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gi | 4507401 | ref | NP_003192.1 | --MAFLRSMWGVLSALGRSGAELCT-CGSRRLRSPFSFVYLPWFSSVLASCPKKPVSSYLRFSEKQLPIFKAQNPDAKTELRIRRIAQRWRELPSKKKIYQDAYRAEWQVYKEEISRFKEQLTFSQIMSLKEEIMDKHLKRRKAMTKKK 147
gi | 114630621 | ref | XP_001164091.1 | --MAFLRSMWGVLSALGRSGAELCT-CGSRRLRSPFSFVYLPWFSSVLASCPKKPVSSYLRFSEKQLPIFKAQNPDAKTELRIRRIAQRWRELPSKKKIYQDAYRAEWQVYKEEISRFKEQLTFSQIMSLKEEIMDKHLKRRKAMTKKK 147
gi | 73953051 | ref | XP_546107.2 | --MALFRGVWSVLNALSALGKSGADLCA-CGSRRLRSPFSFAYVPCFSSSTANYYPKPKPLTSYVRFSEKQLPIFKAQNPDAKNSLIRKIAQLWRELPESEKKIYEDAYRADWQAYKEEINRIQEQLTFSQIMSLKEEILQKRLKKKALIKKR 147
gi | 156151422 | ref | NP_001029188.2 | --MALLRGVWGVNLNALSALGKSGADLCA-CGSRRLRSPFSFAYVPCFSSSTLSGYPKPKMPTSYVRFSEKQLPIFKAQNPDAKNSLIRKIAQLWRELPESEKKIYEDAYRADWQAYKEEINRIQEQLTFSQIMSLKEEIMQKRLKKKALIKKR 147
gi | 6678303 | ref | NP_033386.1 | --MALFRGMWVSLKALGRIGVEMCA-CGGRIPSPSISLVCIKPKCFSS-MGSYVPKKPMSSYLRFSETEQLPKFKAKHPDAKSELVLRKIAALWRELPEAEKKVVEADFKAEWKAVYKYEQLTFSQIMSGEKEARQRRLLKKKALVKKR 146
gi | 13786148 | ref | NP_112616.1 | --MALFRGMWVSLKALGRIGVEMCA-CGGRIPSPSISLVCIKPKCFSS-LGNYPKPKPMSSYLRFSETEQLPKFKAKHPDAKSELVLRKIAAMWRELPEAEKKVVEADFKAEWKAVYKYEQLTFSQIMSGEKEARQRRLLKKKALVKKR 146
gi | 45383910 | ref | NP_989431.1 | --MAAALALLGRAAGLANGARQLFR-CGG--IGRAAEAG-CCRAMSSAER--PKRPLSAYFRFLRDNQPAFRQNPENLNLVKKLAGVWRLEPASQKQVVEARKIDWRKYEEQLAAYKALTPAQAALKERRRRLAKRRSFRIKR 142
gi | 116517272 | ref | NP_001070857.1 | --MAFSLMSVGANLIVKSESLFS-SAS--VVRCSCVAPAIKSFSAIRGPPKRLTAYMTFVVDMPQTVSKQNSIKVVDVWRKIAQQWMLTTEQKQPFQVSLAEAKBQYKLALEKFKALTPAESAAFAEKKRQVAKRKAIRKKK 144
gi | 17738065 | ref | NP_524415.1 | --MIYVTTLMSSRGGGLIGSLINKVRLAAASISNTPAVPSKTLLEEQLGLPPRPKKPLTPYFRFMREDRPKLKAANPQITVIVVVRQLSNWSDADAQLKERLQAEFKRDOQIVVBERIKYDATALTEERAEIKLQKQDLVDAKERRQLRK 148
gi | 118788729 | ref | XP_316944.3 | MQLNAVARLFYSPRLLSLRQPSLSVPSGLHATAIINDAGTAKSVPEKPKRPMNITIRFAISIRSSLASANPQASPTDISKLAAYKWSLQDQATKAKLEBEYKREQAVWLQNAKYLSQLDAQKAEIKLERQRRNEGKVKREQKR 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 4507401 | ref | NP_003192.1 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTVKENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 246
gi | 114630621 | ref | XP_001164091.1 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTVKENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 246
gi | 73953051 | ref | XP_546107.2 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTVKENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 246
gi | 156151422 | ref | NP_001029188.2 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTINENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 246
gi | 6678303 | ref | NP_033386.1 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTINENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 246
gi | 13786148 | ref | NP_112616.1 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTINENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 244
gi | 45383910 | ref | NP_989431.1 | ELTLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKTINENWNKNSDSEKELYIQHAKEDETRHNEMKSWEEOMIEVGRKDLLRRTIKKQRKYGAEBC----- 262
gi | 116517272 | ref | NP_001070857.1 | ELNLLGKPKRPRSAYNVYVAERFOEAKGDSPOEK---LKSRLDDWNRLSDTQKQMYIOLAEDDKVRYKNEIKSWEEHMMIEIGREDLRRKTKSALKAKAKTKTIAATKNRKKTSKVIVIKAKAPKKKSDASGKAVYF 277
gi | 17738065 | ref | NP_524415.1 | RVKELGRPKPASAFRLFIASERINTPQGDKTYREWVHCKTAKWTRLSDSEKEVYMESEKEMELYRKAISVWEEKMIRLGHIDVVRHGSLIDPEPKPRKTLASKDI----- 257
gi | 118788729 | ref | XP_316944.3 | MLKELGRPKRPMNAYLRFCAQNK-PAPGLSKEDNKMOMKMLGMQWKRLEPEGERERYTKEAEAEEMKRYQEMKVVWEDKMLAENVIAVRKKNVLLPSPASVKAAGGIPVVDLAPVAKPKKPTSAARP----- 277
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....

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