

gi | 28893581 | ref | NP_796372.1 |
gi | 114561085 | ref | XP_001174542.1 |
gi | 17298670 | ref | NP_387501.1 |
gi | 62659689 | ref | XP_222902.3 |
gi | 74006229 | ref | XP_851352.1 |
gi | 194665210 | ref | XP_001789234.1 |
MVCDIREIASLFTIRDDQKDVIAVAVHFGSGLAPPLHVHYAPKSDWTRIASAGKEERPSVVPWKTIPRSCPVTVLEHTGGSDHTELAGVRAPRGSSWPPPASCRDAGDPPSPSGTLDLPLSRGKCSRMSALPILTNQTRHLPFHHEEPGL 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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PFSLRQPPFLASLAEDDYRELYKGIAPGQRSLRKRLLSLPVTFLLGGSWCSQPLVCEPSSGYTCGDDPTASAAAAPVHVAETKVPKHPKYVPLQLLWEICTRSHRHPAGGRTPAPRAPSRRRPGSARRRAREGSLSRPRPGPRSSRPPGNMLD 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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GLKMEENFOSAIDTSASFSSLLGRAVSPKSVCEGQORVILDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 153
GLKMEENFOSAIDTSASFSSLLGRAVSPKSVCEGQORVILDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 153
GLKMEENFOSAIEIETSAFSSLLGRAVSPKSVCEGQORVISDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 153
GLKMEENFOSAIEIETSAFSSLLGRAVSPKSVCEGQORVISDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 153
GLKMEENFOSAIEIETSAFSSLLGRAVSPKSVCEGQORVISDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 450
GLKMEENFOSAIEIETSAFSSLLGRAVSPKSVCEGQORVISDRFLLRLNDSFWHEQCVCASCKEPLTTCFYRDKKLYCKYDYEKLFVAVKCGGCFEAIAPNEFVMRAQKSVYHLSCFCCCV CEROLQKGFVFLKEGQLLCKGDYEKERE 153
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 303
LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 303
LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 303
LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 303
LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 600
LLSLVSPAASDSGKSDDEESLCKSAHGAGKGAEEGKDHKRPKRPRITLITQORRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNRQAKMKKLARRQQQQQDQONTORLSSAQTNGGGSAGMEGIMNPYIALPTPQOLLAI 303
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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QSVYSSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 382
QSVYSSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 382
QSVYNSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 382
QSVYNSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 382
QSVYSSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 679
QSVYSSDPFRQGLTPPQMPGDHMHFYGAEPFLFHDLDSDDTLSNLGDCFLATSEAGPLQSRVGNPIDHLYSMONSYFTS 382
.....610.....620.....630.....640.....650.....660.....670.....