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gi|6755506|ref|NP_035497.1|-----MEKRDSVALHWRLLLLLLPPPTHQGRALRHIDPIQSAODPPAKYLSNGPGQEPVVMVTIDLTKISKPHSSFEFRWDPGEGVIFVYGDNTTEDDWFLLGLRAGQLEIQLNHWARLTVGFGPRLD 150
gi|6981532|ref|NP_036782.1|-----MEKGEVASLRCLLLLLLLLLLPPPTHQGRALRHIDPIQSAODSPAKYLSNGPGQEPVTVLTIDLTKISKPHSSFEFRWDPGEGVIFVYGDNTTEDDWFMLGLRDGQLEIQLNHWARLTVGFGPRLN 150
gi|7382460|ref|NP_001031.2|-----MESRGPPLATSRLLLLLLLLLHTRQGWALRPVLPQSAHDPAPVHLSNGPGQEPVAVMTFDLTKIKTSSSFVFRWDPGEGVIFVYGDTPKDDWFMLGLRDGRPEIQLNHWAOQLTVGAGPRLD 150
gi|114666215|ref|XP_511958.2|-----MESRGPPLATSRLLLLLLLLLHTRQGWALRPVLPQSAHDPAPVHLSNGPGQEPVAVMTFDLTKIKTSSSFVFRWDPGEGVIFVYGDTPKDDWFMLGLRDGRPEIQLNHWAOQLTVGAGPRLD 150
gi|57086381|ref|XP_536625.1|-----MDCRGPPLATPQWLLLLLLLPPGHQGLALRQGLSQRIDLPVHLSNGSGGEPVTVMTFNFTKIKKSSSFELRWDPGEGVIFVYGDTPSKDDWFVLGLRDGRPEIQLNHWAOQLTVGAGPRLD 150
gi|194675958|ref|XP_584958.4|-----MVKAAFPHAFAPESLEAKRGPQLIMVSRGPLAIWHG--LLLLLLPLPSHGPPALRPPLPSQTFBSPALHLSGPGQEPVTIMTFNLTIKTKISSFEFRWDPGEGVIFVYGDTPKNDWFMLGLRDGRPEIQLNHWAOQLTVSAGPRLD 150
gi|55742376|ref|NP_001007152.1|-----MKYLKEVITILLCPCLILLCRRRAAGDQISGRGQINLAHRQK-----WTPAMQCANLSDIRSIREFFEFRWDPGEGVIFVYGDTPKEGQDFVLSLRDGIPEMIGKADILVSVKGRKLN 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6755506|ref|NP_035497.1|DGRWHFVLEKMNQDSELLLWVDGKEMLCRQISA-SLADHSQRSMRIALGGLLPTSKLRFPLVPALDGCIRRDIDLGHQAQLSASPRTS-LGNCVDLQPGLEFFPPGTHAEFSLQDIPOPHADPWFTELELGFKLVDSGQLLALGQGTN 300
gi|6981532|ref|NP_036782.1|DGRWHFVLEKMNQDSELLLWVDGKEMLCRQVSA-SLADHPQLSMRIALGGLLPTSKLRFPLVPALDGCIRRDIDLGHQAQLSARTS-LGNCVDLQPGLEFFPPGTHAEFSLQDIPOPHTDPWFTELELGFKLVDSGQRLTLGQGTN 300
gi|7382460|ref|NP_001031.2|DGRWHQVEVKMEGDSVLLLEVDEEVLRLRQVSG-PLTSKRHPIMRIALGGLLFPASNLRPLPVPALDGCIRRDSDWLDKQAEISASAPTS-LRSCDVEINPGIFLPPGTAQAEFNLRDIPOPHAEFPWAFSLDLGLKQAAGSGHLLALGTPEN 300
gi|114666215|ref|XP_511958.2|DGRWHQVEVKMEGDSVLLKVDGEEVLCRQVSG-PLTSKRHPIMRIALGGLLFPASNLRPLPVPALDGCIRRDSDWLDKQAEISASAPTS-LRSCDVEINPGIFLPPGTAQAEFNLRDIPOPHAEFPWAFSLDLGLKQAAGSGHLLALGTPEN 300
gi|57086381|ref|XP_536625.1|DGIWHQVEVKILEDSELLLTVDEEVLRLRQVSGPPATNKPQPIIRIALGGLLFPASNLRPLPVPALDGCVRQGNWLDQAQTSSETPASSLRSCAVQSQPGIFPPGTAQAEFSLQDIPOPHAEFPWAFSLDLGLQLAAGSGHLLALGTPEN 300
gi|194675958|ref|XP_584958.4|DGKWHQVEVKIHGDSVLLLRVDGVEVLCRQVFGQANN-SQLIMRIALGGLLFPASDLRPLPVPALDACLQDDWLDQAQTSASVPTS-VRSCAVESQPGIFPPGTAQAEFGLQEIIPRPHAEFPWAFSLDLQLAAGSGRLLALGTPEN 300
gi|55742376|ref|NP_001007152.1|DGAWHLLELRSEKGFVLELVN-N-EVELVVLGHSKLAEEQLTKIRLALGMLVQKQLFHPFPEMDACIRGGHWLNLSTPWTDSIWE-FRPPSSSIKKGVSFPGTQVAVENTSDLFALKTEAGITVEIFGSGWIGTILSLQSTG---- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|6755506|ref|NP_035497.1|SFWLNTHLQNGSVVLSSEAEKPVVLPDVGGLPQLTLDRVKVVLQSGPKMEVLSMSLLRPAASLWRLWSPQGHLSLGLALPGESSASFCLSDFWVQGORLDDIDQALSRSQDIWTHSCPQRFSDTRFTH 429
gi|6981532|ref|NP_036782.1|SSWLLHLHLDQTVVLSSEAEKPLALPLAVGLPLQLKLDVFKVALSQGPKMEVLSLSLLRLASLWRLWSPQHLSLGLALPGESSASFCLSDFWVQGORLDDIDKALSRSQDIWTHSCPQSFSDTRFTH 429
gi|7382460|ref|NP_001031.2|PSWLSLHLQDQKVVLSGSGPGLDPLVVLGLPLQLKLSMSRVVLSQGSKMKALALPPLGLAPLLNLWAKPQGRFLGLALPGESSSFCNLGLWAGORLDDVDQALNRSHEIWTWSCPQSPFNGTDASH 429
gi|114666215|ref|XP_511958.2|PSWLSLHLQDQKVVLSGSGPGLDPLVVLGLPLQLKLSMSRVVLSQGSKMKALALPPLGLAPLLNLWAKPQGRFLGLALPGESSSFCNLGLWAGORLDDVDQALNRSHEIWTWSCPQSPFNGTDASH 429
gi|57086381|ref|XP_536625.1|PSWLSLHLQDQKVVLSGSGPGLDPLVVLGLPLQLKLAISRVLTPQYKKEIILALPALHGLFLLNLWAKPQGRFLGLALPGEASSASFCLDGLWAGORLDDMDRALRRSQDIWTHSCPQIFPNSGTDTH 429
gi|194675958|ref|XP_584958.4|PSWLSLHLQDQKVVLSGSGPGLDPLVVLGLRLQLNLTVSGVVLSQGAKEIILALPPTGPGSLLDLWVPHGRFLGLALPGEASSASFCLDGLWAGORSLDDMDRAQSRSLNIWTWSCPQNPFGNSDTH 429
gi|55742376|ref|NP_001007152.1|--FLYVLEGDKDDKLGKDGSTEFPSPEATLTFITLKNLSLVNSKPKVSEITLDFLMMWKNMMLTFGGVPG---DSEVAKSNFYLRGCEKIVVQGVIDLDRAYKHTAVSSHSCPTTEAMNELTL-- 429
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....

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