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gi |12963661|ref|NP_075885.1| MNSVLGNQTDVAGLFLVNSSEALERAVRCCTQASVVTDDGFAEGGPDERSLYIMRVVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVKDRRPSKEVEAVVVGPY 109
gi |109468183|ref|XP_001055762.1| MNSVLGNQTDVAGLFLANSSEALERAVRCCTQASVVTDDGFAEGGPDERSLYIMRVVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVKDRRPSKEVEAVVVGPY 109
gi |9790193|ref|NP_062819.1| MNPALGNQTDVAGLFLANSSEALERAVRCCTQASVVTDDGFAEGGPDERSLYIMRVVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVKDRRPSKEVEAVVVGPY 109
gi |114581257|ref|XP_001141560.1| MNPALGNQTDVAGLFLANSSEALERAVRCCTQASVVTDDGFAEGGPDERSLYIMRVVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVKDRRPSKEVEAVVVGPY 109
gi |123959768|ref|NP_001074208.1| MNPALGNQTDVAGLFLANSSEALERAMRCCTQASVVTDDGFAEGGPDERSLYIMRVVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVKDRRPSKEVEAVVVGPY 109
gi |66472424|ref|NP_001018500.1| MNST-FNQTDG--IFSNRTEENLL----CCNFSSVVTDNGFAAAAAPDERSLFIMRIVQIAVMCVLSLTVVFGIFFLGCNLLIKSEGMINFLVTDRRPSKEVEAVIVGAY 103
gi |41387140|ref|NP_957100.1| MNSTGFNDTDSA-LFSN--SFLS----CCNVSSVVTDSGFVSAALDERSVFMRTVQIAVMCVLALTVVFGIFFLGCNLLIKSEGMINFLVTDRRPSKDVEAVIVGSY 102
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....

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