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                                                  *  :*  .      .  .:      .   **  .  .. .                  . .  :          :  .    * *.:****:::**:********.*******::*.
gi|46370060|ref|NP_996915.1|      MEPGLWLLFGLTVTS-----------------------AAGFVPCSQSGDAGRRGVSQAPTAARSEGDCEETVAGPGEETVAGPGEGTV-APTALQGPSPGSPGQEQAAEGAPEHHRSRRCTCFTYKDKECVYYCHLDIIWINTPEQTV   125
gi|114682850|ref|XP_525373.2|     MEPGLWLLFGLTVTS-----------------------AAGFVPCSQSGDAGRSGVSQAPTAARSEGDCEETVAGPGEETVAGPGEGTV-APTALQGPSPGSPGQEQAAEGAPEHHRSRRCTCFTYKDKECVYYCHLDIIWINTPEQTV   125
gi|50950153|ref|NP_001002942.1|   MEPGLWLLFGLTVTS-----------------------AAGLVPCPQPGDAGKSGVPGTPPTARSEGDIQEPVAMT---AVQGPS-----PRSPEQEQELGRFG-EQASKGGPVHGRARRCTCFTYKDKECVYYCHLDIIWINTPEQTV   117
gi|6681267|ref|NP_031929.1|       MEPGLWLLLGLTVTS-----------------------AAGLVPCPQSGDSGRASVSQGPPEAGSERGCEETVAGPGERIVSPTVALPAQPESAGQERAPGRSG-KQEDKGLPAHHRPRRCTCFTYKDKECVYYCHLDIIWINTPEQTV   125
gi|109469319|ref|XP_001072605.1|  MQPVSRHCRSLVESHSGLGGGVVGAKNSVSAAQEPFNPPPARFVPCPQPGGSGRASVSQGLPEAGSERDCPETVAGPHESIVSPTAALPAQPGNAGQERGPGRSG-DQEEKRVPAHHRPRRCTCFTYKDKECVYYCHLDIIWINTPEQTV   149
gi|156120607|ref|NP_001095449.1|  MELGLCFLFGLAVTS-----------------------AAGWVPHPQSGDAGRSSMPRAPSAATSEGDTKETVATMAARGPS--------PRSPWREQGPSQFG-KQGAEGVPVHHRARRCTCFTYKDRECVYYCHLDIIWINTPERTA   117
gi|189535805|ref|XP_001919586.1|  -------------------------------------MAKLIPDALLLIVSLINIFTVDTSFSSEGDLHSSPVFSGG------------SSSVGHQQKE-----AKLVSASHAHTRSKRCTCYSFKDRECVYYCHLGIIWINTPQRTV    94
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                  ***:*.:*  .  * :** *  ..   :       ** *    *  *  **                          .  .
gi|46370060|ref|NP_996915.1|      PYGLSNYRGS-FRGKRSAGPLPGNLQLSHRPHLRCACVGRYDKACLHFCTQTLDVSSNSR------------TAEKTDKEEEGKVRGANRGLCQRRLKSRTNKASRL-----------------------------------------   219
gi|114682850|ref|XP_525373.2|     PYGLSNYRGS-FRGKRSAGPLPGNLQLSHRPHLRCACVGRYDKACLHFCTQTLDVSSNSR------------TAEKTDKEEEGKVRGANRGLCQRRLKSRTNKANRL-----------------------------------------   219
gi|50950153|ref|NP_001002942.1|   PYGLSNYRGS-FRGRRSTGLFPQSPQPSKWT-QRCACVQSQDSACLHFCTRTLAVSRNSR------------TATNPDKEEEPASRG-NGGLRPTR-------------------------------------------------------   198
gi|6681267|ref|NP_031929.1|       PYGLSNYRES-LRGKRSLGPVPESSQPSPWTRLRCTCMGADDKACAHFCARTRDVTSYSG------------RAERPAAEEMRETGGPRQRLMS----RTDKAHRP-----------------------------------------   214
gi|109469319|ref|XP_001072605.1|  PYGLSNHRGS-LRGKRSSGPVPESSQSSPQTRLRCACAGVDDKACAYFCAH---VTSYSR------------RAEKAAAEEKQETGGPRQSVIMSVILECDPECDPKYDLSVIRSVVLSVNLECDPECGPEHD--------PKCYPKCDP   275
gi|156120607|ref|NP_001095449.1|  PYGLSSYRGSGSRGRRSAGQFPQSPQPVKGT-LRCACTESDDDACLQFCTWSLAARGRTAPYGLSSYRGSGSRGRRSAGQFPQSPQPVKGTLRCACTESDDDACLQFCTWSLAARGNSRSAETSDKEVGKQTGGALGGVRPRSCALVATL   266
gi|189535805|ref|XP_001919586.1|  PYGMSSYRSP-QRLRRSSGTISVVLR-------RCLCTDHNDVHCYNFCDASSENVSEGR------------LRGRSPW-------------------------------------------------------------------   153
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

gi|46370060|ref|NP_996915.1|      -----   219
gi|114682850|ref|XP_525373.2|     -----   219
gi|50950153|ref|NP_001002942.1|   -----   198
gi|6681267|ref|NP_031929.1|       -----   214
gi|109469319|ref|XP_001072605.1|  RV---   277
gi|156120607|ref|NP_001095449.1|  RLLSS   271
gi|189535805|ref|XP_001919586.1|  -----   153
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