

gi | 22296589 | ref | NP_083179.1 | MDNKAMYLH-IVS DRDNGS IFEEPPDGRSLSKLNLCEDG--PCHKRRAGGCC TOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESLRDMQLRLLQAPLOADLFEQVWVKVDALONQTD SLLALAGLVG 150
gi | 109501819 | ref | XP_224299.4 | MDNKAMYLH-IVS DRDNGS IFEEPPDGRSLSKLNLCEDG--PCHKRRAGGCC TOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESFRDMQLRLLQAPLOADLFEQVWVKVDALONQTD SLLALAGLVG 150
gi | 47271477 | ref | NP_776194.2 | MENKAMYLH-IVS DCDTSS ICEDSF DGRSLSKLNLCEDG--PCHKRRASICCTOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESFRDLQLRLLQAPLOADLFEQVWVKVDALONQSD SLLALAGAVC 150
gi | 114619471 | ref | XP_519680.2 | MENKAMYLH-IVS DCDTSS ICEDSF DGRSLSKLNLCEDG--PCHKRRASICCTOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESFRDLQLRLLQAPLOADLFEQVWVKVDALONQSD SLLALAGAVC 150
gi | 73993667 | ref | XP_543223.2 | MENKAMYLH-IVS DRD TSS IFEEPPDGRSLSKLNLCEDG--PCHKRRAGGCC TOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESFRDLQLRLLQAPLOADLFEQVWVKVDALONQSD SLLALAGAVC 150
gi | 156523110 | ref | NP_001095969.1 | MENKAMYLH-IVS DRD SSS IFEEPPDGRSLSKLNLCEDG--PCHKGRAGGCC TOLGSL SALKHAVLGLYLLVFLILVGFIFILAVSRPRSSPDDLKALTRNVNRLNESFRDLQLRLLQAPLOADLFEQVWKAHDALONQSD SLLALAGAVC 150
gi | 118089138 | ref | XP_001234366.1 | MENKAMYLH-IVS ERENGS IFEEPPDGRSLSKLNLCEDG--AGHRMKAAGRCGRSLAALKYAVLGLYLLVFLILVGFIFILAVSRPOTSPEDLKALMGNVNRNLNESFRDLQLRLLQAPLOADLFEQVWVMDHWRLLQD LONQSD SLLFLMIGSLG 150
gi | 71834524 | ref | NP_001025361.1 | MENRAMYLTTIHEDRENS FVEESYDGMNLSKLNLCERVNSTKVRRTDNRRCGLDLSL SIKYAVLSYILVLLIFPG-LCIAVSSKSHAWRREALLLENVTRLGEQSETLOMSLSLIPSSD LLENWKLSELFHHTQLRLLGLLTC 150



gi | 22296589 | ref | NP_083179.1 | RLEGTLWGLHAQAQTEQATALLRDRTGQOOSD SAQLELYQLQVESNR SOLLRRHAGLLDGLARRVGVGLGEEADVGGALRGLNHSLSYDVALHSTWLDLQVLVSNASADTRRMRLVHMDMEMQLKQELATLVNVTEDLR LKDWHEHSIA 300
gi | 109501819 | ref | XP_224299.4 | RLEGTLWGLHAQAQTEQAVALLRDRTGQOOSD SAQLELYQLQVESNR SOLLRRHAGLLDGLARRVGVGLGEEADVGGALRGLNHSLSYDVALHSTWLDLQVLVSNASADTRRMRLVHMDMEMQLKQELATLVNVTEDLR LKDWHEHSIA 300
gi | 47271477 | ref | NP_776194.2 | RLEGALWGLQAQAVOTEQAVALLRDRTGQOOSD TAQLELYQLQVESNS OLLRRHAGLLDGLARRVGLGEEADVGGVLRGLNHSLSYDVALHSTRLODLRVLVSNASEDRRLRLAHVGMELQKQELAMLNAVTEDLR LKDWHEHSIA 300
gi | 114619471 | ref | XP_519680.2 | RLEGALWGLQAQAVOTEQAVALLRDRTGQOOSD TAQLELYQLQVESNS OLLRRHAGLLDGLARRVGLGEEADVGGVLRGLNHSLSYDVALHSTRLODLRVLVSNASEDRRLRLAHVGMELQKQELAMLNAVTEDLR LKDWHEHSIA 300
gi | 73993667 | ref | XP_543223.2 | RLEGALWGLQAQAAQTEQAVALLRDRTGQOOSD AAQLELYQLQVESNRTOLLRRHAGLLDGLARRVGVGLGEEADVGGALRGLNHSLSYDVALHSTRLODLQVLVSNASEDARRMRLVHMGELQKQELAVLNTVTEDLR LKDWHEHSIA 300
gi | 156523110 | ref | NP_001095969.1 | RLEGALWGLQAQAAQTEQAVALLRERAAQOOSD AAQLELYQLQVDSNR SOLLRRHAGLLDGLARRVGA LDELADVGGALRGLNHSLSYDVALQCTRLRDLRVLVSNASEDARRLRLAHVGMELQKQELAVLNTVTEDLR LKDWHEHSIA 300
gi | 118089138 | ref | XP_001234366.1 | KLEGLLWSLTQAGQINRAVANLWDSLAAQGDAAQOELYKLSVGGNNSRLLQHHEHLLSHLGSRLGLESEVAVSQAADAMNRF SYDVNHHSTRLODLVLSNATEDARRMRLIHIAMEEQLKHELA TLGNVTEDLR LKDWHEHSIA 300
gi | 71834524 | ref | NP_001025361.1 | GLERDIKDLQAFASHTDSVAQLWDLHLSMISHSARNSTHLGDLASLAGSIREQDALLKTMVGNVEIQLQERLEDMGWLTQLNHS LGGDVSLEHQIKIYELQEKIVNVTHTLGMKILQHLEDLRNEIQVLVNVVADLR LKDWHEHSMA 300



gi | 22296589 | ref | NP_083179.1 | LRNIILAKGPPGPKGDQCNQEKEGKPGSPGLPGSRGLPGERGDPGLPGPKG-----DDGKLGATGPMGMRGFKGDRGPKGEGKERGERAGDMD---FTMIRLVN GSGPHQGRVEVFHDDRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 109501819 | ref | XP_224299.4 | LRNIILAKGPPGPKGDQCNQEKEGKPGSPGLPGSRGLPGERGDPGMPPGPKG-----DDGKLGATGPMGMRGFKGDRGPKGEGKERGERAGDMD---FTMIRLVN GSGPHQGRVEVFHDDRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 47271477 | ref | NP_776194.2 | LRNISLAKGPPGPKGDQCGDEKGEGRPGIPLGLRGLPGERGTPGLPGPKG-----DDGKLGATGPMGMRGFKGDRGPKGEGKERGERAGDASGVEAPMMIRLVN GSGPHEGRVEVFHDDRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 114619471 | ref | XP_519680.2 | LRNISLAKGPPGPKGDQCGDEKGEGRPGIPLGLRGLPGERGTPGLPGPKG-----DDGKLGATGPMGMRGFKGDRGPKGEGKERGERAGDASGVEAPMMIRLVN GSGPHEGRVEVFHDDRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 73993667 | ref | XP_543223.2 | LRNIILAKGPPGPKGDQCGDEKGEGRPGIPLGLRGLPGERGTPGLPGPKG-----DEGKMGATGPMGIRGFKGDRGPKGEGKERGERAGDASGVEA-VMIRLVN GSGPHEGRVEVFHERRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 156523110 | ref | NP_001095969.1 | LRNIILAKGPPGPKGDQPDAGKEGEPGIPGLPGLRGLPGERGTPGLPGPKG-----DEGKMGATGPMGMRGFKGDRGPKGEGKERGERAGDASGVEA-VMVRLV N GSGPHEGRVEVFHERRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 118089138 | ref | XP_001234366.1 | LKNISIIIRGPPGPKGDPGHGEMGEGPGRPGPGLRGMPPGERGLPGPRGLK-----DKGDFGMPGAGMRGFKGDRGPKGEGKERGERAGDASGVEA-VMVRLV N GSGPHEGRVEVFHERRWTVCDDGWDKDKDGDVVCRLMGFRGVVE 450
gi | 71834524 | ref | NP_001025361.1 | LKNLTIIFGPPGPKGEGDVGPLGPDGIPGWIGRGLTGEKGVQGRGLAGRNQDGHNGDKGEVGPPEGKGVRRGERGPKGEGKERGERAGDASGVEA-VMVRLV N GSGPHEGRVEVFHERRWTVCDDVVDIKDGDVVCRLMGFRGAK 450



gi | 22296589 | ref | NP_083179.1 | VVRTARFGGTR IWMDDVNCCKGTESSIFHCQFSKWGVTCGHAEDAGVTCVTP 504
gi | 109501819 | ref | XP_224299.4 | VVRTARFGGTR IWMDDVNCCKGTESSIFHCQFSKWGVTCGHAEDAGVTCAL 504
gi | 47271477 | ref | NP_776194.2 | VVRTARFGGTR IWMDDVACKGTEETIFRCFSFKWGVTCGHAEDASVTCNRH 504
gi | 114619471 | ref | XP_519680.2 | VVRTARFGGTR IWMDDVACKGTEETIFRCFSFKWGVTCGHAEDASVTCNRH 504
gi | 73993667 | ref | XP_543223.2 | VVRTARFGGTR IWMDDVACKGTEETIFRCFSFKWGVTCGHAEDAGVTCNRH 504
gi | 156523110 | ref | NP_001095969.1 | VVRTARFGGTR IWMDDVACKGTEETIFRCFSFKWGVTCGHAEDAGVTCNRH 504
gi | 118089138 | ref | XP_001234366.1 | VVRMARFGGTR IWMDDVSCCKGTESSLLLCFSFKWGVTCGHAEDAGVTCVTP 504
gi | 71834524 | ref | NP_001025361.1 | LHKIGRFGGTGLIWMDDVACKGTESSIDLCKFSKWGVTCGHVEDAGVTCNV- 504

