

gi|45007007|ref|NP\_006178.2| MDLYSIPAAALDRFVARRLQPRKEFEVKARRALGALAAALRERGGRLGAAAPRVLKT V KGGSSGRGTALKGGCDSELVIFLDCFKSVVDQRARRAEILSEMRASLESWVONPVVGLRLTFPEQSVPGALQFRLLTSVDLEDWMDVSLVPAF 150  
gi|114647083|ref|XP\_509393.2| MDLYSIPAAALDRFVARRLQPRKEFEVKARRALGALAAALRERGGRLGAAAPRVLKT V KGGSSGRGTALKGGCDSELVIFLDCFKSVVDQRARRAEILSEMRASLESWVONPVVGLRLTFPEQSVPGALQFRLLTSVDLEDWMDVSLVPAF 150  
gi|73995238|ref|XP\_534688.2| MEVYRIPAEALATLVARRLHRSAEFKRAGRALGALATLGERDRAAAGPWRVLPKPAKGGAGRGTAALRGCCSELVIFLDCFKSVKDHSDVPEILKDLWDLLOSWWQKPIPLNFEFLWDRPVLQFRLLASDLENWMDVSLVPAF 150  
gi|21644585|ref|NP\_660261.1| MDLFHITPAGALDKLVAHNLHPAPETAARVGAALGSLNITLQCHRAR-GSQRPRVIRIAKGGYARGTALRGTTVELVIFLDCFOSEFGDKTCHSETLGAMRMLLESWGHPPGLTFFESQKASRIQFRLLASADGEHMDVSLVPAF 149  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|45007007|ref|NP\_006178.2| NVLGGAGSGVVKPKPQVYSILLNSGCGGGEHAACFTELRRNFVNIIRPAKLNLLLVKHWYHQVCLGLWKEILPPVVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 300  
gi|114647083|ref|XP\_509393.2| NVLGGAGSGVVKPKPQVYSILLNSGCGGGEHAACFTELRRNFVNIIRPAKLNLLLVKHWYHQVCLGLWKEILPPVVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 300  
gi|73995238|ref|XP\_534688.2| DALGQLCAGAKPAPQVYSILLNSGCGGGEHAACFAELRRNFVNIIRPAKLNLLLVKHWYHQVQEAERKREMLPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFENFVRSFLSSQLKKRPRPVILDPAD 300  
gi|21644585|ref|NP\_660261.1| DVLGGPRSGVVKPTPNVYSSLLSSHCAGEYSACFTEPRKNFVNIIRPAKLNLLLVKHWYHQVQTR-AVRAALPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 298  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|45007007|ref|NP\_006178.2| PTVWDLGNGAAWHWDLAEEAASCVYDHP CFLRGMDDPVQSWKGPGLPRAGCSGLGHPILDPNOKTPEN-----SKSLNAVY--PRAGSKPPPCPAP-----GPTGAAS 396  
gi|114647083|ref|XP\_509393.2| PTVWDLGNGAAWHWDLAEEAASCVYDHP CFLRGMDDPVQSWKGPGLPRAGCSGLGHPILDPNOKTPEN-----SKSLNAVY--PRAGSKPPPCPAP-----GPTGAAS 396  
gi|73995238|ref|XP\_534688.2| PTVWDLGNGAAWHWDLAEEAASCVYDHP CFLRGMDDPVQSWKGPGLPRAGCSGLGHPILDPNOKTPEN-----SKSLNAVY--PRAGSKPPPCPAP-----GPTGAAS 396  
gi|21644585|ref|NP\_660261.1| PTVWDLGNGAARWDLAEEAASCVYDHP CFLRGMDDPVQSWKGPGLPRAGCSGLGHPILDPNOKTPEN-----SKSLNAVY--PRAGSKPPPCPAP-----GPTGAAS 448  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|45007007|ref|NP\_006178.2| IIVPSVGMALDLSQIPKELDRFIQDHLKPSQFQEQEVKKAIDILRLCLHENCVHKASRVSKGGSFGRGTDLRDCCDVELIIFLNCFTDYKDGPRRAEILDEMRAOLESWVODQVPSLQFPPEONVPEALQFLVSTALKSWMDVSL 546  
gi|114647083|ref|XP\_509393.2| IIVPSVGMALDLSQIPKELDRFIQDHLKPSQFQEQEVKKAIDILRLCLRENCVHKASRVSKGGSFGRGTDLRDCCDVELIIFLNCFTDYKDGPRRAEILDEMRAOLESWVODQVPSLQFPPEONVPEALQFLVSTALKSWMDVSL 546  
gi|73995238|ref|XP\_534688.2| IIVPSVGMALDLSQIPKELDRFIQDHLKPSQFQEQEVKKAIDILRLCLRENCVHKASRVSKGGSFGRGTDLRDCCDVELIIFLNCFTDYKDGPRRAEILDEMRAOLESWVODQVPSLQFPPEONVPEALQFLVSTALKSWMDVSL 546  
gi|21644585|ref|NP\_660261.1| IIVPSVGMALDLSQIPKELDRFIQDHLKPSQFQEQEVKKAIDILRLCLRENCVHKASRVSKGGSFGRGTDLRDCCDVELIIFLNCFTDYKDGPRRAEILDEMRAOLESWVODQVPSLQFPPEONVPEALQFLVSTALKSWMDVSL 597  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|45007007|ref|NP\_006178.2| PAFDVGQLSSGKTKPNQVYSRLLTSGCGGGEHKACFAELRRNFVNIIRPAKLNLLLVKHWYRVAQAQNGKGPAPASLPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 696  
gi|114647083|ref|XP\_509393.2| PAFDVGQLSSGKTKPNQVYSRLLTSGCGGGEHKACFAELRRNFVNIIRPAKLNLLLVKHWYRVAQAQNGKGPAPASLPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 696  
gi|73995238|ref|XP\_534688.2| PAFDVGQLCAGAKPAPQVYSILLNSGCGGGEHAACFAELRRNFVNIIRPAKLNLLLVKHWYRVAQAQNGKGPAPASLPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 696  
gi|21644585|ref|NP\_660261.1| PAFDVGQLSSGKTKPNQVYSRLLTSGCGGGEHAACFAELRRNFVNIIRPAKLNLLLVKHWYRVAQAQNGKGPAPASLPPVALELLIFAWEGCCKKDAFLAEGRLTVGLIQHQHLCVFWTVNYGFEDPAVGGFLORLKKRPRPVILDPAD 747  
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|45007007|ref|NP\_006178.2| LVLDPADPTWNVGHGSWELLAQEAALGMOACFLSRDGTSVOPWDVMPALLYOTPAGDLDFKISFELQPNRQFLAQNKAVDITCSFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSCFSQFTEQGNKRAEIISEIRAO 846  
gi|114647083|ref|XP\_509393.2| LVLDPADPTWNVGHGSWELLAQEAALGMOACFLSRDGTSVOPWDVMPALLYOTPAGDLDFKISFELQPNRQFLAQNKAVDITCSFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSCFSQFTEQGNKRAEIISEIRAO 846  
gi|73995238|ref|XP\_534688.2| LVLDPADPTWNVGHGSWELLAQEAALGMOACFLSRDGTSVOPWDVMPALLYOTPAGDLDFKISFELQPNRQFLAQNKAVDITCSFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSCFSQFTEQGNKRAEIISEIRAO 846  
gi|21644585|ref|NP\_660261.1| LVLDPADPTWNVGHGSWELLAQEAALGMOACFLSRDGTSVOPWDVMPALLYOTPAGDLDFKISFELQPNRQFLAQNKAVDITCSFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSCFSQFTEQGNKRAEIISEIRAO 897  
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi|45007007|ref|NP\_006178.2| LEACQQRERFEVKFEVSKWENPRVLSFLTSQTLMDQSVDFDVLPAFDALGLVSGSRPSSQVYVDLHYSNAGEYSTCFTELQRFDIISRPPTKLSLIRLVKHWYQCTKISKRGSGLPPQHGLELLIVYAWEGCGGDSQFNMAEGFR 996  
gi|114647083|ref|XP\_509393.2| LEACQQRERFEVKFEVSKWENPRVLSFLTSQTLMDQSVDFDVLPAFDALGLVSGSRPSSQVYVDLHYSNAGEYSTCFTELQRFDIISRPPTKLSLIRLVKHWYQCTKISKRGSGLPPQHGLELLIVYAWEGCGGDSQFNMAEGFR 996  
gi|73995238|ref|XP\_534688.2| LEACQQRERFEVKFEVSKWENPRVLSFLTSQTLMDQSVDFDVLPAFDALGLVSGSRPSSQVYVDLHYSNAGEYSTCFTELQRFDIISRPPTKLSLIRLVKHWYQCTKISKRGSGLPPQHGLELLIVYAWEGCGGDSQFNMAEGFR 996  
gi|21644585|ref|NP\_660261.1| LEACQQRERFEVKFEVSKWENPRVLSFLTSQTLMDQSVDFDVLPAFDALGLVSGSRPSSQVYVDLHYSNAGEYSTCFTELQRFDIISRPPTKLSLIRLVKHWYQCTKISKRGSGLPPQHGLELLIVYAWEGCGGDSQFNMAEGFR 1047  
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



```

****: **** :***:**. :*:*: ** . **:*:**:*****:****:**. **** .*:* **:******
gi |45007007|ref|NP_006178.2| TVLELVTOYRQLCIYWTINYNKDKTVGDFLKOOLQKRPPIILDPA DPTGNLGHNARWDL LAKEAACTSA LCCMGRNGIPIQPWPV KAAV 1087
gi |114647083|ref|XP_509393.2| TVLELVTOYRQLCIYWTINYNKDKTVGDFLKOOLQKRPPIILDPA DPTGNLGHNARWDL LAKEAACTSA LCCMGRNGIPIQPWPV KAAV 1087
gi |73995238|ref|XP_534688.2| TVLELVSOYRQLRVYWTVNYDNEDQTVRDFLSRQLRQPRPIILDPA DPTGNLGHNARWDL LAKEAACTSA LCCMGRNGIPIQPWPV KAAV 1087
gi |21644585|ref|NP_660261.1| TVLELIVQYRQLCVYWTINYS AEDKTI GDFLKMQLRKRPVILDPADPTGNLGHNARWDL LAKEATVYASALCCVDRDGNFIK PWPV KAAV 1138
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.

```

