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gi | 24234699 | ref | NP_002267.2 | ----- MTSYSYROSSATSSFGGLGGGVRFPGPVAFRAPS IHGSGGRCVSVSSARFVSSSSSGAYGGGYGGVLTASDGLLAGNEKLTMONLNDRLASYLKVRALBAANGE 107
gi | 114667194 | ref | XP_511487.2 | MGTVLGTGGHWGQELGRQVRA SPLLPRIAASETRVAPSVLRLAMTSYSYROSSATSSFGGLGGGVRFPGPVAFRAPS IHGSGGRCVSVSSARFVSSSSSGYGGGYGGVLTASDGLLAGNEKLTMONLNDRLASYLKVRALBAANGE 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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gi | 24234699 | ref | NP_002267.2 | ----- LEVKIRDWYQKQGGPSPRDYSHYYTIQDLRDKILGATIENSRIVLQIDNARLAADDFRTKFEETEALRMSVEADINGLRRVLDLTLARTDLEMQIEGLKEELAYLKKNHHEEISTLRGQVGGQVEVEVDSAPGTDLAKILSDMRSQVE 257
gi | 114667194 | ref | XP_511487.2 | LEVKIRDWYQKQGGPSPRDYSHYYTIQDLRDKILGATIENSRIVLQIDNARLAADDFRTKFEETEALRMSVEADINGLRRVLDLTLARTDLEMQIEGLKEELAYLKKNHHEEINTLRGQVGGQVEVEVDSAPGTDLAKILSDMRSQVE 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300
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gi | 24234699 | ref | NP_002267.2 | ----- VMAEQNRKDAAEAWFTSRTEELNREVAGHTEQLQMSRSEVLDLRRTLQGLEIELOSQLSMKAALDTEARFQAQLAHLICALISGIEAQLGDVRADESERONQEVQRMDIKSRLEQEIATYRSLLLEG----- 387
gi | 114667194 | ref | XP_511487.2 | VMAEQNRKDAAEAWFTSRTEELNREVAGHTEQLQMSRSEVLDLRRTLQGLEIELOSQLSMKAALDTEARFQAQLAHLICALISGIEAQLGDVRADESERONQEVQRMDIKSRLEQEIATYRSLLLEGCGDPPGGGRMGALGPGGFPQS 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450
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gi | 24234699 | ref | NP_002267.2 | ----- EDHYNLSASKVL----- 400
gi | 114667194 | ref | XP_511487.2 | ESGGGSTRGGSLLAGGGFGGSLCGGSGGGYGGMRVCGFGGAGSVFGGFRGGVGGGFGGDDGGLLEGNEKLTMONLNDRLASYLKVRALBAANADLEVKIHDWYQKQTPSPPECDYSQYFKTIEELRDKIMATIIDNSRVILEI 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600
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gi | 24234699 | ref | NP_002267.2 | ----- DNARLAADDFRLKYENELALRQGV EADVNLRRVLDLTLARTDLEMQIEGLNEELAYLKKNHHEEVRSDWHEFSSQLAGQVNVEMDAPGVDLTRVLAEMRQVEAMAENRRDVEAWFFSKLEIELOSQLSMKAAGLENSLAETECRY 400
gi | 114667194 | ref | XP_511487.2 | DNARLAADDFRLKYENELALRQGV EADVNLRRVLDLTLARTDLEMQIEGLNEELAYLKKNHHEEVRSDWHEFSSQLAGQVNVEMDAPGVDLTRVLAEMRQVEAMAENRRDVEAWFFSKLEIELOSQLSMKAAGLENSLAETECRY 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750
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gi | 24234699 | ref | NP_002267.2 | ----- ATQLQIQGLIGGLEAQLSELRCMEANQVEYKMLLDIKIRLEQEIATYRSLLLEGQDAKILGGFGGGFAGGFVDFGACDGGLLGNEKLTMONLNDRLASYLKVRALBAANADLEVKIRDWHLQKSPASPERDYSFQYKTIIEELRDKIL 400
gi | 114667194 | ref | XP_511487.2 | ATQLQIQGLIGGLEAQLSELRCMEANQVEYKMLLDIKIRLEQEIATYRSLLLEGQDAKILGGFGGGFAGGFVDFGACDGGLLGNEKLTMONLNDRLASYLKVRALBAANADLEVKIRDWHLQKSPASPERDYSFQYKTIIEELRDKIL 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900
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gi | 24234699 | ref | NP_002267.2 | ----- LAIENNRVILEIDNARLAADDFRLKYENELALRQSV EADINGLRRVLDLTLARTDLEMQIEGLNEELAYLKKNHHEEMKEFSNQVVGQVNVEMDAPGIDLTRVLAEMRQVEAMAENRRDAEWFHAKSAELNKEVSTNTAMIQTS 400
gi | 114667194 | ref | XP_511487.2 | LAIENNRVILEIDNARLAADDFRLKYENELALRQSV EADINGLRRVLDLTLARTDLEMQIEGLNEELAYLKKNHHEEMKEFSNQVVGQVNVEMDAPGIDLTRVLAEMRQVEAMAENRRDAEWFHAKSAELNKEVSTNTAMIQTS 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050
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gi | 24234699 | ref | NP_002267.2 | ----- 400
gi | 114667194 | ref | XP_511487.2 | KTEITELRRTLQGLEIELOSQLSMKAAGLENTVAETECRYALQGLIQGLISSIEAQLSELRSEMCEQNEVYKMLLDIKIRLEQEIATYRSLLLEGQDAK 1148
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....

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