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gi | 37577107 | ref | NP_005118.2 | MMTKHKKCFIIVGVLITNIIILIVKLRDSQSLCPYDWIGFQNKCYFSEKEGDNSSSKYNCSTQHADLIIIDNIEEMNFLRRYKCSFDHWIGLMAKNRTGOWVDGATFKSFGMRSGECCAYLSDDGAAIARCYTERKWI CRKRIR 149
gi | 114643496 | ref | XP_528730.2 | MMTKHKKCFIIVGVLITNIIILIVKLRDSQSLCPYDWIGFQNKCYFSEKEGDNSSSKYNCSTQHADLIIIDNIEEMNFLRRYKCSFDHWIGLMAKNRTGOWVDGATFKSFGMRSGECCAYLSDDGAAIARCYTERKWI CRKRIR 149
gi | 73997675 | ref | XP_854186.1 | -MTGSLVSLIDNSNOGIDAKKQVLEH-RSTOYSCPDDWIGFQNKCYFSEKERDWTSSRHNCTTQADLIIMDTMEEMNFLRRYKCSFDHWIGLEMTENKSGRWVNGIIFKKWFLVRGNEKCAVLDGAAIARCYAERKWCRRKMH 147
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....

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