

gi | 119703753 | ref | NP_005546.2 | *****:***** 150
gi | 114644570 | ref | XP_001143262.1 | MASTSTTIRSHSSRRGFSA NSARLPGVSRSGFSSIVSRERGGGLGGACGGAGFGSRSLYGLGSKRIEIGGSCAIFGGYGRAGGSYGFGGAGSGFGFGGAGIGFGLGGAGLAGGFGGPFVCPGGIQEVTVNSLLTFLNL 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 119703753 | ref | NP_005546.2 | ***** 300
gi | 114644570 | ref | XP_001143262.1 | QIDPAIQRVRAEEREQIKTLNNKFASFDKVRFLFQONKVLDTKWLLQEQGKTVRONLEPLFEQYINNLRRQLDNIVGERGRLDSELRNMODLVEDLKNKYEDEINKRITAAENEFVTLKKDVEDAAYMKNVELQAKADTLTDEINFLRA 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 119703753 | ref | NP_005546.2 | ***** 450
gi | 114644570 | ref | XP_001143262.1 | LYDAELSQMOTHS DTSVVLSDNNRNLDDSIIEVKAQYEEIAQRSRAEESWYQTKYEELQITAGRHGDDLRLNTKQETAEINRMIQRLRSEIDHVKKQCANLQAAIADAEQRGEMALKDAKNKLEGLDALQKAKDLARLLKEYQE 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 119703753 | ref | NP_005546.2 | *****:***** 564
gi | 114644570 | ref | XP_001143262.1 | LMNVKALLDVEIATYRKLLGECECLNGEGVGVNIVVQSTVSSGYGGASGVGSLGLGGSSYSYSGSLGVGGFSSSSGRATGGGLSSVGGGSSTIKYTTTSSSSRKSYPK 564
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....

