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gi |4504725|ref|NP_001562.1|      MGTQKPRILPWLVSQDLGLGLEGVAVVNRSRTRFRIPWKHGLRQDAQOEDFGIFQAWAEATGAYVPGKDKPDLPTWKRNFRSALNRKEGLRLAEDRSKDPDPHKIYEFVNSG-VGDFSQPDTSPTDNGGSGTSDTQEDILDELLGNMVL 150
gi |114678377|ref|XP_001157487.1| MGTQKPRILPWLVSQDLGLGLEGVAVVNRSRTRFRIPWKHGLRQDAQOEDFGIFQAWAEATGAYVPGKDKPDLPTWKRNFRSALNRKEGLRLAEDRSKDPDPHKIYEFVNSG----- 150
gi |73947954|ref|XP_533616.2|      -----MSCGGHG-----WNG-----QAWAEVSGAYTPGKDKPDLPTWKRNFRSALNRKEGLRLAEDRSKDPDPHKIYEFVNSG-AGNLPELDTPDPTNGRYSTSDTQEDTLEELLGDMVL 150
gi |71067136|ref|NP_001025016.1| MGTQKPRILPWLISQLDRGELEGVAVLGESETRFRIPWKHGLRQDAQOEDFGIFQAWAVASGAYTPGKDKPDLPTWKRNFRSALNRKEVLRLEADHSKDSQDPHKIYEFVNSG-VRDIPDPTSDQ-NGRHNTSDTQEDTLEKLLSDMDL 150
gi |8393627|ref|NP_058545.1|      METPKPRILPWLVSQDLGLGLEGVAVLDESRTFRFRIPWKHGLRQDAQMADFGIFQAWAEASGAYTPGKDKPDLPTWKRNFRSALNRKEVLRLEADNSKDPYDPHKVYEFVTPG-ARDFVHLGASPTDNGKSLPHSQEN-LPKLFDGLIL 150
gi |55741687|ref|NP_001006970.1| MGTQKPLILPWLVSQDLGLGQKGVAVLDESRTKFRIPWKHGLRQDAQMADFGIFQAWAEASGAYTPGKDKPDLPTWKRNFRSALNRKEVLRLEADRSKDPDPHKVYEFVTPGGARDFVHLDTSPDPTNGKSLSDHED-LLELLDHMAL 150
gi |189525730|ref|XP_693269.2|      MTQAKPLFVFWLVEIQSGRYPGVCWKNEDCQFSIPWKHALRQDSNSDDVLIFFKAWAQTSAAGD-GRLNGLPESVWKRNFRSALRAKG-FKMTISDKKNDGADPHKVYQFSDP-----SAVHIILNPNLDLYVDPGTIYDFQAVVPIEA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |4504725|ref|NP_001562.1|      APLPDPGPPSLAVAPEPCQPLRSPSLDNPTFFPNLGPSENLKRLLLVPGEEWE--FEVTAFYRGRGVFOOTISCPGGLRLVGS---EVGDRILPGFVTLPPDPMGLIDRGMVSVVRHVLCLGGGLALWRAGQWLWAOQLGHCHTYW 300
gi |114678377|ref|XP_001157487.1|      -----LPAW----- 300
gi |73947954|ref|XP_533616.2|      FPFDEGPPSLVVVPEQTPPLLLSPTIDLPAFCPNSEPPENPLKRLLLVDEEWE--FEVTAFYRGRGVFOOTVSCPRGLRLVAA--AGCDTMLPGQPIILPDPGVLTDKTVMGYVRRVLSCLGGGLALWRAGQQLWARRLGHCHTYW 300
gi |71067136|ref|NP_001025016.1|      SPG---GPSNLTMASERKPPQFLQSPDSIPALCPNSGLSENLKOLLANEEDWE--FEVTAFYRGRGVFOOTVFCPPGGLRLVGS---EAGDRMLPGQPIRLPDPATSLTDKSVTDYVQRVLSCLGGGLALWRAGQWLCAORLGHCHVYW 300
gi |8393627|ref|NP_058545.1|      GPLKDEGSSDLAIVSDPSQQLP-SPNVNN---FLNPAPQENPLKOLLA-EEQWE--FEVTAFYRGRGVFOOTLFCPPGGLRLVGS---TAD-MTLPLWQPVTLPPDEGFLDKLVKEVYVQVVLKGLNGLALWRAGQCLWAORLGHSHAFW 300
gi |55741687|ref|NP_001006970.1|      GPLPDEGSSDLPIASDPSQPLP-SPIVNN---FPNPAPQENPLKOLLA-EEQWE--FEVTAFYRGRGVFOOTLFCPPGGLRLVGS---TSDNGTLPWQPVTLPPDEEFLDRLVREYVRQVLKGLKGLVLRAGQCLWAORLGHSHSFW 300
gi |189525730|ref|XP_693269.2|      SSSDEGAVGGLGQISPTREGAMAVNHISREYQQATQPHLGAVPDHVAIPEPNLAFFFRKVVYKGMVMEQLVENDSGFRMLYHRNMDSEGLQDQAGLFPVVLPPAEGMPDQMQTRLINDILDNLG-GLEIRRDGVVHGHRWSSRIYVW 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |4504725|ref|NP_001562.1|      AVSEELLPSGHGPDGEVPKDKEGGVFDLGPFIVDLITFTEGSGRSPRYALWFCVGESWPD--QPWTKRLVMVKVVPICLRALVEMARVGGASSLENTVDLHISNSHPLSLTSDQYKAYLQDLVEGMDFOGPGET 436
gi |114678377|ref|XP_001157487.1|      -----DLITFTEGSGRSPRYALWFCVGESWPD--QPWTKRLVMVKVVPICLRALVEMARVGGASSLENTVDLHISNSHPLSLTSDQYKAYLQDLVEGMDFOGPGET 436
gi |73947954|ref|XP_533616.2|      ALGSELLPDSRPRPGGEVPKDEDCDLFLRPFVSDLIAFIKGRHSRSPRYTLWFCVGEWPD--QPWTKRLVMVKVVPICLRALLEMARLEGASSLENTVDLHISNSYPLTSLTSDQYKAYLQDLVEDMDFWVTEV 436
gi |71067136|ref|NP_001025016.1|      ATGSELLPSCGHKPDGEVPKDRREGGVFNLGPFIITDLITFTEGSRSPRYTLWFCVGESWPD--QPWTKRLVMVKVVPICLRVLVLIARVGGASSLENTVDLHISNSDPLSLTSDQYMAACLDLAEEDMDF----- 436
gi |8393627|ref|NP_058545.1|      ALGSELLPDSGRGPDGEVHKDKDCAVFDLRRPFVADLIAFMEGSGHSRPRYTLWFCMGEWPD--QPWTKRLVMVKVVPICLKELEEMAREGGASSLK-IVDLHISNSQPISLTSDQYKAYLQDLVEDMDFQATGNI 436
gi |55741687|ref|NP_001006970.1|      ALGSELLPDSGRGPDGEVPKDKNGVFDLRRPFVADLIAFMEGSRHSRPRYTLWFCVGESWPD--QPWTKRLVMVKVVPICLKELEEMAREGGASSLK-IVDLHISNSQPISLTSDQYKAYLQDLVEDMDFQATGET 436
gi |189525730|ref|XP_693269.2|      GLCKHERSQTPR-----ELSKNTPQPIYLMKDYISGLMFIQTGGESPSCHLYFFLGEKWPDKMKPWEKLLIMTEVNLTALEFLKSMAYEQGASSLC-----SDELQLSLEQMMELC----- 436
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....

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