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                                 * :.**:******:: ***  *.*:****::****. **::***:::****** ****   :.***::.::*  ::***:.*:******     *  .  .  :: ::.* .  ***:: :: *:*:. .:  :**.*.:.  .*  *:
gi|112789562|ref|NP_005522.2| ----MGKKYKNIVLLKGLEVINDYHFRMVKSLLSNDLKLNLKMREEYDKIQIADLMEEKFRGDAGLGKLIKIFEDIPTLEDLAETLKKEKLKVKG--PALSRKRKKEVDATSPAPSTSSTVKTEGAEATPGAQKRKKSTKEKAGPKGSKV   144
gi|114560530|ref|XP_513913.2| MSVKMEKKYKNIVLLKGLEVINDYHFRMVKSLLSNDLKLNLKMREEYDKIQIADLMEEKFRGDAGLGKLIQIFKDIPTLEDLAETLKKEKLKVKG--PALSRKRKKEVDATSPAPSTSSTVKTEGAEATPGAQKRKKSTKEKAGPKGSKV   148
gi|119889054|ref|XP_869021.2| ----MGNDYKKIVLLKGFQHINDKCFNMIKSLLAHDLKLTRKMQDEYDRVKIADLMELKFRGPDCVDKLIELVKEIDEIKDLAKVLRKEKLKVIKKNKAKGATPAQNQNTSSLGQSTSTANEALGSESVKDTPVKKKKTTKTNESKRRKL   146
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                :*:*:* *..:  .:.:: *   :*: . * *..***:: . .*.     :*:::      :   *:*.            ::.**:::                 : . *:: .:: ::.
gi|112789562|ref|NP_005522.2| SEEQTQPPSPAGAGMSTAMGRSPSPKTSLSAPPNSSSTENPKTVAKCQVTPRRNVLQKRPVIVKVLSTTKPFEYETPEMEKKIMFHATVATQTQFFHVKVLNTSLKEKFNGKKIIIISDYLEYDSLLEVNEESTVSEAGPNQTFEVPNKI   294
gi|114560530|ref|XP_513913.2| SEKQTQPPSPAGAGMSTAMGRSPSPKTSLSAPPNTSSTENPKTVAKCQVTPRRNVLQKGPVIVKVLSTTKPFEYETPEMEKKIMFHATVATQTQFFHVKVLNTSLKEKFNGKKIIIISDYLEYDSLLEVNEKSTVSEAGPNQTFEVPNKI   298
gi|119889054|ref|XP_869021.2| TEEQSQLPGSSVMSIESTKGLLQTPQMPPSKPSSSSSTKKKSDTATKPKDVKRKIIPYNQSQLPGTSATS-------------LYPTVSSD----------------QRTPIVLPKEFSNFS-------------------------   239
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|112789562|ref|NP_005522.2| INRAKETLKIDILHKQASGNIVYGVFMLHKKTVNQKTTIYEIQDDRGKMDVVGTGQCHNIPCEEGDKLQLFCFRLRKKNQMSKLISEMHSFIQIKKKTNPRNNDPKSMKLPQEQRQLPYPSEASTTFPESHLRTPQMPPTTPSSSFFTKK   444
gi|114560530|ref|XP_513913.2| INRAKETLKIDILHKQASGNIVYGVFMLHKKTVNQKTTIYEIQDDRGKMDVVGTGQCHNIPCEEGDKLQLFCFRLRKKNQMSKLISEMHSFIQIKKKPNPRNNDPKSMKLPQEQSQLPNPSEASTTFPESHLRTPQMPPTTPSSSFFTKK   448
gi|119889054|ref|XP_869021.2| ---------------------------IKKEENAHLSVGKIED-------------------------------------------------------MTTRTADPR-MKLSLEQSQVLGIPAYSTIPTENCLQTPQKLPPTTSSSSSTKK   307
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|112789562|ref|NP_005522.2| SEDTISKMNDFMRMQILKEGSHFPGPFMTSIGPAESHPHTPQMPPSTPSSSFLTTLKPRLKTEPEEVSIEDSAQSDLKEVMVLNATESFVYEPKEQKKMFHATVATENEVFRVKVFNIDLKEKFTPKKIIAIANYVCRNGFLEVYPFTLV   594
gi|114560530|ref|XP_513913.2| SEDTISKMNDFMRMQILKEESHFPGPFMTSIGPAESHPHTPQMPPSTPSSSFLTTLKPRLKTEPEEVSIEDSAQSDLKEVMVLNATESFVYEPKEQKKMFHATVATENEVFRVKVFNIDLKEKFTPKKIIAIANYVCRNGFLEVYPFTLV   598
gi|119889054|ref|XP_869021.2| ------------------------------------------------------------PRLKSVPKEASREEGFQRGPKEVMVLKATEPFTYDVIGGKRMFHATVATESQFFQVKIFNAALKEKFIPNKAIAISDYIGRNGFLEVFNVISV   400
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

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gi|112789562|ref|NP_005522.2| ADVNADRNMEIPKGLIRSASVTPKINQLCSQTKGSFVNGVFEVHKKNVRGEFTYYEIQDNTGKMEVVVHG-RLTTINCEEGDKLKLTCFELAPKSGNTGELRSVIHSHIKVIKTRKNKKDILNPDSSMETSPDFFF   729
gi|114560530|ref|XP_513913.2| VDVNADRNMEIPKGLIRSASVTPKINQLCSQTKGSFVNGVFEVHKKNVRGEFTYYEIQDNTGKMEVVVHG-RLTTINCEEGDKLKLTCFELAPKSGNTGELRSVIHSHIKVIKTRKNKKDILNPDSSMETSPDFFF   733
gi|119889054|ref|XP_869021.2| SDVKPDRKMEISKSLIQKAKATPKISHLYLQDLGTFVNGVFVVHKKSVYNEFIYYEIKDDTGVMEVVVYGQRLTSVNCDEGDRLTLVCFELG-ESGPKRQLRSVIHSFIKVTKVKQR--------TTTQS------   521
                                .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.....
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