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                                                                                                                                                     *   :  *               :.:: *  : * *   .:::*
gi|31982262|ref|NP_032343.2|          ---------------------------------------MLGLTQHAQKVWRMKPFS--PEVSPGSSPATAGHLLRISTLFLTLLELAQVCRGSVVSNRPFITVWNGDTHWCLTE-YGVDVDVSVFDVVANKEQSFQG-SNMTIFYREEL   107
gi|46485726|ref|NP_997499.1|          ----------------------------------------------------MKPFS--PEVSPDPCPATAAHLLRTYTLFLTLLELAQGCRGSMVSNRPFITVWNADTHWCLKD-HGVDVDVSVFDVVANKEQNFQG-PNMTIFYREEL    94
gi|24497564|ref|NP_695013.1|          ---------------------------------------------------------------------MAAHLLPICALFLTLLDMAQGFRGPLLPNRPFTTVWNANTQWCLER-HGVDVDVSVFDVVANPGQTFRG-PDMTIFYSSQL    79
gi|114587044|ref|XP_001168739.1|      ---------------------------------------------------------------------MAAHLLPICALFLTLLDMAQGFRGPLLPNRPFTTVWNANTQWCLER-HGVDVDVSVFDVVANPGQTFRG-PDMTIFYSSQL    79
gi|62988300|ref|NP_001017941.1|       ----------------------------------------------------MRPFS--LEVSLHLPWAMAAHLLPVCTLFLNLLSMTQGSRDPVVPNQPFTTIWNANTEWCMKK-HGVDVDISIFDVVTNPGQTFRG-PNMTIFYSSQL    94
gi|73985710|ref|XP_850767.1|          MTPALPSAYTEAVAPSVQTCDNITFQEDLEDSLMEGAGTATAVDGESESSEPALSFASPGQVSLDSSSAMAVHLLPTYALFLTLLGTAQGSRSSVVPNQPFTTIWNANTQWCLEK-YGVDVDVSVFDVVANPGQTFRG-PDMTIFYSYQL   148
gi|50805781|ref|XP_424356.1|          ---------------------------------------------------------------------MAPGWLCWALLLLPAPVRAAGPGPVLVNRPFVTVWNIPSEPCAQQ-YNVTLPLGVFDVVANTEEAFIG-QDIALFYSSHL    79
gi|189518429|ref|XP_696383.3|         ---------------------------------------------------------------------MDRSGRRTCLLMVFSMCSASVLSQPLIK-LPFISIWNAPTERCKSR-FGVELDLSVFDIVHNPNQTFMG-DNITIFYSDKL    78
gi|158297620|ref|XP_317823.4|         --------------------------------------------------------------------------------------------------RSFEVYWNIPTFMCNQFGFEFSSVNRTYSVVQNRNDTFRG-NAVSILYDPGK    51
gi|17536397|ref|NP_495830.1|          -----------------------------------------------------------------MVIVWYHQLLLVLLIFIGAAKGAQYIGSGASQPNRTDVVWMVPSWTCKNE---YSIDVEKYGILQNEDQHFVGGKQFAIFYEHSF    82
                                      1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                             .  :.       *:**  ..*  **    ..:    :*   :.*:.::* * :** :  .:.. .  *    *   :  : .** *     :*  *    :: :   ::   ** *..  ** . **:* ** *  .              *.
gi|31982262|ref|NP_032343.2|          GTYPYYTPTGEPVFG---GLPQNASLVTHLAHTFQDIKAAMPEPDFSGLAVIDWEAWRPRWAFNWDSKDIYRQRSMELVQAEHPDWPETLVEAAAKNQFQEAAEAWMAGTLQLGQVLRPRGLWGYYGFPDCYNNDFL-SLNYTGQCPVFV   253
gi|46485726|ref|NP_997499.1|          GTYPYYTPTGEPVFG---GLPQNASLVTHLAHAFQDIKAAMPEPDFSGLAVIDWEAWRPRWAFNWDSKDIYQQRSMELVRAEHPDWPETLVEAEAQGQFQEAAEAWMAGTLQLGQVLRPRGLWGYYGFPDCYNYDFL-SPNYTGQCSLSI   240
gi|24497564|ref|NP_695013.1|          GTYPYYTPTGEPVFG---GLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGLWGFYGFPDCYNYDFL-SPNYTGQCPSGI   225
gi|114587044|ref|XP_001168739.1|      GTYPYYTPTGEPVFG---GLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGLWGFYGFPDCYNYDFL-SPNYTGQCPSGI   225
gi|62988300|ref|NP_001017941.1|       GTYPYYTSAGEPVFG---GLPQNASLNAHLARTFQDILAAMPEPRFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQKQHPDWLAPRVEAAAQDQFEGAAEEWMAGTLKLGQALRPQGLWGFYNFPECYNYDFK-SPNYTGRCPLNI   240
gi|73985710|ref|XP_850767.1|          GTYPYYTSAGEPVFG---GLPQNASLDTHLVHSFQDIQAAIPESDFSGLAVIDWEAWRPRWAFNWDSKDIYRQRSRALVRGQHPDWPATRVEAAARDQFQKAAQAWMAGTLKLGQALRPRGLWGFYGFPDCYNYDFL-SPNYTGECPPGI   294
gi|50805781|ref|XP_424356.1|          GLFPYYTAQGQPVDG---GLPQNASLVAHLQRARRDIGAALPSTRYDGLAVVDWEQWRPLWARDWSSMDIYREKSEELVRRQHPLWPHSHVEEVAQQQFQKAARAFMEQTLRLGEAMRPAGYWGFYGFPDCYNNNFS-DPLYNGSCPVVE   225
gi|189518429|ref|XP_696383.3|         GKYPHYGPNDEPIYG---GVPQNASLNEHLKKADEDLRKNIPDPEFQGLAIIDWEKWRPLWERNWDSKEVYWKASRAIVKAKHPTWSPDQIETEAVKEFEASSMAFMVETLKLGRRERPGGLWGFYGFPCCYNYQYKKNETYTGECPALE   225
gi|158297620|ref|XP_317823.4|         FPALLEKPSTKTLYKRNGGVPQEGNLTEHLEIFERHLDELIPDRNFSGIGIIDFESWRPIYRQNFGSLQPYKDLSVKIERERHPYWSGNHLEREATRRFEATGREFMEQTLLLAKQRRPQAAWGYYAFPYCFNMNGA-ASTRSENCSPEV   200
gi|17536397|ref|NP_495830.1|          GKIPYFKAQNESDPK-NGGLPQMGDLEAHLIQAEKDINETIPDENFNGIAVIDIEEFRPMWELSWGPFSVYKTESIRLTRQQHPYWSTKQIEWQAERDYEKACQKFFIETLRLGKRLRPNAKWGYYLFPKCNGDVGQ---KSDTDCSTLF   228
                                      .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|31982262|ref|NP_032343.2|          RDQNDQLGWLWNQSYALYPSIYLPAALMGTEK-SQMYVRHRVQEALRVAIVSRDPHVPVMPYVQIFYE---MTDYLLPLEELEHSLGESAAQGVAGAVLWLSSDKTSTKESCQAIKAYMDSTLGPFIVNVTSAALLCSEALCSGHGRCVR   399
gi|46485726|ref|NP_997499.1|          HDQNDQLGWLWNQSYALYPSIYLPAALMGTGK-SQMYVRYRVQEAFRLALVSRDPHVPIMPYVQIFYE---KTDYLLPLEELEHSLGESAAQGAAGAVLWISSEKTSTKESCQAIKAYMDSTLGPFILNVTSAALLCSEALCSGRGRCVR   386
gi|24497564|ref|NP_695013.1|          RAQNDQLGWLWGQSRALYPSIYMPAVLEGTGK-SQMYVQHRVAEAFRVAVAAGDPNLPVLPYVQIFYD---TTNHFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSGHGRCVR   371
gi|114587044|ref|XP_001168739.1|      RAQNDQLGWLWGQSRALYPSIYMPAVLEGTGK-SQMYVQHRVAEAFRVAVAAGDPNLPVLPYVQIFYD---TTNHFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSGHGRCVR   371
gi|62988300|ref|NP_001017941.1|       CAQNDQLGWLWGQSRALYPSIYLPAALEGTKK-TQMFVQHRVAEAFRVAAGAGDPKLPVLPYMQLFYD---MTNHFLPAEELEHSLGESAAQGAAGVVLWVSWLSTSTKESCQAIKEYVDTTLGPSILNVTSGARLCSQVLCSGHGRCAR   386
gi|73985710|ref|XP_850767.1|          GAQNDQLGWLWRQSRALYPSIYLPTELEGTGK-GQMYVRHRVGEAFRVAEDVGDPYLPVLPYAQIFYD---NTNRVLPLDELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYVDTTLGPFILNVTSGVLLCSQALCSGHGRCVR   440
gi|50805781|ref|XP_424356.1|          QQRNQELGWLWNCSRALYPSIYLPQQLQGTDK-VLRYVRYRVAEAFAVQKGILSNAVPVLPYTEIIYA---NTSDFLSEEDLVNTIGESAAQGAAGIIIWGRSADTASKEKCLKLRDYLDGALGHYIVNVTTSAQLCSQSLCSGNGRCVR   371
gi|189518429|ref|XP_696383.3|         MKRNDKLAWMWNVSSALYPDIYLDLGLRGRGQDILLYSRYRILEAMRVREKTTHQMPSVFPYARIAFT---YSMEFLSQDDLVHTIGESVALGASGVVLWGDGNFSRTKRACEAVRDYLDITLGRYIVNVTEAAFLCSRKVCSSQGRCVR   372
gi|158297620|ref|XP_317823.4|         QRENNRIMWLFDGSDIIFPSVYLREKLSPSER--EQLIRGRVREAVRVAQRTK-PRRKVLTYLRYVYT---DSIQYLTESDWINALAAMKSTGSDGIILWGSSFDLNTR-------------------------------------   303
gi|17536397|ref|NP_495830.1|          QKFNDNLHWLWGESTALFPSIYLYPSQKQNPE-YNFVNSGALITETKRIKRNYCPSCEIHVFTKIEYNPYYTPDDFYSKQNLASTLDLAIKMNANSVVIWSTSQSIGSR--CGSLQTYVDNTLGPYLQLTDRNLDKCRMERCEGRGECYL   375
                                      .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|31982262|ref|NP_032343.2|          HPSYPEALLTLNPASFSIEL--------THDGRPPSLKGTLSLK-DRAQMAMKFRCRCYRGWRGKWCDKRGM----------------   462
gi|46485726|ref|NP_997499.1|          HPSYPEALLTLSPASFSIEP--------THDGRPLSLKGTLSLK-DRAQMAMKFKCRCYRGWSGEWCKKQDM----------------   449
gi|24497564|ref|NP_695013.1|          RTSHPKALLLLNPASFSIQL--------TPGGGPLSLRGALSLE-DQAQMAVEFKCRCYPGWQAPWCERKSMW---------------   435
gi|114587044|ref|XP_001168739.1|      RTSHPKALLLLNPASFSIQL--------TPGGGPLSLQGALSLE-DQAQMAVEFKCRCYPGWQGPWCEQKSMW---------------   435
gi|62988300|ref|NP_001017941.1|       RPSYPKARLILNSTSFSIKP--------TPGGGPLTLQGALSLE-DRLRMAVEFECRCYRGWRGTRCEQWGMW---------------   450
gi|73985710|ref|XP_850767.1|          RPSYPEALLFLNPTSFSIQL--------PPGGRPLTLQGALSRE-DRMRMAVEFQCRCYRGWKGVRCEQQGMR---------------   504
gi|50805781|ref|XP_424356.1|          KEGK-VAFLQLDPNRFAINL--------KAK-KPQPMVWILNADSDMSQLAEGFTCQCYSGWRGEHCDSHGSSNK-------------   436
gi|189518429|ref|XP_696383.3|         RDPSASVYLHLNPEMWSIIPRAQLPGAITGGPSYVAHRRLWTGQEETSRFTDSFRCQCFPGWEGEQCQKPVPVETFT-----------   449
gi|158297620|ref|XP_317823.4|         ----------------------------------------------------------------------------------------   303
gi|17536397|ref|NP_495830.1|          PRPKTNPAIYNFACRCERPYFG-----KSCEYRGRRMGVSMPKASQTPQVIPDVTAYFSTSSNGTKKYNAPNQFYSRTGGDIKLARKL   458
                                      .......460.......470.......480.......490.......500.......510.......520.......530.........
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