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gi | 8394248 | ref | NP_058656.1 | -MACGGKRLFLALAW-VLLAHLCSQAEAA SNYDCCLSYIQTPLP-SRAIVGFTRQMADEACDINAIIFHTKKRKSVCADPKQNWVKRAVNLLSLRVKKM-- 102
gi | 9507069 | ref | NP_062106.1 | -MAC--KHLPLALAG-VLLAYLCSQSEAA SNFDCCLTYTKNVYHHARNFVGFTRQMADEACDINAIIFHLKSKRSVCADPKQIWKRIHLHLLSLRTKKM-- 102
gi | 4759076 | ref | NP_004582.1 | --MCCTKSLLLAALMS-VLLLHLCSQSEAA SNFDCCLGYTDRILH-PKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPKQTWVKYIVRLLSCKVKNM-- 102
gi | 114583733 | ref | XP_516133.2 | --MCCTKSLLLAALMS-VLLLHLCSQSEAA SNFDCCLGYTDRILH-PKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPKQTWVKYIVRLLSCKVKNM-- 102
gi | 52546710 | ref | NP_001005254.1 | --MCSSKNLLAALMMSVLLLHLCSKSEAA SNFDCCLRYTEHMFV-PGSIMGFTQQLANEACDINAVIFYTKKKKAVCADPKKKWVKRIVRLLSHRVKKM-- 102
gi | 27806273 | ref | NP_776688.1 | -MMSSKNLLAALMS-VLLLFHCSKSE-ASNFDCCLRYTERILH-PSILVGFTRQLANEACDINAVIFYTRKKLAVCADPKKKWVKQVHMLSQRVKRM-- 102
gi | 45383285 | ref | NP_989769.1 | MPGLSTKSLILASLLG-LLLLLLCSQSQSNQDCCLSYSKVRLP-RKVIKGFTEQLSGEVCDIDAIIFHTVIRGLKACVNPKEDWVKKHLFLSQKLRMSM 102
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100..

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