

gi|6681243|ref|NP_031917.1|-----MAVA--PAGGOHAPA 13
gi|109469084|ref|XP_230765.4|-----MAVA--PAGGOHAPA 13
gi|73992245|ref|XP_542963.2|MEEMAGKFTIEMIKSHVSAALKAGTRPCTEERTILVKSADLSNEKWLMERWRSLGCHGRSEYGVKRRDIDPKGSTCRDPEASGRRCASRAITPGWPGLCRQRPGAERDRALAAACRHGPAPPPPPATRAARAVSAMAVAGAPAGGCPAPA 150
gi|194672360|ref|XP_615437.4|-----MAVAGAPAGGSCAPA 15
gi|12669911|ref|NP_005216.1|-----MALAGAPAGGCPAPA 15
gi|45382583|ref|NP_990550.1|-----MALAGGAAG----- 9
gi|189536305|ref|XP_695874.3|-----MALAGGAAG----- 9
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|6681243|ref|NP_031917.1|LEALLGAGALRLLDSSQIVIIISTAPDVGAPQLF---AAPPTGPRDSVLLFATPQAPRPAPAPRPALGRPPVKRRLDLETDHQYLAGSSGPPFRG---RGRHPGKGVKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 156
gi|109469084|ref|XP_230765.4|LEALLGAGALRLLDSSQIVIIISTAPDVGAPQVPTGPAAPAGPRDPVLLFATPQAPRPAPAPRPALGRPPVKRRLDLETDHQYLAGSSGPPFRG---RGRHPGKGVKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 159
gi|73992245|ref|XP_542963.2|LEALLGAGALRLLDSSQIVIIISTAQDASAPPAPAGPAAPAGPRDPVLLFATPQAPRPPTAPRPALGRPPVKRRLDLETDHQYLAESSGGPARG---RGRHPGKGVKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 296
gi|194672360|ref|XP_615437.4|LEALLGAGALRLLDSSQIVIIISTAQDASAPPAPAGPAAPAGPRDPVLLFATPQAPRPPTAPRPALGRPPVKRRLNLETDHQYLAESSGPARG---RGRHPGKGVKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 161
gi|12669911|ref|NP_005216.1|LEALLGAGALRLLDSSQIVIIISTAQDASAPPAPAGPAAPAGPRDPVLLFATPQAPRPPTAPRPALGRPPVKRRLDLETDHQYLAESSGGPARG---RGRHPGKGVKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 161
gi|45382583|ref|NP_990550.1|LAALLGG-----APHLIVSABEEP-----AGGCRP-DADLLFATPQPSRPGPAPRRPALGRPPVKRRLNLETDHQYIAESLPAARG---RARIPGRGAKSPGKESRYETSLNLTTKRFLELLSRADGVVDLNWAAEVLK 138
gi|189536305|ref|XP_695874.3|LAALLGG-----APHLIVSABEEP-----AGGCRP-DADLLFATPQPSRPGPAPRRPALGRPPVKRRLNLETDHQYICTRTASNGPTPPATPAPRVPKLAVEKSRYDTSNLTTKRFLLDLSADGVVDLNWASQVLD 78
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|6681243|ref|NP_031917.1|VQKRIYDITNVLEGIQLIAKSKNHIQWLGSHTMVIGIKRLEGLTQDLQQLQESQQLDHLMHICITTLQLLSESDSITQRLAYVTCODLRSIADPAEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESADGISPGKT 306
gi|109469084|ref|XP_230765.4|VQKRIYDITNVLEGIQLIAKSKNHIQWLGSRTMVIGIQRLLEGLTQDLQQLQESQQLDHLMHICITTLQLLSESDSITQRLAYVTCODLRSIADPAEQMVIVIKAPPETQLOAVDSSAETFQISLKSQKGPIDVFLCPESAEGISPGKT 309
gi|73992245|ref|XP_542963.2|VQKRIYDITNVLEGIQLIAKSKNHIQWLGSAAVIGISGRLEGLTQDLQQLQESQQLDHLMHICITTLQLRLLAEDSDSORLAYVTCODLRSIADPAEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESAAGGISPGKT 446
gi|194672360|ref|XP_615437.4|VQKRIYDITNVLEGIHLIAKSKNHIQWLGSHTATVIGISGRLEGLTQDLQQLQESQQLDHLHICITTLQLRLLAEDSDSORLAYVTCODLRSIADPAEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESVGGTISPGKT 311
gi|12669911|ref|NP_005216.1|VQKRIYDITNVLEGIQLIAKSKNHIQWLGSHTVIGVGRLEGLTQDLQQLQESQQLDHLMHICITTLQLRLLAEDSDSORLAYVTCODLRSIADPAEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESVGGTISPGKT 311
gi|45382583|ref|NP_990550.1|VQKRIYDITNVLEGIQLIAKSKNHIQWLGSVAAGASSRQRLLEKELRDLGAERQLDLDLIQCTVRLRLLEDPVSNCHAAVVTQODLRSIVDPSEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESVGGTISPGKT 288
gi|189536305|ref|XP_695874.3|VQKRIYDITNVLEGIHLIAKSKNHIQWLGNRIDGASLARFQELQKEVSELTAEKLEDELINKSLQLRLLEDPVSNCHAAVVTQODLRSIVDPSEQMVIVIKAPPETQLOAVDSSSETFOISLKSQKGPIDVFLCPESVGGTISPGKT 166
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|6681243|ref|NP_031917.1|SQEETS--GEDRTADSGPAGPPP--SPPSTSPALDPSQSLLEQEAFLPRMGH--LRVPMEDQLSPLVAADSLLEHVKEDFSGLLPGEFISLSPPEALDYHFGLEEGEGIRDLDFCDFGDLTPLDF 430
gi|109469084|ref|XP_230765.4|SYQETS--GEDRNADSGTAGPPP--SPPSTSPALDPSQSLLEQEAFLPRIGN--LRAPMEEDRLSPLVAADSLLEHVKEDFSGLLPGEFISLSPPEAVDYHFGLEEGEGIRDLDFCDFGDLTPLDF 432
gi|73992245|ref|XP_542963.2|PSQGTASGEEDRPVDPATITVPPP--SPPSPASDPSQSLLEQEPPLSRMGH--LRAPVDEDRLSPLVAADSLLEHAREDFSGLLPEEFISLSPPEALDYHFGLEEGEGIRDLDFCDFGDLTPLDF 571
gi|194672360|ref|XP_615437.4|PSQGAASGEEDRTADLAIAVPPPPP--SPPSPATDPSQSLLEQEPPLSRMGH--LRAPVDEDRLSPLVAADSLLEHVKEDFSGLLPGEFISLSPPEALDYHFGLEEGEGIRDLDFCDFGDLTPLDF 437
gi|12669911|ref|NP_005216.1|PSQEVTSERENRATDIAIIVSPPPP--SPPSSLTDPQSLLLEQEPPLSRMGH--LRAPVDEDRLSPLVAADSLLEHVREDFSGLLPEEFISLSPPEALDYHFGLEEGEGIRDLDFCDFGDLTPLDF 437
gi|45382583|ref|NP_990550.1|P-----FKAPEELSPGSGQORASPLLSAQDVNMLLEPALLPGLTALPKCPEDVSLSPPLASMDLLEHGKDDFPGLADEFTALSP--QPDYHFGLEEGEGISELDFCDFDFTHLDF 403
gi|189536305|ref|XP_695874.3|-----FKAPEELSPGSGQORASPLLSAQDVNMLLEPALLPGLTALPKCPEDVSLSPPLASMDLLEHGKDDFPGLADEFTALSP--QPDYHFGLEEGEGISELDFCDFDFTHLDF 166
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....

