```
gi|50540036|ref|NP_001002483.1| ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPG-PQT   17
gi|83415189|ref|NP_001032751.1| ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPG-AQT   17
gi|30179900|ref|NP_005977.2|   ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPGGAQA   18
gi|117606322|ref|NP_033259.2|  ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPGGAQA   18
gi|76631951|ref|XP_875555.1|   ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPGGAQA   18
gi|73989544|ref|XP_849239.1|   ----------------------------------------------------------------------------------------------------MYSMMMETDLSSSGGAQA   18
gi|45383488|ref|NP_989664.1|   ----------------------------------------------------------------------------------------------------MYSMMMETDLHSPGGAPA   18
gi|17975569|ref|NP_524735.1|   MLTMESDMKGSLLHATMPPHHTSAALHGHAASPYSALAPLMNLGQSHLTHSQLSHHNHHHHMSAHIAASQSPNPLSSLQSSMANTLNGSQVGQQQQQQQQQSSPLHSSSELSPTQSSIGSHHMTSPVSHQQHTQQQQHGQQQMLGAGS  150
gi|158298957|ref|XP_319093.4|  ----------------------------------------------------------------------------------------------------
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                 .   *    ..                    :   **********************.:***************:** :**:**************:******************* * *:**.:.    .   ..
gi|50540036|ref|NP_001002483.1| NTN--PGQTGPNS-----------------GSKANQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRAMHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLGGAGGG----------VG  136
gi|83415189|ref|NP_001032751.1| NTN--TGHTGPNS-----------------GSKVNQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKLMSEAEKRPFIDEAKRLRAMHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLAGSGGGG------GVGLG  140
gi|30179900|ref|NP_005977.2|   PTN-LSGPAGAGGGGGG------GGGGGGGGGAKANQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLAAGAGGGGAAVAMGVGVG  160
gi|117606322|ref|NP_033259.2|  PTN-LSGPAGAGGGGGG------GGGGGGGGGTKANQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLAAGAGGGGAAVAMGVGVG  160
gi|76631951|ref|XP_875555.1|   PTN-LSGPAGAGGGGGG------GGG-----GSKANQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLAAGAGGG-----AAVAVG  150
gi|73989544|ref|XP_849239.1|   PTN-PLGPAGAGGGGGGGGGGGGGGGGGGGVAKASQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLAAGAGGGGAAVAMGVGVG  166
gi|45383488|ref|NP_989664.1|   PGGGLSGQSGAGGGGGG------GGGG----GGKAGQDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKVMSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLLK-KDKYSLAGGLLGAGPAAGGPP-AVGVGMG  156
gi|17975569|ref|NP_524735.1|   ALSSLTGGSSNNNNNSATAN-----------KNQQHADRVKRPMNAFMVWSRGQRRKMASDNPKMHNSEISKRLGAQWKDLSESEKRPFIDEAKRLRAVHMKEHPDYKYRPRRKTKTLTKTKEKYPMGGLMPGQTVGGGAPGEPVTPTRV  289
gi|158298957|ref|XP_319093.4|  -TGGLLGVNHNNNNTSKAA-------------QQNADRVKRPMNAFMVWSRGQRRKMASDNPKMHNSEISKRLGAQWKDLSETEKRPFIDEAKRLRAVHMKEHPDYKYRPRRKTKTLTKAKEKYPLG---VGSLLGAGQTNE------G  126
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                 .   . ..    .   .  :... *   . :     .:    .. . * :.    : .....           : :  : :   :                 : . * ** ..*     ..*   *.  .
gi|50540036|ref|NP_001002483.1| MS--PAGVGQRLESPGGHGSSASAGYAHMNGWANGTYSGQVAAAAAAAAMMQEAQLAYSQHPGSGS----------HHHHAHHHH--PHNPQPMHR---------YDMTALQYSPISNSQS--YMSASPSGYGGISYT-----------  249
gi|83415189|ref|NP_001032751.1| MG--AAGVGQRLESPVGHGGSTAASYAHMNGWTNGAYSGQVAAAAAAAAMMQEAQLAYGQHPGSGA----------HHHHGHHHH--PHNPQPMHR---------YEMTALQYSPLSNSQS--YMSASPSGYGGISYT-----------  253
gi|30179900|ref|NP_005977.2|   VG--AAAVGQRLESP---GGAAGGGYAHVNGWANGAYPGSVAAAAAAAAMMQEAQLAYGQHPGAGGAHPH----AHPAHPHPHHPHAHPHNPQPMHR---------YDMGALQYSPISNSQG--YMSASPSGYGGLPYGAAAAAAAAAGG  290
gi|117606322|ref|NP_033259.2|  VG--AAAVGQRLESP---GGAAGGGYAHVNGWANGAYPGSVAAAAAAAAMMQEAQLAYGQHPGAGGAHPH----AHPAHPHPHHPHAHPHNPQPMHR---------YDMGALQYSPISNSQG--YMSASPSGYGGIPYGAAAAAAAAAGG  290
gi|76631951|ref|XP_875555.1|   VG--AAAVGQRLESP---GGAAGGGYAHVNGWANGAYPGSVAAAAAAAAMMQEAQLAYGQHPGAGGAHPH----AHPAHPHAHHPHAHPHNPQPMHR---------YDMGALQYSPISNSQG--YMSASPSGYGGLPYG-------AAGG  273
gi|73989544|ref|XP_849239.1|   VGVGAAAVGQRLESP---GGAAGGGYAHVNGWANGAYPGSVAAAAAAAAMMQEAQLAYGQHPGAGGAHPHPHPHAHPAHPHPHHPHAHPHNPQPMHR---------YDMGALQYSPISNSQG--YMSASPSGYGGLPYGAAAAAAAAAGG  302
gi|45383488|ref|NP_989664.1|   VGVIPGGVGQRLESP---GGAAGGGYAHMNGWANGAYPGSVAAAAAAAAMMQEAQLAYGQHPGGGG---------HPHHPHPHHPH-HPHNPQPMHR---------YDMGALQYSPISNSQG--YVSASPSGYGALPYG---------SQ  273
gi|17975569|ref|NP_524735.1|   QG--QPGQNQSLNGS---GGSAAAAAAAAAAAAQQARQ-DMYQMNAPNGYMPNGYMMHADPAGAAAYQTS-----YMGQHYAAQRYDMGHMYNNGYA-------MYQTVSGGQTSPYGSS---LQQPGSPSPYGGSSLQQ----------  408
gi|158298957|ref|XP_319093.4|  SG--MRGSGSSTTLA---AQQAAAAAAAAAAAAANR---DMYHQMPPNGYMPNGYTMMHDPSSAAAYQSQQ---HYMSNYHHHHRYEMGQMAAAAAASGTTAGSLNSTVSGGQTSPYGGSGGGLQQPGS--PYS-TTIQQ----------  252
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                 .           ..  :  : .. .* :****   **  . : ..         *   *   .                 *  :   *: .
gi|50540036|ref|NP_001002483.1| QHQN----------SSVATPAAIGTLSSLVKSEPNI-SPPVTTHSRGPCPGDLREMISMYLPTGESGDP------SVQSRLHALPQHYQSTTAGVN-------------------------------------------------  328
gi|83415189|ref|NP_001032751.1| QHQN----------SSVASSGAIGALGSLVKSEPSV-SPPVNAHSRAPCSGDLREMISMYLPTAEAGDP------SVQSRLHAVPQHYQSSTTSVN-------------------------------------------------  332
gi|30179900|ref|NP_005977.2|   AHQN--SAVAAAAAAAAASSGALGALGSLVKSEPSG-SPPAPAHSRAPCPGDLREMISMYLPAGEGGDPAAAAAAAAQSRLHSLPQHYQGAGAGVN-------------------------------------------------  383
gi|117606322|ref|NP_033259.2|  AHQN--SAVAAAAAAAAASSGALGALGSLVKSEPSG-SPPAPAHSRAPCPGDLREMISMYLPAGEGGDPAAAAAAAAQSRLHSLPQHYQGAGAGVN-------------------------------------------------  383
gi|76631951|ref|XP_875555.1|   AHQN--SAVAAAAAAAAASSGALGALGSLVKSEPSG-SPPAAHSRAPCPGDLREMISMYLPAGEGGDP-----AAAQSRLHSLPPHYQGAGAGAN-------------------------------------------------  361
gi|73989544|ref|XP_849239.1|   AHQN--SAVAAAAAAAAASSGALGALGSLVKSEPSG-SPPAPAHSRAPCPGDLREMISMYLPGGETGDPAAAAAAAAQSRLHSLPQHYQGAGAGVN-------------------------------------------------  395
gi|45383488|ref|NP_989664.1|   PHQNSAAAAAAAAAAAASSGALGALGSLVKSEPSV-SPPVTSHSRAPCPGDLREMISMYLPGGEGGDP---AAAAAQSRLHSLPQHYQSASTGVN-------------------------------------------------  365
gi|17975569|ref|NP_524735.1|   QPGSPTPYGGGGGGGGQVSCQSHSPSDSSIKSEPVSPSPSAIALNNNNNINNNHIMKREYSSAAAAAAAAAAAAAAGGGELNHLMNMYHLPDEQRHLLHYQTDSPDLQQQHQSMQQQQQHLPQQHLSQQHQQIPQQHHTMQQQQQQHHLQ  558
gi|158298957|ref|XP_319093.4|  QPGS--PYGLNHQPGSALSCQSHSPSDSSVKSEPVSPSPIASATNNN------LTMKREYIVGGGHQQQSTAA------DLSHLINMYHVPDMQQ-------------------------------------------------  333
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

gi|50540036|ref|NP_001002483.1| ------GTVPLTHI   336
gi|83415189|ref|NP_001032751.1| ------GTVPLTHI   340
gi|30179900|ref|NP_005977.2|   ------GTVPLTHI   391
gi|117606322|ref|NP_033259.2|  ------GTVPLTHI   391
gi|76631951|ref|XP_875555.1|   ------GTVPLTHI   369
gi|73989544|ref|XP_849239.1|   ------GTVPLTHI   403
gi|45383488|ref|NP_989664.1|   ------GTVPLTHI   373
gi|17975569|ref|NP_524735.1|   HQQSLRAMAPLAHM   572
gi|158298957|ref|XP_319093.4|  --------------   333
                                .......610....
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