

gi|45383740|ref|NP_034462.1| MSIFCLAAFYFLLMVG-GVMADNPERYSANLSHSHMEDFTPPPGTEINFLGTHRRPPNLALPSNGSMHGYPQOQKITTAFKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 149
gi|7549758|ref|NP_036682.1| MGVLCLLASFWLALVG-GAIADNAERYSANLSHSHVEDFTPPPGTEFDLGLTTLRPPNLALPSNGSMHGYPQOQKITTAFKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 149
gi|4503465|ref|NP_001948.1| METLCLRASFWLALVG-CVISDNPERYSANLSHSHVEDFTPPPGTEFDLGLTTLRPPNLALPSNGSMHNYCPQOQKITTAFAKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 149
gi|114596313|ref|XP_001149597.1| METLCLRASFWLALVG-CVISDNPERYSANLSHSHVEDFTPPPGTEFDLGLTTLRPPNLALPSNGSMHNYCPQOQKITTAFAKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 149
gi|73977858|ref|XP_853465.1| METFCLKVTFFVALVG-YVIGDHPESYSTNLSPTVD-FTTFHGTELSFLVTTHRRPNTLALPSNGSMHYSYCPQOQKITTAFAKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 148
gi|27805817|ref|NP_776733.1| METFWLRLSFVALVG-GVISDNPERYSANLSHSHVEDFTPPPGTEFDLGLTTLRPPNLALPSNGSMHNYCPQOQKITTAFAKYINTVISCTIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 149
gi|45383868|ref|NP_989450.1| MBALVLRVSSLLLLL-GFVLCSSDKYALNNSDVGIYLPSSSGTESLLPTTRRP-----VSNQIVK--CSQOIKLAEIFKYINTVISCAIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 143
gi|150832510|ref|NP_001092915.1| MAITLQLFLMLAVLACGLCLINGTEEAQDALYPNSTSTKTNVHKGFQPTTKDAS---VFNMKHPKRDPSIKLYFKYINTVISCAIFIVGMVGNATLLRIIYONKCMRNGPNALIASLALGDLIYVVIDLPIVFKLLAGRWPFD 146
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|45383740|ref|NP_034462.1| HNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLIATIEIVSIWILSFILAIPEAIGFVMVPEYKGEHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 299
gi|7549758|ref|NP_036682.1| HNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLIATIEIVSIWILSFILAIPEAIGFVMVPEYKGEHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 299
gi|4503465|ref|NP_001948.1| HNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLVTAIEIVSIWILSFILAIPEAIGFVMVPEYKGEHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 299
gi|114596313|ref|XP_001149597.1| HNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLVTAIEIVSIWILSFILAIPEAIGFVMVPEYKGEHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 299
gi|73977858|ref|XP_853465.1| HNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLIATIEIVSIWILSFILAIPEAIGFVMVPEYKGEHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 298
gi|27805817|ref|NP_776733.1| QNDGCVFLCKLFPFLQKSSVGIIVLNLCAVSDRYRAVASWSRVGGIGIPLVTAIEIVSIWILSFILAIPEAIGFVMVPEYKGAHRHTCMLNATSKFMFEYQDVKDWWLFGFYFCMPLVCTAIFYTLMTCEMLNRRNGSLRIALSEHLK 299
gi|45383868|ref|NP_989450.1| DSEFGQFLCKFLPFIQKASVGIIVLNLCAVSDRYRAVASWSRVGGIGIPMTAIEIVSIWILSFILAIPEAIGFVAVPFRYKDSYVVCMLNPNKFMFLFYKDAKDWLFGFYFCMPLACTAIFYTLMTCEMLNRRNSLRIALSEHLK 293
gi|150832510|ref|NP_001092915.1| DSSFGLFLCKLVPFLQKASVGIIVLNLCAVSDRYRAVASWSRVGGVGPLLTAIEIVSIWILSIILAVPEAMVFNMTFTYNNQTRICMLKPEIDFMNFYVYKDWLFGFYFCPLACTAIFYTLMTCEMLHHRDGLRIALSEHLK 296
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|45383740|ref|NP_034462.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 427
gi|7549758|ref|NP_036682.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 426
gi|4503465|ref|NP_001948.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 427
gi|114596313|ref|XP_001149597.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 427
gi|73977858|ref|XP_853465.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 426
gi|27805817|ref|NP_776733.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMKNRCCELLSFLLLMDYIGINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLMTSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 427
gi|45383868|ref|NP_989450.1| QRREVAKIVFCLVVIFALCWFLHLRILKKNVYDEMPGRCELLSFLLLPLDYISINLATMNSCINPIALYFVSKKFKNCFOSCLCCCHQSKSLATSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 421
gi|150832510|ref|NP_001092915.1| QRREVAKAIFFCLVLIFALCWFLHLRILKKNVYVNDERRCDLLNFFLLMDYFGINLATVNSCINPILYFVSKKFKNCFOSCLCCCHQSKSLATSVPMNGTISIQWKNQEQNNHNTDRSSHKDSMN 422
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....

