

gi | 4504533 | ref | NP_000854.1 | -----MEEPGAOCAPPPAGSETWVQPANLSSAPSONCSA-KDYIYODSIS----- 150
gi | 57114071 | ref | NP_001009102.1 | -----MEEPGAOCAPPPAGSETWVQPANLSSAPSONCSA-KDYIYODSIS----- 150
gi | 6754258 | ref | NP_034612.1 | -----MEEQGIOCAPPPAASQTGVPLTNLS-----HNCSA-DGYIYODSIA----- 150
gi | 11560016 | ref | NP_071561.1 | -----MEEQGIOCAPPPAASQTGVPLTNLS-----HNCSA-DDYIYODSIA----- 150
gi | 76625410 | ref | XP_583895.2 | -----MEAVAAOCQPPASSTQGLSQANLSSAGPSSHNCSSAAEYIYODFIA----- 150
gi | 50744790 | ref | XP_419875.1 | -----MEPASPCAPLPPANDSYHG-----RNCSA-EBGIYODAMP----- 150
gi | 192447383 | ref | NP_001122181.1 | -----MERSGYFKPAPHFVILNLSSTG-----TNVTL-TPKDPDEKQES----- 150
gi | 17864132 | ref | NP_524599.1 | -----MALSQDWRRCQSHRQHRNRHCGNQKQLISTATLTLFVFLSSWIIYAAGKATVPAPLVEGETESASQDFNSSSFLGATIASASSTGSGSGSGSGSGSGSYGLASMNSSPILAIVSYQCIITSSNLGDSNITLVPLSDTFLLL 150
gi | 31208325 | ref | XP_313129.1 | -----MDSDTVASASKHRTDQDAGRTDGVVALIVATTIANLLASPSPLAATSTAWAVT---TEFAAQPPYLVYGNLSSLAYLDANTH-----ASLYSP-----FFVGPASATPAPGPP----- 150
gi | 58384228 | ref | XP_313127.2 | MLLWLPDSDSTSSITLAVTVGGSAIVGLEPGSSIPFPFAVLIAHNLQITGDHGFHGHTDGGDAGGSGSGEAIVGAASITIGGSLGVPLAG-----GTTVAIVVSS-----TLNANLSEHLLDLD----- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 4504533 | ref | NP_000854.1 | -----LPWKVLLVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITMYTVTGRWTLGOVVCDFWLSDDITCCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAVMIALVWVFSISISLPP 300
gi | 57114071 | ref | NP_001009102.1 | -----LPWKVLLVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITMYTVTGRWTLGOVVCDFWLSDDITCCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAVMIALVWVFSISISLPP 300
gi | 6754258 | ref | NP_034612.1 | -----LPWKVLLVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITMYTVTGRWTLGOVVCDFWLSDDITCCTASIMHLCVIALDRYWAITDAVEYSAKRTPKRAAIMIVLVVWFSISISLPP 300
gi | 11560016 | ref | NP_071561.1 | -----LPWKVLLVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITMYTVTGRWTLGOVVCDFWLSDDITCCTASIMHLCVIALDRYWAITDAVEYSAKRTPKRAAIMIVLVVWFSISISLPP 300
gi | 76625410 | ref | XP_583895.2 | -----LPWKVVVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITMYTVTGRWTLGOVVCDFWLSDDITCCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAGMIALVWVFSICISLPP 300
gi | 50744790 | ref | XP_419875.1 | -----LSGKIVLAVLLALILALITLNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITLYTVTGRWTLGOVVCDFWLSDDITCCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAGMIALVWVFSICISLPP 300
gi | 192447383 | ref | NP_001122181.1 | -----FAFQVILSIVLGLILALILNAFVIATVYTRKRLHTPANYLIASLAVTDLVLSILVMPISITLYTVTGRWTLGOVVCDFWLSDDITCCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAGMIALVWVFSICISLPP 300
gi | 17864132 | ref | NP_524599.1 | EFFAAGEFVLPPLSIFVSVLVLLVILGVVGNLVLCIACVMRKLRRPCNYLLVSLALSDLCVALLVMPMALLYEVLEKWNFGPLLCDIIVVFDVLCCTASILNLCASIVDRYLAITKPLEYGVKRTPRRMMLCVGVIVWLAACISLPP 300
gi | 31208325 | ref | XP_313129.1 | DVTVSTVISIILLAVIVGIVGNLVLCVAVCLVRKLRPCNYLLVSLALSDLCVALLVMPMALLYEVLEKWNFGVFCDIIVVAFDVLCTASILNLCASIVDRYLAITKPLEYGVKRTPRRMIACIVLVWLAACISLPP 300
gi | 58384228 | ref | XP_313127.2 | IIRKVIICIVLLAVIFGIVGNLVLCVAVCLVRKLRPCNYLLVSLALSDLCVALLVMPMALLYEVLEKWNFGVFCDIIVVAFDVLCTASILNLCASIVDRYLAITKPLEYGVKRTPRRMMLCVGVIVWLAACISLPP 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 4504533 | ref | NP_000854.1 | FFWR---QAKAEEEVSECVNIDHILYIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 57114071 | ref | NP_001009102.1 | FFWR---QAKAEEEVSECVNIDHILYIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 6754258 | ref | NP_034612.1 | FFWR---QAKAEEEMLDCEVNIIDHVLIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 11560016 | ref | NP_071561.1 | FFWR---QAKAEEEVLDCEVNIIDHVLIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 76625410 | ref | XP_583895.2 | FFWR---QAKA---EAMNVCVNIIDHVLIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 50744790 | ref | XP_419875.1 | FFWR---QAKA---EAMNCAVNIIDHVLIVYSTVGFYFPLLLLIYALYGRIVYVARSRIKQTPNRTGKRLTRAQLITDPPGTSSTSVTSINSRVDPVPS-----EGSPVVVNVQKVRVSDALLEKK 450
gi | 192447383 | ref | NP_001122181.1 | FFWR---QVKA---GELTCVNIIDHIFVIVYSTVGFYFPLLLLIYALYGRIVYVARKRILKQSPKPKGKRLTSAHLSNPPAVASTPSLHCGRODLCS-----DGLGSDNIRVTVSDSALLEKK 450
gi | 17864132 | ref | NP_524599.1 | LLLILGNEHEDEE---GQPICTVQCNFAYQIYATLGSFYIPLVLMFVYVYIFRAARRIVLEE--KRAQTHLQDALNGTGPSAPQAPPLGHTLASSNGGQRHSSVGNISLTYSTCGGLSSGGGALAGHSGGGVSGSTGLGSPHKKL 450
gi | 31208325 | ref | XP_313129.1 | LLLILGNEHEIN---GQPACVQCNFFYQIYATLGSFYIPLVLMFVYVYIFRAARRIVMEE--KRAQKRLESAINGATQAVALEKPPG-----MVG-----EKVGPFGKVTTS-----SPQNKRL 450
gi | 58384228 | ref | XP_313127.2 | LLLILGNKHTIGEGPDQRPFCAVCEVGVYIYATLGSFYIPLVLMFVYVYIFRAARRIVKDE--KRAQTRLENSLAVDKLSTAAITITIT-----ITS-----MSLKPPDSIVPAMSVGGGSPHOKKL 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 4504533 | ref | NP_000854.1 | KLMAARERKAKKTLGIILGAFIVCWLPFFIISLVMPICKDACWFHLLAIFDFFFWLGYLNSLINPIIYIMSNEDFKQAFHKLIRFKCTS----- 575
gi | 57114071 | ref | NP_001009102.1 | KLMAARERKAKKTLGIILGAFIVCWLPFFIISLVMPICKDACWFHLLAIFDFFFWLGYLNSLINPIIYIMSNEDFKQAFHKLIRFKCTS----- 575
gi | 6754258 | ref | NP_034612.1 | KLMAARERKAKKTLGIILGAFIVCWLPFFIISLVMPICKDACWFHMAIFDFFFNWLYLNSLINPIIYIMSNEDFKQAFHKLIRFKCAG----- 575
gi | 11560016 | ref | NP_071561.1 | KLMAARERKAKKTLGIILGAFIVCWLPFFIISLVMPICKDACWFHMAIFDFFFNWLYLNSLINPIIYIMSNEDFKQAFHKLIRFKCAG----- 575
gi | 76625410 | ref | XP_583895.2 | KLMAARERKAKKTLGIILGAFIVCWLPFFIISLVMPICKDACWFHMAIFDFFFWLGYLNSLINPIIYIMSNEDFKQAFHKLIRFKCTG----- 575
gi | 50744790 | ref | XP_419875.1 | KLTAARERKAKKTLGIILGAFIVCWLPFFIISLVLPICKDACWFHMAIFDFFFWLGYLNSLINPIIYIMSNEDFKQAFHKLIRFKCTG----- 575
gi | 192447383 | ref | NP_001122181.1 | RISAARERKAKKTLGIILGAFIVCWLPFFIYIILLPLGCS--SCFSPLEDFDFFFWLGYVNSLINPIIYIMSNDDPKAFHKLIRFKCRR----- 575
gi | 17864132 | ref | NP_524599.1 | RFQLAKEKASTTLGIIMSFAVICWLPFFIILALIRPFET--MHVPASLSSLFWLGYANSLLNPIIYATLNRDFRKPFFQIILYFRCSLNTMMRENYQDQYGEPPSORVMLGDER--HGARESFL 575
gi | 31208325 | ref | XP_313129.1 | RFQLAKEKASTTLGIIMSFAVICWLPFFIILALVRFPMK--DDH--RILSSFFLWLGYANSLLNPIIYATLNRDFRKPFFQIILYFRCSLNTMMREDFYHSQYDPPGQRVITND--GGARESFL 575
gi | 58384228 | ref | XP_313127.2 | RFQLAKEKASTTLGIIMSFAVICWLPFFIILALVRFPLMD--DDY--PILSSFFLWLGYANSLLNPIIYATLNRDFRKPFFQIILYFRCSLNTMLMREDFYHSQYGEPPSORVMLEGHTARESFL 575
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....

