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gi|31543675|ref|NP_033153.2|     MPAHMLQ-EISSSYTTTTTITAPPSG---NEREKVKTVPLHLEEDIRP-EMKEDIHDPTYQDEEG-PPPKLEYVWRNIILMVLLHLGGLYGIILVPS-CKLYTCLFGIFYYMTSALGITAGAHRLWSHRTYKARLPLRIFLIIANTMAFQ   143
gi|21070936|ref|NP_631931.1|     MPAHMLQ-EISSSYTTTTTITEPPSGNLQNGREKMKKVPLYLEEDIRP-EMREDIHDPSYQDEEG-PPPKLEYVWRNIILMALLHVGALYGITLIPS-SKVYTLLWGIFYYLISALGITAGAHRLWSHRTYKARLPLRIFLIIANTMAFQ   146
gi|53759151|ref|NP_005054.3|     MPAHLLQDDISSSYTTTTTITAPPSRVLQNGGDKLETMPLYLEDDIRP-DIKDDIYDPTYKDKEG-PSPKVEYVWRNIILMSLLHLGALYGITLIPT-CKFYTWLWGVFYYFVSALGITAGAHRLWSHRSYKARLPLRLFLIIANTMAFQ   147
gi|114632351|ref|XP_001168563.1| MPAHLLQDDISSSYTTTTTITAPPSRVLQNGGDKLETTPLYLEDNIRP-DIKDDIYDPTYKDKEG-PSPKVEYVWRNIILMSLLHLGALYGITLIPT-CKFYTWLWGVFYYFVSALGITAGAHRLWSHRSYKARLPLRLFLIIANTMAFQ   147
gi|73998637|ref|XP_543968.2|     MPAHLLQEEISSSYTTTTTITAPPSRILQNGGGKLEKPSLYLEEDIRP-EIKDDIYDPTYKDPEGRPKPKVEYVWRNIILMSLLHVGALYGITLIPT-CKTYTWLWVFSYYLISAVGITAGAHRLWSHRTYKARLPLRLFLIIANTMAFQ   148
gi|45382443|ref|NP_990221.1|     MPAHLLQEEEFSSASSTTTVI---SRVTKNGNVIMEKDLLNHDDVAAERGMVDDLFDETYREKEG-PKPPLRYVWRNIILMSLLHLGAIIGLTLIPS-AKIQTLAWAILCFVLSALGITAGSHRLWSHRSYKATLPLRIFLTIANSMAFQ   145
gi|66472330|ref|NP_001018541.1|  ----------MADVTTTT--------------------------------EDVFDDSYVEKPG-PSPPVQIVWRNVILMTLLHLGALYGMTILPF-VSSLTLIWTGVCFMVSALGITAGAHRLWSHRSYRASLPLRIFLAVANSMAFQ   104
gi|24646500|ref|NP_731781.1|     MSPNIIGSTFILAEIAIA----------DGNNNKMAATPAASAAPSAATPSQKVAKKAEAKTPENKP-YELEIVWRNVGLFVILHSMALYGLYLVFAESAYWELLPVYATMFLGGLGITAGVHRLWSHKAYKAKLPLRIFLMLCQSLAFQ   139
gi|158290105|ref|XP_311704.4|    MAPNVLGNTILLAEACIE----------QEDNNNNAS---IGTQQYKSKSFLNVAPKPAPITEELKRRYHHVYVWRNIIAFIYLHLGFLYGSYLLVTSAKWSTFFFALALGSCGALGITAGAHRLWSHRAYKAKWPLRLFLMLAQTLAFQ   137
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 *.::**.****.****:.*.*****: **:**:*:.**: :*** *  :*  : :.*:: : :****:: *   : : ** :* :..::   .::  .      ::*: : *: *********:* :*** *:.. :* :*:  : ***:
gi|31543675|ref|NP_033153.2|     NDVYEWARDHRAHHKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGGKLDMSDLKAEKLVMFQRRYYKPGLLLMCFILPTLVPWYCWGETFVNSLFVSTFLRYTLVLNATWLVNSAAHLYGYRPYDKNIQSRENILVSLGAVGEGF   293
gi|21070936|ref|NP_631931.1|     NDVYEWARDHRAHHKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGGKLDMSDLKAEKLVMFQRRYYKPGLLLMCFILPTLVPWYCWGETFLHSLFVSTFLRYTLVLNATWLVNSAAHLYGYRPYDKNIQSRENILVSLGSVGEGF   296
gi|53759151|ref|NP_005054.3|     NDVYEWARDHRAHHKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYYKPGLLMMCFILPTLVPWYFWGETFQNSVFVATFLRYAVVLNATWLVNSAAHLFGYRPYDKNISPRENILVSLGAVGEGF   297
gi|114632351|ref|XP_001168563.1| NDVYEWARDHRAHHKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYYKTGLLLMCFILPTLVPWYFWGETFQNSVFVATFLRYAVVLNATWLVNSAAHLFGYRPYDKNISPRENILVSLGAVGEGF   297
gi|73998637|ref|XP_543968.2|     NDVYEWARDHRAHHKFSETDADPHNSRRGFFFSHVGWLLVRKHPAVKEKGGLLDLSDLKAEKLVMFQRRYYKPGILLMCFILPTFVPWYFWGETFLHSVCVATLLRYAIVLNATWLVNSAAHLYGYRPYDKNISPRENILVSLGAAGEGF   298
gi|45382443|ref|NP_990221.1|     NDIYEWARDHRVHHKFSETHADPHNAMRGYFFSHMAWLLVRKHPDVIEKGQKLDLSDLKADKVVMFQRRYYKPSVVLLCFTLPTLVPWYFWDESIIISFFIPAILRYTLGLNATWLVNSAAHMFGNRPYDQNINPRENPLVSVGALGEGF   295
gi|66472330|ref|NP_001018541.1|  NDIYEWARDHRVHHKFSETDADPHNARRGFFFAHIGWLLVRKHPEVIDKGRKLTFEDLKADSVVMFQRRHYKLSVVVMCFLIPTLVPWFFWEESLWTAYLVPCLLRYAVVLNATWLVNSAAHMWGMRPYDHNINPRENKFVAFSAIGEGF   254
gi|24646500|ref|NP_731781.1|     NSIWEWTRDHRVHHKFTDTHADPHNSRRGFFFAHMGWLMCKKHPDVTSKGKQISMEDIEQDPVVMFQKKMYFVVMPICCFALPMIFPYYVMGSSLRVCFFTCSMLRFCLSLHFTWLVNSAAHFYGMKPYDVNVSAMNNKLVSTLTIGEGW   289
gi|158290105|ref|XP_311704.4|    NSVYEWVRDHRVHHKFTDTDADPHNATRGFFFSHIGWLMVKKHPDVKARGRAVDMSDLEQDGIVMFQKRYYALLMPLFCFILPTFLAYYYLDETFSNAWYVVAIFRYVLSLNATWLVNSAAHIWGTKPYDRNISPTNNTFVAIAAYGEGW   287
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 ***** ** ** ::*      * *.  ** :. :* * * : *:.  :  *  *****.:
gi|31543675|ref|NP_033153.2|     HNYHHTFPFDYSASEYR-WHINFTTFFIDCMAALGLAYDRKKVSKATVLARIKRTGDGSHKSS-------------------------------------------------------   355
gi|21070936|ref|NP_631931.1|     HNYHHAFPYDYSASEYR-WHINFTTFFIDCMAALGLAYDRKKVSKAAVLARIKRTGDGSHKSS-------------------------------------------------------   358
gi|53759151|ref|NP_005054.3|     HNYHHSFPYDYSASEYR-WHINFTTFFIDCMAALGLAYDRKKVSKAAILARIKRTGDGNYKSG-------------------------------------------------------   359
gi|114632351|ref|XP_001168563.1| HNYHHSFPYDYSASEYR-WHINFTTFFIDCMAALGLAYDRKKVSKAAILARIKRTGDGNYKSG-------------------------------------------------------   359
gi|73998637|ref|XP_543968.2|     HNYHHSFPYDYSASEYR-WHINFTTFFIDCMAALGLAYDRKKVSKAAILARIKRTGDGSYKSG-------------------------------------------------------   360
gi|45382443|ref|NP_990221.1|     HNYHHTFPYDYSTSEFG-WRFNLTTAFIDLMCLLGLASDRKKVSKEVILARKMRTGDGSHKSG-------------------------------------------------------   357
gi|66472330|ref|NP_001018541.1|  HNYHHTFPHDYATSEFG-SRLNVTKAFIDLMCFLGLANDCRRVTHETILARVQRTGDGSHKSG-------------------------------------------------------   316
gi|24646500|ref|NP_731781.1|     HNYHHVFPWDYKAAELGTYSFNWTTAFIDVMAKIGQAYDLKFVSQEMVYKRVLRTGDGSHIAALLDANNNSAIPTSELVAHLDHEKEEHAIWGWDDKDISEEDRKGANVVNKESECKLD   408
gi|158290105|ref|XP_311704.4|    HNYHHVFPWDYKTSELGTYSTNFTTAAIDFFARIGWAYDLKSVSDELIRKRVLRTGDGSHQYNEQELQAR----MVDYVNQLDHE-SEQAVWGWDDKDMNEQDRQDATVRNK-------   394
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410........
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