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* . : : * . *
gi |4503463|ref|NP_001947.1| MVSVPITWCSVALALLVALHEGKGOAAAT--LEQPASSSHAQGTHLRLRRCSSSWLDKECVYFCHLDIIWVNTPEOTAPYGLGNPPRRRRRSLPRRCQSSARDPACATFCLRRP-WTEAGAVPE-RKSPADVFPOTGKTGATGELLOR 146
gi |114555867|ref|XP_524683.2| MVSVPITWCSVALALLVALHEGKGOAAAT--LQOPASSSHAQGTHLRLRRCSSSWLDKECVYFCHLDIIWVNTPEOTAPYGLGNPPRRRRRSLPRRCQSSARDPACATFCLRRP-WTEAGAVPE-RKSPADVFPOTGKTGATGELLOR 146
gi |28372485|ref|NP_783645.1| --MPHALCSIALALLVALHEGKGOAAATPIPEQPAPLFRARGSHLRTRRCSSSWLDKECVYFCHLDIIWVNTPGOTAPYGLGNPPRRRRRSLPRRCQSSARDPACATFCHRRP-WTDAVAVPG-SGSPAAPAFDQGTQTATGELLOR 145
gi |50950247|ref|NP_001003002.1| MPAAGVHEPNTASPLKVAAGKGOVAAA--PEHPAP SARARGSHLRTRRCSSSWLDKECVYFCHLDIIWVNTPGOTAPYGLGNPPRRRRRSLPKRCESGGDPACATFCHRRP-WAEAVVVPG-SRSPADVFPAGRTWTSAGELLOR 146
gi |122937365|ref|NP_031928.2| --MVS-AWC SIALALLVALHEGKGOAAAT--LEQPASAPKGRGPLRFRRCSSNSWLDKECVYFCHLDIIWVNTAGOTAPYGLGNPPRRRRRSLPKRCESSTAGDSACATFCHRRH-WPEAVVVPG-SQAPAAVLKTKMWTAEGLLRK 143
gi |6978793|ref|NP_036681.1| --MVSFAWCSIALALLVALHEGKGOAAAT--MEQPASAPKGRGPLRFRRCSSNSWLDKECVYFCHLDIIWVNTAGOTAPYGLGNPPRRRRRSLPKRCESSTAGDSACATFCHRRP-WPEAEVTSI-SQPAAVLETSTWTAAGDLLK 144
gi |50759617|ref|XP_417707.1| MPEHPAGAALLALALCVLLEDGMQ-----PPLQSHLGTAAMLRTRKRCSSNSWLDKECVYFCHLDIIWVNTPGHETAPYGLGNPPRRRRRSLPKRCESSTAGDSACATFCHRRP-WPEAEVTSI-SQPAAVLETSTWTAAGDLLK 141
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |4503463|ref|NP_001947.1| LRDISTVKSFLFAKRQOEAMREPRSTHSRWRKR----- 178
gi |114555867|ref|XP_524683.2| LRDISTVKSFLFAKRQOEAMREPRSTHSRWRKR----- 178
gi |28372485|ref|NP_783645.1| LRVISATKIHFARQOKPQRETRPQTHSRQRKR----- 177
gi |50950247|ref|NP_001003002.1| LRNISAAKIRFPRRPQEAGRQLRPTPFRRRKR----- 178
gi |122937365|ref|NP_031928.2| LRDISATKLRFARLQPEVTRKAIIPAYSRWRKR----- 175
gi |6978793|ref|NP_036681.1| LRDISAAKLRQVLRPELREAIPIAHSRRRRKR----- 176
gi |50759617|ref|XP_417707.1| LRDLAASRLQFVKQVHRAQCSAPPVAVLPWKKSIVKKKR 179
.....160.....170.....180.....

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