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                                 ***:*********** *.:* **  .** *: *******:***********:******:::*           . .:  .: .  :  ***: .*:********: :   **.* .  ****:***:.* ****:**::*****:****
gi|25952111|ref|NP_000585.2|     MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREEFP----------RDLSLISPLAQ--AVRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV   138
gi|114606345|ref|XP_001152827.1| MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREEFP----------RDLSLISPLAQ--AVRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV   138
gi|73972180|ref|XP_858423.1|     MSTESMIRDVELAEEPLPKKAGGPPGSRRCFCLSLFSFLLVAGATTLFCLLHFGVIGPQREEVSQSSGIFSRKLKDLTIFFPLPS--SE-SSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLIVPSDGLYLIYSQV   147
gi|145279649|ref|NP_776391.2|    MSTKSMIRDVELAEEVLSEKAGGPQGSRSCLCLSLFSFLLVAGATTLFCLLHFGVIGPQREEQSP---------GGPSINSPLVQ--TLRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQV   139
gi|7305585|ref|NP_038721.1|      MSTESMIRDVELAEEALPQKMGGFQNSRRCLCLSLFSFLLVAGATTLFCLLNFGVIGPQRDEKFP---------NGLPLISSMAQTLTLRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQV   141
gi|6981662|ref|NP_036807.1|      MSTESMIRDVELAEEALPKKMGGLQNSRRCLCLSLFSFLLVAGATTLFCLLNFGVIGPNKEEKFP---------NGLPLISSMAQTLTLRSSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLIYSQV   141
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gi|114606345|ref|XP_001152827.1| LFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL   233
gi|73972180|ref|XP_858423.1|     LFKGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGTEAKPWYEPIYLGGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL   242
gi|145279649|ref|NP_776391.2|    LFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL   234
gi|7305585|ref|NP_038721.1|      LFKGQGCP-DYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL   235
gi|6981662|ref|NP_036807.1|      LFKGQGCP-DYVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPWYEPMYLGGVFQLEKGDLLSAEVNLPKYLDITESGQVYFGVIAL   235
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