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gi |5453676|ref|NP_006135.1| MRNSYRFLASSLSVVVSLLLIPEDVCEKIIGGNEVTPHSRPMVLLSLDRKNICAGALIAKDWVLTAAHCNLNKRSQLVILGAHSITREBPTKQIMLVKKEFPYPCYDPAIREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQV 150
gi |114600290|ref|XP_001148261.1| MRNSYRFLASSLSVVVSLLLIPEDVCEKIIGGNEVTPHSRPMVLLSLDRKNICAGALIAKDWVLTAAHCNLNKRSQLVILGAHSITREBPTKQIMLVKKEFPYPCYDPAIREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQV 150
gi |154707908|ref|NP_001092565.1| MRNSSTFLAAILSIIVV-FLLIPEDLCEKIIGGNEVTPHSRPMVLL--DGNNICAGALIAKDWVLTAAHCNLNKRSQLVILGAHSITREBPTKQIMLVKKEFPYPCYDPAIREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQV 147
gi |6754102|ref|NP_034500.1| MRNASGPRGSLAIFLLFLLLIPEGGCERIIIGGDTVVPHSRPMALLKLSNTICAGALIEKNVLTAAHCNVGKRSEKIFILGAHSINKE-PEQIILTVKKAFFPYPCYDEYIREGDLQLVRLKKKATVNRNVAIHLHLPKKGDDVKPGTMCQV 149
gi |23618883|ref|NP_703198.1| MRNFCAPWVSSLTIVIFLLIPEGGCERIIIGGDTVVPHSRPMVLLKLPDSICAGALIAKNVLTAAHCNIPGKSEVILGAHSIKKE-PEQIILSVKKAFFPYPCYDPAIREGDLQLVRLKKKATVNRNVAIHLHLPKKGDDVKPGTMCQV 149
gi |73949707|ref|XP_544335.2| MRNSCTFPASSFSLAIFLLVLPGDFCVEIIGGNEVTPHSRPMVLLK--GKKICAGALIAEDWVLTAAHCNLDKNSQVILGAHSITREBPTKQIMLVKKEFPYPCYDPAIREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQV 148
gi |45383251|ref|NP_989788.1| MG---VFFTLSTAAIVLLIPLGDLVDIIGGHEVAPHSRPFMAMLK--GKEFCGGALIKPSWVLTAAHCNLDKNSQVILGAHSITREBPTKQIMLVKKEFPYPCYDPAIREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQV 144
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |5453676|ref|NP_006135.1| AGWGRTHNS-ASWSDTLREVNIIIDRKCNDNRNHYNFNPVIGMNMVCAGSLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 262
gi |114600290|ref|XP_001148261.1| AGWGRTHNS-ASRSDTLREVNIIIDRKCNDNRNHYNFNPVIGMNMVCAGSLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 262
gi |154707908|ref|NP_001092565.1| AGWGQFYNN-SPVSKILREVNIIIDRKCNDNRNHYNFNPVIGLNMICAGSLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 259
gi |6754102|ref|NP_034500.1| AGWGRFGNK-SAPSETLREVNIIIDRKCNDNRNHYNFNPVIGLNMICAGDLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 260
gi |23618883|ref|NP_703198.1| AGWGRFHNK-SPPSDTLREVNIIIDRKCNDNRNHYNFNPVIGLNMICAGNLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 261
gi |73949707|ref|XP_544335.2| AGWGRIHNN-SPQSDTLREVNIIIDRKCNDNRNHYNFNPVIGLNMICAGSLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 260
gi |45383251|ref|NP_989788.1| AGWGQISKRNKMSDTLREVNIIIDRKCNDNRNHYNFNPVIGLNMICAGSLRGGKDSNCGDSGSPLLCEGVFRGVTISFLENKCGDPRGPGVYIILLKHHLNWIIMIKGAV---- 260
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....

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