

gi|15559207|ref|NP_254275.1|MIRTLLLS-----TLVAGALS--CGDPTIYPP--VIVRVVGGEEARPNWPVQVSLQYS-NGKWYHTCGGSLIANSWVLTAAHCIS----- 76
gi|114554264|ref|XP_001156270.1| MKPEGMGVKDasDFPAPSHKLRITGPPYGPRLONSHGHTMIRTLLLS--TLVAGALS--CGDPTIYPP--VIVRVVGGEEARPNWPVQVSLQYS-NGKWYHTCGGSLIANSWVLTAAHCIRLITKAHKVLLCCSLIPFFVRDLCSSGLELTGV 147
gi|6681297|ref|NP_031945.1|MIRTLLLS--ALVAGALS--CGYPTIYEVEDVDVSRVVGGEAEATPNTWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 78
gi|6978803|ref|NP_036685.1|MIRTLLLS--ALVAGALS--CGYPTIYEVQHDVSRVVGGEAEPNWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 78
gi|27807285|ref|NP_777139.1|MIRALLLS--TLVAGALS--CGVPTIYPP--QLSRVVGGEEDARPNWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 76
gi|118101212|ref|XP_001231962.1|MLGILFAVLTAAAALCGVPAIYPP--AVSRVVGGEEDARPNWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 77
gi|189522428|ref|XP_001923718.1|-MKLVILA-LFIAGAYCGGPTIYKP--IDSRVVGGEEDARPNWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 75
gi|41054047|ref|NP_956180.1|-MMKFVVLA-VLVVVGAYSCGLPTIYPP--VIVRVVGGVDRPNWPVQVSLQVLS-SGRWRHTCGGSLVANNWVLTAAHCIS----- 76
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|15559207|ref|NP_254275.1| ---SSRTYRVGLGRHNLVYA-ESGSLAVSVSKIVVHKDWNQISKGNDAIALKLKANPVSLDKIQIOLACLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSSAWVGSSVKTSMTICAGGDGVISSCNGDSGGPLNC 222
gi|114554264|ref|XP_001156270.1| SAGSSRTYRVGLGRHNLVYA-ESGSLAVSVSKIVVHKDWNQISKGNDAIALKLKANPVSLDKIQIOLACLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSSAWVGSSVKTSMTICAGGDGVISSCNGDSGGPLNC 296
gi|6681297|ref|NP_031945.1| ---NYQTYRVLLGAHSLSNP-GAGSAAVQVSKLVVHQRWNSQNVNGYDIALIKLASPVLTKNIQIOLACLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSSAWVGSSVKTSMTICAGGDGVISSCNGDSGGPLNC 224
gi|6978803|ref|NP_036685.1| ---NSRTYRVLLGRHSLSTS-ESGSLAVQVSKLVVHKKWNAQKLSNGNDIALVKLASPVALTSKIQTACLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSSAWVGSSVKTSMTICAGGDGVISSCNGDSGGPLNC 224
gi|27807285|ref|NP_777139.1| ---SSRTYRVVVGQSLSTV-ESGSLTIAVSKSIVHEKWNQVLAQVNDIALIKLASSVPLTDKIQIOLGCLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSNPSWVGSTVKTNNMTCAGGDGVISSCNGDSGGPLNC 222
gi|118101212|ref|XP_001231962.1| ---STRKYRVLLGKYNLEAE-ESGSVIASETKIIVHEKWNQVLAQVNDIALIKLASSVPLTDKIQIOLGCLPAGTILPNNYPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSNPSWVGSTVKTNNMTCAGGDGVISSCNGDSGGPLNC 223
gi|189522428|ref|XP_001923718.1| ---SSRTYRVLLGKHNPLPS-ESGSAIISPARIIIVHENWDSYNIIRN--DIALIKLSPVFTDKISPACLPDSGSLILPHNTPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSKSDWWGSLVVDLMTVCAGGDGVISSCNGDSGGPLNC 220
gi|41054047|ref|NP_956180.1| ---SSRTYRVVFLGKHSLSQE-ENGSVAIGAGKIIIVHEAWNSTIRN--DIALIKLSPVFTDKISPACLPDSGSLILPHNTPCYVTVGWRLQVNGAVPDVLCQGRLLLVVDYATCSSKSDWWGSLVVDLMTVCAGGDGVISSCNGDSGGPLNC 220
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|15559207|ref|NP_254275.1| QASDGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIANN 269
gi|114554264|ref|XP_001156270.1| QASDCQWVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIANN 343
gi|6681297|ref|NP_031945.1| RASNGQWVHGIVSFGSSLCNYPKPSVFTRVSNYIDWINSVIMARK 271
gi|6978803|ref|NP_036685.1| QASNGQWVHGIVSFGSRLGCNYPKPSVFTRVSNYIDWINSVIANN 271
gi|27807285|ref|NP_777139.1| QANRQWVHGIVSFGSSLCNYPKPSVFTRVSNYIDWINSVIANN 269
gi|118101212|ref|XP_001231962.1| QNADGAWVHGIVSFGSSLCNYYQKPSVFTRVSAFDSWIKKIANN 270
gi|189522428|ref|XP_001923718.1| QRRDGTWVHGIVSFGSSLCNYPKPSVFTRVSYIPWIKVMYSY 267
gi|41054047|ref|NP_956180.1| AGSDGAWVHGIVSFGSGLSCNYYKPKPSVFTRVSAVSDWIKKMASY 267
.....310.....320.....330.....340.....

