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gi | 6753404 | ref | NP_034013.1 | MHRLLEAWDAACLPP--PPPAAFRPMEVANFYYPDCLA--YGAKAARAAP-----RAPAAEP-AIGEHERAIDFSPYLEPLAP-----AADFAAP--APA---HHDFLSDLFADDYGAKPSKPPADYGYVSLGRA 114
gi | 81295402 | ref | NP_077039.3 | MHRLLEAWDAACLPP--PPPAAFRPMEVANFYYPDCLA--YGAKAARAAP-----RAPAAEP-AIGEHERAIDFSPYLEPLAP-----AADFAAP--APA---HHDFLSDLFADDYGAKPSKPPADYGYVSLGRA 115
gi | 28872796 | ref | NP_005185.2 | MQRLLVAVDPAACLPLPPPPPAFKSMEVANFYYPDCLAAA--YGGKAAPAAPPAARPGPRPPAGELGSI GDHERAIDFSPYLEPLGAPQAPAPATAIDTFAAPPAPAP---APASSGQHDFLSDLFSDDYGGKNCCKPAEYGYVSLGRL 145
gi | 114682609 | ref | XP_525353.2 | MQRLLVAVDPAACLPLPPPPPAFKSMEVANFYYPDCLAAA--YGGKAAPAAPPAARPGPRPPAGELGSI GDHERAIDFSPYLEPLGAPQAPAPATAIDTFAAPPAPAP---APASSGQHDFLSDLFSDDYGGKNCCKPAEYGYVSLGRL 145
gi | 45383936 | ref | NP_990584.1 | MQRLLVAVDPAACLPP--IQPPAFKSMEVANFYYPDCLAAA--LNKLHPRAAG-----GRSMTTEL-TVGDHERAIDFSPYLEPLAASQPPAQP-----PPFAAAGGNFEFACSSGGQDFLSDLFEDYKSGGGKPKDYTVIISLTRH 130
gi | 42476260 | ref | NP_571959.2 | -----MEVAGFY-EGDYLAFHSTNASSSPVVDGVCKQPVNNGSMTKLHDISEHEKAIDFETIYLDLSPQY-----QHLASQ-----DESHRHRALGIYDFLSEGNKSKRAALQNYKNVLSLT-- 105
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 6753404 | ref | NP_034013.1 | GAK---AAPPACFP-----PPPPAALKAEPGFEPAD---CK--RADDAPA-----MAAGFPFALRAYLGYQATPSGSSGSLSTSS--SSPPGTPSPADAKAAPAACFAGPPAAP--AKAKAKKTVDKLSDEYKMRNRNIAV 236
gi | 81295402 | ref | NP_077039.3 | GAK---AAPPACFP-----PPPPAALKAEPGFEPAD---CK--RADDAPA-----MAAGFPFALRAYLGYQATPSGSSGSLSTSS--SSPPGTPSPADAKAAPAACFAGPPAAP--AKAKAKKAVDKLSDEYKMRNRNIAV 237
gi | 28872796 | ref | NP_005185.2 | GAAKG--ALHPGCFAPLHPPPPPPPPAELKAEPGFEPAD---CK--RKEEAGAPGGGAGMAAGFPVALRAYLGYQAVPSGSSGSLSTSS--SSPPGTPSPADAKAPPTACYAGAAPAPSOVKSKAKKTVDKHSDEYKIRRNRNIAV 285
gi | 114682609 | ref | XP_525353.2 | GAAKG--ALHPGCFAPLHPPPPPPPPAELKAEPGFEPAD---CK--RKEEAGAPGGGAGMAAGFPVALRAYLGYQAVPSGSSGSLSTSS--SSPPGTPSPADAKAPPTACYAGAAPAPSOVKSKAKKTVDKHSDEYKIRRNRNIAV 285
gi | 45383936 | ref | NP_990584.1 | GHPGSGSHKPGVLPG---CFPPQIVETKVEPVFETLDS---CKGPRKEEGGAGPGPGMSSPYGSTVRSYLYGQSVPSGSSGNLSTSS--SSPPGTPNPSSESSKSAAG--AGGYSGPPAGKNPKKCVDKHSDEYKLRNRNIAV 268
gi | 42476260 | ref | NP_571959.2 | -----ERDPNQLAV-----PELQETRIDAVFSEDFMGSFAKNGRHEETP-----MDGPGGDMRSYLYGQIAPSGSLGNISTASSSCSSPPGTPAPSGKGRSPQAG--GKMTSS---GKGGKRLDKDSDEYRQRNRNIAV 228
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 6753404 | ref | NP_034013.1 | RKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSLTLRNLFKQLPEPLLASAGHC 296
gi | 81295402 | ref | NP_077039.3 | RKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSLTLRNLFKQLPEPLLASAGHC 297
gi | 28872796 | ref | NP_005185.2 | RKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSLTLRNLFKQLPEPLLASGHC 345
gi | 114682609 | ref | XP_525353.2 | RKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSLTLRNLFKQLPEPLLASGHC 345
gi | 45383936 | ref | NP_990584.1 | RKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSLTLRNLFKQLPEPLLASPRC 328
gi | 42476260 | ref | NP_571959.2 | RKSRDKAKMRNLETQHKVLELAAENDRLQKRVEQLSRELSLTLRNL--LLSATGQC 280
.....310.....320.....330.....340.....350.....360

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