

gi | 156151420 | ref | NP_079406.3 | MFAVHLMAFYFVSKLKEDQIKKVDRLFYHMLRSLDDLLDIMRRFRAEMEKGLAKDTPNTASVKMLPTFVRAIPDGESENGEFLSLDLGGSKFRVLKVVQVABEGKRVHVMESOFYPPNEIIRGNGTELFYVADCLADFMKTKDLKHKKLP 150
gi | 73953327 | ref | XP_546137.2 | MFAIHLMAFYFVSKLKEDQIKKVDRLFYHMLRSLDELLDIMARFQAEKQGLGKDTNPTASVKMLPTFVRAIPDGESENGEFLSLDLGGSKFRVLKVVQVABEGKRVHVMESOFYPPNEIIRGNGTELFYVADCLADFMKTKDLKHKKLP 150
gi | 21703836 | ref | NP_663394.1 | MFAVHLVAFYFVSKLKEDQIKKVDRLFYHMLRSLDELLDIMARFQAEKQGLGKDTNPTASVKMLPTFVRAIPDGESENGEFLSLDLGGSKFRVLKVVQVABEGKRVHVMESOFYPPNEIIRGNGTELFYVADCLADFMKTKDLKHKKLP 150
gi | 118092591 | ref | XP_421579.2 | MFAVHLLAFHFVAKLKEDQIKKVDRLFYHMLRSLDDVLLDMARFQAEKQGLGKDTNPTATVTKMLPTFVRAIPDGESENGEFLSLDLGGSKFRVLKVVQVABEGKRVHVMESOFYPPNEIIRGNGTELFYVADCLADFMKTKDLKHKKLP 150
gi | 169403990 | ref | NP_001108597.1 | MFAVHLLSFFVSKLKEDQIKKVDRLFYHMLRSLDDVLLDMARFQAEKQGLGKDTNPTATVTKMLPTFVRAIPDGESENGEFLSLDLGGSKFRVLKVVQVABEGKRVHVMESOFYPPNEIIRGNGTELFYVADCLADFMKTKDLKHKKLP 150
gi | 115435012 | ref | NP_001042264.1 | ----- 150
gi | 39971149 | ref | XP_366965.1 | ----- 150
gi | 85114646 | ref | XP_964736.1 | ----- 150
gi | 19114777 | ref | NP_593865.1 | ----- 150
gi | 6319809 | ref | NP_009890.1 | ----- 150
gi | 45199235 | ref | NP_986264.1 | ----- 150
gi | 50304581 | ref | XP_452246.1 | ----- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 156151420 | ref | NP_079406.3 | GLTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLTKAMRRHKMDVDLALVNDIVGIMMTCAYDDPYCEVGVIIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 73953327 | ref | XP_546137.2 | GLTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLTKAVKKHKDIDVDLILVNDIVGIMMTCAYDDPYCEVGVIIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 21703836 | ref | NP_663394.1 | GLTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLATAMKHKHDLVDLILVNDIVGIMMTCAYDDPYCEVGVIIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 118092591 | ref | XP_421579.2 | GFTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLNALQKHKDIDVDLILVNDIVGIMMTCYDDPRECEIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 169403990 | ref | NP_001108597.1 | GFTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLNALQKHKDIDVDLILVNDIVGIMMTCYDDPRECEIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 115435012 | ref | NP_001042264.1 | GFTFSPFCROTKLEEGVLLSWTKKFKARGVQDTDVVSRLLNALQKHKDIDVDLILVNDIVGIMMTCYDDPRECEIIGTGNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGLEDIRTEFDRELDLGLSLNPGKQLFEKMI SGL 300
gi | 39971149 | ref | XP_366965.1 | ----- 300
gi | 85114646 | ref | XP_964736.1 | ----- 300
gi | 19114777 | ref | NP_593865.1 | ----- 300
gi | 6319809 | ref | NP_009890.1 | ----- 300
gi | 45199235 | ref | NP_986264.1 | ----- 300
gi | 50304581 | ref | XP_452246.1 | ----- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi | 156151420 | ref | NP_079406.3 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 73953327 | ref | XP_546137.2 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 21703836 | ref | NP_663394.1 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 118092591 | ref | XP_421579.2 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 169403990 | ref | NP_001108597.1 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 115435012 | ref | NP_001042264.1 | YLGEVLRILLLKMAKAGLLPFGGKSSALHTKGGIETRHVAAMEKYKEGLANTREILVLDLGLPESADCIAVQHVCTIVSFRSANLCAAALAILTRLENKVKERLRITVGMGDTLYKIHPOYPKRLHKVVRRLVPSCDVRFLLSESGST 450
gi | 39971149 | ref | XP_366965.1 | ----- 450
gi | 85114646 | ref | XP_964736.1 | ----- 450
gi | 19114777 | ref | NP_593865.1 | ----- 450
gi | 6319809 | ref | NP_009890.1 | ----- 450
gi | 45199235 | ref | NP_986264.1 | ----- 450
gi | 50304581 | ref | XP_452246.1 | ----- 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi | 156151420 | ref | NP_079406.3 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVDVQAKMRAELEYGLKKKSHGLATVRLMPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 73953327 | ref | XP_546137.2 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVDVQAKMRAELEYGLKKRTHLMAVTKMLPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 21703836 | ref | NP_663394.1 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVGRDQAKMRAELEYGLKKKTHLMAVTKMLPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 118092591 | ref | XP_421579.2 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVGRDQAKMRAELEYGLKKRTHLMAVTKMLPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 169403990 | ref | NP_001108597.1 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVGRDQAKMRAELEYGLKKRTHLMAVTKMLPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 115435012 | ref | NP_001042264.1 | KGAAMVTAASRVQAQRKIDRVLALFQLTREOLVGRDQAKMRAELEYGLKKRTHLMAVTKMLPTVVCGLPDGTEKG-KFLALDLGGTNRVLLVLRIRSG-RRSRVMYKIFAIPLEIMQG--TGEELFDHIVQCIADFLDYMG----- 600
gi | 39971149 | ref | XP_366965.1 | ----- 600
gi | 85114646 | ref | XP_964736.1 | ----- 600
gi | 19114777 | ref | NP_593865.1 | ----- 600
gi | 6319809 | ref | NP_009890.1 | ----- 600
gi | 45199235 | ref | NP_986264.1 | ----- 600
gi | 50304581 | ref | XP_452246.1 | ----- 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

