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                                 *.     :.* :    *                     *:                   .                   .                  :*    :*  :  ::.*::       .  :*
gi|24642168|ref|NP_573023.2|     MSGSGLDENPFGEPNLDNPFADPAIQQARRLQSGAALVSLEDYNPFEEQAKPQLQIN--STNTAAVVQPLSQNIPPP-------QTSSLGASAPSTS-----IQITSEELQRRQEELDRKAAELDRREQ-----QLQG-NVP----QLNN   126
gi|158290380|ref|XP_311983.4|    MAG--LNDNPFGEPEIDNPFADPSIQQITRNTT-SLQQTLDDYRPFDNDRNVLGNGS--GASQPATLHPSTQSPPVYNQSGAQFQTNSNGAMAASGSKPDGMTQISTAELERAQEELERKTRELERREA-----NMMR-STNG---QPNN   136
gi|116256358|ref|NP_004857.4|    MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGGV--KMPNVPNTQPAIMKPTEEH------PAYT--QIAKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHG---RKNN   119
gi|114599518|ref|XP_001141573.1| MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGSV--KMPNVPNTQPAIMKPTEEH------PAYT--QIAKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHGTSSRKNN   122
gi|58037395|ref|NP_083429.1|     MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGSV--KMPNVPNTQPAIMKPTEEH------PAYT--QITKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHG---RKNN   119
gi|34853043|ref|XP_342175.1|     MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGGV--KMPNVPNTQPAIMKPTEEH------PAYT--QITKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHG---RKNN   119
gi|73952187|ref|XP_859726.1|     MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGTV--KMPNVPSTQPAIMKPTEEH------PAYT--QIAKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHGTLSRKNN   122
gi|115496974|ref|NP_001069522.1| MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTPPPGNV--KMPNVPSTQPAIMKPTEEH------PAYT--QIAKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQNLSQHG--RKNN   119
gi|118103846|ref|XP_414682.2|    MSD--FDSNPFADPDLNNPFKDPSVTQVTRNVP----PGLDEYNPFSDSRTAPPGNV--KMPNVPSTQPAIMKPTEEP------PAYT--QIAKEHA-------LAQAELLKRQEELERKAAELDRRER-----EMQSLNQQG--GRKNN   120
gi|45387801|ref|NP_991255.1|     MSD--FDSNPFADPDFSNPFQDPSVTQVTRTAP----PGLEEYNPFTDTKPVPPGSAPKSVPPTTNTQPAIMKPTEEP------PAYTQSQQTPDQS-------RAQAELLRRQEELERKAAELDRRER-----EMQSLNASG--GRKNN   124
gi|17508301|ref|NP_490911.1|     MSD-----NPFADP-FSAPPPPPAAAAAASKPTSGGTIETEDFNPFANRAG--------GSNAQPTTHQSTGSLGNKS-------AGMDDELFRKQQ-----------DLERRAQELRMREEELDRRQRSAAGGNNLNTNAQNNAPRPHN   118
gi|15219893|ref|NP_176320.1|     MAN-RYDPNPFAEEEEVNPFANARGVPPASNSR---------LSPLP-------------PEPVGFDYGRTVDIPLDR--------AGTQDLKKKEK-----------ELQAKEAELKRREQDLKRKED--------AAARAGIVIEVKN   100
gi|15220305|ref|NP_172584.1|     MGG-RYDRNTFDEQDEVNPFANPGSVPAASNSR---------LSPLP-------------PEPAGFGYGRTVDIPLDRP------GSGAQDLKKKEK-----------ELQAKEADLRRREQDLKRKQD--------AAARAGIVIEAKN   102
gi|15226410|ref|NP_179680.1|     MS--RYQSHSFDD-GEINPFANPTSVP-AATSK---------LSPLP-------------PEP--YDRGATMDIPLDS----------GKDLKAKEK-----------ELREKEAELKRREQEIKRKED--------AIAQAGIVIEEKN    93
gi|18379111|ref|NP_563686.1|     MA--RHDPNPFAD-EEINPFANHTSVPPASNSY---------LKPLP-------------PEP--YDRGATVDIPLDS----------GNDLRAKEM-----------ELQAKENELKRKEQELKRRED--------AIARTGVVIEEKN    94
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 **       . * :::*:  :*  . *:     :   :  .  :. *:.  :                *: :      * .:: *:** * * :.**:: *  **:    :      . : .    :      * : ::  :      :.:
gi|24642168|ref|NP_573023.2|     WPPLPDNFCVKPCFYQDFEVEIPPEFQKLVKRLYYIWIFYTMTLLANVIGGLILLFHAG-EFETFFLAIFYTMLFSPASYVCWFRPAYKAFRNDSSFNFMVFFFIYFFQTLYSIVQAVG----FNKMGYCGFITAIGQFDGQASGIIVGI   271
gi|158290380|ref|XP_311983.4|    WPPLPAFCPMQPCFYHDISLDIPSEFQKTVTRLYKLWMFYALVMVVNILGGLVILIHSG-EFRTFGLSIFYAVLFTPASFLCWYRPAYKAFKTDSSFNFMMFFFIFSFQALVTTIQTIG----FPGSGTCGVIMAISQFS-SGWGVVVGL   280
gi|116256358|ref|NP_004857.4|    WPPLPSNFPVGPCFYQDFSVDIPVEFQKTVKLMYYLWMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---QNIPVGI   262
gi|114599518|ref|XP_001141573.1| WPPLPSNFPVGPCFYQDFSVDIPVEFQKTVKLMYYLWMCDTLTLFLNIFGCLAWFCVDSARAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---QNIPVGI   265
gi|58037395|ref|NP_083429.1|     WPPLPSNFPVGPCFYQDFSVDIPVEFQKTVKLMYYLWMFHAVTLFLNIFGCLAWFCVDSSRAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---KNIPVGI   262
gi|34853043|ref|XP_342175.1|     WPPLPSNFPVGPCFYQDFSVDIPVEFQKTVKLMYYLWMFHAVTLFLNIFGCLAWFCVDSSRAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---KNIPVGI   262
gi|73952187|ref|XP_859726.1|     WPPLPGNFPVGPCFYQDFSVDIPVEFQKTVKIMYYLWMFHAVTLFLNIFGCLAWFCVDPTRGVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---QSIPVGI   265
gi|115496974|ref|NP_001069522.1| WPPLPDNFPVGPCFYQDFSVDIPVEFQKTVKIMYYLWMFHAVTLFLNIFGCLAWFCVDPPRGVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FHNWGNCGWISSLTGLN---KSIPVGI   262
gi|118103846|ref|XP_414682.2|    WPPLPENFPVGPCFYQDFSVDIPVEFQKTVKIMYYLWMFHTVTLFLNIFGCLAWFYVDATRGVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFAVHVLQAAG----FQRWGNCGWISSLTGLN---KSIPVGI   263
gi|45387801|ref|NP_991255.1|     WPPLPEKFPVGPCFYHDISVDIPVEYQKTVKIMYYLWMFHTGTLFANIFGCLSWFCVDASRGVDFGLAMLWFMLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFFVYICQFGVHVLQAIG----ITGWGASGWISALTGLN---TSIPVGI   267
gi|17508301|ref|NP_490911.1|     WPPLPTIIPIEPCFYQDIEVEIPVQFQKTVTFAYYVFLMYVLALVVNVLASLFYMIFAGGSIGQLFLACIQLALFSPCSFLFWFRPVYKAFRNDSSFNFMVFFFVLFFHCIFTFVQTLG----LSNY-ACGWINALDTFN---VSVPIAL   260
gi|15219893|ref|NP_176320.1|     WP------PFFPLIHHDIANEIPVHLQRLQYVTFATYLGLVLCLFWNII-AVTTAWIKGEGVTIWLLALIYFIAGVPGGYVLWYRPLYRAFRTDSALSFGWFFLFYMLHIAFCVFAAVAPPVVFKGKSLAGILPAIDVLS---GQAIVGI   240
gi|15220305|ref|NP_172584.1|     WP------TFFPLIHHDIANEILVRLQRLQYIAFATYLGLVLALFWNII-AVTTAWIKGEGVTIWLLAVIYFISGVPGGYVLWYRPLYRAFRSDSAFNFGWFFLFYMLHILFCLFAAVAPPIVFKGKSLAGILPAIDVLS---AQALVGI   242
gi|15226410|ref|NP_179680.1|     WP------PFFPLIHHDISNEIPIHLQRIQYVAFTSMLGLVVCLLWNIV-AVTTAWIKGEGPTIWFLAIIYFISGVPGAYVMWYRPLYRAMRTDSALKFGWFFFTYLFHIAFCVFAAVAPPIIFKGKSLTGILPAIDVLS---GNILVGI   233
gi|18379111|ref|NP_563686.1|     WP------EFFPLIHHDIPNEIPIHLQKIQYVAFTTLLGLVGCLLWNIV-AVTVAWIKGEGPTIWLLSIIYFLAGVPGAYVLWYRPLYRATRTDSALKFGAFFFFYVFHIAFCGFAAVAPPVIFQGKSLTGFLPAIELLT---TNAAVGI   234
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 : :     :       :  : :::  :*  .                  : *:  :
gi|24642168|ref|NP_573023.2|     LLLNVAFCFTAVAVANVLMITKIHSIYRSTG-ASMAKAQAEFTTEFLRNQHVQEAASSAVNTAINSQFNNSRY--------------------   343
gi|158290380|ref|XP_311983.4|    FLMCIALAYGTCAAGNIFMLTKIHQIYRSGDKITMGKAREEFQSQFMSNSIVRDAAAGAARASVSSTLN--RY--------------------   351
gi|116256358|ref|NP_004857.4|    MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAASSAAQNAFKG---------NQI-------   338
gi|114599518|ref|XP_001141573.1| MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAASSAAQNAFKG---------NQI-------   341
gi|58037395|ref|NP_083429.1|     MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAATSAAQNAFKG---------NQM-------   338
gi|34853043|ref|XP_342175.1|     MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAATSAAQNAFKG---------NQM-------   338
gi|73952187|ref|XP_859726.1|     MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASSAATSAAQNAFKG---------NQI-------   341
gi|115496974|ref|NP_001069522.1| MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAASSAAQNAFKGTMDSRKQFSNQEKKYSVYF   354
gi|118103846|ref|XP_414682.2|    MMIIIAALFTASAVISLVMFKKVHGLYRTTG-ASFEKAQQEFATGVMSNKTVQTAAANAASTAATSAAQNAFKG---------NRM-------   339
gi|45387801|ref|NP_991255.1|     IMILIAALFTASAVISLIMFKKVHALYRTTG-ASFEKAQQEFATGVMANKTVQTAAANAAS----SAARGAFKE----------QI-------   338
gi|17508301|ref|NP_490911.1|     LMLISAITFTVALTGMVTALVKVHRLYRGAG-FSIDKARQEFTNGVMSDAGVQRATQAATQAAAGAAFNQATQGRF-----------------   335
gi|15219893|ref|NP_176320.1|     FYFIGFAFFCLESVVSIWVIQQVYMYFRGSG--------------KQDQMRREAARGALRAAV----------------------------   289
gi|15220305|ref|NP_172584.1|     FYFIGFGLFCLESVVSIWVIQQVYMYFRGSG--------------KADDMRRDAARGAMRAAI----------------------------   291
gi|15226410|ref|NP_179680.1|     FYFIGFGFFCLESLVSIWVIQQVYMYFRGSG--------------KAAEMKQEATRRAMMAAL----------------------------   282
gi|18379111|ref|NP_563686.1|     MYFIGAGFFCIETLLNIWVIQQVYAYFRGSG--------------KAAEMKREATKSTLMRAL----------------------------   283
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390...
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