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gi|4507751|ref|NP_001062.1|-----150
gi|114672493|ref|XP_001150558.1|-----150
gi|83716002|ref|NP_001032905.1|-----150
gi|57100565|ref|XP_533309.1|-----150
gi|73961995|ref|XP_849163.1|-----150
gi|46358062|ref|NP_067263.1|-----150
gi|9507217|ref|NP_062052.1|-----150
gi|118086858|ref|XP_419147.2|-----150
gi|18859519|ref|NP_571835.1|-----150
gi|30690081|ref|NP_195183.2|-----150
gi|15227185|ref|NP_179230.1|-----150
gi|115485535|ref|NP_001067911.1|-----150
gi|115488458|ref|NP_001066716.1|-----150
gi|118781473|ref|XP_311491.3|-----150
gi|17137556|ref|NP_477367.1|-----150
gi|50302825|ref|XP_451349.1|-----150
gi|45188092|ref|NP_984315.1|-----150
gi|83578104|ref|NP_014717.2|-----150
gi|19115217|ref|NP_594305.1|-----150
gi|39944952|ref|XP_362013.1|-----150
gi|32405614|ref|XP_323420.1|-----150
gi|71993377|ref|NP_491532.3|-----150
gi|124505475|ref|XP_001351479.1|-----150
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MRCLQN-----SAKTLPLAFKS-----ALLPLS-----QRWFCKFSPKPSLITN-----

MTWPNKRYLLPSLLSIRTKSLKKRKENPPFHTNLSPSPQFPICSGGGERDTAAAAAALRRTRPGGARRGTDTSITLPLFLSFLTPQPPTPDPRPPSRFIRAASIPSRRLSESNRRICMLVAIVFRAGAYISRFSRHACQVAFVSGISCS
MPVPPNP-----HSPGLSGKN-----PMPVPMSDGNG-----YARR-----ATHFFRKSNIILLRLOS-----

-----MQQPLHARFATRAVKNPMTLEKERQLTDSKVHTLVAAATGVAATKL-----

-----MMEQVCDV-----

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gi|4507751|ref|NP_001062.1|-----300
gi|114672493|ref|XP_001150558.1|-----300
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gi|57100565|ref|XP_533309.1|-----300
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gi|9507217|ref|NP_062052.1|-----300
gi|118086858|ref|XP_419147.2|-----300
gi|18859519|ref|NP_571835.1|-----300
gi|30690081|ref|NP_195183.2|-----300
gi|15227185|ref|NP_179230.1|-----300
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gi|115488458|ref|NP_001066716.1|-----300
gi|118781473|ref|XP_311491.3|-----300
gi|17137556|ref|NP_477367.1|-----300
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gi|45188092|ref|NP_984315.1|-----300
gi|83578104|ref|NP_014717.2|-----300
gi|19115217|ref|NP_594305.1|-----300
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gi|32405614|ref|XP_323420.1|-----300
gi|71993377|ref|NP_491532.3|-----300
gi|124505475|ref|XP_001351479.1|-----300
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-----IFKVISISTMANTLNGNVIMTKPKCSFYQVVVAATKEMGIGKDGKLPWNLPDLDKFFKDLTLSTSDSAKKNVAVMGRKTWESIPKKYRPLSGRLNVVLSRSGFDIANTENVVTCSEIDSALDLLAAPP-----

-----MATTTLNDSVT--TLASEPQRTYQVVVAATKEMGIGKDGKLPWNLPDLDKFFKDLTLSTSDSAKKNVAVMGRKTWESIPKKYRPLSGRLNVVLSRSGFDIANTENVVTCSEIDSALDLLAAPP-----

APISQFRRPQSLEGSRLRCCFIQTRLIAMATILS-NGVSONGPQRNYQVVVAATKEMGIGKDGKLPWLLGDLKFFKELVITLADPVKKNVAVMGRKTWESILPKARPLPGRLNIIILTRSGSFEFATVENVVICGSMNSALELLSSTP
-----LKYLEFRDKLNFSRPHKSVIVMSINVN-NGNSEENLKRSYQVVVAATKEMGIGKDGKLPWLLGDLKFFKELVITLADPVKKNVAVMGRKTWESILPKARPLPGRLNIIILTRSGSFEFATAENVVICGSLDSALQLLATP-----

-----LLIVKSLLYKGVQVQVLLDPAARNFVEKEDLALGVNVVNNADDWKNWDGLECPITHIELRRWAHLLLIAPLSANIMAKMANGLCNLLTSLIRAWAPLKPILLAPAMNLMWLNPIIQEHLSAISRIYKNSSEFIMPIEKVLACGDIGM-----

-----FDIYAICACCKVEISKNEGKKNEVFNNYTRFGLGNKGVLPWKCNSLDMKYFCAVLYVNESKYEKLYKRCXYLNKEIVDNDVNDMPNSKKLQNVVVMGRTSWESIPKKFKPLSNKINVILSRILKKE-DFDEDVLIINKVEDLIVLLG--------

