

gi | 119395716 | ref | NP_001444.2 | MQARYSVSSPNSLGVVYPLGGEQSYRRAAAAAGGGYTAMPAPMSVYSHPAHAEOYPGGMARAYGPTTPOPKDMVKPPYSYIALITMAIQNAPDKKITLNGIYQFIMDRFPFPRDNKQGWNSIRHNLNLCFVKVPRDDKPKGKS 150
gi | 114605184 | ref | XP_001174718.1 | MQARYSVSSPNSLGVVYPLGGEQSYRRAAAAAGGGYTAMPAPMSVYSHPAHAEOYPGGMARAYGPTTPOPKDMVKPPYSYIALITMAIQNAPDKKITLNGIYQFIMDRFPFPRDNKQGWNSIRHNLNLCFVKVPRDDKPKGKS 150
gi | 50345972 | ref | NP_032618.2 | MQARYSVSSPNSLGVVYPLGGEQSYRRAAAAAGGGYTAMPAPMSVYSHPAHAEOYPGGMARAYGPTTPOPKDMVKPPYSYIALITMAIQNAPDKKITLNGIYQFIMDRFPFPRDNKQGWNSIRHNLNLCFVKVPRDDKPKGKS 150
gi | 18858697 | ref | NP_571803.1 | MQARYSVSSPNSLGVVYPLGGEQSYRRAAAAAGGGYTAMPAPMSVYSHPAHAEOYPGGMARAYGPTTPOPKDMVKPPYSYIALITMAIQNAPDKKITLNGIYQFIMDRFPFPRDNKQGWNSIRHNLNLCFVKVPRDDKPKGKS 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 119395716 | ref | NP_001444.2 | YWTLDPDSYNMFENGSLRRLRRRFFKKKDAVKDKKEKDRHLHKEPPPP--GRQPPAPPEQADGNAPGPPPPVRIQDIKTENGTCPSPPOPLSPAALGSGSAAVPKIESPDSSSSSLSSGSSPPGSLPEARPLSLDGADSA PPPPAPS 300
gi | 114605184 | ref | XP_001174718.1 | YWTLDPDSYNMFENGSLRRLRRRFFKKKDAVKDKKEKDRHLHKEPPPP--GRQPPAPPEQADGNAPGPPPPVRIQDIKTENGTCPSPPOPLSPAALGSGSAAVPKIESPDSSSSSLSSGSSPPGSLPEARPLSLDGADSA PPPPAPS 300
gi | 50345972 | ref | NP_032618.2 | YWTLDPDSYNMFENGSLRRLRRRFFKKKDAVKDKKEKDRHLHKEPPPP--GRQPPAPPEQADGNAPGPPPPVRIQDIKTENGTCPSPPOPLSPAALGSGSAAVPKIESPDSSSSSLSSGSSPPGSLPEARPLSLDGADSA PPPPAPS 300
gi | 18858697 | ref | NP_571803.1 | YWTLDPDSYNMFENGSLRRLRRRFFKKKDAVKDKKEKDRHLHKEPPPP--GRQPPAPPEQADGNAPGPPPPVRIQDIKTENGTCPSPPOPLSPAALGSGSAAVPKIESPDSSSSSLSSGSSPPGSLPEARPLSLDGADSA PPPPAPS 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 119395716 | ref | NP_001444.2 | APPPHSQGFVVDNIMTSLRGSPOGAAELSSGLLASAAAASRAGIAPPLALGAYSPGQSSLYSSPCQTSAGSSGGGGGAGAAGG----AGGAGTYHCNLOAMSLYAAGERGGHLOGPAGGAGSAVDDPLPDYSLPPVTSSSSS 450
gi | 114605184 | ref | XP_001174718.1 | APPPHSQGFVVDNIMTSLRGSPOGAAELSSGLLASAAAASRAGIAPPLALGAYSPGQSSLYSSPCQTSAGSSGGGGGAGAAGG----AGGAGTYHCNLOAMSLYAAGERGGHLOGPAGGAGSAVDDPLPDYSLPPVTSSSSS 450
gi | 50345972 | ref | NP_032618.2 | APPPHSQGFVVDNIMTSLRGSPOGAAELSSGLLASAAAASRAGIAPPLALGAYSPGQSSLYSSPCQTSAGSSGGGGGAGAAGG----AGGAGTYHCNLOAMSLYAAGERGGHLOGPAGGAGSAVDDPLPDYSLPPVTSSSSS 450
gi | 18858697 | ref | NP_571803.1 | QHHQAPAGFVVDNIMTSLRGSPOGAAELSSGLLASAAAASRAGIAPPLALGAYSPGQSSLYSSPCQTSAGSSGGGGGAGAAGG----AGGAGTYHCNLOAMSLYAAGERGGHLOGPAGGAGSAVDDPLPDYSLPPVTSSSSS 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 119395716 | ref | NP_001444.2 | SLSHGGGGGGGGGQEAQHHPAAHQGRLTSWYLNQAGDGLHLASAAAAAAGYPGQQQNFHVSREMFEQRIGLNNSPVNGNSSCOMAFPSQSLYRTSGAFVYDCSKF 561
gi | 114605184 | ref | XP_001174718.1 | SLSHGGGGGGGGGQEAQHHPAAHQGRLTSWYLNQAGDGLHLASAAAAAAGYPGQQQNFHVSREMFEQRIGLNNSPVNGNSSCOMAFPSQSLYRTSGAFVYDCSKF 561
gi | 50345972 | ref | NP_032618.2 | SLSHGGGGGGGGGQEAQHHPAAHQGRLTSWYLNQAGDGLHLASAAAAAAGYPGQQQNFHVSREMFEQRIGLNNSPVNGNSSCOMAFPSQSLYRTSGAFVYDCSKF 561
gi | 18858697 | ref | NP_571803.1 | SLSHGQLS----SAQEGHHP--HQGRLASWYLNQAG--DIGHLG-----ATYPAQQQNFHVSREMFEQRIGLNNSPVNGNSSCOMAFPSQSLYRTSGAFVYDCSKF 561
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560

