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                                 **:*:*****:*****************************************  .*  * . .  .        *    **:     ..   *    *    .
gi|6754284|ref|NP_034630.1|      MEFKLEAHRIVSISLGKIYNSRVQRGGIKLHKNLLVSLVLRSARQVYLSDPCPGLYLAGPAGTPAVPPPQQPGEPVAGPPSGWGEPPPPVARAAWPEPEPQPQPQPQRPSVCHTPGAGSSEPVAAVAGSGEALRGGEEDSAAAAWGRVER   150
gi|68342001|ref|NP_001020308.1|  MEFKLEAHRIVSISLGKIYNSRVQRGGIKLHKNLLVSLVLRSARQVYLSDPCPGLYLAGPAGTPAVPPPQQPGEPVAGPPSGWGEPPPPVAR----EDEPRP-------------------------------------------------   98
gi|142976757|ref|NP_057629.2|    MEFKLEAHRIVSISLGKIYNSRVQRGGIKLHKNLLVSLVLRSARQVYLSDPCPGLYLAGPAGTPAPPPQQQPGEPAAGPPAGWGEPPPPAARASWPETEPQPE----RSSVSDAPRVGDEVPVATVTGVGDVFQGGEADATEAAWSRVEG   146
gi|194674218|ref|XP_601920.3|    MEFKLEAHRIVSISLGKIYNSRVQRGGIKLHKNLLVSLVLRSARQVYLSDPCPGLYLAGHPGAPAPP--QQPEESAAGPPAGWGEPPPPAGRAAWPEPEPQPE----RPAVPEVPRAGDAQPAATVTAAGDTLQGGEAEAPEAAWRRVEG   144
gi|55742142|ref|NP_001007198.1|  MEYKVEAHRIMSISLGKIYNSRVQRGGIKLHKNLLVSLVLRSARQVYLSDYYSGACLNAQSEREGNEWDITDSEREKFPPS-----TTECDRVESPEEPQLTE----QPEASEKEREYRENDAEKSERVDCTSTSEQESNQNSSLDSVST   141
                                 1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150
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gi|6754284|ref|NP_034630.1|      PRAASS------GGGSDACPEGPRAVRRPCGCPPAVEE----------------RSSEDGSPAPPAPCPRKRGAAGVGGGRASCSAPGSTPLKKPRRNSEEQP--VTGEDDTDEEMETGNVANLISIFGSSFSGLLRKSPAGGREEEEA   275
gi|68342001|ref|NP_001020308.1|  ----------------------------------------------------------------------------------------------------------------------------------------   98
gi|142976757|ref|NP_057629.2|    PRQAAAREAEGTAGGWGVFPEVSRAARRPCGCPLGGEDPPGTPAATPRAACCCAPQPAEDEPPAPPAVCPRKRCAAGVGGGPAGCPAPGSTPLKKPRRNLEQPP--SGGEDDDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEG   294
gi|194674218|ref|XP_601920.3|    PRETAIGGAGGPAEVSGVFPQGPEAARGPCGCPPGDED---RLSAAPRVDGCRAPRPAAAEPPASPPVCARKRGAAGVGGGPADCPAPGSTPLKKPRRNSEEQPGGAAAAAEEEEEMETGNVANLISIFGSSFSGLLRKSPGGGREEAEG   291
gi|55742142|ref|NP_001007198.1|  ETTTES-------------PSDTTVAERDS-TPVVVNG--------------------ESHQPPKTHVCSSNRKRS------AEESESGDAPQKRTKVASSNTK----EDEEEAEEMDTGNVSNLITIFGSSFSGLLSKD--GTKPEAEA   245
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6754284|ref|NP_034630.1|      EEGGPEAAEPGQICCDKPVLRDMSPWSTAIVAF   308
gi|68342001|ref|NP_001020308.1|  --------------------------------    98
gi|142976757|ref|NP_057629.2|    EESGPEAAEPGQICCDKPVLRDMNPWSTAIVAF   327
gi|194674218|ref|XP_601920.3|    EESGPEAAEPGQICCDKPVLRDINPWSTAIVAF   324
gi|55742142|ref|NP_001007198.1|  EESG-------QICCDQ-MLKNLNPWSTAIVAF   270
                                 .......310.......320.......330...
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