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                                 *****:***.:*.:* *****.******:**:*** **:********* :.*       *  . :        . * *  **:******:: ::.*:* **..  . *            :*:* ****.: .*        .. :.
gi|6677939|ref|NP_033194.1|      MAKWLRDYLNLGSRRPPPQPPTPDYTESDILRAYREQKDLDFEDPYEDSNGR-------AEPEVTG--------SGDPKYNSPRHRLIKVEAADMARAKALLGSPGEEP-----------EAETEYSDPFDAQPQP---------PAPMS   115
gi|62718074|ref|XP_237255.3|     MAKWLRDYLNLGSRRPPPQPPTPDYTESDILRAYREQKDLDFEDPYEDSNGR-------PESEITE--------SSDPKYNSPRHRLIKVEAVNLARAKTLLGSLGEEP-----------EADTEYSDPFDAQPQP---------PAPNN   115
gi|222537752|ref|NP_064594.3|    MAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAYRAQKNLDFEDPYEDAESR-------LEPDPAG--PGDSKNPGDAKYGSPKHRLIKVEAADMARAKALLGGPGEEL-----------EADTEYLDPFDAQPHP---------APPDD   121
gi|55647979|ref|XP_512284.1|     MAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAYRAQKNLDFEDPYEDAESR-------LEPDPAG--PGDSKNPGDAKYGSPKHRLIKVEAADMARAKALLGGPGEEL-----------EADTEYSDPFDAQPHP---------APPDD   121
gi|194668816|ref|XP_001790650.1| MAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAYREQKDLDFEDPYEDADSR-------LEPDSSGG-PGDSKGPGDAKYDSPKHRLIKVEAVDIARAKVLLGSPGEES----------KVDTEYSDPFDAQPHP---------PPPDD   122
gi|113682292|ref|NP_001038542.1| MAKWLKDYLSFGSKRVPPQPPKPDYTESEILKAYRAQKNLDFEDPYEDFENRGRNDNGSNEVSHTGFGSPMKSSSLDIKVVSPKHRLIKVDSQDLGRSKILLSSVSLEEPTDPVVPSAPVMGDTDYSDPFDVRLDPRPESAQGQITPENN   150
gi|292626403|ref|XP_002666302.1| MAKWLKDYLSFGSKRVPPQPPKPDYTESEILKAYRAQKNLDFEDPYEDFENRGRNDNGSNEVSHTGFGSPMKSSSLDIKVVSPKHRLIKVDSQDLGRSKILLSSVSLEEPTDPVVPSAPVMGDTDYSDPFDVRLDPRPESAQGQITPENN   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 ******:*: : :*   *           **********:     *   .*:    ** * :*:**************:***:******...:*:*:  .::             :  :*      .****.:*.**** : :
gi|6677939|ref|NP_033194.1|      GYMEPYDARSVSSEQPSRA-----------VQLYDTPYEEQATKPEDGGSSGQ----SRRPLEDERPADEYDQPWEWKKDHISRAFAVQFDGPDWERTPCSTK--------------EPWRP-----QPAERVDTALALEKQPWFHGPLS   231
gi|62718074|ref|XP_237255.3|     GYMEPYDARNISSEQPSRA-----------VQLYDTPYEEQDMKPEDGGSSGQ----SRRPLEDERPADEYDQPWEWKKDHISRAFAVQFHGPDWERTPCSTK--------------EPWRP-----QPAERVDTALALEKQPWFHGPLS   231
gi|222537752|ref|NP_064594.3|    GYMEPYDAQWVMSELPGRG-----------VQLYDTPYEEQDPETADGPPSGQKPRQSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPGSAK--------------ELRRPPPRSPQPAERVDPALPLEKQPWFHGPLN   246
gi|55647979|ref|XP_512284.1|     GYMEPYDAQWVMSELPGRG-----------VQLYDTPYEEQDPETADGPPSGQKPRQSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPGSAK--------------ELRRPPPRSPQPAERVDPALPLEKQPWFHGPLN   246
gi|194668816|ref|XP_001790650.1| GYMEPYDAQRVMSELPCRR-----------VQLYDTPYEEQDQELGDGPPSGQKPRQSRLPQEDERPADEYDQPWEWKKDHISKAFAVQFDSPDWERTSGSAK--------------ELRRPPPRSPQPAERVDPTLPLEKQPWFHGLLS   247
gi|113682292|ref|NP_001038542.1| GYMEPYEAQKVITELQRRAGGGAGGWGRGEVQLYDTPYEERVPGQPDLPEEGR---ESRLPQDDDRPADEYDQPWEWKKEHISKAFAVQFEGAEWDRSCSPTERLRCSRAPPTTGSMKLRKPSDPHSMIGERVDPSLPLEKQVWYHGSLS   297
gi|292626403|ref|XP_002666302.1| GYMEPYEAQKVITELQRRAGGGAGGWGRGEVQLYDTPYEERVPGQPDLPEEGR---ESRLPQDDDRPADEYDQPWEWKKEHISKAFAVQFEGAEWDRSCSPTERLRCSRAPPTTGSMKLRKPSDPHSMIGERVDPSLPLEKQVYVQ----   293
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6677939|ref|NP_033194.1|      RAEAENLLSLCKEGSYLVRLSETRAQDCILSLRSNQGSMHLKFARTRENQVVLGQHSGPFPSIPELVLHYSARPLPVQGAEHLALLYPVTSSQSSQGPCTLAAKPERGQGDP   343
gi|62718074|ref|XP_237255.3|     RVEAENLLSLCKEGSYLVRLSETRAQDCILSLRSNQGSMHLKFAKTRENQVVLGQHSGPFPSVPELVLHYSARPLPVQGIEHLALLYPVTSSQSSQGPCTLAARPEKGQGDP   343
gi|222537752|ref|NP_064594.3|    RADAESLLSLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVVLGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVT----QTP--------------   340
gi|55647979|ref|XP_512284.1|     RADAESLLSLCKEGSYLVRLSETSPQDCSLSLRSSQGFLHLKFARTRENQVVLGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVT----QTP--------------   340
gi|194668816|ref|XP_001790650.1| RADAENLLSLCKEGSYLVRLSESSPQDCSLSLRSSQGFLHLKFARTRENQFVLGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVS----QTP--------------   341
gi|113682292|ref|NP_001038542.1| RSEAESLLTLCKECSYLVRNSETSRLDYSLSLRSCQGFMHMKFSQCKDGRYILGQNSPPFETIPEVIHYYTTHKLPIKGAEHLSLLFPVLVQTL-----------------   391
gi|292626403|ref|XP_002666302.1| ---------------HLTTNY-------------------------------------------------------------------------------------   299
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410..
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