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gi | 45555716 | ref | NP_996485.1 | MEHFHQIQDTIQHYQOQLAAQOQQVQOQQLDQHQVVVVQOQOQAHQNSNTIAGVGTQOLFVYKMASSFPNPATTMAQV-VATSNAGTIGYDYLRLNMAQAAAAAVPGSQWVYSAANCGVDANTAAQLQHQOQQOQQQQQQOQH 149
gi | 158289425 | ref | XP_311155.3 | -----QLFSYKMANSEFQNPVITMSGVTVSTSNAP-----YDYRLGMSVTVARPGDPPMSSITAPITQCKHRLTYREIHHQNVNHNKSLIIGTEFIFL 87
gi | 4504425 | ref | NP_002119.1 | -----
gi | 50950133 | ref | NP_001002937.1 | -----
gi | 41386729 | ref | NP_788785.1 | -----
gi | 114649257 | ref | XP_001140879.1 | -----
gi | 109459982 | ref | XP_001055841.1 | -----
gi | 51762947 | ref | XP_485920.1 | -----
gi | 45382473 | ref | NP_990233.1 | -----
gi | 17553928 | ref | NP_498375.1 | -----

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1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 45555716 | ref | NP_996485.1 | OQQMOQQOQNVINSASPMSEVRKADAKP-RGRMTAYAYFFVQTCREEHKKKHPDETVIFAEFSRKAERWKMVLDKERFRHMAEKDKQRYEAEMQNVVPPKGAUVVGRGKRRQIKDPNAPKRSLSAFFWFCNDRNKVKALNPEFG 297
gi | 158289425 | ref | XP_311155.3 | SQAHVQNNVILNKMVTTGGTVAGGKVKDNKP-RGRMTAYAYFFVQTCREEHKKKHPDETVIFAEFSRKAERWKMVLDKERFRHMAEKDKQRYEAEMQNVVPPKGAUVVGRGKRRQIKDPNAPKRSLSAFFWFCNDRNKVKALNPEFG 235
gi | 4504425 | ref | NP_002119.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 50950133 | ref | NP_001002937.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 41386729 | ref | NP_788785.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 114649257 | ref | XP_001140879.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 109459982 | ref | XP_001055841.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 51762947 | ref | XP_485920.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 45382473 | ref | NP_990233.1 | -----MGKGDPKKP-RGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----GETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
gi | 17553928 | ref | NP_498375.1 | SPTLYQSHQLCPNPSATMYQATPRDMGKPPVVGKTSYPYGFVVMCYEEHKKKYPNENVQVTEISKKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPK-----AMRKRRAKDPHAPKRALSAFFVVSQDKRPEIQAGHPDWK 161

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gi | 45555716 | ref | NP_996485.1 | VGDIAKELGRKWSVDPEVKQYESMAERDKARYER-EMTEYKTSKGIAMSAFMSQASMOAQAQKAAALLAAAAQQHQOLEE@HDDDDGDDDDENC 393
gi | 158289425 | ref | XP_311155.3 | VGDIAKELGRKWSMDMAEIKCKVE@MAEKDKQRYEQ-VRLTIPALAPRHVQAAAQLAQVVAQAAAAVAAAAAAAVQQHDDDDDEDEDDEDDNE-- 329
gi | 4504425 | ref | NP_002119.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 50950133 | ref | NP_001002937.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 41386729 | ref | NP_788785.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 114649257 | ref | XP_001140879.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 216
gi | 109459982 | ref | XP_001055841.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 51762947 | ref | XP_485920.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAKKGVVKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 45382473 | ref | NP_990233.1 | IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEK-DIAAYRAKGPDAAGKRVVAKAESKSKKKEEEDDEEEDDEEEDDEEEDDEEEDDDDE-- 215
gi | 17553928 | ref | NP_498375.1 | VQVACELGKMWKLVQETKDMYEQKAQADKDRVAD-----EMRNVKAEMQKMSGMDHYDDNIHVVVHVEDINS@NIS----- 235

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