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gi |166158922|ref |NP_001107227.1| MAALMTPGTGAPPAGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLSEADIRGFVAAVVNSAOGAIGAMLMAIRLRGMDLEETSVLTAALASGOOLEWPEAWRQQLVDKHS TGGVGDKVS LVLAPALAAACGCKVPMISGRGLGH 150
gi |114687130|ref |XP_515224.2| MAALMTPGTGAPPAGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLSEADIRGFVAAVVNSAOGAIGAMLMAIRLRGMDLEETSVLTAALASGOOLEWPEAWRQQLVDKHS TGGVGDKVS LVLAPALAAACGCKVPMISGRGLGH 150
gi |19923857|ref |NP_612175.1| MAAPGTPPPSA-----SGGGG-----EPRQLPELIRLKRGGHLSREADIRNFVHAVIDGRAODTOIGAMLMAIRLQGMNLEETSVLTAALAESGOOLEWPKAWHQQLVDKHS TGGVGDKVS LVLAPALAAACGCKVPMISGRSLGH 136
gi |58865814|ref |NP_001012122.1| MAAPGTPPPLAPETAGADSGGGG-----EHRQLPELIRLKRGGHLSREADIRNFVHALMDGRAODTOIGAMLMAIRLQGMNLEETSVLTAALAESGOOLEWPKAWHQQLVDKHS TGGVGDKVS LVLAPALAAACGCKVPMISGRSLGH 143
gi |292612461|ref |XP_694448.4| MSSEDT-----DTISFPELIKLRNGGQLSLAEIHTFVQGVITGAIKRSQIGAMLMAIWQKGMTDEETLALIREMNSGDTFKWPNW--LVLDKHS TGGVGDKVS LVLAPALAAACGCKVPMISGRGLAH 122
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |166158922|ref |NP_001107227.1| TGGTLDKLESIPGFNVIOSPEQMQLLDAGCCIVGQSEQLVPADGILYAARDVATVDSLPLITASILSKKLVGELSAVVVDVKFGGAAVFPNDEKARELAKTLVGVGASLGLRVAAALTAMDKPLGRCVGHAEVVEALLCMDGAGPP 300
gi |114687130|ref |XP_515224.2| TGGTLDKLESIPGFNVIOSPEQMQLLDAGCCIVGQSEQLVPADGILYAARDVATVDSLPLITASILSKKLVGELSAVVVDVKFGGAAVFPNDEKARELAKTLVGVGASLGLRVAAALTAMDKPLGRCVGHAEVVEALLCMDGAGPP 300
gi |19923857|ref |NP_612175.1| TGGTLDKLESIPGFNVIOSPEQMLHILBEVGGCCIVGQSEKLVLPADGILYAARDVATVDSVPLITASILSKKAVEGLSTLVVDVKFGGAAVFPDQEKARELAKMLVRVGVSLGLKVAALTAMDNPLGRSVGHTEVVEALLCLDGAGPP 286
gi |58865814|ref |NP_001012122.1| TGGTLDKLESIPGFNVIOSPEQMLLLEEVGGCCIVGQSEKLVLPADGILYAARDVATVDSVPLITASILSKKAVEGLSTLVVDVKFGGAAVFPDQEKARELAKMLVRVGVSLGLKVAALTAMDNPLGRSVGHTEVVEALLCLDGAGPP 293
gi |292612461|ref |XP_694448.4| TGGTLDKLESIPGFNVIOSVQVKQILEDVGGCCIVGQTESLVLPADRVLYAIRDATSTVDSLPLITSSIIKKGAGELSAVVVDVKFGRAALYKLDLRARSLAQCLVTAGNELGIKTCAVLSRMDAPIGITVGNAVEVCEALECLKGRGPD 272
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |166158922|ref |NP_001107227.1| DLRDLVITLGGALLWLSGHAGTQAQGAARVAAALDDGSAALGRFERMLAAQGVDPGLARALCSGSPAREROLLPRAREQBELLPADGTVELVRLPLALVHLHELGAGRSRAGEPLRLGVGAELLVDVGRRLRGTPLWRVHRDGPALSGP 450
gi |114687130|ref |XP_515224.2| NLRDLVITLR-----SEDP-----CA-----LP-----VNVWRPLSLRRRGRAQGAG-----GRRFLSG-----LVH----- 347
gi |19923857|ref |NP_612175.1| DLRDLVIRLGGAILWISGQAETODQGAARVAAALDDGSAARRRFQMLLSAQGVDPGLAKALCSGSPTORROLLPHAREQBELLPADGIVECVRALPLARVLDLHLAGRSRAGQPIRPGVGAELVVDVGCCLSRGTPWLRVHLDGPALSSQ 436
gi |58865814|ref |NP_001012122.1| DLRDLVIRLGGAILWLSGQAETODQGAARVAAALDDGSAALHRFQMLLSAQGVDPGLARALCSGSPTORROLLPHARKQBELLPADGIVECVRALPLACVHLHELGAGRSRAGQPIRPGVGAELVVDVGCWLRSRGTPLWRVHLDGPALSSQ 443
gi |292612461|ref |XP_694448.4| DLRELVINLGGHLLWMCCHSSILENGKHEIAVKLNKEALNKFQAMLEAGVTDVARSLCSDE-SRYFVYMKRAANQTELKVPKDGAVLIDGLALAEVHLKLGAGRTKSGEKIDHSVGAEMLVEMGQLVQKQGTWIRIHHSSVDLSAQ 421
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |166158922|ref |NP_001107227.1| SRALQELVLSDRAPFAAPSPFAELVLPQQ--- 482
gi |114687130|ref |XP_515224.2| ----- 347
gi |19923857|ref |NP_612175.1| QRRLLGALVLSDRAPFKVPSPPFAELVLPPTIAQP 471
gi |58865814|ref |NP_001012122.1| QRRLLGALVLSDRAPFKAPSPFAELVLPPTIP-- 476
gi |292612461|ref |XP_694448.4| QRSDLQKALVIGRQDYKAASRIVEFIHPNHMS- 455
.....460.....470.....480.....

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