQDDPLCMIIDYMEGND 708
gi | 73972142 | ref | XP_532062.2 | PPPPQNSVPHYAEADIVTLQGVVGGNTYAVPALPPGAVGDPGRVDFPFRSRLRFKEKLGEGQFGEVHLCEVENPQDLVSDFFPISVQKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVQDDPLCMIIDYMEGND 715
gi | 292622258 | ref | XP_001345829.3 | ---GASVPHYAEADITSLQGVVGGNTYAVPALSPATP---DCPPPELPRRRLRFKEKLGEGQFGEVHLCEVENPQDLVSDFFPISVQKGHPLLVAVKILRPDAIKNARNDFLKEVKIIMSRLKDPNIIRLLGVCVSSDPLCMTVEYMEGND 728



gi | 6680828 | ref | NP_031610.1 | LNOFLSAHOLENKATQGLSDTSDGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVG---ENFTIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILMGKFTTASDVWAFGVTLWEVLMLCRAOPFGQL 846
gi | 6978585 | ref | NP_037269.1 | LNOFLSAHOLENKATQGLSDTSDGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVG---ENFTIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILMGKFTTASDVWAFGVTLWEVLMLCRAOPFGQL 845
gi | 83977450 | ref | NP_054699.2 | LNOFLSAHOLEDKAAEGAPDGGQAAQGPPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVG---ENFTIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILMGKFTTASDVWAFGVTLWEVLMLCRAOPFGQL 848
gi | 114606277 | ref | XP_001150123.1 | LNOFLSAHOLEDKAAEGAPDGGQAAQGPPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVG---ENFTIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILMGKFTTASDVWAFGVTLWEVLMLCRAOPFGQL 848
gi | 73972142 | ref | XP_532062.2 | LNOFLSAHOLEDKAAEGAPDRBAAGPPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVG---ENFTIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILMGKFTTASDVWAFGVTLWEVLMLCRAOPFGQL 855
gi | 292622258 | ref | XP_001345829.3 | LXOYLSHRVLLDKSGP---SONTPTISYPALISMASQIASGMKFLASLNFVHRDLATRNCLVGGEGESSEERGERHIKIADFQMSRNLVAGDYRVOGRAVLPIRWMWAWECILM----- 840



gi		6680828		ref		NP_031610.1		TDEQVIENAGEFFRD	GROVYLSRPPAC	POTLYELMLRCWSREPEQ	RPPFA	LHRFLADDALNTV	911
gi		6978585		ref		NP_037269.1		TDEQVIENAGEFFRD	GROVYLSRPPAC	POTLYELMLRCWSREPEQ	RPPFS	LHRFLADDALNTV	910
gi		83977450		ref		NP_054699.2		TDEQVIENAGEFFRD	GROVYLSRPPAC	PGLYELMLRCWSRESEQ	RPPFS	LHRFLAEDALNTV	913
gi		114606277		ref		XP_001150123.1		TDEQVIENAGEFFRD	GROVYLSRPPAC	PGLYELMLRCWSRESEQ	RPPFS	LHRFLAEDALNTV	913
gi		73972142		ref		XP_532062.2		TDEQVIENAGEFFRD	GROVYLSRPPS	CPLGLYELMLRCWSREPEQ	RPS	LHRFLAEDALNTV	920
gi		292622258		ref		XP_001345829.3		-----					840
							910.....920.....930.....940.....950.....960.....					

