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                                                  *..                                  . :****************:************* ************************************************.***:** ::*:*:::*:**:::::
gi|12669915|ref|NP_001941.2|                      MAEAG-----------------PQAP--------------PPPGTPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIELKAEIEELQQREQELDQHKV   119
gi|114663112|ref|XP_511025.2|                     MASPSLLPGRPTDALLIPPQLHPNSPVY------------PPPGTPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIELKAEIEELQQREQELDQHKV   138
gi|73957515|ref|XP_853975.1|                      MAEAG-----------------PQAP--------------PPPGTPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIELKAEIEELQQREQELDKHKV   119
gi|115497534|ref|NP_001069341.1|                  MAEAG-----------------PQAP--------------PPPGTPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIELKAEIEELQQREQELDQHKV   119
gi|22507329|ref|NP_683754.1|                      MAEAG-----------------PQAP--------------PPPGTPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIELKAEIEELQQREQELDQHKV   119
gi|118096144|ref|XP_001231948.1|                  MAECG-----------------PQPPGAGGGGGGGGGGSGGAGAPSRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIAHKLIELKADIEDLEQQEQELEKQKM   133
gi|47087407|ref|NP_998597.1|                      MGESL-----------------------------------QPQTPSRHEKSLGLLTTKFVTLLQEAKDGVLDLKAAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWKGVGPGCNTREIADKLIDLKLELEDLDRREHELDQQRV   114
                                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                                  ******:***:*  *. ******:*:*.** ************* ****:**    . ********** :***:******:. **.**.:*****:*::*   .. .:  .   .    .    ::: . :.    *..    .    .
gi|12669915|ref|NP_001941.2|                      WVQQSIRNVTEDVQNSCLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPE-GLNGQKKYQIHLKSVSGPIEVLLVNKEAWSSPPVAVPVPPPEDLLQSPSAVSTPPPLPKPALAQSQEASRPNSPQLT-PTAVPG---SAEVQGMAGP   264
gi|114663112|ref|XP_511025.2|                     WVQQSIRNVTEDVQNSCLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPE-GLNGQKKYQIHLKSVSGPIEVLLVNKEAWSSPPVAVPVPPPEDLLQSPSAVSTPPPLPKPALAQSQEASRPNSPQLT-PTAVPG---SAEVQGMAGP   283
gi|73957515|ref|XP_853975.1|                      WVQQSIRNVTEDVQNSCLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPE-GLNGQKKYQIHLKSVSGPIEVLLVNKEAWSSPPVAVPVPPPEDLLQSPPAVSTPPPLPKPTLAQPHDTSRPSSPQLTTPTPVTG---ITEAQGVPGP   265
gi|115497534|ref|NP_001069341.1|                  WVQQSIRNVTEDVHNSCLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPE-GLNGQKKYQIHLKSVSGPIEVLLVNKEAWSSPPVAVPVPPPEDLLQNPPAVSTPPLLPKPSLAQPQDASRPSSPQATTPNPVPS---STEAQGVAGP   265
gi|22507329|ref|NP_683754.1|                      WVQQSIRNVTEDVQNSCLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPE-GLNGQKKYQIHLKSMSGPIEVLLVNKEAWSSPPVAVPVPPPDDLLQSPPAVSTPPPLPKPALAQPQESSPPSSPQLTTPTPVLG---STQVSEVACQ   265
gi|118096144|ref|XP_001231948.1|                  WVQQSIKNVTEDVQNNWLAYVTHEDICKCFTGDTLLAIRAPSGTRLEVPIPE-GPSRQKKYQIHLKSTSGPIDVLLVNKDAWSSPPVVLPVPPPEDLIQCQAVAPSKPQIP--PLAHFQEASVPSSTQPSTPTPSSTQDHSPPEQKDTST   280
gi|47087407|ref|NP_998597.1|                      WVQQSIKNVTDDSLNSPLAYVTHQDLCNCFKGDTLLAIRAPSGTQLEVPVPESHVNGQKKYQIHLKSSAGPIEVLLVNKDPSSSSPVVLPVPPPDDMLQNLSTPASTTSAAAAPTKPTANSTPSPASTCQSPSTTTT----SNTAITTTT   260
                                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|12669915|ref|NP_001941.2|                      AAEITVSGGPGTDSKDSGELS--SLPLGPTT-LDTRPLQSSALLDSSSSSSSSSSSSSNSNSSSSSGPNPSTSFEPIKADPTGVLELPKELSEIFDPTRECMSSELLEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVL   411
gi|114663112|ref|XP_511025.2|                     AAEITVSGGPGTDSKDSGELS--SLPLGPTT-LDTWPLQSSALLDSSS------SSSSNSNSSSSSGPNPSTSFEPIKADPTGVLELPKELSEIFDPTRECMSSELLEELMSSEVFAPLLRLSPPPGDHDYIYTLDESEGVCDLFDVPVL   424
gi|73957515|ref|XP_853975.1|                      AAEIAVSGGPGTDSKDGGELG--SLPPGLAA-LDTRPLQSSALLDSSS-----SSSSSSSSNSSSSGPNPSTSFEPIKADPTGVLELPKELSEIFDPTRECMSSELLEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVL   407
gi|115497534|ref|NP_001069341.1|                  AAEIPVSGGHGTESKDSGELS--SLPLGLAA-LDTRPLQSSALLDSSS-----SSS-----NSSSSGPNPSTSFEPIKEDPTGVLELPKELSEIFDPTRECMSSELLEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVL   402
gi|22507329|ref|NP_683754.1|                      TSEIAVSGSPGTENKDSGEVS--SLPLGLTA-LDTRPLQSSALLDSSSS----SSSSSSSSSSSSSGPNPSTSFEPIKADPTGVLDLPKELSEIFDPTRECMSSELLEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVL   408
gi|118096144|ref|XP_001231948.1|                  ECSISVVESKSSSS-DLDPLSNVSAPSGHTARLDTQLLQSSASLDSSS-----------------VLPSPSASFEPIKPDPAGMLELPKELSEMFDPTRECMNSELLEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVL   412
gi|47087407|ref|NP_998597.1|                      VPPNTNSGPPAVADTDISSTSTPDITANPTPSTDTQQLQSSASLDSSS-----------------LPDSSTLFEPIKTDPSDLLDFPKELSEMFDP-KEIMSTDLLEELMSSEVFSPLLRLSPPPGDHDYIYNLDETEGLCDLFDVPVA   391
                                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|12669915|ref|NP_001941.2|                      NL   413
gi|114663112|ref|XP_511025.2|                     NL   426
gi|73957515|ref|XP_853975.1|                      NL   409
gi|115497534|ref|NP_001069341.1|                  NL   404
gi|22507329|ref|NP_683754.1|                      KL   410
gi|118096144|ref|XP_001231948.1|                  NL   414
gi|47087407|ref|NP_998597.1|                      NL   393
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