

gi|116007922|ref|NP\_001036659.1|-----  
 gi|158287035|ref|XP\_309088.3|-----  
 gi|7949135|ref|NP\_038815.1|-----  
 gi|109464488|ref|XP\_226817.4|-----  
 gi|16306595|ref|NP\_005974.2|-----  
 gi|114600587|ref|XP\_526948.2|-----  
 gi|73954319|ref|XP\_546346.2|-----  
 gi|156120751|ref|NP\_001095522.1|-----  
 gi|56118960|ref|NP\_001007983.1|-----  
 gi|130496750|ref|NP\_001076306.1|-----  
 gi|25148653|ref|NP\_741137.1|-----

MIRIMONKMKIATSVKISGSPFVDFARSSDLECGILPALAAPRLSRAATGSOQLAFQTAIPPDVVGGARAAQRPRAWRSAPHRPTDRPLSCSOARLGCQAAQLSHRTPWRKQLRGGGGGGGGGGGGASGTPAALIVSPGRRIGLPPPI 150

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|116007922|ref|NP\_001036659.1|-----MGIGMLDSESSSSALSAIALAVSATSDDNSNETTPCASVSRMAHQLQHTQ 51  
 gi|158287035|ref|XP\_309088.3|-----  
 gi|7949135|ref|NP\_038815.1|-----  
 gi|109464488|ref|XP\_226817.4|-----  
 gi|16306595|ref|NP\_005974.2|-----  
 gi|114600587|ref|XP\_526948.2|-----  
 gi|73954319|ref|XP\_546346.2|-----  
 gi|156120751|ref|NP\_001095522.1|-----  
 gi|56118960|ref|NP\_001007983.1|-----MP 2  
 gi|130496750|ref|NP\_001076306.1|-----  
 gi|25148653|ref|NP\_741137.1|-----

GGRRRRPAAAAAARGLRGLDLRORPASDRRRPRAHALPIRPDSVTRTRGNPAAATAVPDLRPAIRGDDGGRSAAHFRFPAYRVDGPA SRARGLVGISEAGSGAADGGGGGGGGGRVEEPPARRRGWVARVRGSRCWGSELHALSRR 300

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

gi|116007922|ref|NP\_001036659.1|-----RLSLGSSTGDTILDSPAVEDLSMSRQSAEKLILAQAKRSLSGSESGNSNSPSKRLRNPLAAVLCNNIDGTASLNFQPTSLRLAQVRQAKKPSLTNITLRIVAADSFVFRTPAMSAHNSGINYFERLSDLELLDIPKWLPKKTLRL 201  
 gi|158287035|ref|XP\_309088.3|-----MDPPSNKGRLLPLNVSNVNRQCKSNVPPPHDPLSSEQLKAPHGSEBFAFFMYRKNQRKATYGEEDLFSLLSDEVLLHLKWLPKKTLRLS 92  
 gi|7949135|ref|NP\_038815.1|-----MHRKHLQEIIPD-QSGNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 119  
 gi|109464488|ref|XP\_226817.4|-----MHRKHLQEIIPD-QSSNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 119  
 gi|16306595|ref|NP\_005974.2|-----MHRKHLQEIIPD-LSSNVAITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 119  
 gi|114600587|ref|XP\_526948.2|-----MHRKHLQEIIPD-QSSNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 119  
 gi|73954319|ref|XP\_546346.2|-----PKRESRRRAVLQLMHAFKTPAIVDAMHRRKHLQEIIPD-QSSNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 444  
 gi|156120751|ref|NP\_001095522.1|-----MHRKHLQEIIPD-QSSNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 119  
 gi|56118960|ref|NP\_001007983.1|-----RVRRDARLGEHCHEEQESPQASAMLRKHLQEIIPS-SGSNVITTSFTWGWDSSTKTELLSGMGVSALEKEEVDSENIPHGLLNLGHQPSPPRKRLKSKGSKDKDFVIVRRPKLNRENFPVGSWDSLPDELLLGIFSCLCLEPELLR 140  
 gi|130496750|ref|NP\_001076306.1|-----MSNERVFLSENLEGLSCLRSQRKWK--KRFPCSSGLDIENTPNELIQWSPPHKALTTAKGENEENLFLVLRARRPKRRRESSANLCSWDSLPDELLLGIFSRLLQDLLR 110  
 gi|25148653|ref|NP\_741137.1|-----MSRVIQRLSTLENGPSENHCVETVFSDEITISIFPCYNLVPKKSLRLSVSGNSEKLSLNLNCKN--LVDEIAPIKRKRARSIQNPFKKLS-IPDEITQIFSNLKKKDLLS 112

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



gi|116007922|ref|NP\_001036659.1|-----MATVCRRFNRCSRDETLWTRLDLGLRTIRPGALEQIVRRGVLVIRLAQTSIQEPAFAPY---TEVFR--LRLOQLDLSMASITRSLTLTLHCRQLKKIILENIEELDDICAEIAKNEALEAVNLTMASGLTNSVRLMMEIILSISSL 346  
 gi|158287035|ref|XP\_309088.3|-----CGQVNRRENVRKDETLWYRLDLSNRTLQDFGLVEVLRGVIIVLRLAQTSIVNPTPSN---YLEFPACTIKVOYLDLSMCTVSLAVLIGALLANRALVKLSENVPLDGRICAEIAENRKLALNLMCSGIDATCMRLMAKALRHLHS 239  
 gi|7949135|ref|NP\_038815.1|-----VSGVCKRWYRLSLDESLSQSLDLGKNLHPDVTVIRLLSRGVAFRCPRSFMEQPLGES---FSSFRVQHMDLSNSVINVNLHKLSECSKLNLSLEGLQLSDPIVKTLAGQENLVRNLNLCGCGFSFSAVATLLSSCSRDEL 261  
 gi|109464488|ref|XP\_226817.4|-----VSGVCKRWYRLSLDESLSQSLDLGKNLHPDVTVIRLLSRGVAFRCPRSFMEQPLGES---FSSFRVQHMDLSNSVINVNLHKLSECSKLNLSLEGLQLSDPIVKTLAGQENLVRNLNLCGCGFSFSAVATLLSSCSRDEL 261  
 gi|16306595|ref|NP\_005974.2|-----VSGVCKRWYRLASDESLSQTLDDLTKGNLHPDVTGRLLSQGVIAFRCPRSFMDQPLAEH---FSPFRVQHMDLSNSVIEVSTLHGILSQCSKLNLSLEGLRLSDPIVNTLAKNSNLVRLNLSGCCGFSFALQTLSSCSRDEL 261  
 gi|114600587|ref|XP\_526948.2|-----VSGVCKRWYRLASDESLSQTLDDLTKGNLHPDVTGRLLSQGVIAFRCPRSFMDQPLAEH---FSPFRVQHMDLSNSVIEVSTLHGILSQCSKLNLSLEGLRLSDPIVNTLAKNSNLVRLNLSGCCGFSFALQTLSSCSRDEL 261  
 gi|73954319|ref|XP\_546346.2|-----VSSVCKRWYHLAFDESLSQTLDDLTKGNLHPDVTGRLLSRGVAFRCPRSFMDQPLVEH---FSSFRVQHMDLSNSVIDVSTLHGILSQCSKLNLSLEGLQLSDPIVNNLACNSNLVRLNLSGCCGFSFSAKTLSSCSRDEL 586  
 gi|156120751|ref|NP\_001095522.1|-----VSSVCKRWYHLAFDESLSQTLDDLTKGNLHPDVTGRLLSRGVAFRCPRSFMDQPLVEH---FSPFRVQHMDLSNSVIDVSTLHGILSQCSKLNLSLEGLRLSDPIVNDLACNTNLLRLNLSGCCGFSFSAKTLSSCSRDEL 261  
 gi|56118960|ref|NP\_001007983.1|-----VSMICKRWHLRSLFDESLSQTLDDLTKRSLLPGVIGQLPAGVIAFRCPRSFCIGNPLFKT---MKPLRVOHMDLSNCTVSVADLQSLCERLENLSEGLVLSDDIILKIAKNPSLIRLNLCCGCGFSFAELMLSKCSMLDEL 282  
 gi|130496750|ref|NP\_001076306.1|-----FSRVCKRWHLAFDESLSQTLDDLTKRSLLPGVIGQLPAGVIAFRCPRSFCIGNPLFKT---FSPFRVQHMDLSNCTVSEVLEDVLRCKHNLNLSLEGLVLSDDIILYLAQNPETIIRLNLCCGCGFSFESITELMIACTRIEM 252  
 gi|25148653|ref|NP\_741137.1|-----AMLVCHRFPYGIHKSRNWITDAQDRPISEISLIALSRKIKVLRLAGAADRILRADERLVEALLSTSLRELLDLSRNLNLTARQMQLKPCOKLKLCEIGNQLDDHVAICTAENRGLRELDISMNGITANGASLIFRNCKDQL 262

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



