

>AraTPT_AT5G46110
 --MESRVLLRATANVVG-----IPKLRRPIGAIHRQFS-----TASSSS
 FSVKPIGGIGEGANLI-----SGRQLRPILLDSSAINGGEKREILKPVKAAAAEGGDTAG
 DAKVGF-----LAKYPWLVTGFFFFMWFYFLNVIFNILNKKIYNY--FPYPYFVS
 VIHLFVGVVYCLISWSVGLPK--RAPIDSNLLKVLIPVAVCHALGHVTSNVSFAAVAVSF
 THTIKALEPFFNAASQFIMGQSIPTLWLSLAPVVLGVAMASLTLSFNWLGFIAMIS
 NISFTYRSIFSKKAMTD-----MDSTNVYAYISIIALFVCIPPAIVEG-----
 -P-----KLLNHGFADAIKVGMTKFISDLFWVGMFYHLYNQLATNTLERVAPLTHAVGNV
 LKRVFVIGFSIVIFGNKISTQTGIGTGIAIAGVAMYSIIKAKIEEEKRVTR--KESIESS
 >Alyr_477360_380
 --MFALTFTPNPRLPS-----PLFV
 AKSIPESA-----LSRRSIAFSSYHWRP----NLRFNFGFKLSATVPENVEGG
 DSESGS-----LVKGLKL--GGMFGVWYLLNIYYNIFNKQVLRV--YPYPATVT
 AFQLGCGTLMIAVMWLLKLHP--RPKFAPSQFTAIQVLAHAHTLGNLLTNVSLGRNVVSF
 THTIKAMEPFFTVLLSVLLLGEWPSLWTVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
 NVTNQSRNVLSKKFMVGKE-----AMDNINLFSVITIIISFISLVPVAILIDG--FKL
 TP-----WDLQIATSQGLS--VKEFCIMSLLAGVCLHSYQQVSYMILEMVPVTHSVGNC
 VKRVVVITSSILFFKTPVSPVLSIGTATALAGVYLYSRAKRV-----KVKPNPKTS-----
 >Alyr_493573_406
 --MQSSAVFSLSPSLPL-----LKPRRLSLRHSLTTAS-----SDLNIS
 PNVVSIPLSRRSWRL-----ASSDSPLRAWGVPSSISHSLDTNRFKTAATAVPESAEEG
 DNSGK-----LTKILEL--GLLFAMWYLFNIYFNIYNKQVLKA--LHAPMTVT
 LVQFVAGSVLITIMWVLNLYK--RPKISGAQLAAILPLAVVHTLGNLFTNMSLGKVSVSF
 THTIKAMEPFFSVLLSAMFLGETPTPWLGAIVPIVGGVALASISEVSFNWAGFLSAMAS
 NLTNQSRNVLSKKVMVKKD--D-----SLDNITLFSIITLMSLVLMAPVTFFTEG--IKF
 TP-----SYIQSA--GVN--VQQIYTKSLIAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVVIVSSVIFKTPVSPVNAFGTGIALAGVFLYSRVKGI-----KPKP--KTA-----
 >Atha_AT3G01550.1_383
 --MFALTFTLPNPRLPS-----PLFL
 AKSTPESALSR-----RSRAFSSSNSYPWRP----NLRFNFGFKLSATVPENVEGG
 DLESGS-----LVKGLKL--GGMFGVWYLLNIYYNIFNKQVLRV--YPYPATVT
 AFQLGCGTLMIAIMWLLKLHP--RPKFSPSQFTVIVQLAVAHTLGNLLTNVSLGRNVVSF
 THTIKAMEPFFTVLLSVLLLGEWPSLWIVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
 NVTNQSRNVLSKKFMVGKD-----ALDNINLFSIITIIISFILLVPLAILIDG--FKV
 TP-----SHLQVATSQGLS--VKEFCIMSLLAGVCLHSYQQVSYMILEMVPVTHSVGNC
 VKRVVVITSSILFFKTPVSPVLSIGTATALAGVYLYSRAKRV-----QVKPNPKMS-----
 >Atha_AT5G33320.1_408
 --MQSSAVFSLSPSLPL-----LKPRRLSLRHHPITTAASS-----SDLNVS
 PNVVSIPLSRRSWRL-----ASSDSPLRAWGVPSPISHSLDTNRFRTAATAVPESAEEG
 DNSGK-----LTKVLEL--GLLFAMWYLFNIYFNIYNKQVLKA--LHAPMTVT
 LVQFVAGSVLITIMWVLNLYK--RPKISGAQLAAILPLAVVHTLGNLFTNMSLGKVSVSF
 THTIKAMEPFFSVLLSAMFLGEKPTPWLGAIVPIVGGVALASISEVSFNWAGFSSAMAS
 NLTNQSRNVLSKKVMVKKD--D-----SLDNITLFSIITLMSLVLMAPVTFFTEG--IKF
 TP-----SYIQSA--GVN--VKQIYTKSLIAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVVIVSSVIFKTPVSPVNAFGTGIALAGVFLYSRVKGI-----KPKP--KTA-----
 >Cgra_Cagra.1561s0021.1_381
 --MFPLTFVTSNPRLPS-----PF
 FVVKSTA-----LSRRSIPFSSSTSFPWRPNLYRSNGFKLSATAPEDVDGG
 DSKSAS-----LVKGLKL--GGMFGVWYLLNIYYNIFNKQVLRV--YPYPATVT
 AFQLGCGTLMIAIMWLLKLHP--RPKFAPSQFTAIQVLAHAHTLGNLLTNVSLGRNVVSF
 THTIKAMEPFFTVLFSVLLLGEWPSLWIVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
 NVTNQSRNVLSKKFMVGKE-----ALDNINLFSVITIIISFVLLVPVAIIMDG--FKL
 TP-----SQLQIATSQGV--VKEFCVMSLLAGVCLHSYQQVSYMILEMVPVTHSVGNC
 VKRVVVITSSIMFFQTPVSPVLSIGTATALAGVYLYSRAKRV-----KVKPNPKGC-----
 >Cgra_Cagra.0647s0002.1_413
 --MQSSAVFSLSPSLPL-----LKPRRLSLRHPLTTAASSSSSSNL----NDLNVS
 PNVVSIPLSRRSWRL-----ASSDSPLRAWGVPSSISHSFDNRFKTAATAVPESADDG
 EKSGK-----LTKMLEL--GLLFAMWYLFNIYFNIYNKQVLKA--LHAPMTVT
 LVQFVAGSVLITVMWALNLYK--RPKISGAQLAAILPLAVVHTLGNLFTNMSLGKVSVSF
 THTIKAMEPFFSVLLSAMFLGEAPTWPVIGAIPIVGGVALASISEVSFNWAGFTSAMAS
 NLTNQSRNVLSKKVMVKKD--D-----SLDNITLFSIITLMSLVLMAPVTFFSEGE--IKF
 TP-----SYIQSV--GVN--VQQIYTKSLIAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVVIVSSVIFKTPVSPVNAFGTGIALAGVFLYSRVKGI-----KPKP--KTA-----
 >Crub_Carubv10013948m_381
 --MFPLTFVTSNPRLPS-----PF
 FVVKSTA-----LSRRSIPFSSSTSFPWRPNLYRSNGFKLSATAPEDVDGG
 DSKSES-----LVKGLKL--GGMFGVWYLLNIYYNIFNKQVLRV--YPYPATVT
 AFQLGCGTLMIAILWLLKLHP--RPKFAPSQFTAIQVLAHAHTLGNLLTNVSLGRNVVSF
 THTIKAMEPFFTVLFSVLLLGEWPSLWIVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
 NVTNQSRNVLSKKFMVGKE-----ALDNINLFSVITIIISFVLLVPVAIIMDG--FKL
 TP-----SQLQIATSQGV--VKEFCVMSLLAGVCLHSYQQVSYMILEMVPVTHSVGNC
 VKRVVVITSSIMFFQTPVSPVLSIGTATALAGVYLYSRAKRV-----KVKPNPKGC-----
 >Brap_Brara.C02942.1_383
 --MLLITPY-----PRLVSPL-----LA

TKSTPESSFTRRARA-----SSSSSSSSSSSYHWPFLTPKRRLNGFKLSATVPGDVESG
S-----LVKGLKL--GGMFGVWYLLNIYYNIFNKQVLRV--FPYPATVT
AFQLGCGTLMISIMWLLKLHP--RPKVTPSQLPAILQLAAHTLGNLLTNVSLGRNVVSF
THTIKAMEPFFTIVLFSVLLLGEWPSLWIVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
NVTNQSRNVLSKKFMVEKE-----ALDNINLFSIITIIISFVLLVPVAILIDG--FKF
TP-----SHLQLATSQGLT---VKEFCLMSLLAGVCLHSYQQVSYMILEMVSPTVTHSVGNC
VKRVVVIASSILFFKTPVSPNSIGTATALAGVLYTRAKRI-----KPNPNKSS-----
>Brap_Brara.H00677.1_407
--MQSSAVFSLSPSLPL-----LKPRRLSLRHPVTVTASS-----NLNVSP
PNVVSVPPLPRRSWRL-----ASSDSPLRASGLPSVSSPSLDTNRFKTAATAVPENAEEG
EGSGK-----MTKVLEL--GLLFAMWYLFNIYFNIYNKQVLKA--LHAPMTVT
LVQFAVGSVLITFMWALNLYH--RPKISAAQLAAILPLAVVHTLGNLFTNMSLGKVSVSF
THTIKAMEPFFSVVLSAMFLGEVPTPWIGSIPIVGGVALASVTEVSFNWAGFLSAMAS
NLTNQSRNVLSKKVMVKKD--D-----SLDNITLFSIITLMSLFLMAPVTFSEF--IKF
TP-----SYIQSA---GVN---VQIYTKSLIAALCFHAYQQVSYMILARVSPVTHSVGNC
VKRVVIVSSVIFFKTPVSPVNAFGTGIALAGVFLYSRVKRI-----KPKP--KTA-----
>Tcac_Thecc1EG016925t1_408
--MQSTA-LALSPTIPF-----FKPLNKNTNPRYSPLSNLSS-----LKPLDL
SSIHGLSCQKACY-----LSSWSSFNARISESFVVSNGRNDSSFVKVRAASVPENKGET
KDSSG-----LSGTLQL--GAMFAIWYLLNIYFNISNKQVLKV--YTFPATVT
AFQLGCGTLMILIMWALNLYH--RPKLTRSQAAILPLAVIHTLGNLFTNMSLGQVNVVSF
THTIKAMEPFFTIVLFSVLLLGEWPTLWILSSLIPVVGVALASVTEVSFNWIGFSSAMAS
NVTNQSRNVLSKKFMVRKE--D-----TLDNINLFSVITIIISFILLVPTAILLEG--VKF
TP-----SYLQSAANQGLN---VKELCIRSLLAGFCFHSYQQVSYMILQMVSPVTHSVGNC
VKRVVIVSSVIFFTQTPVSPINSLGTAVALAGVFLYSKAKRM-----KPKP--KAA-----
>Esa1_Thha1v10020920m_382
--ML-----LTPYPRLPs-----PLLA
AKSNPESSLTR-----RARASYSTSNYYWFLRPNRRFNGFKLSATVPENVEGD
VESGG-----LVKGLKL--GAMFGVWYLLNIYYNIFNKQVLRV--YPYPATVT
AFQFGCGTLMIAIMWLLKLHP--RPKIAPSQPLAIVQLAAHTLGNLFTNMSLGQVNVVSF
THTIKAMEPFFTIVLFSVLLLGEWPSLWIVCSLLPIVAGVSLASFTEASFNWIGFCSAMAS
NVTNQSRNVLSKKFMVEKD-----ALDNINLFSVITIIISFILLVVPVAILIDG--FKF
TP-----SHFQLATSQGLT---VKEFCFMSLLPGVCLHSYQQVSYMILEMVSPTVTHSVGNC
VKRVVVIASSILFFQTPVSPNSIGMATALAGVLYTRAKRA-----KVKPNPKSC-----
>Tcac_Thecc1EG012088t1_412
--MQSAA-FSLSSPSSF-----PSLKPRIFGSNLRFPVRVSSFSASKRHDLSAS
SNVVSVPSPKRSWRLS---SSSGLPLRAWNSVPS---DSKAERFEVRATAAESAGEGE
KAGN-----LMKTLEL--GLLFGLWYLFNIYFNIYNKQVLKV--FHYPVTVT
VIQFAVGTVLVALMWTFNLYK--RPKITGVQLAAILPLALVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSAMFLGELPTVWVVGSLVPIVGGVALASVTEASFNWAGFWSAMAS
NLTNQSRNVLSKKVMVKKE--D-----AMDNITLFSIITVMSFILLAPAAIFMEG--VKF
TP-----SYLQSA---GLN---VKEVVVRSLIAALCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVIVSSVFFFKTPVSPINSLGTGIALAGVFLYSRVKRI-----KPKA--KAA-----
>Ptri_Potri.0016347300.2_411
--MLRTA-LALSSTPV-----LRPQKPLYVHSSPRF-----SPCINL
PSLKPLDTCCHGFSRRKT--SLSGCCLSCNTRISAFICRNHGYGSIKVRAASVPDSTGEF
EKSSD-----AARTMQL--GAMFGIWYLLNIYFNIFNKQVLKV--YFPATIT
AFQVCGTVMIIIMWALNLCN--RPKLTRPQILAILPLAVAHTFGNLLTNVSLGKVAVSF
THTIKALEPFFTIVLFAALFLGETPAFWLSSVLPLVGGVGLASLTVSFNWIGFCSAMAS
NVTNQSRNVLSKKLMVKE--E-----TLDNVNLFVITIIISFILLVPAIIFMEG--FKF
TP-----SYLQSAANQGLN---VKELCIRSLLAGFCFHSYQQVSYMILQMVDPVTHAVGNC
VKRVVIVSSVIFFTQTPVSPINSLGTGIALAGVFLYSRAKRV-----KSKTKPKAA-----
>Ptri_Potri.0120082100.1_414
--MQSTA-FTPSSSSSL-----SPLKPRRLVANPIYSLPSRFDPIRAFSSSSSKRH
DPDSNNVFPRRSWS-----LSSASNSSLSRPWNPLVS--ERKMERFEVKATAVPESAGEG
KEKSS-----LTKTLEL--GLLFGLWYLFNIYFNIYNKQVLRV--FPNPVTIT
AAQFTVGTVLVACMWTFNLYK--KPKVSGAQLAAILPLAVVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSAMFLGEMPTLWVVGSIPIVGGVALASVTEASFNWAGFWSAMAS
NLTNQSRNVLSKKVMLKKE--E-----SMDNITLFSIITIMSFIILLAPVTIFMEG--VKF
TP-----AYLQSV---GLN---VKEVYTRFLAALCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVIVSSVLFFKTPVSPINSLGTGIALAGVFLYSRVKSI-----KPKP--KTA-----
>Ptri_Potri.0150077900.1_416
--MQSTA-FTFSPSPSL-----LKPRRLISSSSTATYSLPPRFDPIRAFSSSKRYDL
DSNNVFPRRSWSLSS---ASNSSLSRPNPLPLVS--ESKTERFEVRATAVPESAGEG
EEKSS-----LVKTLEL--GLLFGLWYLFNIYFNIYNKQVLKV--FPNPVTVT
AVQFAVGTVLVFMWTFNLYK--KPKISGAQLAMILPLAVVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSAMFLGEMPTLWVVGSLPIVGGVALASVTEASFNWAGFWSAMAS
NLTNQSRNVLSKKVMVKNE--E-----SMDNITLFSIITIMSLVLLAPVTIFMEG--VKF
TP-----AYLQSA---GLN---VKQVYTRSLIAALCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVIVSSVFFFKTPVSPINSLGTGVALAGVFLYSRVKRI-----KPKP--KTA-----
>Gmax_Glyma.19G005900.1_408
MSPYSLSLLASVSPKMH-----TLLSFSSSHSPLPNHNITK-----SNNKLS
HSINGLSSC-----PSSPLLPSATKSSPFLISTSKIASFRVLAASSIPDARSDE
PAKTS-----FLKTLQL--GAMFATWYLLNIYYNIFNKQVLKV--YFPATIT

AFQFGFASLVINLVWTLNLHP--RPSISGSQFAAILPLAVAHTMGNLLTNISLGKVAVSF
THTIKAMEPFFTUVLSALLLGEMPTFWVSSLVVVGVALASMTVEVSFNWIGFTTAMAS
NVTNQSRNVLSKKLMVNEE--E-----TLDNINLYSVITIIISFLLLVPCAILVEG--VKF
SP-----SYLQSAASQGLN-----VRELCVRSVLAACFHAYQQVSYMILQMVSPVTHSVGNC
VKRVVVIVSSVIFFFQIPVSPVNTLGTGLALGVFLYSRAKRI-----KSVQ--KTN-----
>Gmax_Glyma.06G181600.1_406
--MQSAA-FTFSPSLPL-----RNPSPNWRRPSLSL-----RLHAKH
SNNNNNSNSTEGVNSNGVSSSTFTRRSWTLPPSSSFKFRPLPSSPPRAAENAVPESAAAP
VENP-----LFKTLEL--GALFGLWYLFNIYFNIYNKQVLKA--FHYPVTVT
VVQFVAVGTVLVAFMWGLNLYK--RPKLSGAMLGAILPLAAVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVILSAMFLGEFPTPWVVGSLVPIVGGVALASVTEASFNWAGFWSAMAS
NVTNQSRNVLSKKAMVKKE--D-----SMDNITLFSIITVMSFLLAPVAIFMEG--VKF
TP-----AYLQSA--GVN--VRQLYIRSLLAALCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVVIVSSVIFFFQTPVSPVNAFGTAIALAGVFLYSRVKRI-----KAKP--KTA-----
>Gmax_Glyma.04G184300.1_396
--MQSAA-FTFSPSLPL-----RNPSPNYWRPSSLSL-----RLSAKH
GNSNDDVNSNG-----VSSTFFTRRSWTLPPSSSFKFRPLPRAAESAVPESAPVE
NP-----LFKTLEL--GALFGLWYLFNIYFNIYNKQVLKA--FHYPVTVT
VVQFVAVGTVLVAFMWGLNLYK--RPKLSGAMLGAILPLAAVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSAMFLGEFPTPWVVGSLVPIVGGVALASVTEASFNWAGFWSAMAS
NVTNQSRNVLSKKAMVKKE--D-----SMDNITLFSIITVMSFLLAPVAIFMEG--VKF
TP-----AYLQSA--GVN--VRQLYIRSLLAALCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVVIVSSVIFFFQTPVSPVNAFGTAIALAGVFLYSRVKRI-----KAKP--KTA-----
>Gmax_Glyma.17G088500.1_382
--MQSTV-FSLSPSLSL-----PKQPL-----KRSVSV
STSKLNVILTP-----SSFPCQPCSLAYSPSPFKLAPSHFHPFHARATSVPESSAGN
T-----LLNTLEL--GALFGLWILFNIYFNIYNKQVLKV--YHPLTVS
TLQFVAVGSLFVAFMWFLNLYK--RPKVSGAQLAAILPLALVHTLGNLFTNMSLGQVAVSF
THTIKAMEPFFSVLLSAMFLGEAPTAWVVGSLVPIVGGVALASATEASFNWAGFWSAMAS
NLTNQSRNVLSKKVMVKKE--E-----SMDNITLFSIITVMSFLLSVPVTLMEG--VKF
TP-----AYLQSA--GLN--VNEVYIRSLLAALCFHAYQQVSYMILQKVSPVTHSVGNC
VKRVVVIVSSVIFFFQTPVSPINALGTALAGVFLYSRVKRL-----KP-----KTT-----
>Acoe_Aquca_061_00001.1_408
--MSSTTAFTFSSTSSP-----FLKTRKTSFQNP-----PNCYRF
NPVRLSTTSKSLDLCLRS--SPLCSSSRWSSIPSLVTDREMKNDFKTKASSSDGGASAD
EVETEKAGA-----LTKTLQL--GAYFGLWYLFNIYFNIYNKQVLKV--FPPVTTIT
TVQFVAVGTVIIVFFMWALNLHK--KPQITTSQLVAILPLAMVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVLFSALFMGEMPSLLVVSSLLPIVGGVALASMTASFNWAGFWAAMAS
NVTNQSRNVLSKKFMVKKD--Q-----SMDNINLFSIITVMSFLLFPVAFMEG--VKV
SP-----AYLQSA--GLN--VRDLGKALLAGLCFHAYQQVSYMILQRVSPVTHSVGNC
VKRVVVIVTSLVFFRTPVSPINSGLGTALAGVFLYSRIKSL-----KPKP--KAA-----
>Acoe_Aquca_002_00108.1_405
--MEST--FALSPSIPF-----LKSARNPNLNRFNYNLNLSS-----NPSFNL
NSVNGVSSY-----SSSLQFSSWCYFPCIVNDRRMEKFNVKATLASHDTNEE
EVERPSTTST-----LIKTLQL--GVLIGLWYILTIMFNIYNKQVLTV--YFPLTIS
TLHFMGTVIIVLLMWTFNLHK--KPKISRSQLLAIPLAIAHTLGNLFTNMSLGKVSVSF
THTIKAMEPFFSVVLSAMFLGEIPTFWVSSLLPVVGGVALASFTVEVSFNWIGFSTAMAS
NLTNQSRNVLSKKFMVKKE--E-----YLDNVTLFSIITVMSFLLAPVTFTEG--VKI
TP-----AGLLSS--GLD--VKDIYVKTFFVAGLFYHAYQQVAYIILERVSPVTHSVSNC
VKRIAIIVASVLFFQSPVSLINSFGTGVAIAGVFLYSRLKQV-----KSKP--KID-----
>Sita_Si013874m_398
--MQSAAAFRCPARPL-----VSRNPSRPLPARPL-----RVGAAA
AATTSTRCGA-----VGPRGHGLGLQVSPDREGKARQVACGAAGAAGKVEEE
GGG-----LMKTLQL--GLFFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
EIQFVAGAAVALFMWITGIK--RPKISGAQLVAILPLAIVHTMGNLFTNMSLGKVAVSF
THTIKAMEPFFSVLLSAIFLGELPTVWVLSLLPIVGGVGLASLTEASFNWAGFWSAMAS
NVTNQSRNVLSKKFMVKKE-----SLDNINLFSIITVMSFLLAPVTFTEG--VKI
TP-----TFLQSA--GLD--VKLVLTRSLLAALCFHAYQQVSYMILERVSPVTHSVGNC
VKRVVVIVTSLVFFRTPVSPINSGLGTALAGVFLYSQKRL-----KPKP--KTA-----
>Sita_Si030085m_396
--MQSAAAIGLVRPCAA-----RPLVACPSHRR-----GGAVAG
EGIRPVLQR-----GIRLSARAGLVASPLEEEEEKRRCAERDVSAAAAAAQEA
GEEAGGG-----FAKTLQL--GALFGLWYLFNIYFNIYNKQVLKV--LPYPINIT
TVQFVAGTAIAMFMWITGILK--RPKISGAQLLAILPLAIVHTMGNLFTNMSLGKVAVSF
THTIKAMEPFFSVLLSAIFLGELPTVWVLSLLPIVGGVALASLTEASFNWAGFWSAMAS
NVTNQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFLLAPVTLTEG--VKV
SP-----AVLQSA--GLN--LKQIYTRSLIAACFHAYQQVSYMILARVSPVTHSVGNC
VKRVVVIVTSLVFFRTPVSPVNSLGTGVALAGVFLYSQKRL-----KPKA--KAA-----
>Sita_Si022164m_417
--MQSMAASCSSSRAW-----AAARRSYAPALPPSSHVAFSS-----SPPSTH
GCRWPVAGSGGPALPLGIRGGLRPLPSPLLPAGVGRAGAAARTRAAAAAASLPAEDGGG
KPEGAAG-----ISRTLQL--GAMILVWYMLNIYFNIYNKVLKA--VPFPYTIT
TFQFASGSFFITLMWLLNLHP--KPRLSLKQYAKILPLALHMLGNVFTNLSLGKVAVSF
THTIKAMEPFFSVLLSVLFLGETPSLLVLGSLVPIVGGVLLASMTVEVSFNWIGFWSAMAS

NLTNQSRNVFSKLLADKE--D-----NLDDINLFSIMTIMAFLLSAPLMLSVEG--IKF
SP-----SYLQSA---GVN---VKELCVKAALAGTCFHFYQQVSYSLARVSPVTHSVTNS
LKRVVIVSTVLFFRTPISPINALGTGVALAGVFLYSQFKA-----KPKA--KAA-----
>Phal_Pahal.F02194.1_403
--MQSAAAFRCPARPL-----VGRSPSRPLLARPIRD-----STGAGA
GAVAAAASTRCGA-----VGPRGLGHGLLPVSTDREGKARQRTVACAAAGKAGKAE
GGG-----FLKTLQL--GAFFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
EVQFAVGAAVAVFMWITGILK--RPKISGAQLLAIVPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVGLSLLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKEDE-----SLDNINLFSIITVMSFFLLAPVTFFTEG--VKM
TP-----SFLQSA---GLN---VNQVLTRSLAALCFHAYQQVSYMILAVVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKP--KTA-----
>Phal_Pahal.B02192.1_398
--MQSAAAIGLVRPCAA-----RQLVACPSHRRGG-----AVAVAG
GGIRPVLPLR-----GLRLSARAGLVPASPLEEEEEKRRCRDVAASASAAAAAQA
GEEAGG-----LLKTLQL--GALFGLWYLFNIYFNIYNKQVLKV--LPYPINIT
NVQFAVGTAIALFMWITGILK--RPKISGAQLLAIVPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVLSLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFLLAPVTLLTEG--VKV
SP-----AVLQSA---GLN---LKQIYTRSLIAAFCFAYQQVSYMILARVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKA--KAA-----
>Zmay_GRMZM2G174107_T01_395
--MQSAAAFRCPTRLL-----VSSPCRPLLSARPL-----RASAAG
AVATRSSA-----VGPRGLGLLPPASPRDGGKCRQRQVSCSAAGDAVAAPKA
EEGG-----LMKTLWL--GSLFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
EVQFAVGTAIALFMWITGILK--RPKISGAQLVAILPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVLSLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFLLAPVTLLTEG--VKI
TP-----TFLQSA---GLN---VNQVLTRCLFAGLCFAYQQVSYMILAMVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKP--KTA-----
>Zmay_GRMZM2G047404_T01_390
--MQSAAAIGLLRPCAA-----RPLAAYTSPRR-----GAGACS
GGTQPLITPR-----GIRLSARGLVPASPLEEKENRRCRASMHAAASAGEEAGG
G-----LAKTLQL--GALFGLWYLFNIYFNIYNKQVLKV--LPYPINIT
TVQFAVGSIAIALFMWITGILK--RPKISGAQLFAILPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVLSLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFLLAPVTLLTEG--VKV
SP-----AVLQSA---GLN---LKQVYTRSLIAAFCFAYQQVSYMILARVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKP--KTA-----
>Zmay_GRMZM2G103047_T01_397
--MQSTAAIGLVRPCAA-----RPLPTYSPRR-----GAGACS
GAAQPI LAPR-----GLCLSARASLLPDSPLEEEYRRCRAGRHVAAAGKVAADG
AVEEAGG-----LVKTLQL--GSLFGLWYLFNIYFNIYNKQVLKV--LPYPINIT
TVQFAVGSIAIALFMWITGILK--RPKISGAQLFAILPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVLSLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFLLAPVTLLTEG--VKV
SP-----AVLQSA---GLN---LKQIYTRSLIAACCFAYQQVSYMILARVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKP--KAA-----
>Zmay_GRMZM2G066413_T01_415
--MMQGAAGGTSVSGA-----SWARATRGRAAVLASRHVGV-----GASSSD
YYNHFGPRGATAAPLLRARGGRLRPLPLSSGSGKNGEVAKAAAAASVPADDASAAV
TDDGG-----IAATAQL--GAMIVAWYLLNIYFNIYNKQVLGALPLPLPYTIT
AFQLAFGSLILFLMWATRHLHP--APRLSAAQLGKIAPLAVGHMLGTFTNMSLGKVA
VSTHTTIKASEPFFTVVLSALFLGEVPSLPVLGSLVPIVGGVALASFTEVSFNWTFWSAMAS
NLTNQSRNVLSKLLAGDK--D-----VMDDINLFSVITVLSFLLSCPLMIFAEG--IKF
TP-----GYLQST---GLN---LQELCVRAALAGLCFHGYQKLSYLILSRVSPVTHSVANC
VKRVVIVTSLVFFRTPISPVNALGTGAALAGVFLYSRLTRT-----KKP--KDA-----
>Sbic_Sobic.004G353100.1_397
--MQSAAAFRCPAGAG-----AGAGQLVSRNPS-----RGPLLP
VPARPLRVVSA-----ATTRALGLRLRLSASPDDRSGQRQVSCGAAGDAVAAPSA
EEGG-----FMKTLWL--GSLFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
EAQFAVGSVVSLLFFWTGIIK--RPKISGAQLAAILPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVASLLPIVGGVALASL TEASFNWIGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFVLAPVTFFTEG--VKI
TP-----TFLQSA---GLN---VNQVLTRSLLAGLCFAYQQVSYMILAMVSPVTHSVGNC
VKRVVIVTSLVFFRTPVSPINSLGTALAGVFLYSQKRL-----KPKP--KTP-----
>Sbic_Sobic.002G159900.1_393
--MQSAAAVGLVRPCAA-----RPLPTYPS-----PRRGAG
ACSPPLLTTPR-----GLRLSARAGLVPASPLEEENRRCRHVAAAAGKVAADTAG
EEAGG-----LAKTLQL--GALFGLWYLFNIYFNIYNKQVLKV--LPYPINIT
TVQFAVGSIAIALFMWITGILK--RPKISGAQLFAILPLAIVHTMGNLFTNMSLGKVA
VSTHTTIKAMEPFFSVLLSAIFLGEFPTVWVLSLPIVGGVALASL TEASFNWAGFWSAMAS
NVTTFQSRNVLSKKLMVKKE--E-----SLDNINLFSIITVMSFFLLAPVTLLTEG--VKV
SP-----AVLQSA---GLN---LKQVYTRSLIAAFCFAYQQVSYMILARVSPVTHSVGNC

VKRVVIVT SVLFFRTVPSPINSLGTGIALAGVFLYSQLKRL-----KPKP--KAA-----
>Sbic_Sobic.003G050800.1_418
--MQRGAAGTTTSVSG-----ASSWTRAATRGLASRHVGVA-----SSSSSF
FGPRGATAAAQRLPLLRVRGGDGRRLRPLSLLSDSGGKNGEVAKAVAAAAAASVPADDASA
AAVTGDRGG-----IAATAQL--GAMIVAWYLLNIYFNIYNKQVLGALPLPLPYTIT
AFQLAFGSLLI FLMWATRLHP--VPRLSAAQLGKIAPLAVGHMLGT VFTNM SLGKVAVSF
THTIKASEPFFTVVLSALFLGEVPSLPVLGSLVPIVGGVALASFT EVSFNWTGFW SAMAS
NLTNQSRNVLSKKLLADKE--D-----VMDDINLFSVITVLSFLLSCPLMFFAEG--IKF
TP-----GYLQST--GLN--LQELCVRAALAGLCFHGYQKLSYLILSRVSPVTHSVANC
VKRVVVIVSSV LFFSTPISPVNALGTGAALAGVFLYSRLTRT-----KKP--KDA-----
>Sbic_Sobic.009G062500.1_401
--MQSMAASCSSSSSS-----SSRAWAAARRSPSP-----SLAFSS
SSSFPSSSHGCRWPV-----APRGIRGVLRLPLSPLLAPCARAGAAAAA SPPAAGKPEG
AAG-----ISRTLQL--GAMILVWYLLNIYFNIYNKLVKA--IPFPYTIT
TFHFASGSFFITLMWLLNLHP--KPRLSLKQYAKLLPLALIHMLGNVFTNM SLGKVAVSF
THTVKAMEPFFSVLLSVLFLGQTPSLLVLGSLVPVVGGVVLASMT EVSFNWIGFWSAMAS
NLTNQSRNVLSKKLLADKE--D-----SLDDINLFSIITIMAFLLSAPLMLSVEG--IKF
SP-----SYLQSA--GVS--VKELCVRAALAGTCFYFYQQVSYSLARVSPVTHSVANS
LKRVVIVSSV LFFRTPISPINALGTGVALAGVFLYSQFKKL-----KPKT--KAA-----
>Bdis_Bradi4g27550.1_405
--MQSAAAIGLLRPCAA-----RPFLKNPSPGGA-----RLPASR
SALRLSAVAPRAGIA-----AAAGLGRIRLVPLSPEQEERSGRCSR DVAAAAA ASGKAAAG
EESGEEGGAA-----LAKTLQL--GVFFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
TVQFVAGTVISLFLWITGILK--RPKISGAQLVAIPLAIVHTMG NLF TNM SLGKVAVSF
THTIKAMEPFFSVLLSAMFLGELPTPWVLSLLPIVGGVALASISEASFNWAGFLSAMAS
NVTFAQSRNVLSKKLLADKE--A-----SLDNINLFSIITVMSFLLAPVTLLTEG--VKV
TP-----TFLQSA--GLN--LQQVYTRSLIAAFCFHAYQQVSYMILARVSPVTHSVGNC
VKRVVVIVT SVLFFKTPVSPINSIGTAIALAGVFLYSQLKRL-----QPKP--KAA-----
>Bdis_Bradi2g04447.3_397
--MQRAAASLSSSRAA-----WAAAASSRHAAG-----ASCSAA
AGRRENTMAPP-----PLRILRGQQLLPLLPLLSGNRARRAVTASAAAAAELPAGD
DAAAGG-----IAGAVEL--GAMIVAWYLLNIYFNIYNKLVQA--LPFPYTMT
AFQLGFGSLVIFFMWAARLHP--APKLSAAQLARIAPLAAGHMLGT VFTNM SLGKVAVSF
THTVKASEPFFTVLLSAFFLGETPSLLVLGSLVPIVGGVALASL TEVSFNWVGFW SAMAS
NLLNQTRNVLSKKLLADKE--E-----SMDDINLFSVITVLSFLLMSCPLMLLAEG--VKF
SP-----AYLQST--GLN--LPELCVRAALAGLCFHGYQKISY MILARVSPVTHSVANC
VKRVVVIVSSV LFFRTPISAVNALGTGAALGGVYLYSRLKKS-----KP--KSI-----
>Bdis_Bradi2g34300.1_418
--MQSMA-ATAAPAASSSYASKGWAALRRCPSPSLAA--RHVAFSSSSSARCTVAAAG
APVLP LGIRG-----SCLLLQSPLLTDGGKNGAATRTVAEEAAV ASPSAEGDG
EPEAAG-----IPRTVKL--GAMILVWYLLNIYFNIYNKLVKA--VPFPYTIT
TFQFASGSFFITLMWLLNLHP--KPRLSLQQYAKILILALIHMMGNVFTNM SLGKVAVSF
THTIKAMEPFFSVLLSVLFLGETPPLPVLGSLVPVVGGVVLASMT EVSFNWIGFWSAMAS
NVTFAQSRNVLSKKLLADKE--E-----TLDDINLFSIMTVMSFLLAPVTLLTEG--VKV
TP-----TVLQSA--GLN--LQQVYTRSLIAAFCFHAYQQVSYMILARVSPVTHSVGNC
VKRVVVIVT SVLFFKTPVTPINSIGTAIALAGVFLYSQLKRL-----QPKP--KAA-----
>Bsta_Brast05G093500.1_405
--MQSTAAGI LLRPCAA-----RPLLKNPSPGGA-----RLPAAR
GALRLSAVAPRAGIS-----AAAGLGRIGLLPLSPEQEERSGRCSR DVAAAAA ASGKAAAG
EGSGEEGGAA-----LAKTLQL--GVFFGLWYLFNIYFNIYNKQVLKV--FPYPINIT
TVQFVAGTVISLFLWITGILK--RPKVSGAQLVAIPLAIVHTMG NLF TNM SLGKVAVSF
THTIKAMEPFFSVLLSAMFLGELPTPWVLSLLPIVGGVALASISEASFNWAGFLSAMAS
NVTFAQSRNVLSKKLLADKE--A-----SLDNINLFSIITVMSFLLAPVTLLTEG--VKV
TP-----TVLQSA--GLN--LQQVYTRSLIAAFCFHAYQQVSYMILARVSPVTHSVGNC
VKRVVVIVT SVLFFKTPVTPINSIGTAIALAGVFLYSQLKRL-----QPKP--KAA-----
>Bsta_Brast01G368500.1_401
--MQRAAASLSSSRAA-----WAAAAASSRHAPG-----ASSCSA
ADRRDAAIAPP-----PLRVLRGQQLLPLRPLSGNRARRAVTASAAAAAELPAGD
EAAVDTDGG-----IAGAVEL--GAMIVAWYLLNIYFNIYNKLVQA--LPFPYTMT
AFQLAFGSLVIFFMWAARLHP--APKLSAAQLARIAPLAAGHMLGT VFTNM SLGKVAVSF
THTVKASEPFFTVLLSAFFLGETPSLPVLGSLVPIVGGVALASL TEVSFNWVGFW SAMAS
NLLNQTRNVLSKRLGGQEEEE-----SMDDINLFSVITVLSFLLMSCPLMLLAEG--VKF
SP-----AYLQST--GLN--LPELCVRAVLAGLCFHGYQKISY MILARVSPVTHSVANC
VKRVVVIVSSV LFFRTPISPVNALGTGAALGGVYLYSRLKKS-----KP--KSI-----
>Bsta_Brast08G188700.1_413
--MPSMAATAASSSYAA-----SKGWAVLRRCPSPSLAARHVAFSSSSSSRCPVA
GAVAPVLSLGIR-----GGRLLQSPLLPDGGKNGAATGRVAAAASVSPSAEGGGE
PKAAG-----IPRTVQL--GAMILVWYLLNIYFNIYNKLVKA--VPFPYTIT
TFQFASGSFFITLMWLLNLHP--KPRLSLQQYAKILILALIHMMGNVFTNM SLGKVAVSF
THTIKAMEPFFSVLLSVLFLGETPPLLVLGSLVPVVGGVVLASMT EVSFNWIGFWSAMAS
NVTFAQSRNVLSKKLLADKE--E-----TLDDINLFSIMTVMSFLLAPVTLLTEG--VKV
TP-----SYLQST--GIN--LQDLCLKAAIAGTCFHGYQQVSYSLARISPVTHSVANS
VKRVVVIVSSV LFFRTPISINAFGTGLALLGVFLYSRFFKA-----KPKV--KAA-----
>osat_LOC_0s08g25624.1_407

-MQSAAAFGLVRPCPA-----RPPLQLGPGSSSCR-----ILLHAR
 PLAAGIASSSRGPAVAARSLGRLLLLPPPPPISPDRAGRGRARHVACGAAAGDAKAE
 ESG-----LAKTLQL---GALFGLWYLFNIYFNIYNKQVLKV---FPYPINIT
 TVQFAVGTVALFMWITGILR---RPKISGAQLFAILPLAVVHTMGNLFTNMSLGKVA
 VSFTHTIKAMEPFFSVLLSAIFLGELPTVWVILSLLPIVGGVALASLTFASFNWAGFWSAMAS
 NVTFFQSRNVLSKKLMVKKE---E-----SLDNINLFSIITVMSFLLAPVAFLE
 TEG---IKITP-----TVLQSA---GLN---VKQVLTSLLAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTAIALAGVFLYSQKRL-----KPKP---KAA-----
 >Osat_LOC_0s08g25624.2_401
 -MQSAAAFGLVRPCPA-----RPPLQLGPGSSSCR-----ILLHAR
 PLAAGIASSSRGPAVAARSLGRLLLLPPPPPISPDRAGRGRARHVACGAAAGDAKAE
 ESG-----LAKTLQL---GALFGLWYLFNIYFNIYNKQVLKV---FPYPINIT
 TVQFAVGTVALFMWITGILR---RPKISGAQLFAILPLAVVHTMGNLFTNMSLGKVA
 VSFTHTIKAMEPFFSVLLSAIFLGELPTVWVILSLLPIVGGVALASLTFASFNWAGFWSAMAS
 NVTFFQSRNVLSKKLMVKKE---E-----SLDNINLFSIITVMSFLLAPVAFLE
 TEG---IKITP-----TVLQSA---GLN---VLTRSLLAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTAIALAGVFLYSQKRL-----KPKP---KAA-----
 >Osat_LOC_0s09g12600.1_408
 -MQSAAAVGLLRPCGA-----TTAAAPLQLRNP-----PRGFGV
 GVGQPLPPRGLRLSAPVPRAGISARRIGLVPASPEQEDERRRGARDVAVATAAAAGEA
 GAEEGG-----LAKTLQL---GALFGLWYLFNIYFNIYNKQVLKV---FPYPINIT
 NVQFAVGTVALFMWITGILK---RPKISGAQLAAILPLAMVHTMGNLFTNMSLGKVA
 VSFTHTIKAMEPFFSVLLSALFLGEMPTPFVVLSPVIVGGVALASLTFASFNWAGFWSAMAS
 NVTFFQSRNVLSKKLMVKKE---E-----SLDNITLFSIITVMSFLLAPVTLLTE
 G---VKVTP-----TVLQSA---GLN---LKQIYTRSLIAAFCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTGVALAGVFLYSQKRL-----KPKP---KTA-----
 >Osat_LOC_0s05g07870.1_414
 -MQAVAAATSRWAAS-----PRRRRHVASCSSPPPTTTATTTSSLRNCPVAGAG
 APVLP-----GIRGGRMLLAPLLWNSGAAARKAAVATAAAASPPAEGGG
 KANGGAVAGG-----ISRTVQL---GAMILVWYLLNIYFNIYNKQVLKV---VPFPYTIT
 TFQFASGSFFITLMWLLNLHP---KPRLSLQGYAKILPLALVHTMGNVFTNMSLGKVA
 VSFTHTIKAMEPFFSVLLSVLFLGETPSFLVLGSLVPIVGGVVLASMTVEVSFNWIGFWSAMAS
 NLTNQSRNVLSKKLLADKE---E-----TLDDINLFSIMTMSFLLSAPLMLSVEG---IKF
 SP-----SYLQSN---GVN---LQELCMKAALAGTCFHFYQQVSYSLARVSPVTHSVANC
 VKRVVIVTSVLFFRTPISPINALGTGVALAGVFLYSRKKKA-----KPKA---KTA-----
 >Osat_LOC_0s01g07730.1_393
 -MQRAAAASRATA-----WSTARHGAARVTA-----SASFSG
 GGGIVAGAA-----LPLRVGGQMLSLPLLSGGRVARTARVAAAEAPLPADDADA
 AAGRERGA-----LAETAQL---GAMIVAWYLLNIYFNIYNKQVLQP---LPFPYTIT
 AFQLAFGSFVIFLMWALKLHP---APRISISQLAKIAPLAAGHMLGTVFTNMSLSKVAVSF
 THTIKASEPFFTVLLSAFFLGETPSLLVLGSLVPIVGGVALASLTFELSFNWIGFWSAMAS
 NLLYQSRNVLSKKLLGGEE---E-----ALDDINLFSILTILSFLSLPLMLFSE
 G---VKFSP-----GYLRST---GLN---LQELCVRAALAGFCFHGYQKLSYLILARVSPVTHSVANC
 VKRVVIVTSVLFFRTPISPINALGTGVALGGVFLYSRLKRT-----KP-----KNA-----
 >Macu_GSMUA_Achr2T14180_001_420
 MHLRSAAFSAARPLPM-----LRAGSNLPDGHSCSVPTVSSSSSSSFSTDLPSFL
 PRIRPLSCRPTRFLL-----TPRLANQKSSLGLTTVVKAAEDVAAAAAGGTENHGEAAVS
 SYGSSSTSG-----MVKKLQL---GFLFGLWYLFNIYFNIYNKQVLKV---YPFPYTIT
 TIHFAIGTVLIWLMWVTNLK---RPKISSQKLAAILPLAIVHTLANLFTNMSLGKVA
 VSFTHTIKALEPFFTVLLSAMFLGELPTLWVLISLVPIVGGVAMASLTFASFNWAGFWSAMAS
 NLTNQSRNVLSKKIMDKDE---E-----TMDHITLFSIITVMSFLLAPVSLLE
 G---IKFTP-----SYMRF---GLN---LKEVYVRSFLAGVCFHAYQQASYMILAEVSPITHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTGVALIGVFLYSRVKRT-----KS-----KSA-----
 >Macu_GSMUA_Achr3T28500_001_368
 -MGAIVILSTVTFASC-----AVAAAS
 -----LTAATVRAGTVVAPDLAASDVQSWGTVTNSQAAAAASLRER
 RD-----LLQTLLL---GSLFGLWYLFNIYFNIYNKQVLKV---FQFPLTIT
 LLQFSIGTFLVLFMWTTNLK---RPKISPMQLAAILPLALVHTMGNLFTNMSLGRVSVSF
 THTIKAMEPFFSVLLSALFLGEVPTIWWILSLMPIVGGVALASLTFASFNWAGFWSAMAS
 NLTFQSRNVLSKKVMVKKE---E-----SLDNINLFSIITIMSFFLLAPVTLFVE
 G---IKITP-----TYLESA---GLN---LKQIYLRSLIAGLCFHAYQQVSYMILSRVSPVTHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTGVALGGVFLYSRVKRI-----KP-----KST-----
 >Macu_GSMUA_Achr1T25520_001_398
 -MQSAAISPSAAPLL-----RSSTKPPAPRWSPLLL-----PLHRGG
 PRLRPLAAVPSFSGCCRCSSGRCLVSGTSSTSTSTSTISRHVSPRRLDAFSCPKGTGYS
 NSSWD-----TVTLKKAEPGRIFA-----NTRVLKG---FTFPLTIT
 TVQFAVGTFLVLFMWTTNLK---RPKISASQLAVILPLAMVHTMGNLFTNMSLGKVA
 VSFTHTIKAMEPFFSVLLSALFLGEMPTIWWLLSLVPIVGGVGLASLTFASFNWAGFWSAMAS
 NLTFQSRNVLSKKAMVKKE---E-----SLDNINLFSIITIMSFFLLAPATFFVE
 G---IKVTP-----SYLQSA---GLN---FKEIYLRSLAALCFHAYQQVSYMILARVSPVTHSVGNC
 VKRVVIVTSVLFFRTPVSPINSLGTGVALAGVFLYSRVKKI-----KP-----KSA-----
 >Atri_v1.0_scaffold00096.30_407
 -MQSSA-ISLSSCNPF-----LKSKSPCKPTSG-----FPPRFS
 RGLDPLPPKGLHLRASIGRSDLRQRISFGNGVSPSMQKPLFEGPDFRVGASASVPESADS

KSSSSS-----LIQTLQL--GALFGLWYLFNIYFNIYNKQVLKV--FPFPITIT
TLQFAVGTVLVLIMWSTGLYK--KPKINSSQLIAILPLAAVHTLGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSALFMGELPTLWVSSLVPIVGGVALASLTFASFNWAGFWSAMAS
NLTNQSRNVLSKKFMLKKE--E-----SLDNITLFSIITIMSLIMLAPVTVFTEG--IKF
TP-----SYMELA--GLN--VEQVIQRSLLAGLCFHAYQQVSYMILARVSPVTHSVGNC
VKRVVVIVSSVLFCKTPVSPINSLGTGIALAGVFLYSRVKKI-----KPKPEAKSA-----
>Smoe_172535|172535_307

-----MMRTLQL--GSLFGLWYLFNIYFNIYNKQVLKV--FPFPITIT
EIQFAIGSAAVLFMWTGLYK--RPSLTAAQVVAIPLALVHTMGNLFTNMSLGKVAVSF
THTIKAMEPFFSVVLSALFMGELPTLWVSSLVPIVGGVALASLTFASFNWAGFWSAMAS
NVTQSRNVLSKKLMVKKE--G-----SLDNINLFSVITILSFFLLAPVTLFFEG--VKF
TP-----EYLTSM--GLD--VKVVMRLALVAGLCFHSYQQVSYMILQRVSPVTHSVGNC
VKRVIVIVTSVIFFRTPVSTINALGTALALAGVFAYSRAKRI-----KPAK--KSA-----
>Mpus_3748_320

-----KTLIL--GVLFAGWYACNIVFNICNKQVLGA--YFPPLTST
LWQFAAGVAFTALLQMTGIHRINKDALTMESLRAIPLAIVHTLGNLTVNSLGKVAVSF
THTIKAMEPFFSVVLSALFLGDVPSAAVIATLVPIVGGVAAASVTEASFNWPGFLAAMGS
NVTQSRNVLSKKLIGDGCSEQACPAIPMDNIDLFSIITIMSLALTLPAAVVLEG--VRF
TPGAIAAAYAASAGA-AFS--PAVIFQKAMIAGACFHMYYQISYMILARVSPVTHSVGNC
VKRVVVISFVSLFFKNAVSPVNAVGTAAALGGVYAYTRVKRA-----ERDA--AAA-----
>Crei_Cre06.g263850.t1.1_401

--MASLLGRKACIPATC-----VQKSLTPPAPL-----RLGLAC
SALQRHQVQ-----TAIASRVARQEEENGRAAAIVPRQRTVCQAAAVPADGESD
KGKD-----MSGMMVL--GLMFVAWYGTNIFFNIYNKQLFKV--FPFPLTTT
NIQFFIGSCLSMVFWVTGIVK--LPKIDMALVKSIIYPLAIVNLGNLTVNSLGHVAVSF
THTVKAMEPFFSVIFSAIFLGDVPPVPVLLTLVPIVGGVVIASLTFATFNWTFGLSAIFS
NMTQSRNVLSKKLMIKKG-----AVDNMNLFQIITIMSFLMLLPVSTMVEGGAALL
TP-----ESLANL--GLNEAAREQFMRLLSAGICFHSYQQLSYMILSRVAPVTHSIGNC
VKRVVVIVASLIAFQNPISMQNAIGTGIALFGVFLYSQAKRKYKGKGDVKP--EAA-----
>Crei_Cre08.g379350.t1.1_399

--MSSLLKTRVPSLAA-----RDVAF
HPLVFTTSSQR-----VARASGQSSAFPLRSVAVSGVSSRRPFTCLAVAASAGDVSD
GSSHT-----MMQTLVL--GSMFAGWYAANIAFNIYNKQLLKA--FAFPLTIT
EAQFLVGSCVTLVAWGSLQR--APKITWSTIKNVLPLAVVHTLGNLFTNMSLGAVAVSF
THTIKAMEPFFSVLSALFLGDQPSPLVLATLLPIIGGVAMASMTATFNWTFGLSAMGS
NLTQSRNVLSKKLMKKDKDGNAPLDNMALFSVITLLSAALLPATLLFEG--WKL
SP-----VGLAEM--GVR--SPNGVLAHAAMAGLCFHLYQQVSYMILSRVSPVTHSIGNC
VKRVVVIAASVLFRRNPVSLQNALGTALALAGVFLYGTVKRQ-----QAIAGKKIAASE
>Mpol_Mapoly0083s0074.1_440

--MVSQALAMLQPQACCVSSSRC--AGLSGAAFSSASGVKSIVSSYAVSRRDGRALSSKA
AASKFGSSFLSGPAV-----SRSGLFPLNASLNSRLEERRPRKGSVVVRASAVESGADEG
AAPDGTSPVVPAPQPSLAKTLQL--GSLFGLWYLFNIYFNIYNKQVLKV--YTFPVMT
NMQFAVGGVIVMIMWLTGLHK--RPKITTSQLLAILPLAIVHTMGNLFTNMSLGKVAVSF
THTIKAMEPFFSVLLSALFLGEVNPWVVASLLPIVGGVALASLTFVSFNWAGFLAAMAS
NVTQSRNVLSKKLMVKKE--G-----SLDNINLFSVITVMSFFLLAPVTYLMEG--VKF
TP-----AVIQAA--GLD--VKVIATRALLAGLCFHSYQQVSYMILQRVNPVTHSVGNC
VKRVVVIVTSVLFCKTPVSPINALGTGIALSGVFAYSRVKALGKGSKKEK--KEA-----