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gi | 41152241 | ref | NP_957034.1 | -----MATFRFGQHIHKS AVFLKTELSFALVNRKPVVPGHVLVCLRPVVERFRDLRPEVDLDFMTORVSVQIEKHFQAE----- 150
gi | 189524912 | ref | XP_001923175.1 | -----MATFRFGQHIHKS AVFLKTELSFALVNRKPVVPGHVLVCLPVSVEKFRDLHPDEVDLDFMTORRVSSLIEKHFQAE----- 150
gi | 6753862 | ref | NP_034340.1 | -----MSFRFGQHLIKP VVFLKTELSFALVNRKPVVPGHVLVCLRPVVERFRDLHPDEVDLDFQVTRVGVVVEKHFQGT----- 150
gi | 11120730 | ref | NP_068542.1 | -----MSFKFGQHLIKP VVFLKTELSFALVNRKPVVPGHVLVCLRPVVERFRDLRPEVDLDFQVTRVGVVVEKHFQGT----- 150
gi | 4503719 | ref | NP_002003.1 | -----MSFRFGQHLIKP VVFLKTELSFALVNRKPVVPGHVLVCLRPVVERFRDLRPEVDLDFQVTRVGVVVEKHFQGT----- 150
gi | 114587495 | ref | XP_001156390.1 | -----
gi | 99028931 | ref | NP_001035736.1 | -----MSFRFGQHLIKP VVFLKTELSFALVNRKPVVPGHVLVCLRPVVERFRDMSPEEVDLDFQAAQVGVVVEKHFQGT----- 150
gi | 118097032 | ref | XP_414409.2 | -----MLRFGQNLIKP VVFLKTELSFALVNRKPVVPGHVLVCPVRRVVERFRDLCPVEVDLDFRFAQVGVNAVEKHFCAI----- 150
gi | 30697031 | ref | NP_200632.2 | -----MLNLQVIG-----KILILE-----IIRCQRKMSSTCS-----SYAFGPKYKIDPREVFIYAPLSYAMVNLRLPLLPAHVLCPRRLVPRFTDLTADETS DLWLTAQKVGSKLETFHNAS----- 150
gi | 115483895 | ref | NP_001065609.1 | -----MLFVLSADLRRAPTFPELLPLALAPPPPPPLLRRLRPLLLPRAISSSTSPFPVQEMEAAYFGPYKIDAREVFHSPLSYAMVNLRLPLLP-----VCPKREVKRFADLSSNEISDLWVTAKEVGIKLEQYHKAS----- 150
gi | 19075336 | ref | NP_587836.1 | -----MPKQLYFSKFPVVG-----QVFFYRKLKSAAFVNLKPLPGHVLVTPQRAVPRKLDLTPSELDTLFTSVRVVQVVEKVFSAE----- 150
gi | 39951749 | ref | XP_363591.1 | -----MPKIPAPSSITRLCIKPKISATWSYRQRVIPSTITTHITAAAAAATIKNSITKTIVPVRMASNSSSQTAPKTFQGPYEVTHQVFRHTAHSFALVNIKPLLPGHVLVCLPVPHRRLLDILTAEITDLFSAVRRIQHMLARRFPSP----- 150
gi | 32417042 | ref | XP_328999.1 | -----MMNSTSDPSEGNIRPASTQK-----SHYSDDEIHFQPFKVTNQVFLRTPHSFALVNIKPLLPGHVLVCLPVPKRLTDLSPAENVLDFSTVGVVQRMGLGRYVYFHP----- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 41152241 | ref | NP_957034.1 | -----SLTICVODGHEAGQTVKHHVHVHVLPRKAGDFEKN-----DSIYDELQKHD----- 300
gi | 189524912 | ref | XP_001923175.1 | -----SLTICVODGPEAGQTVKHHHLHVLVVKAGDFEKN-----DSIYDELQKLD----- 300
gi | 6753862 | ref | NP_034340.1 | -----SITFSMODGPEAGQTVKHHVHVHVLPRKAGDFERN-----DNIYDELQKHD----- 300
gi | 11120730 | ref | NP_068542.1 | -----SITFSMODGPEAGQTVKHHVHVHILPRKSGDFERN-----DNIYDELQKHD----- 300
gi | 4503719 | ref | NP_002003.1 | -----SLTFSMODGPEAGQTVKHHVHVHVLPRKAGDFERN-----DSIYDELQKHD----- 300
gi | 114587495 | ref | XP_001156390.1 | -----MODGPEAGQTVKHHVHVHVLPRKAGDFERN-----DSIYDELQKHD----- 300
gi | 99028931 | ref | NP_001035736.1 | -----SLTFSMODGPEAGQTVKHHVHVHILPRKAGDFERN-----DSIYDALQKHD----- 300
gi | 118097032 | ref | XP_414409.2 | -----SLTIAIDGPEAGQTVKHHVHVHVLPRKSGDFERN-----DDVYKELQKHD----- 300
gi | 30697031 | ref | NP_200632.2 | -----SLTIAIDGPEAGQTVPHVHIVHILPRKGGDFEKN-----DEIYDALDEKEK----- 300
gi | 115483895 | ref | NP_001065609.1 | -----SLTFAIDGPEAGQTVPHVHIVHILPRKGGDFEKN-----DEIYDALDKKER----- 300
gi | 19075336 | ref | NP_587836.1 | -----ASNIGIDGVDAGQTVPHVHVHILPRKADFSEN-----DLVYSELEKNEGFLA----- 300
gi | 39951749 | ref | XP_363591.1 | -----SSSSGAAE-----ADAAAIVCGGSFNIAVODGPEAGQTVPHVHVHIVIPRKKGEAAARAGEPELNVGMANEDGNVGGALWD----- 300
gi | 32417042 | ref | XP_328999.1 | -----TTTTTRPKREKEKEKEEGGVAEDKVMLETTGGSFNIAVODGPEAGQTVSHVHVHIVIPRIRNVAKDLETPSDALYEWMAEEKGNIGGAFWDRDYGHGHGHGHGNDGGPHHHHHHLOHSSITFCQGRERALGGQQLNGSGSDVQSKE----- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 41152241 | ref | NP_957034.1 | -----RESEDDSSQWRSEEMAKEEASLRSLSF----- 370
gi | 189524912 | ref | XP_001923175.1 | -----REREDVPSQWRSEEMAKEEASLHSLFS----- 370
gi | 6753862 | ref | NP_034340.1 | -----REEDS PAFWRSEKEMAAEAEALRVYFQA----- 370
gi | 11120730 | ref | NP_068542.1 | -----REEDS PAFWRSEEMAAEAEVLRVYFQA----- 370
gi | 4503719 | ref | NP_002003.1 | -----KED--FPASWRSEEMAAEAAALRVYFQ----- 370
gi | 114587495 | ref | XP_001156390.1 | -----KED--SPASWRSEEMAAEAAALRVYFQ----- 370
gi | 99028931 | ref | NP_001035736.1 | -----REDKDS PALWRSEEMAAEAAALRVYFQ----- 370
gi | 118097032 | ref | XP_414409.2 | -----KED--SPDKWRSEEMAAEAAVLRVYFQEN----- 370
gi | 30697031 | ref | NP_200632.2 | -----ELKQLDLDKDRVDRS IQEMADEASQYRSLFDC----- 370
gi | 115483895 | ref | NP_001065609.1 | -----ELKEKLDLDIERKDRIMKEMAHEANEYRGLFS----- 370
gi | 19075336 | ref | NP_587836.1 | -----SLYLTCNERVAGDERPPTSMRQAIKDEDKRPRTLEEMEKEAQWLKGYFSEEQEK----- 370
gi | 39951749 | ref | XP_363591.1 | -----LHSREAG-----RPLPGGGFPKIEDADRVARSMADMETEAAEFRLELLRVMEDEKHRQC----- 370
gi | 32417042 | ref | XP_328999.1 | -----GEALLREEEGEEEEEQVAEMQARPKPGGSPSIEDAARTAREMEEMEREAGEYRRVLEEMGILSV----- 370
.....310.....320.....330.....340.....350.....360.....370

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