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                                 * *** ***::****** *:****   *::***:**.  ** .******:*::* ******************************:****.** **:***********:*******:**************:** ***:***: :*****
gi|54114982|ref|NP_001005757.1|  MAHQLLCCEVETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEILPSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLNRFLSLEPVKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPDELLQMELLLVNKLKW   150
gi|114053227|ref|NP_001039738.1| MAHQLLCCEMETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEILPSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPDELLHMELVLVNKLKW   150
gi|6680868|ref|NP_031657.1|      MEHQLLCCEVETIRRAYPDTNLLNDRVLRAMLKTEETCAPSVSYFKCVQKEIVPSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSLEPLKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPEELLQMELLLVNKLKW   150
gi|31377523|ref|NP_741989.2|     MEHQLLCCEVETIRRAYPDTNLLNRPGLRAMLKTEETCAPSVSYFKCVQREIVPSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSLEPLKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPEELLQMELLLVNKLKW   150
gi|16950655|ref|NP_444284.1|     MEHQLLCCEVETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEVLPSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPEELLQMELLLVNKLKW   150
gi|45382411|ref|NP_990712.1|     MEHQLQCCEVETIRRAYLDANLLNDRVLQTMLKAEETCSPSVSYFKCVQKEILPYMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSFEPLKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPDELLQMELLLVNKLKW   150
gi|18858509|ref|NP_571100.1|     MEHQLFCCEVDTIRRAYQDSNLLNDRVLQTMLKAEENYLPSPNYFKCVQKEIVPKMRKIVATWMLEVCEEQKCEEEVFPLAMNYLDRFLSVEPTKKTRLQLLGATCMFLASKMKETVPLTAEKLCIYTDNSVRPGELLQMELLALNKLKW   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 :**::**********:*:*  :..** :***************:**:.****:*****.** *** * ..:  **    *.***:**:.*.****:******:***********:      : *    *::..*:********::*
gi|54114982|ref|NP_001005757.1|  NLAAMTPHDFIEHFLSKMPVAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIKCDADCLRACQEQIEALLESSLRQAQQQSLDPKAAEEEEE-EEEADLACTPTDVRDVNI   296
gi|114053227|ref|NP_001039738.1| NLAAMTPHDFIEHFLSKMPVAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVAAAAQGLHLGSANGFLSYHRLTRFLSKVIRCDPDCLRACQEQIEALLESSLRQAQQQNLDPKAAEEEEE-EEEVDLACTPTDVRDVNI   296
gi|6680868|ref|NP_031657.1|      NLAAMTPHDFIEHFLSKMPEADENKQTIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLGSPNNFLSCYRTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQN-VDPKATEEEGEVEEEAGLACTPTDVRDVDI   296
gi|31377523|ref|NP_741989.2|     NLAAMTPHDFIEHFLSKMPEADENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLGSPNNFLSCYRTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQN-IDPKATEEEGEVEEEAGLACTPTDVRDVDI   296
gi|16950655|ref|NP_444284.1|     NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAVQGLNLRSPNNFLSYYRLTRFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQN-MDPKAAEEEEEEEEEVDLACTPTDVRDVDI   296
gi|45382411|ref|NP_990712.1|     NLAAMTPHDFIEHFLTKMPLAEDTKQIIRKHAQTFVALCATDVKFISNPPSMIAAGSVVAAVQGLHLGNTNTFLSYQCLTHFLSQVIKCDPDCLRACQEQIESLLESSLRQAQQH----NVSSETKTVEDEADLSCTPTDVRDVNI   296
gi|18858509|ref|NP_571100.1|     DLASVTPHDFIEHFLAKLPIHQSSKQILRKHAQTFVALCATDVNFIASPPSMIAAGSVAAAVQGLYLKSTDSCLSSQNLTNFLSQVIRSDPDCLRSCQEQIESLLESSLRQAQQH-----ISTETKRVEEDVDLSCTPTDVRDINI   296
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290......
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