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                                 *  *::  :**:*  .*.* ::*      .*: :****:***      ***:*:. :********  .   : :: **: :: : * : *.  **::: ** :* :*           * *******.:**.***.** : *** *.
gi|8659568|ref|NP_034775.1|      MWFLILFLALSLGGIDAAPPVQSRIVGGFKCEKNSQPWHVAVYRYKEYICGGVLLDANWVLTAAHCYYE---KNNVWLGKNNLYQDEPSAQHRLVSKSFLHPCYNMSLHRNRIQNPQDDYSYDLMLLRLSKPADITDVVKPIALPTEEPK   147
gi|21426851|ref|NP_034246.1|      MRFLILFLALSLGGIDAAPPVHSRIVGGFKCEKNSQPWHVAVYRYNEYICGGVLLDANWVLTAAHCYYE---ENKVSLGKNNLYEEEPSAQHRLVSKSFLHPGYNRSLHRNHIRHPEYDYSNDLMLLRLSKPADITDVVKPIALPTEEPK   147
gi|52851403|ref|NP_032719.1|      MWFLILFLALSLGGIDAAPPVQSRIVGGFKCEKNSQPWHVAVYRYTQYLCGGVLLDPNWVLTAAHCYDD---NYKVWLGKNNLFKDEPSAQHRFVSKAIPHPGFNMSLMRKHIRFLEYDYSNDLMLLRLSKPADITDTVKPITLPTEEPK   147
gi|31980868|ref|NP_034769.4|      MRFLILFLALSLGGIDAAPPVQSRIVGGFNCEKNSQPWQVAVYRFTKYQCGGILLNANWVLTAAHCHND---KYQVWLGKNNFLEDEPSAQHRLVSKAIPHPDFNMSLLNEHTPQPEDDYSNDLMLLRLKKPADITDVVKPIDLPTEEPK   147
gi|7949064|ref|NP_032482.1|      MWFLILFLALSLGGIDAAPPVQSRIFGGFNCEKNSQPWQVAVYRFTKYQCGGVLLNANWVLTAAHCHND---KYQVWLGKNNFFEDEPSAQHRLVSKAIPHPDFNMSLLNEHTPQPEDDYSNDLMLLRLKKPADITDVVKPIDLPTEEPK   147
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gi|12313877|ref|NP_064664.1|      MRFLILFLALSLGGIDAAPPVQSRIIGGFKCKKNSQPWHVAVLRSNKYICGGVLLDPNWVLTAAHCYGNDTSQHNVWLGKNKLFQREPSAQHRWVSKSFPHPDYNMSLLNDHIPHPED-KSNDLMLLRLSKPADITDAVKPIDLPTEEPK   149
gi|23956056|ref|NP_034772.1|      MRFLILFLALSLGEIDAAPPVQSRIVGGFNCEKNSQPWHVAVFRYNKYICGGVLLNPNWVLTAAHCYGN---QYNVWLGKNKLFQHESSAQHRLVSKSFPHPDYNMSLMNDHTPHPEDDYSNDLMLLRLSKPADITDAVKPIDLPTEEPK   147
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gi|28875780|ref|NP_034770.1|      MWFLILFLALSLGGIDAAPPVQSRIVGGFNCEKNSQPWHVAVYRYNKYICGGVLLDRNWVLTAAHCHVS---QYNVWLGKTKLFQREPSAQHRMVSKSFPHPDYNMSLLIIHNPEPEDDESNDLMLLRLSEPADITDAVKPIALPTEEPK   147
gi|7019443|ref|NP_032480.1|      MWFLILFLALSLGGIDAAPPVQSRIVGGFKCEKNSQPWQVAVYYHKEHICGGVLLDRNWVLTAAHCYVD---ECEVWLGKNQLFQEEPSAQNRLVSKSFPHPGFNMTLLTFEKLPPGADFSNDLMLLRLSKPADITDVVKPIDLPTKEPK   147
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gi|5031829|ref|NP_005542.1|      MWDLVLSIALSVGCTGAVPLIQSRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCLKK---NSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDSSHDLMLLRLSEPAKITDVVKVLGLPTQEPA   147
gi|114678693|ref|XP_001174026.1| MWDLVFSIALSVGCTGAVPLIQSRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCLKK---NSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHRSLRPDEDSSHDLMLLRLSEPAKITDAVKVLGLPTQEPA   147
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|8659568|ref|NP_034775.1|      LGSTCLASGWGSIIPVKFQYAKDLQCVNLKLLPNEDCDKAYVQKVTDVMLCAGVKGGGKDTCKGDSGGPLICDGVLQGLTSWGYNPCGEPKKPGVYTKLIKFTSWIKDTLAQNP   261
gi|21426851|ref|NP_034246.1|      LGSTCLASGWGSTTPFKFQNAKDLQCVNLKLLPNEDCGKAHIEKVTDVMLCAGETDGGKDTCKGDSGGPLICDGVLQGITSWGFTPCGEPKKPGVYTKLIKFTSWIKDTMAKNL   261
gi|52851403|ref|NP_032719.1|      LGSTCLASGWGSITPTKFQFTDDLYCVNLKLLPNEDCAKAHIEKVTDAMLCAGEMDGGKDTCKGDSGGPLICDGVLQGITSWGHTPCGEPDMPGVYTKLNKFTSWIKDTMAKNP   261
gi|31980868|ref|NP_034769.4|      LGSTCLASGWGSITPVKYEYPDELQCVNLKLLPNEDCAKAHIEKVTDDMLCAGDMDGGKDTCAGDSGGPLICDGVLQGITSWGPSPCGKPNVPGIYTRVLNFNTWIRETMAEND   261
gi|7949064|ref|NP_032482.1|      LGSTCLASGWGSITPVIYEPADDLQCVNFKLLPNEDCVKAHIEKVTDVMLCAGDMDGGKDTCMGDSGGPLICDGVLHGITSWGPSPCGKPNVPGIYTKLIKFNSWIKDTIAKNA   261
gi|8659572|ref|NP_035045.1|      LGSTCLASGWGSTTPIKFKYPDDLQCVNLKLLPNEDCDKAHKMKVTDAMLCAGEMDGGSYTCEHDSGGPLICDGILQGITSWGPEPCGEPTEPSVYTKLIKFSSWIRETMANNP   256
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gi|23956056|ref|NP_034772.1|      LGSTCLASGWGSITPTKWQIPNDLQCGFIKPLPNENCAKAYIHKVTDVMLCAGEMGGGKDTCAGDSGGPLICDGVLQGITSWGSIPCAKPNAPAIYTKLIKFTSWIKDTMAKNP   261
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gi|28875780|ref|NP_034770.1|      LGSTCLVSGWGSITPTKFQTPDDLQCVSIKLLPNEVCVKNHNQKVTDVMLCAGEMGGGKDTCKGDSGGPLICDGVLHGITAWGPIPCGKPNTPGVYTKLIKFTNWIKDTMAKNP   261
gi|7019443|ref|NP_032480.1|      LDSTCLVSGWGSITPTKWQKPDDLQCMFTKLLPNENCAKAYLLKVTDVMLCTIEMGEDKGPCVGDSGGPLICDGVLQGTVSIGPDPCGIPGVSAIYTNLVKFNSWIKDTMMKNA   261
gi|6754460|ref|NP_034774.1|      PGSTCLASGWGSITPTRWQKSDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEMGGGKDTCAGDSGGPLICDGILQGTTSNGPEPCGKPGVPAIYTNLIKFNSWIKDTMMKNA   261
gi|7705572|ref|NP_032483.1|      LGSTCLASGWGSITPTKWQKPDDLQCVFLKLLPIKNCIENHNVKVTDVMLCAGEMSGGKNICKGDSGGPLICDSVLQGITSTGPIPCGKPGVPAMYTNLIKFNSWIKDTMTKNS   261
gi|52693913|ref|NP_034244.1|      LGSTCLASGWGSINQLIYQNPNDLQCVSIKLHPNEVCVKAHILKVTDVMLCAGEMNGGKDTCKGDSGGPLICDGVLQGITSWGSTPCGEPNAPAIYTKLIKFTSWIKDTMAKNP   259
gi|5031829|ref|NP_005542.1|      LGTTCYASGWGSIEPEEFLRPRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPLVCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP   261
gi|114678693|ref|XP_001174026.1| LGTTCYASGWGSIEPEEFLRPKSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPLVCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP   261
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