

gi | 109148552 | ref | NP_476429.2 | MSROASKTSGGSGGFSGRSAVVGSSSRMSCVAHSGGAGGGAYGFRSGAGGFGSRRLYNLGNKSEISISVAAGGSRAGGFGGGRSSCAFAGGYGGGFSGYGGFGGGFGGGRMGGGFGGAGGFGGAGGFGGAGGFGGPGGFGGCGGFG 150
gi | 114644544 | ref | XP_522398.2 | MSROASKTSGGSGGFSGRSAVVGSSSRMSCAARS GGAGGGAYGFRSGAGGFGSRRLYNLGNKSEISISVAAGGSRAGGFGGGRSSCGFAGGYGGGFSGGYGGFGGGFGGGRMGGGFGGAGGFGGAGGFGGAGGFGGPGGFGGPGVFG 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 109148552 | ref | NP_476429.2 | GPSSLGSPGGFGPGGFPGGIQEVTINQSLLPPLNVEIDPQIGQVKAQEREQIKTLNKFASFIDKVRFLQONKVLTKWNLQQQCTSSISGTNNLEPLFENHINYLRSYLDN ILGERGRLDSELKNMEDLVDFKKKVEDEINKRTAA 300
gi | 114644544 | ref | XP_522398.2 | GPSSFSPGGFGPGGFPGGIQEVTINQSLLPPLNVEIDPQIGQVKAQEREQIKTLNKFASFIDKVRFLQONKVLTKWNLQQQCTSSISGTNNLEPLFENHINYLRSYLDN ILGERGRLDSELKNMEDLVDFKKKVEDEINKRTAA 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 109148552 | ref | NP_476429.2 | ENEFVTLKKDSDSAYMNKVELQAKVDALIDEIDFLRNLDAELSQMOSHISDTSVVLSDMNNRSLDLDSEIIAEVRAQVEDIAQRSKAEAEALYQTKLGELOTTAGRHGDDL RNTKSEIIELNRMIOQLRAEIEGVKKQANLQTAIAEAE 450
gi | 114644544 | ref | XP_522398.2 | ENEFVTLKKDSDSAYMNKVELQAKVDALIDEIDFLRNLDAELSQMOSHISDTSVVLSDMNNRSLDLDSEIIAEVRAQVEDIAQRSKAEAEALYQTKLGELOTTAGRHGDDL RNTKSEIIELNRMIOQLRAEIEGVKKQANLQTAIAEAE 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 109148552 | ref | NP_476429.2 | OHGEMALKDANAKLQELQALQAKDDLARLLRDYQELMNVKLALDVEIATYRKLLEGEYRMSGECPSAVSISVVSSTTSASAGGYGGYGGMGGGLGGGFAGGSGSGFGRGGGGIGGGFGGSS-GFSGSGFSGISGARYGV 599
gi | 114644544 | ref | XP_522398.2 | OHGEMALKDANAKLQELQALQAKDDLARLLRDYQELMNVKLALDVEIATYRKLLEGEYRMSGECPSAVSISVVSSTTSASAGGYGGYGGMGGGLGGGFAGGSGSGFGRGGGGIGGGFGGSSGFSGSGFSGISGARYGV 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 109148552 | ref | NP_476429.2 | SGGGFSASNRGGSIKFSQSSQSSQRYSR 628
gi | 114644544 | ref | XP_522398.2 | SGGGFSASNRGGSIKFSQSSQSSQRYSR 629
.....610.....620.....

