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                                                                                                  :   :           ..**********:***** : ***:*            :.        .*    * : :.**   .*
gi|6754310|ref|NP_034644.1|      ------------------------------------------------------MGIPVGKSMLVLLISLAFALCCIAAYGPGETLCGGELVDTLQFVCSDRGFYFS------------RPSS----RANRRS--RGIVEECCFRSCD    76
gi|13937375|ref|NP_113699.1|     ------------------------------------------------------MGIPVGKSMLVLLISLAFALCCIAAYRPSETLCGGELVDTLQFVCSDRGFYFS------------RPSS----RANRRS--RGIVEECCFRSCD    76
gi|189083846|ref|NP_001121070.1| MVSPDPQIIVVAPETELASMQVQRTEDGVTIIQIFWVGRKGELLRRTPVSSAMQTPMGIPMGKSMLVLLTFLAFASCCIAAYRPSETLCGGELVDTLQFVCGDRGFYFS------------RPAS----RVSRRS--RGIVEECCFRSCD   132
gi|114635621|ref|XP_001153640.1| MVSPDPQIIVVAPETELASMQVQRTEDGVTIIQIFWVGRKGELLRRTPVSSAMQTPMGIPMGKSMLVLLTFLAFASCCIAAYRPSETLCGGELVDTLQFVCGDRGFYFS------------KASTPAAFPITRPL--RRVGQRCCRGGCP   136
gi|73982638|ref|XP_863200.1|     ------------------------------------------------------MGVPMGKSILVLLTFLALASCCFAAYRPSETLCGGELVDTLQFVCGDRGFYFSDAALLPPVGLPGRPAS----RVTRRSS-RGIVEECCFRSCD    89
gi|110350675|ref|NP_776512.2|    ------------------------------------------------------MGITAGKSVLVLLAFLAFASCCYAAYRPSETLCGGELVDTLQFVCGDRGFYFS------------RPSS----RINRRS--RGIVEECCFRSCD    76
gi|118091260|ref|XP_421026.2|    ------------------------------------------------------MCAAR-QILLLLLAFLAYALDSAAAYGTAETLCGGELVDTLQFVCGDRGFYFS------------RPVG----RNNRRIN-RGIVEECCFRSCD    76
gi|49227275|ref|NP_001001815.1|  ----------------------------------MEDQLKHHSVCHTCSRTDSFVNKVIKMFWSIRMPICILFLTLSAFEVASAETLCGGELVDALQFVCEDRGFYFS------------RPTS---RSNSRRSQNRGIVEECCFSSCN   100
gi|18858889|ref|NP_571508.1|     ----------------------------------MDD---YHVFCASCRKTEETRTTMR------SLIVFVLSLSMLISNVTAGETLCGGELVDTLQFVCGEDGFYIS------------RPN----RSNSRRPQ-RGIVEECCFRSCE    89
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                   *.  .* . :..*.: :.            :       *: ::: * :::: **:* :*.:* *:: :   : ::  .:    ****: ** : *.       :
gi|6754310|ref|NP_034644.1|      LALLETYCATPAKSERDVSTS--------QAVLPDDFPRYPVGKFFQYDTW-RQSAGRLRRGLPALLRARRGRMLAKELKEFREAKR-HRPLIVLPPKDPA-HGGASSEMSSNHQ   180
gi|13937375|ref|NP_113699.1|     LALLETYCATPAKSERDVSTS--------QAVLPDDFPRYPVGKFFKFDTW-RQSAGRLRRGLPALLRARRGRMLAKELEAFREAKR-HRPLIVLPPKDPA-HGGASSEMSSNHQ   180
gi|189083846|ref|NP_001121070.1| LALLETYCATPAKSERDVSTP--------PTVLPDNFPRYPVGKFFQYDTW-KQSTQRLRRGLPALLRARRGHVLAKELEAFREAKR-HRPLIALPTQDPA-HGGAPPEMASNRK   236
gi|114635621|ref|XP_001153640.1| PADLRDASAFPRRESRHLLTS--------PFPSQDNFPRYPVGKFFQYDTW-KQSTQRLRRGLPALLRARRGHMLAKELEAFREAKR-HRPLIALPTQDPA-HGGAPPEMASNRK   240
gi|73982638|ref|XP_863200.1|     LALLETYCATPAKSERDVSTP--------PTVLPDNFPRYPVGKFFQYDTW-KQSAQRLRRGLPALLRARRGRMLAKELEAFREAKR-HRPLIALPTHDPATHGGASPEASGNQK   194
gi|110350675|ref|NP_776512.2|    LALLETYCATPAKSERDVSAS--------TTVLPDDVTAYPVGKFFQYDIW-KQSTQRLRRGLPAFLRARRGRTLAKELEALREAKS-HRPLIALPTQDPATHGGASSKASSD--   179
gi|118091260|ref|XP_421026.2|    LALLETYCAKSVKSERDLSATSLAGL---PALNKESFQKPSHAKYSKYNVWQKKSSQRLQREVPGILRARRYRWQAEGLQAAEEARAMHRPLISLPSQRPP-APRASPEATGPQE   187
gi|49227275|ref|NP_001001815.1|  LALLEQYCAKPAKSERDVSATSLQVIPVMPALKQEVPRKHVTVKYSKYDVWQRKAAQRLRRGIPAILRAKKFRRQAERIKAQEQLLH-HRPLITLPSKLPP--ILLPTENYVSHK   212
gi|18858889|ref|NP_571508.1|     LHLLQQYCAKPVKSERDVSSTSLQVFPVSQALHKDT----INVKYSKYEVWQQKAAQRLRRGVPSILLARKFRRQMEKIQDEEQTSF-HRPLMTLPNRQPA--IVPHVQISTSRK   197
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.....
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