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gi|6678311|ref|NP_033390.1|      MDPAMPLQLWNLPLLLVGSVLGLTSVSAQGNNLEICLLPLDAGPCQALIPKFYYDRDQQKCRRFNYGGCLGNANNFHSRDLCQQTCGSIEKVPPVCRSELK-TYPCDKPNIRFFFNLNTMTCEPLRPGLCSRT--INVFSEEATCKGLCE   150
gi|27465613|ref|NP_775164.1|     MDPATSLRLWNLPLLLVGSALGLASVSAQGNNLEICLLPLDMGPCKALIPKFYYDRDQKKCRRFKYGGCLGNANNFHSRKLCEHTCGNKEKVPWVCRSAVR-TYPCDKPNTEFFFNLKTMTCEPLRPGLCSRT--TNVFPEEAMCKSLCE   150
gi|5730091|ref|NP_006519.1|      MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA   150
gi|114614526|ref|XP_519205.2|    MDPARPLGLSILLLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDEACWRIEKVPKVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA   150
gi|73976317|ref|XP_532462.2|     MDPAGPFGVLLLPLLLMGTALGDGGAGAPASSAETCLLPPDVGPCRALIPSYYYDRYTQSCLPFTYGGCRGNANNFETWEACDEACWRIEKVPKICRLEVN-EEKCGENKEEYFFNLTSMTCEKFLSGGCHSN--ENRFPDEAACMNFCA   150
gi|33354271|ref|NP_877589.1|     MDSVRPLWLMLLSLLLVGTALGDASQAPPGNNAEICLLPPDDGPCRARIPSYYYDRYTQSCREFMYGGCEGNANNFETLEACNEACWKIEKVPKICRLKVN-KKQCGELREQYFFNLSSMTCKKFISGGCHSN--ENRFPDEATCMDFCA   150
gi|118085836|ref|XP_418662.2|    MAAGRRLPLPALLLPLACAALAPRGLTE---KQRACLLPPDDGPCRALVPRWYYDRYTQSCQEFSYGGCHGNANNFLSHDDCEKNCWTIKKVPKLCRMEAD-TGPCRGYIRRYAFNLSSMRCEEFIYGGCYGN--GNNFKDLQSCVDHCL   150
gi|91754176|ref|NP_001035185.1|  -MACDLLGALLLFISVLESAVGLTLQPK-----EVCLLQIEEGTCNDDIQRFYYNTISQQCEEFSYSGCGGNQNNFRSFVECQKTCFRIPKIPQICRFQKK-EGPCRGLFSRYFFNMTSMQCEPFTYGGCQGN--ENNFRNPEECIEYCK   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|6678311|ref|NP_033390.1|      PRKHIPSFCSSPKDEGLCSANVTRFYFNSRNKTCETFTYTGCGGNENNFYYLDACHRACVKGWKKP--KRWKIGDFLPRFWKHLS---------   244
gi|27465613|ref|NP_775164.1|     PRKSIPSFCSSPKDEGLCSANVTRYYFNSRNKTCETFTYTGCGGNENNFYYLDACNRACVKALKKP--KRRKIGDFLPRFWKLRS---------   244
gi|5730091|ref|NP_006519.1|      PKK-IPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKK--KKMPKLRFASRIRKIRKKQF------   244
gi|114614526|ref|XP_519205.2|    PKK-IPSFCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSREDCKRACAKALKKK--KKMPKLRFASRIRKIRKKQF------   244
gi|73976317|ref|XP_532462.2|     PKK-SPSFCYSPKDEGLCSANVTRYYFNPRHRTCEAFAYTGCGGNDNNFVSMKDCKNVCVKALKKERNKKMTKLSLVNRRLKNWKKQS------   244
gi|33354271|ref|NP_877589.1|     PKR-APVFCYSPKDEGLCSANVTRYYFNPRHKACEAFNYTGCGGNDNNFVNLKDCKRTCVKALKKEKNKKMPRLLLANRRLKIKKKQF------   244
gi|118085836|ref|XP_418662.2|    PEKTGPLLCYSPKDEGLCSSSVPRYYYDTTSKSCKEFKYTGCGGNANNFVTEVDCYNVCRKGSQKPTINKSRSLLRRKMMRKLIKKPQTHNPKS   244
gi|91754176|ref|NP_001035185.1|  PPKTIPVICLDNLDKGRCSASIPRYYYNSATKTCEEFMYTGCGGSNNNFISKQSCVDVCGSKRWSPTKKSVRVSKQYLRRVKPQPSREKTNK--   244
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240....
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