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** . . . . . ** *
gi |15029518|ref|NP_036224.1| MKSGLWYFFLFCRLRIKVLTG-----EINGSAANYEMFIFHNGGVOILCKYPDIVQOFKMLLKGGQILCDLTKTKGSGNTVSIKSLKFCBSQLSNNNSVFFFLYNLDHSHANYFCNLSIFDPPPFK-VTLTGGYLHIYESQLC 136
gi |114582825|ref|XP_001173460.1| MKSGLWYFFLFCRLRIKVLTG-----EINGSAANYEMFIFHNGGVOILCKYPDIVQOFKMLLKGGQILCDLTKTKGSGNTVSIKSLKFCBSQLSNNNSVFFFLYNLDHSHANYFCNLSIFDPPPFK-VTLTGGYLHIYESQLC 136
gi |8567362|ref|NP_059508.1| MKPYFCHVFVFCFLIRLLTG-----EINGSAADHRMFSFHNGGVOISCKYPTVQOLKMRLEFREREVLCELTTRTKGSGNAVSIKSNPMLCLYHLSNNNSVFFFLNNDSSQGSYYFCLSLIFDPPPFQERNLSSGVLHIYESQLC 137
gi |50950193|ref|NP_001002972.1| MKSDLRWYFFLFCFQVEALTG-----EINDSTKSEMFTFHDGGVOILCKFNIAIVSOYKMBELLKGTVEVLCDLTTTKENGTVE-KNPKFCQSSSDGVSFFFLYNLDSSHASYYAQLSIFDPPPFQKRNLSREVLNIVESQTC 136
gi |77735505|ref|NP_001029447.1| MKSDLRWYFFLFCFQVEALTG-----EINDSTKSEMFTFHDGGVOILCKYPTVROFKMQLLKGDNVLCDLTKTKENEDTVEIRNLNVCKFQLSNNNSVFFFLYNLDSSYASYIICKLSIFDPPPFQVDILSREVLNIVESQLC 137
gi |50750339|ref|XP_421959.1| MKITVAVTFCLLCFQFEALCGVDTCSSRLCKNIDKLQVSDPQGVIVEFENGKFLIFQNPKNVNEFSMTLLKGRERKAIKALHMNNKKAVPESNVTYQAEHSDTSTTFILTNLDRKHIDTYTCLESLLEPPPIHCHLKETVLYIQDKEDC 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |15029518|ref|NP_036224.1| CQ--LKFWLPICCAAFVVVCILGCILICWLTKK--KYSSSVHDPNGEYMFMAAVNTAKKSRLTDVTL----- 199
gi |114582825|ref|XP_001173460.1| CQ--LKFWLPICCAAFVVVCILGCILICWLTKK--KYSSSVHDPNGEYMFMAAVNTAKKSRLTDVTL----- 199
gi |8567362|ref|NP_059508.1| CQ--LKLWLPVGCFAAFVVVLLFGCILIIWFSSKK--KYSSVHDPNSEYMFMAAVNTAKKSRLAGVTS----- 200
gi |50950193|ref|NP_001002972.1| CQ--LKFWLPICCAAFVVVYIFGCIPLCWLTKK--KYRSSHVDPNSEYMFMAAVNTAKKPGLTGVTHNLELCGTOA 208
gi |77735505|ref|NP_001029447.1| CQ--LKFWLPICCAAFVTVCVFQVLMYWLTKK--KYPTSVHDPNSEYMFMAAVNTAKKPAPTDVTRNLELPGTOA 209
gi |50750339|ref|XP_421959.1| SSGGIMSWIITGLIAPALIFCVCFVACHLRNKNQCCESNSHEYNSYEMFMAAVNAAKKPRI----- 212
.....160.....170.....180.....190.....200.....210.....220.....

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