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gi|33468957|ref|NP_058550.1|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 32
gi|58865716|ref|NP_001012072.1|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 32
gi|4885559|ref|NP_005389.1|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 32
gi|114631775|ref|XP_507911.2|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 32
gi|115495731|ref|NP_001069632.1|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 32
gi|73998207|ref|XP_534961.2|-----MSCTRMIVLDPRLTSSVMPVDMAMRICALH 150
gi|118092827|ref|XP_423102.2|-----MIQLDPRPLNSIMPVDMAMRICALH 27
gi|41152149|ref|NP_957128.1|-----MNCITRVLIINFRPMPSPIMPVDMAMRICALH 32
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|33468957|ref|NP_058550.1|SPLLKSFLLGPNVGFORRNFVNKLLKPLKPLKLSVKQEAQSQS-EWKSHPNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSSLKLHHEEKNLVDFPPOPSTDYLSFRDRFQKNFVCLENCSDRIVTGTIVKKNVSFE 181
gi|58865716|ref|NP_001012072.1|SPLLKSFLLGPNVGLQRRHFVNKPKLPLKPLKLSVKQEAQSQK-EWKSHPNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSSLKLHHEEKNLVDFPPOPSSDYLSFRDRFQKNFVCLENCSDRIVTGTIVKKNVSFE 181
gi|4885559|ref|NP_005389.1|SPPVKSFLGPNVDFORRHFVNKLLKPLKLSCLNIKHKAKSON-DWKCASHNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSALKHHEEKNLILDFPOPSTDYLSFRSHFQKNFVCLENCSDRIVTGTIVKKNVSFE 181
gi|114631775|ref|XP_507911.2|SPPVKSFLGPNVDFORRHFVNKLLKPLKLSCLNIKHKAKSON-DWKCASHNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSALKHHEEKNLILDFPOPSTDYLSFRSHFQKNFVCLENCSDRIVTGTIVKKNVSFE 181
gi|115495731|ref|NP_001069632.1|SPLLKSFLLSPYDDFORRNFVNKLLKPLKLSCLNIKQEARAOD-DWKPASHNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSGLKLHHEEKNLILDFPOPSTDYLSFRNHQKNFVCLENCSDRIVTGTIVKKNVSFE 181
gi|73998207|ref|XP_534961.2|SPLLKSFLLGPNVDDLQRRNFVNKLLKPLKLSCLNIKQEAQSQS-EWKSHPNQAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSGLKLHHEEKNLILDFPOPSTDYLSFRNHQKNFVCLENCSDRIVTGTIVKKNVSFE 299
gi|118092827|ref|XP_423102.2|SPLLKSFLLSPLEGCCORNFVNRFKPLRCLHVKRDSEAKSDWNHSAARAKKRVVFADSKGLSLTAIHVFSDDLPEEPAWDLQFDLLDLNDISSGLKLHHEEKNLILDFPOPSTDYLSFRNHQKNFVCLENCSDRIVTGTIVKKNVSFE 177
gi|41152149|ref|NP_957128.1|SPLLRSFLSSVEDCKSRNLVNOYKPLRSCLISKTEDDIANITWSPETKAKKRVVFADSKGMSLTAHVVFKEFEEDLMLDLQFELSDLEDAIVGLKARKEKNFSLGFPQPAADYLDFRNRLKKNLVCLENCIIQERSVTGTIVKKNVSFE 182
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|33468957|ref|NP_058550.1|KKVQVRIIFDITWKTYTDVDCVMKNNVYSSSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRVENLASYR 317
gi|58865716|ref|NP_001012072.1|KKVQVRIIFDITWKTYTDVDCVMKNNVYSSSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRVENLASYR 317
gi|4885559|ref|NP_005389.1|KKVQIRIIFDITWKTYTDVDCVMKNNVYGGTSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRMENLASYR 317
gi|114631775|ref|XP_507911.2|KKVQIRIIFDITWKTYTDVDCVMKNNVYGGTSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRMENLASYR 317
gi|115495731|ref|NP_001069632.1|KKVQIRIIFDITWKSYTDVDCVMKNNVYGGTSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRMENLASYR 318
gi|73998207|ref|XP_534961.2|KKVQIRIIFDITWKSYTDVDCVMKNNVYGGTSDSDFSFALDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGRMENLASYR 435
gi|118092827|ref|XP_423102.2|KKVQVRIIFDITWKTYTDIECVYMNNVYGDSENDTFSFIDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGGIENSSPYW 314
gi|41152149|ref|NP_957128.1|KVVHVRIIFDITWKSHTDIPCTVMNNVYGCEDVDTFSFIDLPVPIPEEKIEFCISYHANGRIQVFNWNNQNYRIVHVQWPKDGVQVQVAPKDCAFQVPL-KTELEPTVFGSPRLASGLFPEWQSWGGIENSSPYW 317
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....

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