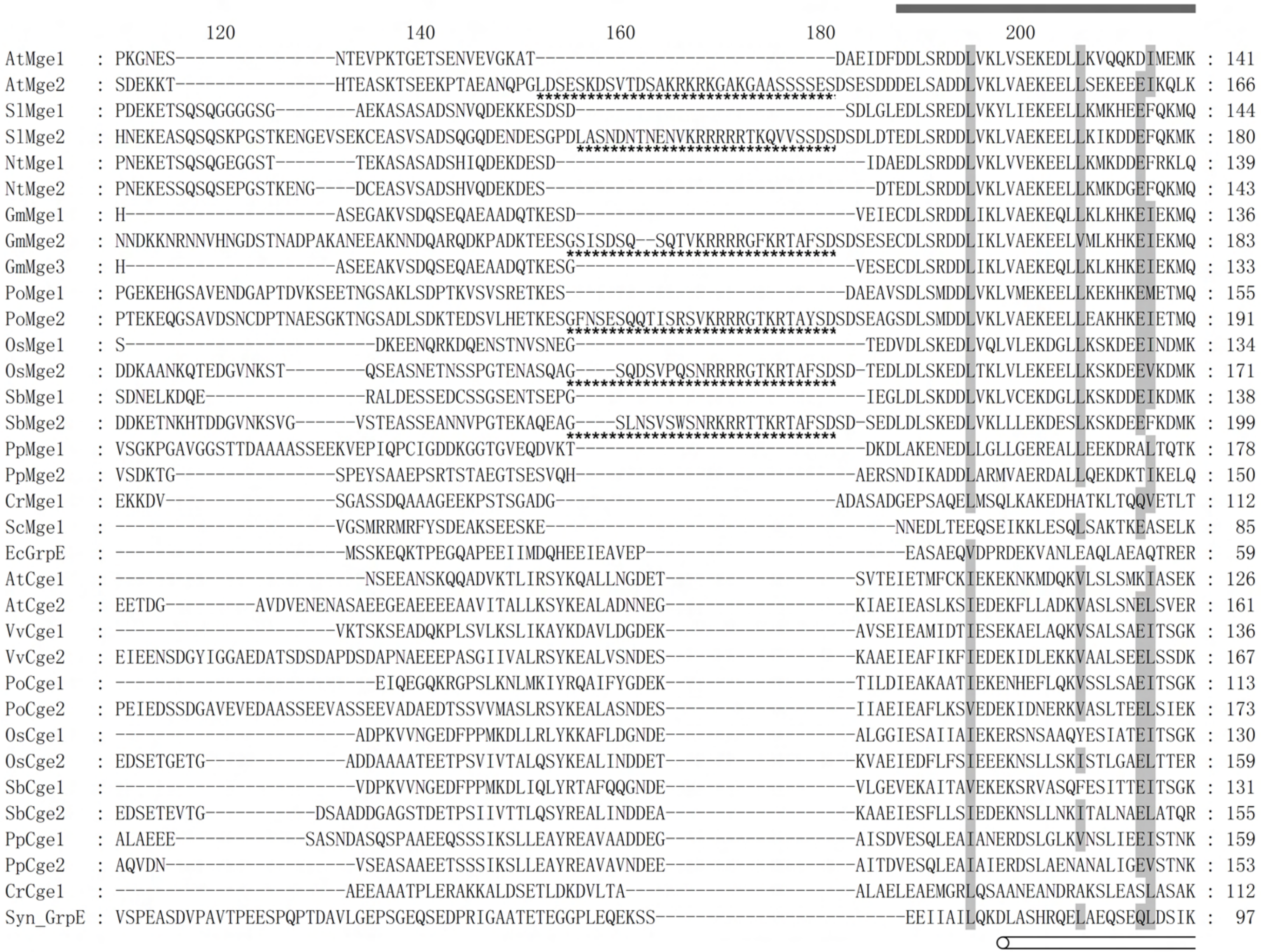
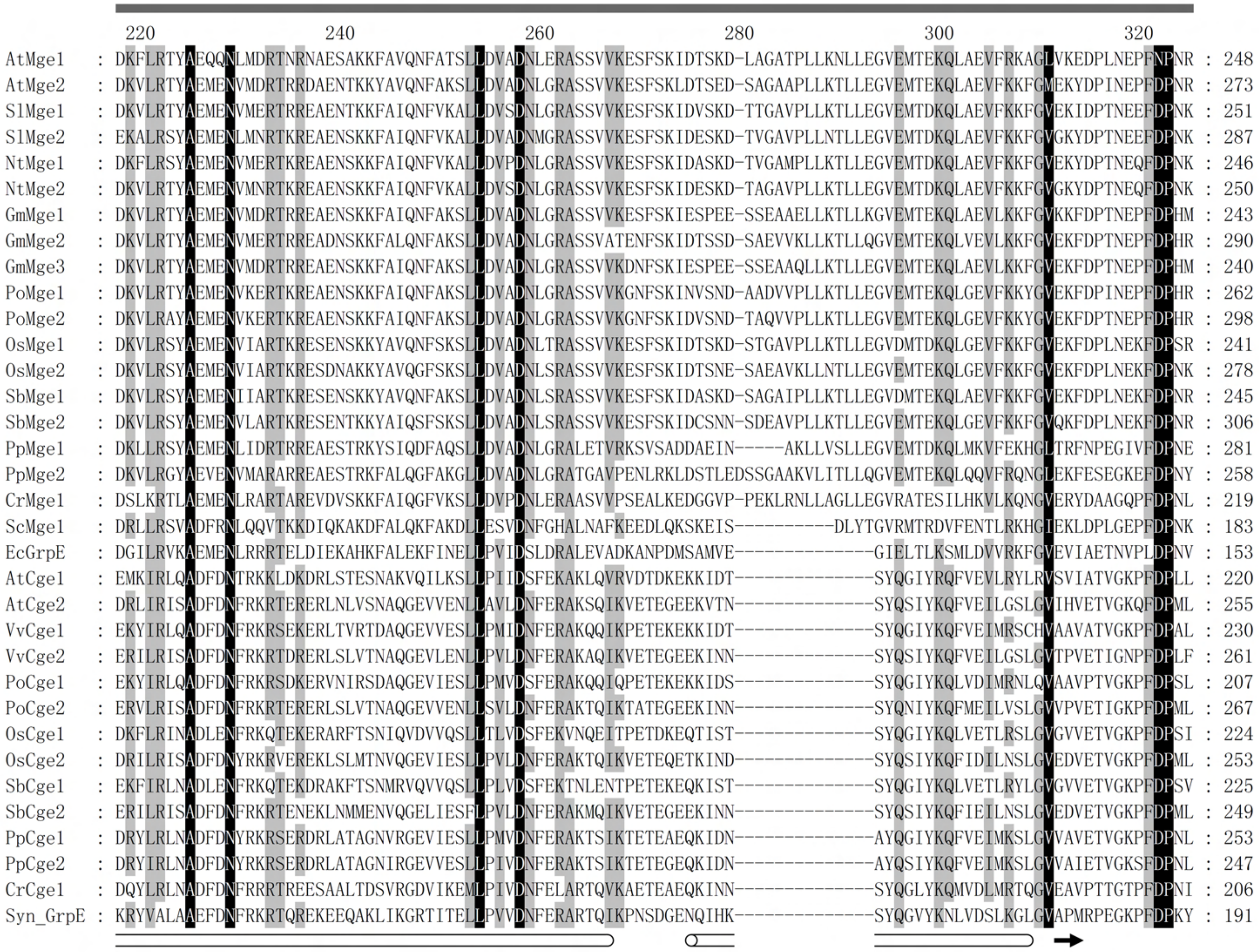
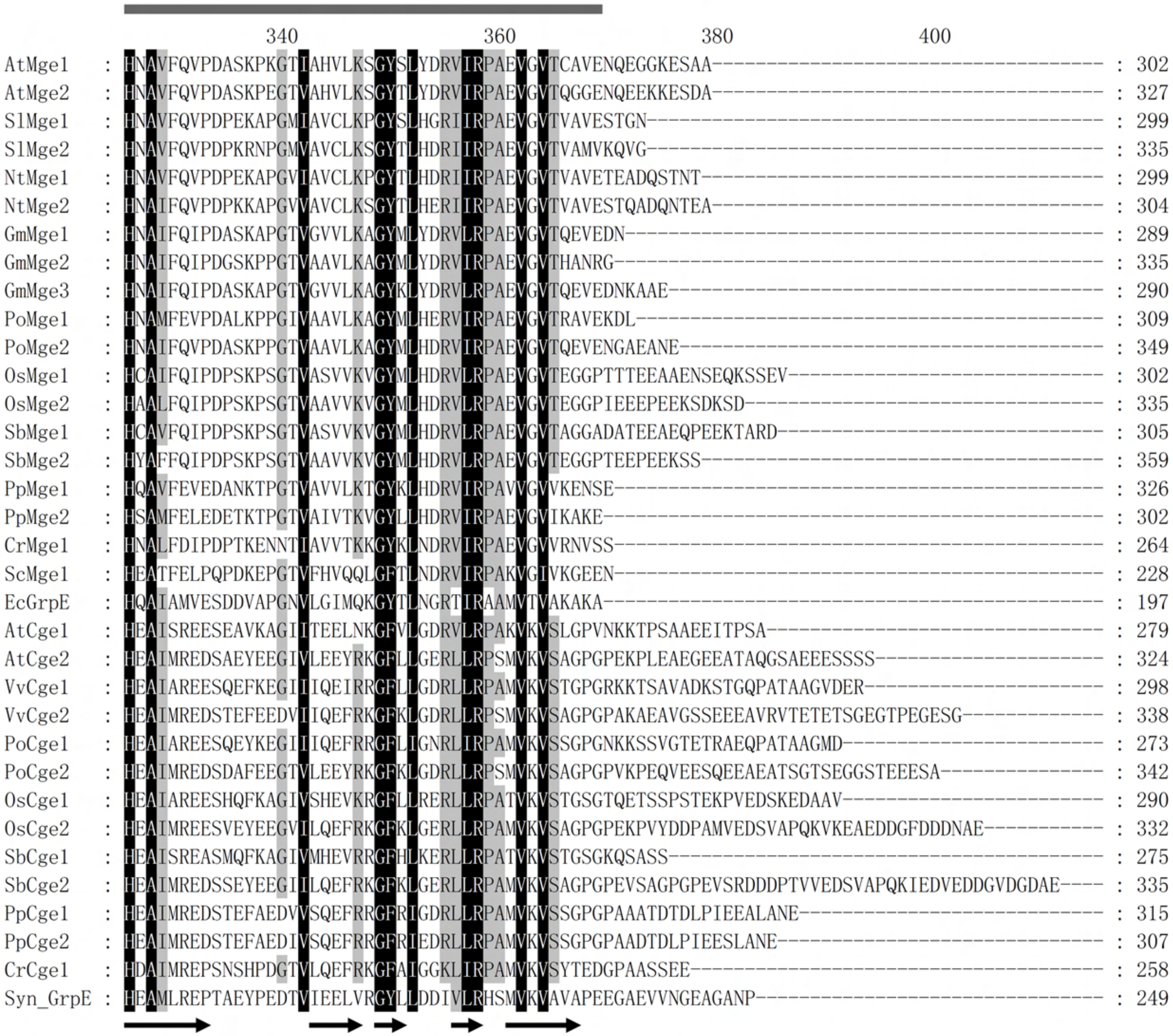
```
                             20                  40                  60                  80                 100
AtMge1   : --------------------------MLVSRVLSRVSRSAGLRSSFSSVVTPKRNQIPIVASR---FHSLVHGTPNKLVAVPVSLRNHGTLDLNVLQRFGFFSSSSAE :  79
AtMge2   : --------------------------MLVLRILSRVTRNAGIRSSLSAVTLPARNQTPVFSSR---FHSLAHDFSHKLVPAQM-----SMMDSFALQRFNFSSSTSPE :  74
SlMge1   : --------------------------MVLSRISSRFSRNVLTQCRNSLLLYYR-QNQQHHVPI----------LSSQFHSIRNIREKVSLVPESALQRFGISSSASPQ :  71
SlMge2   : --------------------------MLVGRISSRFPKSIVAQCRSSLLLYSREQQQQQYVPI----------FASEFHSFREFKEKVTLFRESLLQQFRISSSASPQ :  72
NtMge1   : --------------------------MSVSRISSRFSRNVLTQCR-LYYRQQK-QQQQHHLPI----------LSSQFHSVRDIKEKVSLLPDSALQWFGISSSASPQ :  70
NtMge2   : --------------------------MSVSRISSRFRRAILNQCRSSVLLYSREQQRQQHVPV----------LAFQFHSLRDFKEKVSLFHESALQRFGISSSASPQ :  72
GmMge1   : --------------------------MFAYRVLSRSSATLSRSFTLFSVSRNSQPFSTNLSNN----FNSLLHPSPNKLIPVQTNFLNSMNPSLT-SRFGFSSTASHE :  77
GmMge2   : --------------------------MFFHRVLSRVSTNICR-TSLLSASQTPQHLSSFANIN----LHSLLPHSPNKVIPVQLNLLLPPINSLSAPRFGFSSSASTE :  77
GmMge3   : --------------------------MFAYRVLSRSSAILSRSFTLFSVSRNSQPFSTTLSNN----FHSLLHPSPNKVIPVQTNFLN---SSLT-SRFGFSSTASHE :  74
PoMge1   : --------------------------MLMTRMLSRLSRSVGQRSLHLCSPSQNHHLLLIPSN-------QFHEYPNKCITSKVCLFHHSVLNSSLFQNFGFTSSASPE :  75
PoMge2   : -------------------------MLMTRMLSRLSRSVGRRSLVLHSPSPSHNHHLLPILSYQFHSLVHEYGYPDKCITRKVCLFHHSALNSPPFQNFGFTSSASPE :  83
OsMge1   : ------------------------MVAASRLLARASRQCVAAVAASAARRRRCPAAALSLPV----VTAAKAAAAEPWLGVPYMLNQPLRYSTTIFQRFGFSSTSPEL :  80
OsMge2   : ------------------------MAAAARLLARISR-QG--VASAAAARRQAEAAALLGAS----AGRHLAPPCSSIKALPLLN-QPRLYSTSTFQRFGFSSSAPQQ :  76
SbMge1   : --------------------------MATARLLARVSRQCAGAVAASSAAGRHRRAPAAASVE-------QFAGSCLSARVPRILNHHFRYSTSIFQKFGFSSVSPQQ :  75
SbMge2   : MHRFPFFPHNCFISLSSPRFRPNKMAAAARLLTRISKRAVPSVALAGAARRRPEAASLLGAS----VLAAVEP-CASIKVIPLLN-QLAPYSTSAFQRFGFSTSAPQQ : 102
PpMge1   : ---------MSNAQRSMHYARALLRAFKKEPSRVARGAVRETAPAKPMRECSRPSALQSLRDSDLHLMNSFQKFRWASAASPVSHAAPSFESCPSLYSASFSSATSPE :  99
PpMge2   : ----------------------MSSSKHARLLFKAFQKPPQIRCFRAPSSSAPINEKSVFSTKLSGTEFLSPLSKRWTAFSLHRAVPQVSSISNLNSFTHFSSAASPD :  86
CrMge1   : ----------------------------MTSLLRVGAAVLRTCRLEVSPLMSAQSGLAMPTS-------------------------------RPILQWSRCFATDKD :  49
ScMge1   : ----------------------------MRAFSAATVRATTRKSFIPMAPRTPFVTPSFTKN---------------------------------------------- :  34
EcGrpE   : ------------------------------------------------------------------------------------------------------------ :   -
AtCge1   : ------------------------MAISFAIDPSISPCFSFSSPSSSSKTLPLRNNLHFHGRPSPISPLISKPSRKFPIFSAHQTN---------------------- :  62
AtCge2   : ------------------------MAGLLKTPSLHLTPTLLHAPSVPFKPFCVSFAGGR---NVSVSLSRRASLRSVSSGYPLRLLNLVPFASGEAETTETEVESNEP :  81
VvCge1   : --------------------MAFSLSNHLLFTPKPSKTLALHPPHPSKPILGFRLSTSSPILRRSFKPFLALQDSTPYTNNEEEGSRYD------------------- :  69
VvCge2   : -------------------------MATLLRAPFTAPPPQSLTSICTQSPKAFHLSLTR---RCALNPSRLTSSLRFSPILHIRFLRFDPFASNG--EATETQEVQDS :  78
PoCge1   : ------------------------------------MPLRQCKPINASLLSSSSPIPINNIKRRSLKTYLAPEDSAPTTNGKEENN---------------------- :  50
PoCge2   : ------------------------MATVIKTPPFSAPRIINNSSISLKYANPLCLSFSHNNNRSIPNFSLAKNSLRFPTKPSLRFVKFVPFSSQGETETTETEETIQE :  84
OsCge1   : ------------------------MAATFSAAAAAAAASPTYLHRPRTLAPPASTPARLSPSSSSRRPATPSLLSLRRTHAAPPPLRAAA------------------- :  65
OsCge2   : ------------------------MAALLRTAAALAPPPSPARDPRRPSSAASSLAFARRAAARPLRAQPLLPPAARRVPGFVAGPLLRRRPRVGATEADEAAQTATE :  84
SbCge1   : ------------------------MAATFCAGPAASAVANPSSAG--CRRQNLPRAGVLSACWRPTRPIPAFLSLRRPNAELRPLRVAAGSG---------------- :  66
SbCge2   : ------------------------MAALLRTAAALAPPPSSPLPAREPRGRCLRLACSRRAPARPLRAWLLPTPHVFCRDGARFRRLAA-------TEADEAAQTATQ :  77
PpCge1   : -------------------------MAALASSAATAGMIGQAPRQSTVALRMASSRAFVPAQFGVQCLRWRGRVQVQSSHYRRPVFVAQNSAQTEETEVGEDVETNEE :  83
PpCge2   : -------------------------MPAVACTAAMAGTLIQAPRQSIVVSRMASARAFVPAQFGAQCFRWRGVVQVQSFRYRRLVFVARNSAQTDAKKTEEVAEKKGE :  83
CrCge1   : ------------------------------------MQLLSSRPACVALPRSVQRAAAKPMVARAPVARRFVATRAAEEAEAAAAP---------------------- :  50
Syn_GrpE : ----------------------------------------------------------------------------------------------MNEDQVSLENQTNP :  14
```



```
                    120                 140                 160                 180                 200
AtMge1   : PKGNES----------------NTEVPKTGETSENVEVGKAT------------------------------DAEIDFDDLSRDDLVKLVSEKEDLLKVQQKDIMEMK : 141
AtMge2   : SDEKKT----------------HTEASKTSEEKPTAEANQPGLDSESKDSVTDSAKRKRKGAKGAASSSSESDSESDDDELSADDLVKLVAEKEELLSEKEEEIKQLK : 166
                                                     ******************************
SlMge1   : PDEKETSQSQGGGGSG--------AEKASASADSNVQDEKKESDSD---------------------------SDLGLEDLSREDLVKYLIEKEELLKMKHEEFQKMQ : 144
SlMge2   : HNEKEASQSQSKPGSTKENGEVSEKCEASVSADSQGQDENDESGPDLASNDNTNENVKRRRRRTKQVVSSDSDSDLDTEDLSRDDLVKLVAEKEELLKIKDDEFQKMK : 180
                                                         **************************
NtMge1   : PNEKETSQSQGEGGST--------TEKASASADSHIQDEKDESD-------------------------------IDAEDLSRDDLVKLVVEKEELLKMKDDEFRKLQ : 139
NtMge2   : PNEKESSQSQSEPGSTKENG----DCEASVSADSHVQDEKDES---------------------------------DTEDLSRDDLVKLVAEKEELLKMKDGEFQKMQ : 143
GmMge1   : H---------------------ASEGAKVSDQSEQAEAADQTKESD----------------------------VEIECDLSRDDLIKLVAEKEQLLKLKHKEIEKMQ : 136
GmMge2   : NNDKKNRNNVHNGDSTNADPAKANEEAKNNDQARQDKPADKTEESGSISDSQ--SQTVKRRRRGFKRTAFSDSDSESECDLSRDDLIKLVAEKEELVMLKHKEIEKMQ : 183
                                                        ***************************
GmMge3   : H---------------------ASEEAKVSDQSEQAEAADQTKESG----------------------------VESECDLSRDDLIKLVAEKEQLLKLKHKEIEKMQ : 133
PoMge1   : PGEKEHGSAVENDGAPTDVKSEETNGSAKLSDPTKVSVSRETKES----------------------------DAEAVSDLSMDDLVKLVMEKEELLKEKHKEMETMQ : 155
PoMge2   : PTEKEQGSAVDSNCDPTNAESGKTNGSADLSDKTEDSVLHETKESGFNSESQQTISRSVKRRRGTKRTAYSDSDSEAGSDLSMDDLVKLVAEKEELLEAKHKEIETMQ : 191
                                                        ***************************
OsMge1   : S-------------------------DKEENQRKDQENSTNVSNEG-----------------------------TEDVDLSKEDLVQLVLEKDGLLKSKDEEINDMK : 134
OsMge2   : DDKAANKQTEDGVNKST--------QSEASNETNSSPGTENASQAG----SQDSVPQSNRRRRGTKRTAFSDSD-TEDLDLSKEDLTKLVLEKEELLKSKDEEVKDMK : 171
                                                        ***************************
SbMge1   : SDNELKDQE----------------RALDESSEDCSSGSENTSEPG-----------------------------IEGLDLSKDDLVKLVCEKDGLLKSKDDEIKDMK : 138
SbMge2   : DDKETNKHTDDGVNKSVG------VSTEASSEANNVPGTEKAQEAG----SLNSVSWSNRKRRTTKRTAFSDSD-SEDLDLSKEDLVKLLLEKDESLKSKDEEFKDMK : 199
                                                        ***************************
PpMge1   : VSGKPGAVGGSTTDAAAASSEEKVEPIQPCIGDDKGGTGVEQDVKT-----------------------------DKDLAKENEDLLGLLGEREALLEEKDRALTQTK : 178
PpMge2   : VSDKTG----------------SPEYSAAEPSRTSTAEGTSESVQH----------------------------AERSNDIKADDLARMVAERDALLQEKDKTIKELQ : 150
CrMge1   : EKKDV-----------------SGASSDQAAAGEEKPSTSGADG----------------------------ADASADGEPSAQELMSQLKAKEDHATKLTQQVETLT : 112
ScMge1   : ----------------------VGSMRRMRFYSDEAKSEESKE-----------------------------------NNEDLTEEQSEIKKLESQLSAKTKEASELK :  85
EcGrpE   : -----------------------MSSKEQKTPEGQAPEEIIMDQHEEIEAVEP--------------------------EASAEQVDPRDEKVANLEAQLAEAQTRER :  59
AtCge1   : -------------------------NSEEANSKQQADVKTLIRSYKQALLNGDET-------------------SVTEIETMFCKIEKEKNKMDQKVLSLSMKIASEK : 126
AtCge2   : EETDG---------AVDVENENASAEEGEAEEEEAAVITALLKSYKEALADNNEG-------------------KIAEIEASLKSIEDEKFLLADKVASLSNELSVER : 161
VvCge1   : ----------------------VKTSKSEADQKPLSVLKSLIKAYKDAVLDGDEK-------------------AVSEIEAMIDTIESEKAELAQKVSALSAEITSGK : 136
VvCge2   : EIEENSDGYIGGAEDATSDSDAPDSDAPNAEEEPASGIIVALRSYKEALVSNDES-------------------KAAEIEAFIKFIEDEKIDLEKKVAALSEELSSDK : 167
PoCge1   : --------------------------EIQEGQKRGPSLKNLMKIYRQAIFYGDEK-------------------TILDIEAKAATIEKENHEFLQKVSSLSAEITSGK : 113
PoCge2   : PEIEDSSDGAVEVEDAASSEEVASSEEVADAEDTSSVVMASLRSYKEALASNDES-------------------IIAEIEAFLKSVEDEKIDNERKVASLTEELSIEK : 173
OsCge1   : ------------------------ADPKVVNGEDFPPMKDLLRLYKKAFLDGNDE-------------------ALGGIESAIIAIEKERSNSAAQYESIATEITSGK : 130
OsCge2   : EDSETGETG--------------ADDAAAATEETPSVIVTALQSYKEALINDDET-------------------KVAEIEDFLFSIEEEKNSLLSKISTLGAELTTER : 159
SbCge1   : ------------------------VDPKVVNGEDFPPMKDLIQLYRTAFQQGNDE-------------------VLGEVEKAITAVEKEKSRVASQFESITTEITSGK : 131
SbCge2   : EDSETEVTG-----------DSAADDGAGSTDETPSIIVTTLQSYREALINDDEA-------------------KAAEIESFLLSIEDEKNSLLNKITALNAELATQR : 155
PpCge1   : ALAEEE-------------SASNDASQSPAAEEQSSSIKSLLEAYREAVAADDEG-------------------AISDVESQLEAIANERDSLGLKVNSLIEEISTNK : 159
PpCge2   : AQVDN-------------------VSEASAAEETSSSIKSLLEAYREAVAVNDEE-------------------AITDVESQLEAIAIERDSLAENANALIGEVSTNK : 153
CrCge1   : -----------------------AEEAAATPLERAKKALDSETLDKDVLTA-----------------------ALAELEAEMGRLQSAANEANDRAKSLEASLASAK : 112
Syn_GrpE : VSPEASDVPAVTPEESPQPTDAVLGEPSGEQSEDPRIGAATETEGGPLEQEKSS-------------------------EEIIAILQKDLASHRQELAEQSEQLDSIK :  97
```

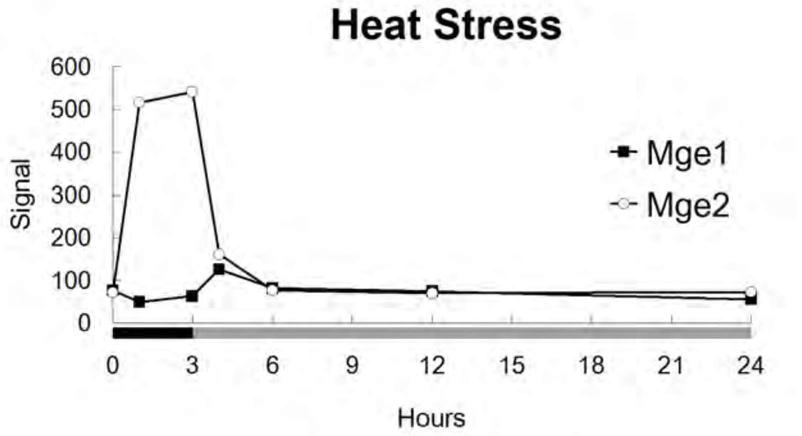


```
            220                 240                 260                 280                 300                 320
AtMge1   : DKFLRTYAEQQNLMDRTNRNAESAKKFAVQNFATSLLDVADNLERASSVVKESFSKIDTSKD-LAGATPLLKNLLEGVEMTEKQLAEVFRKAGLVKEDPLNEPFNPNR : 248
AtMge2   : DKVLRTYAEMENVMDRTRRDAENTKKYAVQNFAKSLLDVADNLGRASSVVKESFSKLDTSED-SAGAAPLLKTLLEGVEMTEKQLAEVFKKFGMEKYDPINEPFDPNR : 273
SlMge1   : DKVLRTYAEMENVMERTRREAENTKKFAIQNFVKALLDVSDNLGRASSVVKESFSKIDVSKD-TTGAVPLLKTLLEGVEMTDKQLAEVFKKFGVEKIDPTNEEFDPNK : 251
SlMge2   : EKALRSYAEMENLMNRTKREAENSKKFAIQNFVKALLDVADNMGRASSVVKESFSKIDESKD-TVGAVPLLNTLLEGVEMTDKQLAEVFKKFGVGKYDPTNEEFDPNK : 287
NtMge1   : DKFLRSYAEMENVMERTKREAENSKKFAIQNFVKALLDVPDNLGRASSVVKESFSKIDASKD-TVGAMPLLKTLLEGVEMTDKQLAEVFKKFGVEKYDPTNEQFDPNK : 246
NtMge2   : DKVLRTYAEMENVMNRTKREAENSKKFAIQNFVKALLDVSDNLGRASSVVKESFSKIDESKD-TAGAVPLLKTLLEGVEMTDKQLAEVFKKFGVGKYDPTNEQFDPNK : 250
GmMge1   : DKVLRTYAEMENVMDRTRREAENSKKFAIQNFAKSLLDVADNLGRASSVVKESFSKIESPEE-SSEAAELLKTLLKGVEMTEKQLAEVLKKFGVKKFDPTNEPFDPHM : 243
GmMge2   : DKVLRTYAEMENVMERTRREADNSKKFALQNFAKSLLDVADNLGRASSVATENFSKIDTSSD-SAEVVKLLKTLLQGVEMTEKQLVEVLKKFGVEKFDPTNEPFDPHR : 290
GmMge3   : DKVLRTYAEMENVMDRTRREAENSKKFAIQNFAKSLLDVADNLGRASSVVKDNFSKIESPEE-SSEAAQLLKTLLEGVEMTEKQLAEVLKKFGVEKFDPTNEPFDPHM : 240
PoMge1   : DKVLRTYAEMENVKERTKREAENSKKFAIQNFAKSLLDVADNLGRASSVVKGNFSKINVSND-AADVVPLLKTLLEGVEMTEKQLGEVFKKYGVEKFDPINEPFDPHR : 262
PoMge2   : DKVLRAYAEMENVKERTKREAENSKKFAIQNFAKSLLDVADNLGRASSVVKGNFSKIDVSND-TAQVVPLLKTLLEGVEMTEKQLGEVFKKYGVEKFDPTNEPFDPHR : 298
OsMge1   : DKVLRSYAEMENVIARTKRESENSKKYAVQNFSKSLLDVADNLTRASSVVKESFSKIDTSKD-STGAVPLLKTLLEGVDMTDKQLGEVFKKFGVEKFDPLNEKFDPSR : 241
OsMge2   : DKVLRSYAEMENVIARTKRESDNAKKYAVQGFSKSLLDVADNLSRASSVVKESFSKIDTSNE-SAEAVKLLNTLLEGVEMTEKQLGEVFKKFGVEKFDPLNEKFDPNK : 278
SbMge1   : DKVLRSYAEMENIIARTKRESENSKKYAVQNFAKSLLDVADNLSRASSVVKESFSKIDASKD-SAGAIPLLKTLLEGVDMTEKQLAEVFKKFGVEKFDPLNEKFDPNR : 245
SbMge2   : DKVLRSYAEMENVLARTKRESENTKKYAIQSFSKSLLDVADNLSRASSVVKESFSKIDCSNN-SDEAVPLLKTLLEGVEMTEKQLGEVFKKFGVQKFDPLNEKFDPNR : 306
PpMge1   : DKLLRSYAEMENLIDRTRREAESTRKYSIQDFAQSLLDVADNLGRALETVRKSVSADDAEIN-----AKLLVSLLEGVEMTDKQLMKVFEKHGLTRFNPEGIVFDPNE : 281
PpMge2   : DKVLRGYAEVENVMARARREAESTRKFALQGFAKGLLDVADNLGRATGAVPENLRKLDSTLEDSSGAAKVLITLLQGVEMTEKQLQQVFRQNGLEKFESEGKEFDPNY : 258
CrMge1   : DSLKRTLAEMENLRARTAREVDVSKKFAIQGFVKSLLDVPDNLERAASVVPSEALKEDGGVP-PEKLRNLLAGLLEGVRATESILHKVLKQNGVERYDAAGQPFDPNL : 219
ScMge1   : DRLLRSVADFRNLQQVTKKDIQKAKDFALQKFAKDLLESVDNFGHALNAFKEEDLQKSKEIS----------DLYTGVRMTRDVFENTLRKHGIEKLDPLGEPFDPNK : 183
EcGrpE   : DGILRVKAEMENLRRRTELDIEKAHKFALEKFINELLPVIDSLDRALEVADKANPDMSAMVE--------------GIELTLKSMLDVVRKFGVEVIAETNVPLDPNV : 153
AtCge1   : EMKIRLQADFDNTRKKLDKDRLSTESNAKVQILKSLLPIIDSFEKAKLQVRVDTDKEKKIDT--------------SYQGIYRQFVEVLRYLRVSVIATVGKPFDPLL : 220
AtCge2   : DRLIRISADFDNFRKRTERERLNLVSNAQGEVVENLLAVLDNFERAKSQIKVETEGEEKVTN--------------SYQSIYKQFVEILGSLGVIHVETVGKQFDPML : 255
VvCge1   : EKYIRLQADFDNFRKRSEKERLTVRTDAQGEVVESLLPMIDNFERAKQQIKPETEKEKKIDT--------------SYQGIYKQFVEIMRSCHVAAVATVGKPFDPAL : 230
VvCge2   : ERILRISADFDNFRKRTDRERLSLVTNAQGEVLENLLPVLDNFERAKAQIKVETEGEEKINN--------------SYQSIYKQFVEILGSLGVTPVETIGNPFDPLF : 261
PoCge1   : EKYIRLQADFDNFRKRSDKERVNIRSDAQGEVIESLLPMVDSFERAKQQIQPETEKEKKIDS--------------SYQGIYKQLVDIMRNLQVAAVPTVGKPFDPSL : 207
PoCge2   : ERVLRISADFDNFRKRTERERLSLVTNAQGEVVENLLSVLDNFERAKTQIKTATEGEEKINN--------------SYQNIYKQFMEILVSLGVVPVETIGKPFDPML : 267
OsCge1   : DKFLRINADLENFRKQTEKERARFTSNIQVDVVQSLLTLVDSFEKVNQEITPETDKEQTIST--------------SYQGIYKQLVETLRSLGVGVVETVGKPFDPSI : 224
OsCge2   : DRILRISADFDNYRKRVEREKLSLMTNVQGEVIESLLPVLDNFERAKTQIKVETEQETKIND--------------SYQSIYKQFIDILNSLGVEDVETVGKPFDPML : 253
SbCge1   : EKFIRLNADLENFRKQTEKDRAKFTSNMRVQVVQSLLPLVDSFEKTNLENTPETEKEQKIST--------------SYQGIYKQLVETLRYLGVGVVETVGKPFDPSV : 225
SbCge2   : ERILRISADFDNFRKRTENEKLNMMENVQGELIESFLPVLDNFERAKMQIKVETEGEEKINN--------------SYQSIYKQFIEILNSLGVEDVETVGKPFDPML : 249
PpCge1   : DRYLRLNADFDNYRKRSERDRLATAGNVRGEVIESLLPMVDNFERAKTSIKTETEAEQKIDN--------------AYQGIYKQFVEIMKSLGVVAVETVGKPFDPNL : 253
PpCge2   : DRYIRLNADFDNYRKRSERDRLATAGNIRGEVVESLLPIVDNFERAKTSIKTETEGEQKIDN--------------AYQSIYKQFVEIMKSLGVVAIETVGKSFDPNL : 247
CrCge1   : DQYLRLNADFDNFRRRTREESAALTDSVRGDVIKEMLPIVDNFELARTQVKAETEAEQKINN--------------SYQGLYKQMVDLMRTQGVEAVPTTGTPFDPNI : 206
Syn_GrpE : KRYVALAAEFDNFRKRTQREKEEQAKLIKGRTITELLPVVDNFERARTQIKPNSDGENQIHK--------------SYQGVYKNLVDSLKGLGVAPMRPEGKPFDPKY : 191
```



```
AtMge1   : HNAVFQVPDASKPKGTIAHVLKSGYSLYDRVIRPAEVGVTCAVENQEGGKESAA------------------------------------ : 302
AtMge2   : HNAVFQVPDASKPEGTVAHVLKSGYTLYDRVIRPAEVGVTQGGENQEEKKESDA------------------------------------ : 327
SlMge1   : HNAVFQVPDPEKAPGMIAVCLKPGYSLHGRIIRPAEVGVTVAVESTGN------------------------------------------ : 299
SlMge2   : HNAVFQVPDPKRNPGMVAVCLKSGYTLHDRIIRPAEVGVTVAMVKQVG------------------------------------------ : 335
NtMge1   : HNAVFQVPDPEKAPGVIAVCLKPGYTLHDRIIRPAEVGVTVAVETEADQSTNT------------------------------------- : 299
NtMge2   : HNAIFQVPDPKKAPGVVAVCLKSGYTLHERIIRPAEVGVTVAVESTQADQNTEA------------------------------------ : 304
GmMge1   : HNAIFQIPDASKAPGTVGVVLKAGYMLYDRVLRPAEVGVTQEVEDN-------------------------------------------- : 289
GmMge2   : HNAIFQIPDGSKPPGTVAAVLKAGYMLYDRVIRPAEVGVTHANRG--------------------------------------------- : 335
GmMge3   : HNAIFQIPDASKAPGTVGVVLKAGYKLYDRVLRPAEVGVTQEVEDNKAAE---------------------------------------- : 290
PoMge1   : HNAMFEVPDALKPPGIVAAVLKAGYMLHERVIRPAEVGVTRAVEKDL------------------------------------------- : 309
PoMge2   : HNAIFQVPDASKPPGTVAAVLKAGYMLHDRVIRPAEVGVTQEVENGAEANE--------------------------------------- : 349
OsMge1   : HCAIFQIPDPSKPSGTVASVVKVGYMLHDRVLRPAEVGVTEGGPTTTEEAAENSEQKSSEV----------------------------- : 302
OsMge2   : HAALFQIPDPSKPSGTVAAVVKVGYMLHDRVLRPAEVGVTEGGPIEEEPEEKSDKSD--------------------------------- : 335
SbMge1   : HCAVFQIPDPSKPSGTVASVVKVGYMLHDRVLRPAEVGVTAGGADATEEAEQPEEKTARD------------------------------ : 305
SbMge2   : HYAFFQIPDPSKPSGTVAAVVKVGYMLHDRVLRPAEVGVTEGGPTEEPEEKSS------------------------------------- : 359
PpMge1   : HQAVFEVEDANKTPGTVAVVLKTGYKLHDRVIRPAVVGVVKENSE--------------------------------------------- : 326
PpMge2   : HSAMFELEDETKTPGTVAIVTKVGYLLHDRVIRPAEVGVIKAKE---------------------------------------------- : 302
CrMge1   : HNALFDIPDPTKENNTIAVVTKKGYKLNDRVIRPAEVGVVRNVSS--------------------------------------------- : 264
ScMge1   : HEATFELPQPDKEPGTVFHVQQLGFTLNDRVIRPAKVGIVKGEEN--------------------------------------------- : 228
EcGrpE   : HQAIAMVESDDVAPGNVLGIMQKGYTLNGRTIRAAMVTVAKAKA---------------------------------------------- : 197
AtCge1   : HEAISREESEAVKAGIITEELNKGFVLGDRVLRPAKVKVSLGPVNKKTPSAAEEITPSA------------------------------- : 279
AtCge2   : HEAIMREDSAEYEEGIVLEEYRKGFLLGERLLRPSMVKVSAGPGPEKPLEAEGEEATAQGSAEEESSSS--------------------- : 324
VvCge1   : HEAIAREESQEFKEGIIIQEIRRGFLLGDRLLRPAMVKVSTGPGRKKTSAVADKSTGQPATAAGVDER---------------------- : 298
VvCge2   : HEAIMREDSTEFEEDVIIQEFRKGFKLGDRLLRPSMVKVSAGPGPAKAEAVGSSEEEAVRVTETETSGEGTPEGESG------------- : 338
PoCge1   : HEAIAREESQEYKEGIIIQEFRRGFLIGNRLIRPAMVKVSSGPGNKKSSVGTETRAEQPATAAGMD------------------------ : 273
PoCge2   : HEAIMREDSDAFEEGTVLEEYRKGFKLGDRLLRPSMVKVSAGPGPVKPEQVEESQEEAEATSGTSEGGSTEEESA--------------- : 342
OsCge1   : HEAIAREESHQFKAGIVSHEVKRGFLLRERLLRPATVKVSTGSGTQETSSPSTEKPVEDSKEDAAV------------------------ : 290
OsCge2   : HEAIMREESVEYEEGVILQEFRKGFKLGERLLRPAMVKVSAGPGPEKPVYDDPAMVEDSVAPQKVKEAEDDGFDDDNAE----------- : 332
SbCge1   : HEAISREASMQFKAGIVMHEVRRGFHLKERLLRPATVKVSTGSGKQSASS---------------------------------------- : 275
SbCge2   : HEAIMREDSSEYEEGIILQEFRKGFKLGERLLRPAMVKVSAGPGPEVSAGPGPEVSRDDDPTVVEDSVAPQKIEDVEDDGVDGDAE---- : 335
PpCge1   : HEAIMREDSTEFAEDVVSQEFRRGFRIGDRLLRPAMVKVSSGPGPAAATDTDLPIEEALANE---------------------------- : 315
PpCge2   : HEAIMREDSTEFAEDIVSQEFRRGFRIEDRLLRPAMVKVSSGPGPAADTDLPIEESLANE------------------------------ : 307
CrCge1   : HDAIMREPSNSHPDGTVLQEFRKGFAIGGKLIRPAMVKVSYTEDGPAASSEE-------------------------------------- : 258
Syn_GrpE : HEAMLREPTAEYPEDTVIEELVRGYLLDDIVLRHSMVKVAVAPEEGAEVVNGEAGANP-------------------------------- : 249
```

**Fig. S1 Protein sequence alignment of Mge homologs.** The gray bar on top of the alignment indicates the section of aligned Mge/Cge sequences used to generate the phylogenetic tree. Solid underlines indicate the sequence segments removed as mTP for long form constructs of AtMges. Dotted underlines indicate the sequence segments, in addition to the solid underlined portion, removed as mTP for short form constructs. The stretch of stars indicates the amino acid sequence derived from retained intron 2 of the AS form of Mge in several plant species. Note that for Arabidopsis, this segment resembles intron 2, but does not splice out to form isoform. For tomato and poplar, the segments are predicted to be retained intron 2; further investigation is required for confirmation. The cylinders and arrows at the bottom of the alignment indicate the alpha helixes and beta sheets, respectively, in E. coli GrpE, as shown in Harrison et al., 1997. Accession numbers of each sequence are as followed: AtMge1: At5g55200; AtMge2: At4g26780; SlMge1: TC226893; SlMge2: TC233922; NtMge1: AF09863; NtMge2: AP09863; GmMge1: Glyma08g43430.1; GmMge2: Glyma02g46390.1; GmMge3: Glyma18g10120.1; PoMge1: TC156480; PoMge2: TC162523; OsMge1: LOC_Os09g11250.1; OsMge2: LOC_Os08g25090.1; SbMge1: Sb02g019590.1; SbMge2: Sb07g017190.1; PpMge1: Pp1s194_146V2.1; PpMge2: Pp1s162_160V2.1; CrMge1: Au9.Cre08.g370450; ScMge1: NP_014875.1; EcGrpE: X07863.1; AtCge1: AT1G36390.1; AtCge2: AT5G17710.1; VvCge1: GSVIVT01008951001; VvCge2: GSVIVT01029905001; PoCge1: POPTR_0002s09060.1; PoCge2: POPTR_0013s06430.1; OsCge1: LOC_Os04g35180.2; OsCge2: LOC_Os02g39870.1; SbCge1: Sb06g016920.1; SbCge2: Sb04g025770.1; PpCge1: Pp1s372_19V6.1; PpCge2: Pp1s273_60V6.1; CrCge1: XM_001692360.1; Syn GrpE: NP_442221.



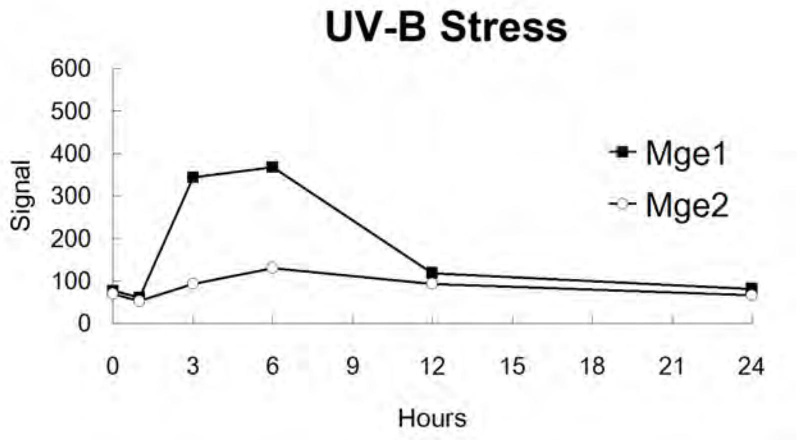


**Fig. S2** ***In silico*** **analysis of the expression of Arabidopsis** ***Mge*****s**. Data were obtained and organized from the public microarray data concerning the transcript expression of *Mge1* and *Mge2* under HS or UV-B stress. The black bar underneath the x-axis indicates heat treatment period at 38$^o$C, while the gray bar indicates the recovery period at 25$^o$C following a 3-h heat treatment. For, UV-B treatment, the plants were exposed to 15 min of irradiation and the expression was determined during recovery.

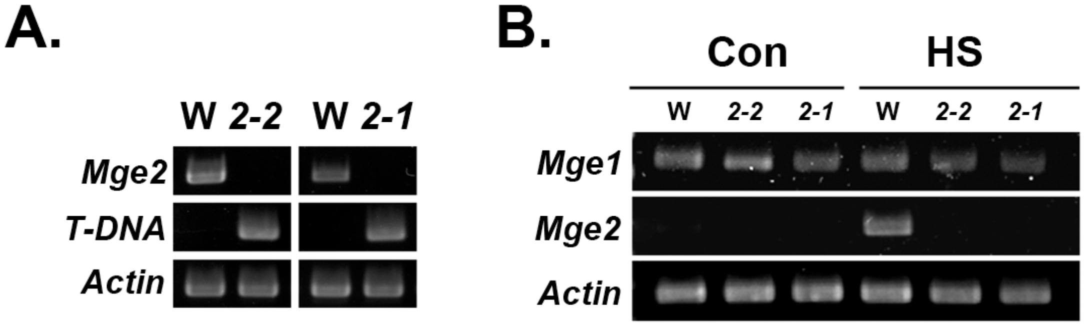
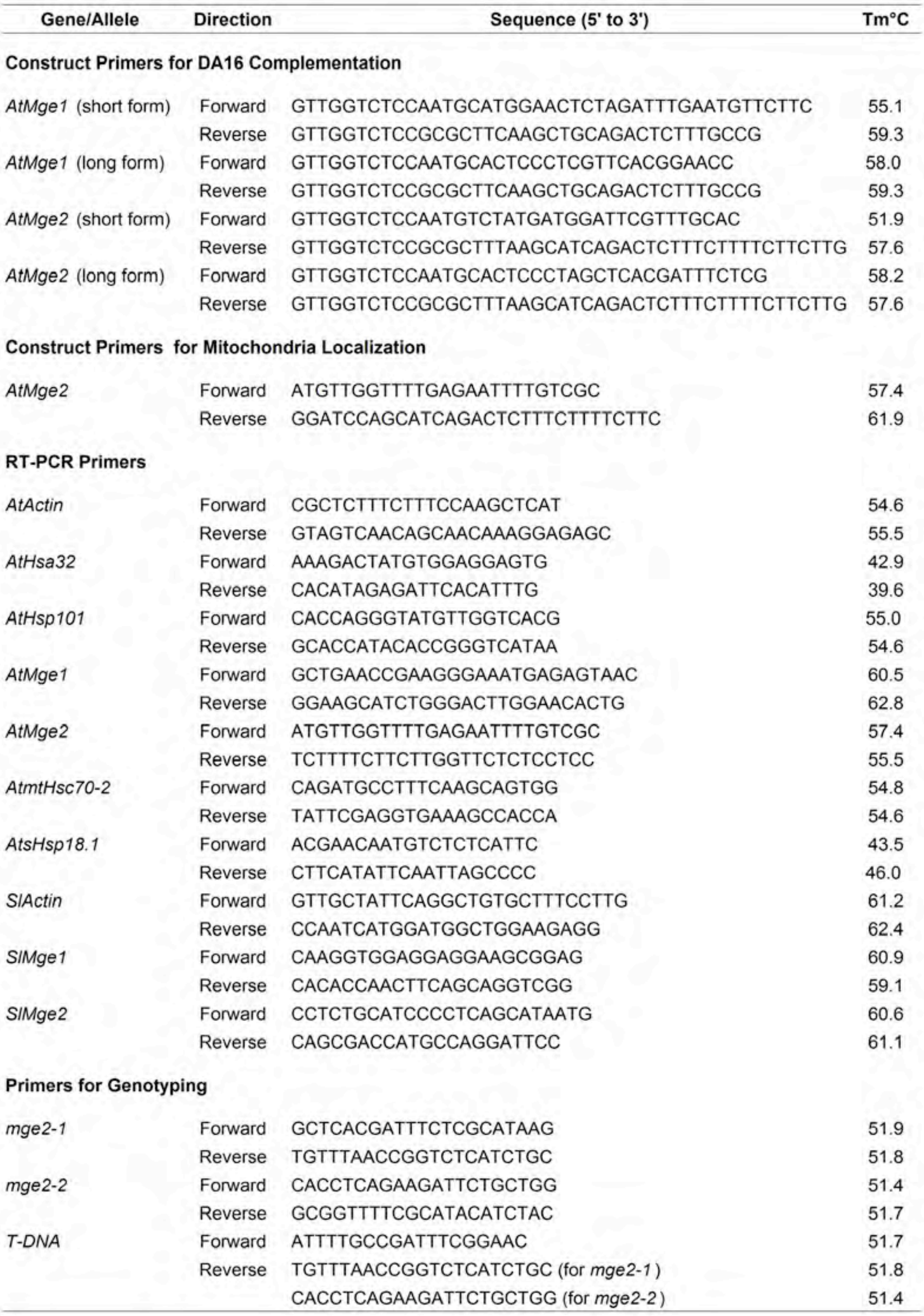


**Fig. S3 Molecular characterization of *mge2-1* and *mge2-2* T-DNA insertion lines**. **(A)** PCR analyses of the genomic DNA of the wild-type and *mge2* KO lines. Presence of T-DNA was detected by use of T-DNA left border primer and gene specific flanking primer as shown in **Table S1**. **(B)** The RT-PCR products of *Mge1* and *Mge2* derived from the wild type or the *Mge* mutants without (Con) or with (HS) heat treatment at 37$^{o}$C for 1 h. W: wild type; 2-1: *mge2*-1; 2-2: *mge2-2*.

**Table S1. List of primers used in this study.**



| Gene/Allele | Direction | Sequence (5' to 3') | Tm°C |
|---|---|---|---|
| **Construct Primers for DA16 Complementation** | | | |
| *AtMge1* (short form) | Forward | GTTGGTCTCCAATGCATGGAACTCTAGATTTGAATGTTCTTC | 55.1 |
| | Reverse | GTTGGTCTCCGCGCTTCAAGCTGCAGACTCTTTGCCG | 59.3 |
| *AtMge1* (long form) | Forward | GTTGGTCTCCAATGCACTCCCTCGTTCACGGAACC | 58.0 |
| | Reverse | GTTGGTCTCCGCGCTTCAAGCTGCAGACTCTTTGCCG | 59.3 |
| *AtMge2* (short form) | Forward | GTTGGTCTCCAATGTCTATGATGGATTCGTTTGCAC | 51.9 |
| | Reverse | GTTGGTCTCCGCGCTTTAAGCATCAGACTCTTTCTTTTCTTCTTG | 57.6 |
| *AtMge2* (long form) | Forward | GTTGGTCTCCAATGCACTCCCTAGCTCACGATTTCTCG | 58.2 |
| | Reverse | GTTGGTCTCCGCGCTTTAAGCATCAGACTCTTTCTTTTCTTCTTG | 57.6 |
| **Construct Primers for Mitochondria Localization** | | | |
| *AtMge2* | Forward | ATGTTGGTTTTGAGAATTTTGTCGC | 57.4 |
| | Reverse | GGATCCAGCATCAGACTCTTTCTTTTCTTC | 61.9 |
| **RT-PCR Primers** | | | |
| *AtActin* | Forward | CGCTCTTTCTTTCCAAGCTCAT | 54.6 |
| | Reverse | GTAGTCAACAGCAACAAAGGAGAGC | 55.5 |
| *AtHsa32* | Forward | AAAGACTATGTGGAGGAGTG | 42.9 |
| | Reverse | CACATAGAGATTCACATTTG | 39.6 |
| *AtHsp101* | Forward | CACCAGGGTATGTTGGTCACG | 55.0 |
| | Reverse | GCACCATACACCGGGTCATAA | 54.6 |
| *AtMge1* | Forward | GCTGAACCGAAGGGAAATGAGAGTAAC | 60.5 |
| | Reverse | GGAAGCATCTGGGACTTGGAACACTG | 62.8 |
| *AtMge2* | Forward | ATGTTGGTTTTGAGAATTTTGTCGC | 57.4 |
| | Reverse | TCTTTTCTTCTTGGTTCTCTCCTCC | 55.5 |
| *AtmtHsc70-2* | Forward | CAGATGCCTTTCAAGCAGTGG | 54.8 |
| | Reverse | TATTCGAGGTGAAAGCCACCA | 54.6 |
| *AtsHsp18.1* | Forward | ACGAACAATGTCTCTCATTC | 43.5 |
| | Reverse | CTTCATATTCAATTAGCCCC | 46.0 |
| *SlActin* | Forward | GTTGCTATTCAGGCTGTGCTTTCCTTG | 61.2 |
| | Reverse | CCAATCATGGATGGCTGGAAGAGG | 62.4 |
| *SlMge1* | Forward | CAAGGTGGAGGAGGAAGCGGAG | 60.9 |
| | Reverse | CACACCAACTTCAGCAGGTCGG | 59.1 |
| *SlMge2* | Forward | CCTCTGCATCCCCTCAGCATAATG | 60.6 |
| | Reverse | CAGCGACCATGCCAGGATTCC | 61.1 |
| **Primers for Genotyping** | | | |
| *mge2-1* | Forward | GCTCACGATTTCTCGCATAAG | 51.9 |
| | Reverse | TGTTTAACCGGTCTCATCTGC | 51.8 |
| *mge2-2* | Forward | CACCTCAGAAGATTCTGCTGG | 51.4 |
| | Reverse | GCGGTTTTCGCATACATCTAC | 51.7 |
| *T-DNA* | Forward | ATTTTGCCGATTTCGGAAC | 51.7 |
| | Reverse | TGTTTAACCGGTCTCATCTGC (for *mge2-1*) | 51.8 |
| | | CACCTCAGAAGATTCTGCTGG (for *mge2-2*) | 51.4 |