

gi|56117838|ref|NP\_003003.3|-----MGIGRSE 7  
 gi|114619896|ref|XP\_001138037.1|-----MGSGRSV 7  
 gi|65301472|ref|NP\_038862.2|-----MGVGRSA 7  
 gi|109503534|ref|XP\_224987.4|MAAQCTILRYPSTHPEGRHMYEDPENFTDCFAELIGCAREIQGSAITRTPRTTRAAAPVQGAARSSPRLCEPGRHSAPRAPRLAPAPPPGAAAEIDPDRLGEORAAPSRITGPGTAPLSPEAPGSLQRDARVKAAWAAPSPSSMGVGRNA 150  
 gi|27806139|ref|NP\_776885.1|-----MGGR-- 5  
 gi|45383069|ref|NP\_989884.1|-----MGVGRSE 7  
 gi|134133216|ref|NP\_001077040.1|-----MKN 3  
 gi|45387599|ref|NP\_991148.1|-----MKS 3

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|56117838|ref|NP\_003003.3|GRRGAALGVLLALGAALLAVGSAEYDVVSFOSDIGPYQSGRFYTKPPQCVDPADLRLCHNVGYKKMVLPLNLEHETMAEVKQOASSWVPLLNKNCHAGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 157  
 gi|114619896|ref|XP\_001138037.1|GRRGAALGVLLALGAALLAVGSAEYDVVSFOSDIGPYQSGRFYTKPPQCVDPADLRLCHNVGYKKMVLPLNLEHETMAEVKQOASSWVPLLNKNCHAGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 157  
 gi|65301472|ref|NP\_038862.2|RGRGGAASGVLLALAAALLAAGSAEYDVVSFOSDIGSYQSGRFYTKPPQCVDPADLRLCHNVGYKKMVLPLNLEHETMAEVKQOASSWVPLLNKNCHMGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 157  
 gi|109503534|ref|XP\_224987.4|RGRGGAASGVLLALAAALLAAGSAEYDVVSFOSDIGSYQSGRFYTKPPQCVDPADLRLCHNVGYKKMVLPLNLEHETMAEVKQOASSWVPLLNKNCHMGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 300  
 gi|27806139|ref|NP\_776885.1|----WAAAGALLAALAAAGSAEYDVVSFOSDIGAYQSGRFYTKPPQCVDPADLRLCHNVGYKKMVLPLNLEHETMAEVKQOASSWVPLLNKNCHMGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 151  
 gi|45383069|ref|NP\_989884.1|GRRGAALGVLLALGVALLAVGSAEYDVVSFOSDLGYPYGGRFYTKPPQCVDPADLRLCHSVGYDKMVLPLNLDHETMAEVKHQOASSWVPLLNKNCHMGTQVFLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 157  
 gi|134133216|ref|NP\_001077040.1|LA-LKWLSTIAPFLCLPLNLALEDEYIWPDDSSDK-----HPPCVDPEDLRLCFNVGYGRMMLPLNLDHETMAEVKQOASSWVPLVHKACHKGTQVLLCSLFAPVCLDRPIYPCRWFCEAVRDSCEPVMQFFGFVWPEMLKC 141  
 gi|45387599|ref|NP\_991148.1|LASLSLWRIII--LILPLVSLGQFQYGNP--DNYDK-----PPQCVDPADLRLCQGVGYHMLLPLNLEHETMAEVKQOASSWVPLLNKNCHMGTQVLLCSLFAPVCLDRPIYPCRWLCEAVRDSCEPVMQFFGFVWPEMLKC 139

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi|56117838|ref|NP\_003003.3|DKFPEGDVCIAMTPPNATEASKPO---GTTVCPPCDNELKSEAIIEHLCASEFALRMKIKEVKKENGDKKIVP-KKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRKVKSQYLLTAIHKWDKKNKFEKFMKKMK 302  
 gi|114619896|ref|XP\_001138037.1|DKFPEGDVCIAMTPPNATEASKPO---GTTVCPPCDNELKSEAIIEHLCASEFALRMKIKEVKKENGDKKIVP-KKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRKVKSQYLLTAIHKWDKKNKFEKFMKKMK 302  
 gi|65301472|ref|NP\_038862.2|DKFPEGDVCIAMTPPNATEASKPO---GTTVCPPCDNELKSEAIIEHLCASEFALRMKIKEVKKENGDKKIVP-KKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRKVKSQYLLTAIHKWDKKNKFEKFMKKMK 302  
 gi|109503534|ref|XP\_224987.4|DKFPEGDVCIAMTPPNATEASKPO---GTTVCPPCDNELKSEAIIEHLCASEFALRMKIKEVKKER-VDEIVP-KKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRKVKSQYLLTAIHKWDKKNKFEKFMKKMK 444  
 gi|27806139|ref|NP\_776885.1|DKFPEGDVCIAMTPPNATEASKPO---GTTVCPPCDNELKSEAIIEHLCASEFALRMKIKEVKKENGDKKIVP-KKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRKVKSQYLLTAIHKWDKKNKFEKFMKKMK 296  
 gi|45383069|ref|NP\_989884.1|DQFPQDYVCIAMTPPNATEVSRPK---GTTVCPPCDNEMKSEAIIEHLCASEFALKMTIIEVKKENGDKVIIIP-RKRKALKLGPTRKKNLKKLVLLKNGADCPCHOLDNLSHHFLIMGRVKKVQHLLTAIYKWDKKNKFEKFMKKVK 302  
 gi|134133216|ref|NP\_001077040.1|DKFPLGVECISS--NATKSNETDLIAGGSSVCPACENEMKTDLILDQMCASEFAIKTKIIEVKKIDNLDKRVILQKRRKLVVRAKSMKODLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRVSVKQYVLLTAIHKWDKSNKFEKFMKKK 288  
 gi|45387599|ref|NP\_991148.1|DKFPPDDMCINAP--NDTISISEFN---GHPPVCPDNEKMDVILDHMCASEFAIKTKIIEVKKRENDKRVILQKRRKLVVRAKSMKODLKKLVLYLKNGADCPCHOLDNLSHHFLIMGRVSVKQYVLLTAIHKWDKSNREFKFMKKK 284

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi|56117838|ref|NP\_003003.3|NHECPTFQSVFK 314  
 gi|114619896|ref|XP\_001138037.1|NHECPTFQSVFK 314  
 gi|65301472|ref|NP\_038862.2|NHECPTFQSVFK 314  
 gi|109503534|ref|XP\_224987.4|NHECPTFQSVFK 456  
 gi|27806139|ref|NP\_776885.1|NHECPTFQSVFK 308  
 gi|45383069|ref|NP\_989884.1|APDCPTFQSVFK 314  
 gi|134133216|ref|NP\_001077040.1|NHECPSVDHVK 300  
 gi|45387599|ref|NP\_991148.1|SHKCPAYENVFK 296

