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gi|5174675|ref|NP_006052.1|-----MILFVLLFLVAGLLPFFPANEDKPA--FTALLTT-QIQVOREIVNKHNELRRRAVSPPARNMLKMEWNKEAANAQKWANOCNTRHSNPKDRMSLK-CGENLY 150
gi|114607750|ref|XP_001148602.1|-----MKRILHPALETTAMLFVLLFLVAGLLPFFPANEDKPA--FTALLTT-QIQVOREIVNKHNELRRRAVSPPARNMLKMEWNKEAANAQKWANOCNTRHSNPKDRMSLK-CGENLY 150
gi|73973254|ref|XP_538955.2|MGHGKPTMTMVDISTEKDKLIMAGEGKEVIANNHFCRLRSNCKSTMALFLELLFLAVLLPFFPAN-CGQPS--FTALLTT-QIQVOREIVNKHNELRKSVPSPASNMLKMEWNKEAANAQKWANOCNTRHSNPKDRMSLK-CGENLY 150
gi|118601862|ref|NP_001073103.1|-----MALFIVVLLFLAAVWLPFFPAK-GODRR--FADLSNT-LKNVQTEIVNKHNDLRRGVSPPPSNMLKMEWNKEAANAQKWANOCNTRHSNPKDRMSLK-CGENLY 150
gi|118089209|ref|XP_420051.2|-----MILPAVLLCLAAVLSP---SAGEIPE--ASLLLSNTRDQKLVLDKHNALRRRVSPPARNMLRMEWNPQAAVNAQNWANOCNTRHSNPKDRMSLK-CGENLY 150
gi|31981914|ref|NP_033768.2|-----MALMLVFLFLAAVLPPLLQDSSQENR--LEKLSIT-KMSVPEEIVSKHNQLRRMVSPSGDILLKMEWNYDAQVNAQWADKCTFSSPIELRTNLR-CGENSF 150
gi|12408314|ref|NP_074050.1|-----MALMLVLLFLAAVLPPLLQDTTDENRDLNLSIT-KLSVQEEIINKHNQLRRITVSPSGDILLRVEWDHDAVNAQKWANRCIYNHSPLOHRTITLK-CGENLF 150
gi|189539007|ref|XP_001922209.1|-----MSAACSVSG-----VCHLSVQQLIVDVHNAFRRAVQPSASNMLKMSWSDAVAESARGWINKNMTHGPPSSRMLNGYEMGENLF 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|5174675|ref|NP_006052.1|MSASASSWSQAICSWFDEYNDFDFGVGPKTPNAVVGHYTVVWYSSYLVCNGNAYCPNQKVLKYYYVCOYCPAGNWANRLYVPEQGAPCAFCPDNCDGLCTNGCKVEDLYSNCKSLKLTLCQKHLVRDSCKASCNCSNSIY---- 299
gi|114607750|ref|XP_001148602.1|MSSAPSSWSQAICSWFDEYNDFDFGVGPKTPNAVVGHYTVVWYSSYLVCNGSAYCPNQKVLKYYYVCOYCPAGNWANRLYVPEKGAFCPCPDNCDGLCTNGCKVEDLYSNCKSLKLTLCQKHLVRDSCKASCNCSNSIY---- 299
gi|73973254|ref|XP_538955.2|MSSYPASWSDAIONWYEEHDFVYGVGPKSSDAVIGHYTVVWYSSYHVGCGIAYCPNQLKYYYVCOYCPAGNLVNMHTPYLKGKSCASCYHCDKGLCTNSCEVEDNYSNCKDLKTLTLCNHYFVSDNCKAAKCKENKIY---- 299
gi|118601862|ref|NP_001073103.1|MSSYPTWNSAICSWYDEVDHDFVFEVGPKSPQAVIGHFTQIVWYSSFLICGCVAYCPKQ-SLKLYLVCOYCPAGNIVGRQHVVPYQKGTPCGSCPNHCDNGLCTNSCEVEDTYSNCKASLKEITWCASDFVKTNCKAACNCGKIY---- 299
gi|118089209|ref|XP_420051.2|MSTAPSSWSDSIQAWFDEEKDFKYGSGATTANAVIGHYTVLWVYNSYQVGCVAVYCPER-TFKYFYVCHYCPA----- 299
gi|31981914|ref|NP_033768.2|MSSYLASWSSAICGWYNEYKDLTYDVGPKQPDVSVGHYTVVWVNSYFQVACGVAECPKN-PLRYYYVCHYCPVGNVQGRLYTPYTAGEPCASCPCDHCEDGLCTNSCGHEDKYTNCKYLLKMLSCHEHELLKRGCKATCLCEGKIY---- 299
gi|12408314|ref|NP_074050.1|MANYPASWSSVIQDWYDESLDFVFGPKKVGKVGHYTVVWVNSYFLVACGVAECPDN-PLKYFYVCHYCPGGNYVGRLYSPYTEGEPDCSCPCNCDGLCTNSCEVEDNYSNCGDLKMMVSCDDPLLKEGCRASCFCCEDKIY---- 299
gi|189539007|ref|XP_001922209.1|KATGISSWTSVVDAWHSEVNNYKYPIGSIN-GQALGHYTVVWYSSYEVGCAVTCGNSN---YFYGGHYVRAGNFR--LVPPYSLGSPCASCPNCCEDNLCNACPYINGFVNCDAKAKLTCENTAVKLCGPASCLCNKIITPIAKK 299
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....

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