```
gi|33942112|ref|NP_898850.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|109493471|ref|XP_221343.4|     MRPLLQELGSQRVSGSVNGSERAGKVVSRGVQSSTRGAPHWPRTHVASTLHIPHPRPHPSLSARRLAPPLPASLGPPPLPPAGRAAWERRALGARGAGRAGRALSAVHTPLQLSGARGASARRRRPGTGRQSERFVRTPARDSARRRQPR   150
gi|64085377|ref|NP_006539.3|      ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|114590853|ref|XP_001151234.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|74003538|ref|XP_535832.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|119879735|ref|XP_597236.3|     ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|195972875|ref|NP_001108030.2| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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                                                                                                                                                                  :*:...   ***:******
gi|33942112|ref|NP_898850.1|      ------------------------------------------------------------MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK--VELHGKIMEVDYSVSKKLRSRRIQIRNI    88
gi|109493471|ref|XP_221343.4|     RVPASASAPGRAGPAAVGGARLRARVGAGAGAGGERRAAEAAGAPGAGPGEPRALGKTRMMNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGEHSLELHGKIMEVDYSVSKKLRSRKIQIRNI   300
gi|64085377|ref|NP_006539.3|      ------------------------------------------------------------MMNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK--VELHGKIMEVDYSVSKKLRSRKIQIRNI    89
gi|114590853|ref|XP_001151234.1| ------------------------------------------------------------MMNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK--VELHGKIMEVDYSVSKKLRSRKIQIRNI    89
gi|74003538|ref|XP_535832.2|     ------------------------------------------------------------------------------------------------------------------------------MDFGTS---RSRKIQIRNI    16
gi|119879735|ref|XP_597236.3|     ------------------------------------------------------------MMNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK--VELHGKIMEVDYSVSKKLRSRKIQIRNI    89
gi|195972875|ref|NP_001108030.2| ------------------------------------------------------------MNKLYVGNLSPSVTVEDLKQLFGERKLPVTDQVLLKSGYAFVDFPDQNWAIKAIETLSGK--VELHGKVIEVDYSVPKKLRSRKIQIRNI    88
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                  **********.***: ********************** *:**** *:***  : **:****:*** * : ::. *       : :***.  ** :     *: :* *****:****************************:********
gi|33942112|ref|NP_898850.1|      PPHLQWEVLDGLLAEYGTVENVEQVNTDTETAVVNVTYMTREEAKLAIEKLSGHQFEDYSFKISYIPDEEVSSPSPP-------HRAREQGHGPGSS-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   226
gi|109493471|ref|XP_221343.4|     PPHLQWEVLDGLLAEYGTVENVEQVNTDTETAVVNVTYMTREEAKVAIEKLSGHQFEDYSFKISYIPDEELSSPSPP-------HRAREQGHGPGSS-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   438
gi|64085377|ref|NP_006539.3|      PPHLQWEVLDGLLAQYGTVENVEQVNTDTETAVVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPPQRAQRGDHSSREQGHAPGGT-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   234
gi|114590853|ref|XP_001151234.1| PPHLQWEVLDGLLAQYGTVENVEQVNTDTETAVVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPPQRAQRGDHSSREQGHAPGGT-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   234
gi|74003538|ref|XP_535832.2|     PPHLQWEVLDGLLAQYGTVENVEQVNTDTETAVVNVTYATREEAKIAIEKLSGHQFENYSFKISYIPDEEVSSPTPPQRAQRGDHSSREQGHAPGGS-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   161
gi|119879735|ref|XP_597236.3|     PPHLQWEVLDGLLAQCGTVENVEQVNTDTETAVVNVTYATREEAKTAIEKLSGHQFENYSFKISYIPDEEVSSPSPPQRAQRGDHSSREQGHAPGGS-----SQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKEN   234
gi|195972875|ref|NP_001108030.2| PPHLQWEVLDSLLAQYGTVENVEQVNTDTETAVVNVTYSTKEEAKVAVEKLIEQTFEDYSFKVSYIMDMDAAAALPGTRNRRGGRTSREQDSQPGTSGSSLGSRQKQPDFPLRMLVPTQFVGAIIGKEGLTIKNITKQTQSKVDIHRKEN   238
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                  :******:***:**** * **:**::****** :**::*::********.:****************.:* ***********:******** *:*::***. **:*********:***: *:***:******.**************.*.
gi|33942112|ref|NP_898850.1|      SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEVPLKILAHNGFVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVRGTIEACANAEIEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLPPP   376
gi|109493471|ref|XP_221343.4|     SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEVPLKILAHNGFVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTIEACASAEMEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLPPP   588
gi|64085377|ref|NP_006539.3|      SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLSPP   384
gi|114590853|ref|XP_001151234.1| SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLSPP   384
gi|74003538|ref|XP_535832.2|     SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTVEACANAEVEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLPPP   311
gi|119879735|ref|XP_597236.3|     SGAAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTVEACANAEIEIMKKLREAFENDMLAVNQQANLIPGLNLSALGIFSTGLSVLPPP   384
gi|195972875|ref|NP_001108030.2| AGAAEKPITIHSTPEGCSTACHMIMDIMQKEAVDTKVTEDIPLKILAHNSLVGRLIGKEGRNLKKIEEDTETKITISSLQDLTIYNPERTIIVKGSIEACCRAEVEIMKKLREAYENDVAAINQQSNLIPGLSLSALGIFSTGLSVLPPA   388
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                                  ***** ** .*  *:**  **. :..**     . :.*:*:  **** * **************** *******************.***::**************..                    :: :*..: :*
gi|33942112|ref|NP_898850.1|      AGPRGVPPSPP--YHPFATHSGYFSSLYPHHHFGPFPHHHS-YPEQETVSLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKVS----------------------AKDHVSPAGSG---------   492
gi|109493471|ref|XP_221343.4|     AGPRGAPPSPP--YHPFATHSGYFSSLYPHHHFGPFPHHHS-YPEQETVSLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKT   735
gi|64085377|ref|NP_006539.3|      AGPRGAPPAAP--YHPFTTHSGYFSSLYPHHQFGPFPHHHS-YPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKT   531
gi|114590853|ref|XP_001151234.1| AGPRGAPPAAP--YHPFTTHSGYFSSLYPHHQFGPFPHHHS-YPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKT   531
gi|74003538|ref|XP_535832.2|     AGPRGAPPAPP--YHPFATHSGYFSSLYPPHQFGPFPHHHS-YPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKT   458
gi|119879735|ref|XP_597236.3|     AGPRGAPPAPP--YHPFATHSGYFSSLYPPHQFGPFPHHHS-YPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKT   531
gi|195972875|ref|NP_001108030.2| AGPRGIPPVPPTGYNPFLGHSSQLGGLYGVPPASGISHQHTQAPEQEVVYLFIPTQAVGAIIGKKGQHIKQLARFAGASIKIAPAESPDVTQRMVIITGPPEAQFKAQGRIFGKLKEENFFTAKEEVKLETHIKVPSSAAGRVIGKGGKT   538
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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gi|33942112|ref|NP_898850.1|      --------------SRADSSEVYSFLLLLVGVRLRPGCAFLCALPSLLRKVGRQSVPILLGIFGF-SS-   545
gi|109493471|ref|XP_221343.4|     VNELQNLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQAQKYPQGVAPQ-RSK   803
gi|64085377|ref|NP_006539.3|      VNELQNLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQ-RSK   599
gi|114590853|ref|XP_001151234.1|  VNELQNLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQ-RSK   599
gi|74003538|ref|XP_535832.2|      VNELQNLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQ-RSK   526
gi|119879735|ref|XP_597236.3|     VNELQNLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQ-RSK   599
gi|195972875|ref|NP_001108030.2|  VNELQNLTSAEVIVPRDQTPDENDEVFVKISGHFFASQTAQRKIREIIQQVKQQEQKHQQGAPTTPRSK   607
                                  .......760.......770.......780.......790.......800.......810.........
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