

gi|8850219|ref|NP\_059066.1| MRALGAVVILLWGLFAVELGNDAMD-----FEDDSCPKPPETANGVVEHLVRYRCRQFYRLRAEGDGVYTLNDEKQWVTVAGEKLPCEAVCGKPKHP 96  
gi|60097941|ref|NP\_036714.2| MRALGAVVILLWGLFAVELGNDAMD-----IEDDSCPKPPETANGVVEHLVRYRCRQFYRLRAEGDGVYTLNDEKQWVTVAGEKLPCEAVCGKPKHP 96  
gi|186910296|ref|NP\_001119574.1| MSALGAVIALLWGLFAVDSGNDVTD-----IADDGCPKPPETANGVVEHVRVYCKNRYKLRTEGSGVYTLNNEKQWVTVAGEKLPCEAVCGKPKHP 96  
gi|73957097|ref|XP\_536799.2| MRALGAVIALLWGLFAEDTGSEAIN-----NTEVSLPKPPVIENTGVVEHMIRYCKPFYKLRTEGSGVYTLNNEKQWVTVAGEKLPCEAVCGKPKHP 96  
gi|94966763|ref|NP\_001035560.1| MSALGAVVILLWGLLAVETGSEAINADSCPKAPEIANSHVEYSVRYQCDKYYKLGAGNVYTFNNKQWINKDIGQQLPECEBDDSCPEPPKIENGVVEYLVRYCKPYYTLRTCGDGVYTFNSKKQWINKNIGKLPCEAVCGKPKHP 150  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|8850219|ref|NP\_059066.1| VDVQRIIGGSMDAGSFPPWQAKMISRHLTIGANLISDWLLTTAKNFLNHSSETASAKDIPTLLTYVGNQQLVEIEKVVLHPNHSVVDIGLIKLRQVLTVERVMPICLPKDYIAPGRVGVVSGWGRNANFRFTDRLKVVMLFPVAD 246  
gi|60097941|ref|NP\_036714.2| VDVQRIIGGSMDAGSFPPWQAKMISRGLTIGANLISDWLLTTAQNLFNHSENATAKDIAPLLTYVGNQQLVEIEKVVLHPERSVVDIGLIKLRQVLTVERVMPICLPKDYVAPGRMGVYVSGWGRNVNFRFTDRLKVVMLFPVAD 246  
gi|186910296|ref|NP\_001119574.1| ANFVQRIIGGSLDAGSFPPWQAKMVSHPHLLTGANLINEQWLLTTAKNFLNHSENATAKDIAPLLTYVGNQQLVEIEKVVLHPNYSQVDIGLIKLRQVLTVERVMPICLPKDYAEVGRVGVVSGWGRNANFKFTDHLKVVMLFPVAD 246  
gi|73957097|ref|XP\_536799.2| VDVQRIIGGSMDAGSFPPWQAKMVSHPHLLTGANLINEQWLLTTAKNFLNHSKDDAKANDIAPLLKLYVGNQQLVEIEKVVLHPDYSKVDIGLIKLRQVLTVERVMPICLPKDYAEVGRVGVVSGWGRNANFNFTDHLKVVMLFPVAD 246  
gi|94966763|ref|NP\_001035560.1| VDVQRIIGGSLDAGSFPPWQAKMVSQHNLLTGANLINEQWLLTTAKNFLNHSKDKAKDIPTLLRLYVGNQQLVEIEKVVLHPDHSKVDIGLIKLRQVLTVERVMPICLPKDYVAVGRVGVVSGWGRNANFNFTDHLKVVMLFPVAD 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|8850219|ref|NP\_059066.1| QDKCVVHYENSTVPEKKNLTSFVGVQPIILNEHTFCAGLTKYQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDRKSCAVAEYGVYVRAIDLKDWVQETMAKN 347  
gi|60097941|ref|NP\_036714.2| QDKCELHYEKSTVPEKKGAVSFPVGVQPIILNKHHTFCAGLTKYEEDTCYGDAGSAFAVHDLEEDTWYAAGILSFDRKSCAVAEYGVYVRAIDLKDWVQETMAKN 347  
gi|186910296|ref|NP\_001119574.1| QDCCIRHYEGSTVPEKKTPKSFPVGVQPIILNEHTFCAGMSKYQEDTCYGDAGSAFAVHDLEEDTWYAAGILSFDRKSCAVAEYGVYVRAIDLKDWVQETIAEN 347  
gi|73957097|ref|XP\_536799.2| QDKCVQHYEGSTVPEKKSPPSFPVGVQPIILNEHTFCAGMSKFOEDTCYGDAGSAFAVHDQEDTWYAAGILSFDRKSCAVAEYGVYVRAIDLKDWVQETIAGN 347  
gi|94966763|ref|NP\_001035560.1| QDKCVKHYEGVDAPKNTAKSFPVGVQPIILNENLFCVGLSKYQDDTCYGDAGSAFVVDKREDDTWYAAGILSFDRKSCAVAEYGVYVRAIDLKDWVQETIANN 401  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400

