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gi|76880478|ref|NP_001029125.1|  MGFOKFS PFLALS ILVLL QAGSLHAA PFRSALES SPADPATLS EDEARLLLAALVQDYVOMKASELEQEQEREGSRIIAQKRAQDTATCVTHRLAGLLSRSGGVVKNNFVPTNVGSKAFGRRRRDLQA 128
gi|115496471|ref|NP_001069808.1| MGFWKFLPFLVLSFLAVYHAGMLQAAPFRSALEN-DFDPAILTEKEMCLLLAAMVNNYVQMKTSSELKP--ETFAFRITAKRSCNRAICVIHKVAGSLSRSGSEIKRNFMTNAFGRAAGTFRTKQ-- 123
gi|50950151|ref|NP_001002947.1|  MGFWKLSPFLAIGLLVMYQAGILQAAPFRSALEN-PLESATLIEDEICVLLTAVVKDYVQMKARELQQEQETEGSSLTAKSSCKDGPVITNRLEGWLRARERMVKNTFMPTDVPDFGHHQKELAA 127
gi|73989342|ref|XP_852201.1|    -----MAG---TTANSGFQEAAYYSILE-----SATLIEDEICVLLTAVVKDYVQMKARELQQEQETEGSSLTAKSSCKDDPCVITNRLEGWLRARERMVKNTFMPTDVPDFGHHQKELAA 104
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....

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