

gi | 19921526 | ref | NP_609946.1 | ...MSGKNRKRRTASSSSSGEEPPDSEESR--LKDLEERDEFA-----SRLKKRDDRTRN----- 150
gi | 158299819 | ref | XP_319843.4 | -----CLLNMSKNTDRRSYSSESDSSDEER-----HRDLKERDEEFS-----KRRLQRDESNTRN----- 150
gi | 17531507 | ref | NP_497027.1 | ...MSVQFINDQLHSIVGIDRSICQVHALAKKASAPDLVEKLRDAGDFPIISPAIQSFADQLMSRMPRCATSARQGPITAEELAEQELNRLNRAVGVLEDEYSASSTTK-----KNVRRKRKSSSEDEEAP----- 150
gi | 30794426 | ref | NP_081263.1 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQEEDDEEAE-----V 150
gi | 47059171 | ref | NP_997661.1 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQE-----E 150
gi | 255982614 | ref | NP_003578.2 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQE-----E 150
gi | 108860675 | ref | NP_001035839.1 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQE-----E 150
gi | 76650576 | ref | XP_872459.1 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQE-----E 150
gi | 73972115 | ref | XP_856794.1 | MATPAGLERWVQDELHSLVGLSERHVAQFLICTAQRCSAEAEFFVQRLRDTLTLDLGGPARDPALKLWSKVPKRAVVEKPARAAEREARALLEK-----NRSYKLLDESE-----SGEEAVARGDSSLOKKR-----KRRKHLRKKHQE-----E 150
gi | 41053341 | ref | NP_956318.1 | MAN---LQHWVSDQLHDLGLSDRYVAQFMIGLVQKSSGGPQDFVSRLODGTITDIDQRTAFAPHELYDKPKKHVVEKPARAETRVMMEMERK-----NRYITLLEDES-----SGDGAAREGGKKEKSKERDKKKRHLRKKHQE-----E 150
gi | 22329903 | ref | NP_174527.2 | MASN---DLKTVVSDKLMMLLGLSQAQVNNVLIAMAKKTSPTLVLGELVDYGFSSGDTTRSPAEEIFAVRNPRTAGVNLNKKHBAEAMLVK-----KQYVALLDADDDDEVVVEKSSVSVSKSSD-----KRRKHLRKKHQE-----E 150
gi | 145360634 | ref | NP_181077.3 | MGSN---DLNTVWSDKLMVLLGFSQTAVVQVLIAMAKKTSPTLVLGELVRELVCEG---FSLSGDTRAFAEIIVARPRKTPGVNLLKQQAEEAAMLLK-----KQYVALLDADDDDEVVVEKSSVSVSKSSD-----KRRKHLRKKHQE-----E 150
gi | 115475958 | ref | NP_001061575.1 | MASDQQLRDVWSDKLMVLLGFSQTAVVQVLIAMAKKTSPTLVLGELVRELVCEG---FSLSGDTRAFAEIIVARPRKTPGVNLLKQQAEEAAMLLK-----KQYVALLDADDDDEVVVEKSSVSVSKSSD-----KRRKHLRKKHQE-----E 150
gi | 39972399 | ref | XP_367590.1 | ...MSNKKYAFVPMQDDEVPQKVKKSSKDRR-----DKKKESSSRSSRHSRHSRSPARESSSKHYRSRAK-----DRRDYDRHSRRDD-----KEDRWADDEPLTDDGADPEF----- 150
gi | 85099496 | ref | XP_960795.1 | ...MAS---KRYAFVPMQDDEPAAPSKSDRDKDRR-----DSKRRDKDRR---SRSPRRHKSRRPD---DSDSTRQSRSR---SPRKDDSR---DSRRD----- 150
gi | 6324338 | ref | NP_014408.1 | ...MSS---ITSETGKRR-----VKRTIEVTRQNDN-----AVRIEPLSSIGEEEDKEAK-----DKNSALILK----- 150
gi | 45188160 | ref | NP_984383.1 | ...MDDP---DVVGTGKRR-----IKRKFDEIEQDIRAPTAVERNIGSEHGAGATEEY-----GTTDPAIMQ----- 150
gi | 50310679 | ref | XP_455361.1 | ...MGTSGDENGTGLGSGQRR-----AKRTYESTELVYNNAN---TNSFSPADQVLDSSPPSLK-----DGKAHYSVN----- 150



gi | 19921526 | ref | NP_609946.1 | ...VVSTGGRRRAIEATKRLKLEHEDRDKIVP-----HIRLQSRROYLEKRRKDDKVALEADILDD---EYLFDESVLTKREKEREYKQOLLNIAKEHEKAR 300
gi | 158299819 | ref | XP_319843.4 | ...VAASSDKR---GADAAKRLRLTEADREKLLP-----ELRQSRROYLEKREKDDKVALEADIRDD---EYLFPEAETTERERRDRHKKRLLQIAKDHAKAR 300
gi | 17531507 | ref | NP_497027.1 | ...IKASKPKGSVKPKSDDSESDIEAMEAKLDADTAERDALAARINKKEKDKTRNVME-----KRDNDKDKEGSSMDKLRRESROYLAKRKKVVKLEBAIVHDD---QTLFAREKLTREKADMEYKRVLEVYKAKHGKAG 300
gi | 30794426 | ref | NP_081263.1 | ESGKRRKAGGSKSPTEKPKASEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 47059171 | ref | NP_997661.1 | ESGKRRKAGGSKSPTEKPKASEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 255982614 | ref | NP_003578.2 | EKGKKTGGSKQQLTEKPESEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 108860675 | ref | NP_001035839.1 | EKGKKTGGSKQQLTEKPESEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 76650576 | ref | XP_872459.1 | EKGKKTGGSKQQLTEKPESEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 73972115 | ref | XP_856794.1 | EKGKKTGGSKQQLTEKPESEDEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 41053341 | ref | NP_956318.1 | KSITFPKDEPKKAGKE---DEEIEEWEWERTERERLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 22329903 | ref | NP_174527.2 | VREDS---RHVRRKVE---EDGSESEEE---RVRDQERELEEHLKDRDARTRKLTE---TLKSKKEEBAVRRANALEKDD---LYSLKRVSRROYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 145360634 | ref | NP_181077.3 | VREDK---RNVRRKVE---EDDTESEEE---RLRDQERELEEHLRERDARTRKLTE---TPKMSKKEE---EFVRRSQAMDKGD---IESLRKFSWQBYMKRKKQKVLKEDDLEDE---PYLFGDEKLTREHIREFRYKREIYDLKKTQEE 300
gi | 115475958 | ref | NP_001061575.1 | IKQDSGRNVKRTREVDDEDDGNDTDEEIRLQDLEERDFAFAERVRQDKDRTRNVLERSDKKAYEEAQKRLKMAEEDRKAMVPELRKKSRRREYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 39972399 | ref | XP_367590.1 | EQSASKRVKISHGDDAEDADLSDGAREELQAQRDAERAFAFNRKEDDGRSKKGGKEDLATSIR---RSLADDAKGRSEAVADLRERSROYLAKREREKLEDLEAELEADE---EYLFQDVELSRHERELKVKRRVRLDAREVRAAG 300
gi | 85099496 | ref | XP_960795.1 | ...REDPK-----MSDLRLKRYDYLKREBAEKLLAKKQVABET---AELRSVGLSEKKAFAFNRKLLALIEERLID 300
gi | 6324338 | ref | NP_014408.1 | ...RSRYDPNKVFNNTNGPEKNLKGQSGKSSKYN---DEKITSNN---ELTKKGLLGD---ENETKY 300
gi | 45188160 | ref | NP_984383.1 | ...ELRRARQVLRDREREKLDWAIRDALLLEEDVVKYGDWDLTERERREIGKRRQLVQIVREDAAY 300
gi | 50310679 | ref | XP_455361.1 | ...SKSMVEQKVLTKRQSLHVLVKDQLLEDDIKRYGWNLLVSEREIEISLKKLQLENEPKDY 300



gi | 19921526 | ref | NP_609946.1 | ...ELERI---QRVMP---QDLKKG---ERSEYVE---VDEFEKQPNSEKKNWEAEOLASARFHFCAKDAKA---EEVELLLDDG---IDFIC---ALTLDSGREKSS---RQPELTKERKRLTDEI---RRSLPVVFPFK 450
gi | 158299819 | ref | XP_319843.4 | ...ELERV---QRVMP---KDVKKG---EMEEYVE---VDERERMPHSEKKNWEAEOLASAVYGFSGKDAKERA---AQQVEVELLDDG---IDFVE---ALQMGACTKKDD---KPELTEAORCKMITEET---KTLPIVFPFK 450
gi | 17531507 | ref | NP_497027.1 | ...DVMKM---KRYHLP---DASTKC---LPSQYVE---DDEEDFRPGGDGAKWEEQLMASMLHLAGDAKRR---EQEFELLDEK---VDFIG---ALQMPGTN---EEVVE---TEAKKMIET---RKSLPVVAFRD 450
gi | 30794426 | ref | NP_081263.1 | EQEKLEAT---NRYHMP---KETRGC---PARTVDIV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---AAQQLQGDSEPS---GPPLSAQAC---QKESIQA---RRSLPVVFPFR 450
gi | 47059171 | ref | NP_997661.1 | EQEKLEAT---NRYHMP---KETRGC---PARATDIV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---AAQQLQGDSEPS---GPPLSAQAC---QKESIQA---RRSLPVVFPFR 450
gi | 255982614 | ref | NP_003578.2 | EQEKLEAT---NRYHMP---KETRGC---PARAVDLV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---ATQLQGDSEPS---APPTSTQAC---QKESIQA---RRSLPVVFPFR 450
gi | 108860675 | ref | NP_001035839.1 | EQEKLEAT---NRYHMP---KETRGC---PARAVDLV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---ATQLQGDSEPS---APPTSTQAC---QKESIQA---RRSLPVVFPFR 450
gi | 76650576 | ref | XP_872459.1 | EQEKLEAT---NRYHMP---EETRGC---PARTVDIV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---ATQLQGDSEPS---APPAPTQAC---QKESIQA---RRSLPVVFPFR 450
gi | 73972115 | ref | XP_856794.1 | EQEKLEAT---NRYHMP---EETRGC---PSRAVDLV---EES---GAPGEE---RRWEEARLGAASLKFPGARDAAS---QEPKYQLVLEEBEETIEFVR---ATQLQGDSEPS---GPPSPQAC---QKESVQA---RRSLPVVFPFR 450
gi | 41053341 | ref | NP_956318.1 | AKEQEERK---NRYMP---EEKNKSS---IPQKMDLLE---FEETPREGGGEGRWEEARVATATLQFARGQERERRIKEEQERYQLILEEEMITFVSTAITMKTGLSEKE---SEPQSQAQKQSIQEV---RRSLPIFVYRD 450
gi | 22329903 | ref | NP_174527.2 | DNVEYRIPDAVDQGE---GGVDQEKRFVAVQRYRDLSTEKMNPFPAEQEAWEDHIGKATLKFQAKN---KQA---SDDYQVFEDEG---INFIK---ESVMAGENYEDAM---DAKQSGDQLAEKTALEEL---QVRRSLPIVYTRD 450
gi | 145360634 | ref | NP_181077.3 | DNVEYRIPDAVDQGE---GGVDQEKRFVAVQRYRDMGSAEKMNPFPAEQEAWEDHIGKATLKFQAKN---KEV---SDNYEVEFDEG---IDFIK---ASVLGADNYEDAM---HAKP---SDSAGKSAFHM---EDRKALPIVYTRD 450
gi | 115475958 | ref | NP_001061575.1 | DVDVAYKMPPEAMDG---DSVNQEKRFVAVQRYRDKPARDKMNPFPAEQEAWEDHIGKATLKFQAKN---KQV---SDDYQVFEDEG---IDFIK---SSVLEGTIHEDE---DQEDIDKMLKRELHSLNLDKERTKLEPIVYTRD 450
gi | 39972399 | ref | XP_367590.1 | DHRDGYMPEDYIIKGGKIDRKKED---ALYKRYVVERDEYQGEKVFVEHEEWEEREAQAKAQIK---VAERD---BAG---IDYVMDDEYIYQWRD---RLPGEKVLQGEVLYLQAOIDAAREKRLSMOET---RKSLPIVYTRD 450
gi | 85099496 | ref | XP_960795.1 | DYDGYRIPDQYGI---DTKKKEE---ALYQRYVVERDEYQGEKVFVEHEEWEEREAQAKAQIK---TASGERE---DGGEDYVFLDDE---AINFVRDAAAKFIQPTDGLPEQIRLKEKTEAAREAKSIQEV---RKSLPIVYTRD 450
gi | 6324338 | ref | NP_014408.1 | ASS---NSKFNVEV---KIKN---AKEIDKINR---WEMWEEQOLRNAMAGQSDHPDITILE---GSDKYVFDLDDTDAMDYNEEDLLPEEKLYQ---EARLAQALETEKRIITQEA---RKLPVYVYKD 450
gi | 45188160 | ref | NP_984383.1 | AAA---ERRFHPGGET---VVAA---TARQEKSS---WEEQVQKVARAG---RSDIIEVE---GSEQYFVLDSDRSVDFI---EETELAPE---RV---EKQLEQLEKEIKRVASIQET---RRQLPVVYVYRD 450
gi | 50310679 | ref | XP_455361.1 | AENQDTSGEFKMDEV---ASKKQL---LAKLRNKTDRVNNWEEQMKKSVKAD---ADBIKVK---DSDNYEVEFVDEPSMDFDITDILEPVE---DGRLEAELEQKINKMSIKET---RKSLPVVYVYRD 450



