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gi|30425358|ref|NP_780772.1|     MPKYKQRRRKLKAKAKRMSKKKE-AAVVSPKLLTPSPPLPEPERVVTSAADIPQSRNWLRPS----------------WNLRFPNIKDAINLWTNRAWCIYSCCQTCVAQSLEVLKDALFPSRVYHRELHSLKQQLCVLKRELCKLREN   150
gi|109488736|ref|XP_340872.3|    MPKFKQRRRKLRAKAKRLCKTKE-ASRVLPKLLAPPPPPPTPERVVTSSADIPQSRNWLRPS----------------WNLRLPNFKAAINLWTNRAWCIYSCCQTRVAQSLEVLKDAIFPSRVYHRELHSLKQQLCVLKSELCELQEN   150
gi|88703045|ref|NP_060774.2|     MPKFKQRRRKLKAKAERLFKKKE-ASHFQSKLITPPPPPPSPERVGISSIDISQSRSWLTSS----------------WNFNFPNIRDAIKLWTNRVWSIYSWCQNCITQSLEVLKDTIFPSRICHRELYSVKQQFCILESKLCKLQEA   150
gi|114669567|ref|XP_001172831.1| MPKFKQRRRKLKAKAKRLFKKKE-ASHFQSKLITPPPPPPSPERVGISSIDISQSRSWLTSS----------------WNFNFPNIRDAIKLWTNRVWSIYSWCQNCITQSLEVLKDTIFPSRICHRELYSVKQQFCILESKLCKLQEA   150
gi|73966734|ref|XP_852527.1|     MPKFKQRRRKLKAKAKRLFKKKE-ASNSQPKLIIPPPPPPSPERVIILSADTALSRSLLRSS----------------WNFRFPNIKDTVKLWTNRVWSIYKWCQNCMAQSLEVLKDTIFPSHFCHRELHNLRQQFCILESELHKLQET   150
gi|148232834|ref|NP_001091606.1| MPKFKQRRRKLKAKAKRLFKRKE-ASHLQSKLVTPPPPPPSPARAVIPSTDIPISRSWLRLS----------------WNFRFPSFTNAIKLLANRVWSIYSWCQSCMTQSFEVLKNTIFPSRLCHRELRSLKQRFCVLENEVCKLQEA   150
gi|118100300|ref|XP_001235261.1| MAKHKQRRRKPRGRTKPGRRREAGAAASQPQLSAFHTTPPSAQRRTAAPRGRGDRSAAIRPGPAHLPPDAAAAAARASLCSLPLHGVKHVVKLLAAVAALLYCWCHSAVAQSFTAVKEMIFPSQVYLKELNAFKEQLEKLEMEFSRIQGI   150
gi|125828137|ref|XP_695751.2|    MGGYRGLGCAYQRRRKRNGSSRR---WALKSKMAPTAPDPDSKTKVVGMGEMSIQTTKRSSP------------------------LSITALLSAFRSVVQKCRRTIYQTCRGFFNVFLFWRGYAERVESLHQKVDELQRELALLHST   150
                                 1.......10.......20.......30.......40.......50.......60.......70.......80.......90.......100.......110.......120.......130.......140.......150
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gi|30425358|ref|NP_780772.1|     LKS--ISENSSCSSCCHKCCPSDKLTTVPACAPTTNGESQTVLSSTQPQPANHPPSPPPLPPPPPPPPPLPPPPPPLAPLLLRKSGTTKALQVEPLK--KDGPMHITVKDLLNVKLKKTQSVDERKKLVPSPPEERTPLVTVSDLQHVTL   300
gi|109488736|ref|XP_340872.3|    LKS--ISEHSSRSSCCHTCCGGDRLTTVPACAPTTHGESQTALPPTLPQPASHPPPPPPLLPLPPPPPPLPPPPPPLAPLLLRKSGSTKALQVEPLK--KDGPMHITVKDLLTVKLKKTQNIDERRKFVPSPPEERTPLVTVSDLQRITL   300
gi|88703045|ref|NP_060774.2|     LKT--ISESSSCPSCGQTCHMSGKLTNVPACVLITPGDSKAVLPPTLPQPASHFP-------PPPPPPPLPPPPPPLAPVLLRKPSLAKALQAGPLK--KDGPMQITVKDLLTVKLKKTQSLDEKRKLIPSP-KARNPLVTVSDLQHVTL   300
gi|114669567|ref|XP_001172831.1| LKT--ISESSSCPSCGQTCHMSGKLTNVPACVLITPGDSKAVLPPTLPQPASHLP-------PPPPPPPLPPPPPPLAPVLLRKPSLAKALQAGPLK--KDGPMQITVKDLLTVKLKKTQSLDERRKLIPSP-KARNPLVTVSDLQHVTL   300
gi|73966734|ref|XP_852527.1|     MKA--VLENSSCPSCGQMCHISGKLTNVPACVLTTPGESQAVLPPSLPQSATHLPPLPPP-PPPPPPPPLPPPPLPRAPLLLRKFDHTKALQAGSLK--KDGPMQITVEDLLTVKLKKTQCFDEKKKFAPSP-KARNPLVTVSDLQRVTL   300
gi|148232834|ref|NP_001091606.1| LKA--ISENSSCTSCGQACHTGGEHPDVPACALASPADSAALRPPSPAQPASRPPP--PL-PPPPPPPPLPPPPPPTAPLLLRKPALTKALQAGPLK--KNGPMQITVKDLLTVKLKKTQSLDERRKLVPSP-KAQKALVTISDLQRVTL   300
gi|118100300|ref|XP_001235261.1| LQKSGITTLSSESSHCQRCS--KTVLGAPVEVQPDPPPSVPGPPAVQLQPTAVPPPLPP--PPPPPPPPLPPPKLPAAPLLLKRGNGSKALLEPSVK--KDAPMHITLKDLLNVKLRKTDSS-LRTDKAGSPARTRRALITVSDLQSVNL   300
gi|125828137|ref|XP_695751.2|    LKLS-------------------------QEAKTSDGQWEMPDGVRPLVSPPPPP----PPPPPPPPLPPPQILVTLPPKVASFSKKTAQANSLKEKQNGPVAVTLRDLQAVQLRKVTVS---QKTLMSPEKRRSPLVTLADLQKVKL   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|30425358|ref|NP_780772.1|     KPNSRVSATRIKNVLITPGKSQIDLRKLLRKVQVERSPGGTPLNNKENMDTGTGLTPVMTRALRRKFQLAHPQSPTQSLPLSTSSFDEQN   390
gi|109488736|ref|XP_340872.3|    KPNSRVLATRIKNVLITPGKSQIDLRKLLRKVEVERSPGGTPLNNKENMDTGTGLTPVMTRALRRKFQLAHPQSPTQSLPLSTSNFDEQN   390
gi|88703045|ref|NP_060774.2|     KPNSKVLSTRVTNVLITPGKSQMDLRKLLRKVDVERSPGGTPLTNKENMETGTGLTPVMTQALRRKFQLAHPRSPTPTLPLSTSSFDEQN   390
gi|114669567|ref|XP_001172831.1| KPNSKVLSTRVTNVLITPGKSQMDLRKLLRKVDVERSPGGTPLINKENMETGTGLTPVMTQALRRKFQLAHPRSPTPTLPLSTSSFDEQN   390
gi|73966734|ref|XP_852527.1|     KPNSKMLSTRVTNVLITPGKSQIDLRKLLRKVDVERSPGGTPLTNKENMETGTGLTPVMTRALRRKFQMAHPRSPTQTLPLSTSSFDEQN   390
gi|148232834|ref|NP_001091606.1| KPKSKALSTRVTNVLITPGKSQLDLRKLLRKVDVERSPGGTPLTNKENVETGTGLTPVMTQALKRKFQLAHPRSPPQTLPVSTSSFDEQN   390
gi|118100300|ref|XP_001235261.1| RSKSKP-SAHVTSSLNTPPKNQLDLRKHLKKVNIQRSPGGTPLN-KENTECGTGLTPIMTQALRRKFQMAHPKSPSPARLSAANSFDEHK   390
gi|125828137|ref|XP_695751.2|    RRSNSDLPLKLRSSLRTPTKNGMSLRVPLRKVNLTRSPGGTPRCNKENNVTDSSLDPSMTKGLGNKYLNSLTKGLSPFKCA--------   390
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390
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