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gi|29837648|ref|NP_828847.1|     ----------MEFSWLETRWARPFYLAF-VFCLALGLLQAIKLYLRRQRLLRDLRPFPAPPTHWFLGHQKFIQDDN-----------------------MEKLEEIIEKYPRAFPFWIGPFQAFFCIYDPDYAKTLLSRTDP---KSQY   150
gi|114556395|ref|XP_001162991.1| ----------MEFSWLETRWARPFYLAF-VFCLALGLLQAIKLYLRRQRLLRDLRPFPAPPTHWFLGHQKFIQDDN-----------------------MEKLEEIIEKYPRAFPFWIGPFQAFFYIYDPDYAKTLLSRTDP---KSQY   150
gi|73977808|ref|XP_539622.2|     ----------MESSWLETRWARPLYLAF-AFCLALGLLQAIKLYLRRLRLLRDLCPFPAPPTHWFYGHQKLLQDGK-----------------------IEKLEELVEKYPCAFPYWVGPFQAFFYIYDPDYAKTFLGRTDP---KSKY   150
gi|194665816|ref|XP_592978.4|    MESSWMESSWMESSWLETHWARPFYLTL-VFCLALGLLQAIKLYLQRQRLLRDLRLFPSPPTHWLYGHSKLFKDGK-----------------------MEILEKIVEKYPCAFPRWIGPFQAFLYIYDPDYAKTFLSRTDP---KSNF   150
gi|51592065|ref|NP_001003947.1| ----------MEASWLETRWARPLHLAL-VFCLALVLMQAMKLYLRRQRLLRDLSPFPGPPAHWLLGHQKFLQEDN-----------------------METLDEIVKKHPCAFPCWVGPFQAFFYIYDPDYAKIFLSRTDP---KMQY   150
gi|21728402|ref|NP_663708.1|     ----------MEASWLENRWARPLHLAL-VFCLALVLMQAVKLYLRRQRLLRDLRPFPGPTAHWLLGHQKFLQEDN-----------------------MEKLDEIVKEYPCAFPCWVGPFQAFFYIYDPDYAKIFLSRTDP---KTQY   150
gi|18420859|ref|NP_568463.1|     ----------MENFMVEMAKTISWIVVIGVLGLGIRVYGKVMAEQWRMRRKLTMQGVKGPPPSLFRGNVPEMQKIQSQIMSNSKHYSGDNIIAHDYTSSLFPYLDHWRKQYGRVYTYSTG-VKQHLYMNHPELVKELNQANTLNLGKVSY   150
gi|15238644|ref|NP_197872.1|     ----------MESLVVHTVNAIWCIVIVGIFSVGYHVYGRAVVEQWRMRRSLKLQGVKGPPPSIFNGNVSEMQRIQ----SEAKHCSGDNIISHDYSSSLFPHFDHWRKQYGRIYTYSTG-LKQHLYINHPEMVKELSQTNTLNLGRITH   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|29837648|ref|NP_828847.1|     LQKFSPPLLGKGLAALDGPKWFQHRRLLTPGFHFNILKAYIEVMAHSVKMMLDKWEKICSTQD---TSVEVYEHINSMSLDIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPQG-YRFQKLSRVLNQYT   300
gi|114556395|ref|XP_001162991.1| LQKFSPPLLGKGLAALDGPKWFQHRRLLTPGFHFNILKAYVEVMAHSVKMMLDKWEKICSTQD---TSVEVYEHINSMSLDIFMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPQG-YRFQKLSRVLNQYT   300
gi|73977808|ref|XP_539622.2|     LYKFLIPCLGNGLVNLEGSKWFQHRCLLTPGFNVNILKSYIKVMAHSVNTMLGKWEKICGTQD---TVVEVFEHINLMTLDVLMKCAFSQETNCQISSNHDLYVKTTFEASKINFYRLYSFLHHHDIIFKFSPQG-HRLQELVKILHQYT   300
gi|194665816|ref|XP_592978.4|    LYKFMTASVGKGLVNLSGPKWSQHRRLLTPGFHFNTLKSFVEVMAQSVNIMLNKWEKICGSQN---TLLDIYEHINLMTLDVLMKCIFSWETNCQTDSSHDNYVKATSEGSNILMQRLFNYFYHYDLIFKLSPLG-HRLREVNKILHHHT   300
gi|51592065|ref|NP_001003947.1| LHQLLTPCIGRGLLNLDGPRWFQHRCLLTPAFHQDILKPCVDTMAHSVKVMLDKWEKMWTTQE---TTIEVFEHINLMTLDIIMKCAFGQETNCQINGTYESYVKATFELGEIISSRLYNFWHHHDIIFKLSPKG-HCFQELGKVIHQYT   300
gi|21728402|ref|NP_663708.1|     LHQLMTPFLGRGLLNLDGPRWFQHRCLLTPAFHQDILKPCVDMMAHSVNMMLDKWEKTWTTQE---TTIEVFEHINLMTLDIIMKCAFGQETNCQINGTYESYVKATFELGEIISSRLYNFWHHHDIIFKLSPKG-HCFQELGKVIHQCT   300
gi|18420859|ref|NP_568463.1|     VTKRLKSILGRGVITSNGPHWAHQRRIIAPEFFLDKVKGMVGLVVESAMPMLSKWEEMMKREGEMVCDIIVDEDLRAASADVISRACFG---SSFSKGKEIFSKLRCLQKAITHNNILFSLNGFTDVVFGTKKHGNGKIDELERHIESLI   300
gi|15238644|ref|NP_197872.1|     ITKRLNPILGNGIITSNGPHWAHQRRIIAYEFTHDKIKGMVGLMVESAMPMLNKWEEMVKRGGEMGCDIRVDEDLKDVSADVIAKACFG---SSFSKGKAIFSMIRDLLTAITKRSVLFRFNGFTDMVFGSKKHGDVDIDALEMELESSI   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|29837648|ref|NP_828847.1|     DTIIQERKKSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDIDVHSEVSTFLLAGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCRLIPAVPSISRDLSKPLTFPDGCTLPAGITVVL   450
gi|114556395|ref|XP_001162991.1| DTIIQERKKSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDIDVHSEVSTFLLAGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCRLIPAVPSISRDLSKPLTFPDGCTLPAGITVVL   450
gi|73977808|ref|XP_539622.2|     EKVIQDRKKLLKDEKKHGNTQKRKDQDYLDIILSAQAENGNSFSDTDLRSEVNTFILAGHDTMAGSISWLLYHLALNPEHQERCRQEIRGILRDRSSITWDQLGEMSYTTMCIKESLRLAPPIPSISRELSKPITFPDGRSLPAGITVVL   450
gi|194665816|ref|XP_592978.4|    DKIVKNRRNSLKDENKQTNTQKRKYRDFLDIVLSAQAEN-DSFTDADLWSEVNTFMVAGHDSVSAGISWLLYHLALYPEHQEKCREEIRAILGDGSSITWDQLSEMSYTTMCIKESLRLAPPAVSISRQLSKPITFPDGRSLPAGMTVVL   450
gi|51592065|ref|NP_001003947.1| EKIIQDRKKILKNQVKQDDTQTS--QIFLDIVLSAQAEDERAFSDADLRAEVNTFMWAGHDASAASISWLLYCLALNPEHQDRCRTEIRSILGDGSSITWEQLDEMSYTTMCIKETLRLIPPVPSISRELSKPLTLPDGHSLPAGMTVVL   450
gi|21728402|ref|NP_663708.1|     EKIIQDRKKTLKDQVNQDDTQTS--QNFLDIVLSAQAGDEKAFSDADLRSEVNTFMWAGHDASAASISWLLYCLALNPEHQDRCRTEIRSILGDGSSITWEQLDEIPYTTMCIKETLRLIPPIPSISRELSKPLTLPDGHSLPAGMTVVL   450
gi|18420859|ref|NP_568463.1|     WETVKERERECVGDHKKDLMQLILEGARS--SCDGNLEDKTQSYKSFVVDNCKSIYFAGHETSAVAVSWCLMLLALNPSWQTRIRDEVFLHCKNG-IPDADSISNLKTVTMVIQETLRLYPPAAFVSREALEDTKLGN-LVVPKGVCIWT   450
gi|15238644|ref|NP_197872.1|     WETVKEREIECKDTHKKDLMQLILEGAMR--SCDGNLWDKS-AYRRFVVDNCKSIYFAGHDSTAVSVSWCLMLLALNPSWQVKIRDEILSSCKNG-IPDAESIPNLKTVTMVIQETMRLYPPAPIVGREASKDIRLGD-LVVPKGVCIWT   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|29837648|ref|NP_828847.1|     SIWGLHHNPAVWK-NPKVFDPLRFSQ-ENSDQRHPYAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLKKLSEC   553
gi|114556395|ref|XP_001162991.1| SIWGLHHNPAVWK-NPKVFDPLRFSQ-ENSDQRHPYAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLKKLSEC   553
gi|73977808|ref|XP_539622.2|     SIWGLHHNSAIWE-NPKVFDPLRFSQ-ENSDQRHTHSFLPFSAGPRNCIGQHFAMVKLKVAIALILLHFKVSPDPTRPLVFLHQIVLKPKNGVHLHLKKLP--   553
gi|194665816|ref|XP_592978.4|    SIWGLHHNPAVWE-NPEVFDPLRFSQ-ECN-KRHSHAYLPFSSGPRNCIGQNFAIAEIKVIVALILLRFQMRVEPTKPVVFVPYIFIKPKKGIYLHLKKLP--   553
gi|51592065|ref|NP_001003947.1| SIWGLHHNPAVWN-DPKVFDPLRFTK-ENSDQRHPCAFLPFSSGPRNCIGQQFAMLELKVAIALILLHFQVAPDLTRPPAFSSHTVLRPKHGIYLHLKKLLEC   553
gi|21728402|ref|NP_663708.1|     SIWGLHHNPAVWK-DPKVFDPLRFTK-ENSEQRHPCAFLPFSSGPRNCIGQQFAMLELKVAIALTLLRFRVAADLTRPPAFSSHTVLRPKHGIYLHLKKLPEC   553
gi|18420859|ref|NP_568463.1|     LIPTLHRDPEIWGADANEFNPERFSEGVSKACKHPQSFVPFGLGTRLCLGKNFGMMELKVLVSLIVSRFSFTLSPTYQHSPVFRMLVEPQHGVVIRVLRQ---   553
gi|15238644|ref|NP_197872.1|     LIPALHRDPEIWGPDANDFKPERFSEGISKACKYPQSYIPFGLGPRTCVGKNFGMMEVKVLVSLIVSKFSFTLSPTYQHSPSHKLLVEPQHGVVIRVV-----   553
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550...
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