

gi | 24655582 | ref | NP_611409.1 | -MTSSWVIGNVG-TLQTLGPKGLDLPNNFETMWRHTIQSTRYLGNASLCRQIAT---HSFKLGAENRSKKEKASENESEPMANIFRGSILVSVQVFPVPPDVLTAEOKELENSLIDPFERFFS-DVNDAAARNDAKSIDDTSTALWELGAFG 144
gi | 158293556 | ref | XP_314893.4 | ---LITTIIFPLLPSSRCLAS-AAPQAKQAEA---QQATPSEAEKRP-----NMSFLNIFRQVQPAQVFPPEALDABOKEYIASFVDPVTKFFEEEDYDVPKAKHGGPDDEAFISMWEMGLMG 113
gi | 23956084 | ref | NP_059062.1 | -MQSARMTPSVGRQLLRGARSRSITVLQGGPRPISAQRLYAREATAVLQDK---PELTSDDASTREKPARAESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 144
gi | 6978435 | ref | NP_037023.1 | -MQSARMTPSVGRQLLRGARSRS-AALQGGPRPISAQRLYAREATAVLQDK---PELTSDDASTREKPARAESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 143
gi | 4557235 | ref | NP_000009.1 | -MQAARMAASLGRQLLRGGSSRL-TALLGQPRFPARRPAGGAAALALDK---SDSHSPEASTREKPARAESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 143
gi | 27806205 | ref | NP_776919.1 | -MQAARMAASLGRQLLRGGSSRL-TALLGQPRFPARRPAGGAAALALDK---SDSHSPEASTREKPARAESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 143
gi | 73955386 | ref | XP_546581.2 | ---MAPSVGRQLLRGARSRS-SALLGQPRFPACRPAASGAAVLEK---SDSHSPEASTREKPARAESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 138
gi | 47086807 | ref | NP_997776.1 | MLLRKYVTSPTAICSSVLRQPATIGA-QRQSGALVQMNVRVLYASQTAARVLDKNNVTRITATAAEVDRKAVVSVESKSFVAVGMFKGQLTIDOVFPYPSVLSBECAQFLKELVGPVARRFFE-EVNDPAKNDALKEVEDDITLQGLKELGAFG 148
gi | 71985184 | ref | NP_001022062.1 | ---MLSTLSEARLNTRFIRLS---HSAAAADAKPKKVAADVSPFVNMFRGKAVLDOVFPYPLNMTDEKQETLPLDMVMSPLEKMLV-EVNDVVKNDSEDIIPRAVLQDFEALGTEG 112



gi | 24655582 | ref | NP_611409.1 | IOVPSFEFGLLNNTQVGRCAIVGVNDLGLGITIGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWIENGGIAEIMTVFAQTEQVDPKTEGKDKVTAFAIVERFSGGVTN 294
gi | 158293556 | ref | XP_314893.4 | MQAPEYGGALPNTGYARMGELVGAADLGLAVVFGAHQSIGGWKVVLLYGEQEKRYLQVVTGGTIAFCFLTEPSSGSDAGSIRCAVKSADGSHYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 263
gi | 23956084 | ref | NP_059062.1 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 294
gi | 6978435 | ref | NP_037023.1 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 293
gi | 4557235 | ref | NP_000009.1 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 293
gi | 27806205 | ref | NP_776919.1 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 293
gi | 73955386 | ref | XP_546581.2 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 288
gi | 47086807 | ref | NP_997776.1 | LQVPSBELGGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFGKILLYGTPEQKEKYLKVAEAVVAAFALTEPSSGSDAGSIRCAVKSADGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 298
gi | 71985184 | ref | NP_001022062.1 | VLVPPELEGGFNNQMARVAEIVGADLGFVVMGAHQSIGYKILLLEGDAQKQKYLPLDLATGRKFAAFALTEPTTGSASVTRRAELSDGKHVYVNLGSKIWISGGGLADIFVFAQTEVTPDKTGQKDKVTAFAIVERFSGGVTN 261



gi | 24655582 | ref | NP_611409.1 | GPEKKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 444
gi | 158293556 | ref | XP_314893.4 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 413
gi | 23956084 | ref | NP_059062.1 | GLPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 444
gi | 6978435 | ref | NP_037023.1 | GLPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 443
gi | 4557235 | ref | NP_000009.1 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 443
gi | 27806205 | ref | NP_776919.1 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 443
gi | 73955386 | ref | XP_546581.2 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 438
gi | 47086807 | ref | NP_997776.1 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 448
gi | 71985184 | ref | NP_001022062.1 | GPEKMGIKASNTAEVYFDDVKIPIENVLKGEGDGFKVAMNINNGRFGMGATLSTGTMKCTEQAETHANRVRVDFGQKLVNYSIQEKLQMNILQYATESMAPTTIQNMDAGSKDYHLEAAISKIYAESAWVCDDEATQILGGMGYM 411



gi | 24655582 | ref | NP_611409.1 | VDNGLERVLRLDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSGHVVGELLPYAKKTAHCIDLFGQSVSEELLRLRNKNVNEQILLRLANAAIDYAMVVVTSRASSRAVNLNL 593
gi | 158293556 | ref | XP_314893.4 | KSSGLEKFLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 562
gi | 23956084 | ref | NP_059062.1 | KEPGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 594
gi | 6978435 | ref | NP_037023.1 | KEPGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 593
gi | 4557235 | ref | NP_000009.1 | KEPGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 593
gi | 27806205 | ref | NP_776919.1 | KEPGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 593
gi | 73955386 | ref | XP_546581.2 | KEPGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 588
gi | 47086807 | ref | NP_997776.1 | KDAQGVVERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 598
gi | 71985184 | ref | NP_001022062.1 | RTGLERVLRDIRIFRIFEGNDILRLFLIALTGIQYAGSHLKEQLRAFKNPNSANLGLIFKEASRRRAASTVGLG-GTDLSTFVVDPLKESAAALCADDIDRFSTIEALLIKHKGIVDQFLLRLRADSADIDYGMCVLSRASKAVRNN 551



gi | 24655582 | ref | NP_611409.1 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 655
gi | 158293556 | ref | XP_314893.4 | PSAHEHLLMAKAWCVANDRVIRIRRVNNG-VFVKNYDTMSAIAKNICARQGVQSNPVGIA 624
gi | 23956084 | ref | NP_059062.1 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 656
gi | 6978435 | ref | NP_037023.1 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 655
gi | 4557235 | ref | NP_000009.1 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 655
gi | 27806205 | ref | NP_776919.1 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 655
gi | 73955386 | ref | XP_546581.2 | PTAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 650
gi | 47086807 | ref | NP_997776.1 | SSAQHEKMLCDWCIEAARIREMNTALQSDPPQOELFRNFKSISKALVERGGVVTSNPLGF 659
gi | 71985184 | ref | NP_001022062.1 | SSADFERKVVATYVVDKAMKSNRFLKDGAGSVENASKVATIESLAKEVCCNGGLTLQHPVEL 613

