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gi | 54114982 | ref | NP_001005757.1 | MAHQLLCCVEETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEILPSMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPDELLQMELLLVNKLKW 150
gi | 114053227 | ref | NP_001039738.1 | MAHQLLCCVEETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEILPSMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPDELLHMLVLVNKLKW 150
gi | 6680868 | ref | NP_031657.1 | MEHQLLCCVEETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEIVPSMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPLKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPELLOMELLLVNKLKW 150
gi | 31377523 | ref | NP_741989.2 | MEHQLLCCVEETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQREIVPSMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPLKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPELLOMELLLVNKLKW 150
gi | 16950655 | ref | NP_444284.1 | MEHQLLCCVEETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEVLPVPSMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPELLOMELLLVNKLKW 150
gi | 45382411 | ref | NP_990712.1 | MEHQLCCVEETIRRAYLDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEILPYMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSLEPLKKSRLQLLGATCMFVASKMKEIPLTAEKLCIYTDNSIRPDELLQMELLLVNKLKW 150
gi | 18858509 | ref | NP_571100.1 | MEHQLFCCVEETIRRAYQDSNLLNDRVLRAMLKAEENYLPSPNYFKCVQKEIVPKMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSVEPTKKTTRQLLGATCMFLASKMKEIPLTAEKLCIYTDNSVRPGELLOMELLALNKLKW 150
gi | 292616296 | ref | XP_002662962.1 | MEHQLFCCVEETIRRAYQDSNLLNDRVLRAMLKAEENYLPSPNYFKCVQKEIVPKMRKIVATWMLLEVCEEKCEEEVFLAMNYLDRFLSVEPTKKTTRQLLGATCMFLASKMKEIPLTAEKLCIYTDNSVRPGELLOMELLALNKLKW 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 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMVAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIKCDADCLRACQEQIEALLESRLQAQQQLDPKAAEEEE-EEEADLACTPTDVRDVI 295
gi | 114053227 | ref | NP_001039738.1 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMVAAGSVVAAAQGLHLGSSNSFLSYHRLTRFLSKVIRCDPCLRACQEQIEALLESRLQAQQQLDPKAAEEEE-EEEVDLACTPTDVRDVI 295
gi | 6680868 | ref | NP_031657.1 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMVAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIRCDPCLRACQEQIEALLESRLQAQQQLDPKAAEEEE-EEEVDLACTPTDVRDVI 295
gi | 31377523 | ref | NP_741989.2 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMVAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIRCDPCLRACQEQIEALLESRLQAQQQLDPKAAEEEE-EEEVDLACTPTDVRDVI 295
gi | 16950655 | ref | NP_444284.1 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMVAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIRCDPCLRACQEQIEALLESRLQAQQQLDPKAAEEEE-EEEVDLACTPTDVRDVI 295
gi | 45382411 | ref | NP_990712.1 | NLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCANDVKFISNPPSMIAAGSVVAAVQGLHLGSSNSFLSYHRLTRFLSKVIRCDPCLRACQEQIESLLESRLQAQQH---NVSETKTVEEADLACTPTDVRDVI 292
gi | 18858509 | ref | NP_571100.1 | DLASVTPHDFIEHFLAKLPVHSSKQILRKHQTFVALCANDVNFIAASPPSMIAAGSVVAAVQGLYLYKSDCLSSQNLNFLSOVIRSDPCLRSQEQIESLLESRLQAQQH---ISTETKRV EEDVDLACTPTDVRDVI 291
gi | 292616296 | ref | XP_002662962.1 | DLASVTPHDFIEHFLAKLPVHSSKQILRKHQTFVALCANDVNFIAASPPSMIAAGSVVAAVQGLYLYKSDCLSSQNLNFLSOVIRSDPCLRSQEQIESLLESRLQAQQH---ISTETKRV EEDVDLACTPTDVRDVI 291
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....

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