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gi|6755775|ref|NP_035707.1| MPPSGRLRLPLLLPLPWLWLVTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP-LPEAVLALYNSTRDRVAGESADPEPEPEAD---YYAKEVTRVLMVDRNNAIYEKTKDISHSIYMFNTSDIREAV 144
gi|11024652|ref|NP_067589.1| MPPSGRLRLPLLLPLPWLWLVTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP-LPEAVLALYNSTRDRVAGESADPEPEPEAD---YYAKEVTRVLMVDRNNAIYDKTKDISHSIYMFNTSDIREAV 144
gi|63025222|ref|NP_000651.3| MPPSGRLRLPLLLPLPWLWLVTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP-LPEAVLALYNSTRDRVAGESADPEPEPEAD---YYAKEVTRVLMVDRNNAIYDKTKDISHSIYMFNTSDIREAV 144
gi|114677451|ref|XP_512687.2| MPPSGRLRLPLLLPLPWLWLVTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP-LPEAVLALYNSTRDRVAGESADPEPEPEAD---YYAKEVTRVLMVDRNNAIYDKTKDISHSIYMFNTSDIREAV 144
gi|50979134|ref|NP_001003309.1| MPPSGRLRLPLLLPLPWLWLVTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP-LPEAVLALYNSTRDRVAGESADPEPEPEAD---YYAKEVTRVLMVDRNNAIYDKTKDISHSIYMFNTSDIREAV 144
gi|189534498|ref|XP_001923657.1| -----MKAESLLLALQCLLGFV--QYSRALSTCNPLDLELIKRRKRIEIRGQILSKLRLPKPEVEEKEKLIENIPAELISVYNSTMELNEEAANPVQHTIEDPHEEYAKEIHKFTMKLR-----EKPEKY-LVFNIIDIKHKL 133
gi|68397085|ref|XP_692338.1| -----MKAESLLLALQCLLGFV--QYSRALSTCNPLDLELIKRRKRIEIRGQILSKLRLPKPEVEEKEKLIENIPAELISVYNSTMELNEEAANPVQHTIEDPHEEYAKEIHKFTMKLR-----EKPEKY-LVFNIIDIKHKL 132
gi|33504525|ref|NP_878293.1| -----MRLVCLVLTALCLV-----TCTGSMSTCKKLDLEVRKKRIEIRGQILSKLRLPKPEVEEKEKLIENIPAELISVYNSTMELNEEAANPVQHTIEDPHEEYAKEIHKFTMKLR-----EKPEKY-LVFNIIDIKHKL 128
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6755775|ref|NP_035707.1| PEPVLLSRABELRLQRLMSSV---EQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVVROWLNQGDGIGGFRFSAHCSCD-KDNK--LHVEINGISPKRRGDLGIHDMNRPFLLMATAFLERAQHLHSSRRRRALDINYCFSS 288
gi|11024652|ref|NP_067589.1| PEPVLLSRABELRLQRFKSTV---EQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVVROWLNQGDGIGGFRFSAHCSCD-KDNV--LHVEINGISPKRRGDLGIHDMNRPFLLMATAFLERAQHLHSSRRRRALDINYCFSS 288
gi|63025222|ref|NP_000651.3| PEPVLLSRABELRLRLKLV---EQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVVROWLNQGDGIGGFRFSAHCSCD-KDNT--LQVDINGFTTGRGDLATIHGMNRPFLLMATAFLERAQHLHSSRRRRALDINYCFSS 288
gi|114677451|ref|XP_512687.2| PEPVLLSRABELRLRLKLV---EQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVVROWLNQGDGIGGFRFSAHCSCD-KDNT--LQVDINGFTTGRGDLATIHGMNRPFLLMATAFLERAQHLHSSRRRRALDINYCFSS 288
gi|50979134|ref|NP_001003309.1| PEPVLLSRABELRLRLKLV---EQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVVROWLNQGDGIGGFRFSAHCSCD-KDNT--LQVDINGFTTGRGDLATIHGMNRPFLLMATAFLERAQHLHSSRRRRALDINYCFSS 288
gi|189534498|ref|XP_001923657.1| GANHVLVQAEFRRLRIKEPKMGDSEQRLELYQVTVGNKS-RYLNSRFISLQTAGKWSFDVTSILKDWLQMPBEKQEFQLQACCKPESQNT-EFLFKIAGLSRNRGDTGLLADQVAKPYILVMSPAD-GHSPAKSRKRRE--TDAVCTE 278
gi|68397085|ref|XP_692338.1| GANHVLVQAEFRRLRIKEPKMGDSEQRLELYQVTVGNKS-RYLNSRFISLQTAGKWSFDVTSILKDWLQMPBEKQEFQLQACCKPESQNT-EFLFKIAGLSRNRGDTGLLADQVAKPYILVMSPAD-GHSPAKSRKRRE--TDAVCTE 277
gi|33504525|ref|NP_878293.1| PDVRLLSQAEFRRLRIKNTM-DQEQRLLELYRQVGDQA-RYLGTRFVSKDLNRWLSFDVTKQIMIEWLQSGDEETLRLRYCCKKANQSTDKFLFTISGLDKQRGDTAGLADMMVKPYILALSLEFN-GNSLAVRKRRAVGDIDEICDE 275
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|6755775|ref|NP_035707.1| TEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
gi|11024652|ref|NP_067589.1| TEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
gi|63025222|ref|NP_000651.3| TEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
gi|114677451|ref|XP_512687.2| TEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
gi|50979134|ref|NP_001003309.1| TEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
gi|189534498|ref|XP_001923657.1| KSEGCCVRSLYIDFRKDLGWKWIHEPSGYANYCTGSCSYVVTSENKYSQVLALYRHHNPGASAQPCCVPPQVLDPLPIIYVYVGRQHKVQQLSNMIVKTKCKC 380
gi|68397085|ref|XP_692338.1| KSEGCCVRSLYIDFRKDLGWKWIHEPSGYANYCTGSCSYVVTSENKYSQVLALYRHHNPGASAQPCCVPPQVLDPLPIIYVYVGRQHKVQQLSNMIVKTKCKC 379
gi|33504525|ref|NP_878293.1| KTETCCMRKLYIDFRKDLGWKWIHEPKGYFANYCMGSCYIWNANKEYSQLALYKHHNPGASAQPCCVPPALDPLPIIYVYVGRQHKVQQLSNMIVRNCKCS 377
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400..

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