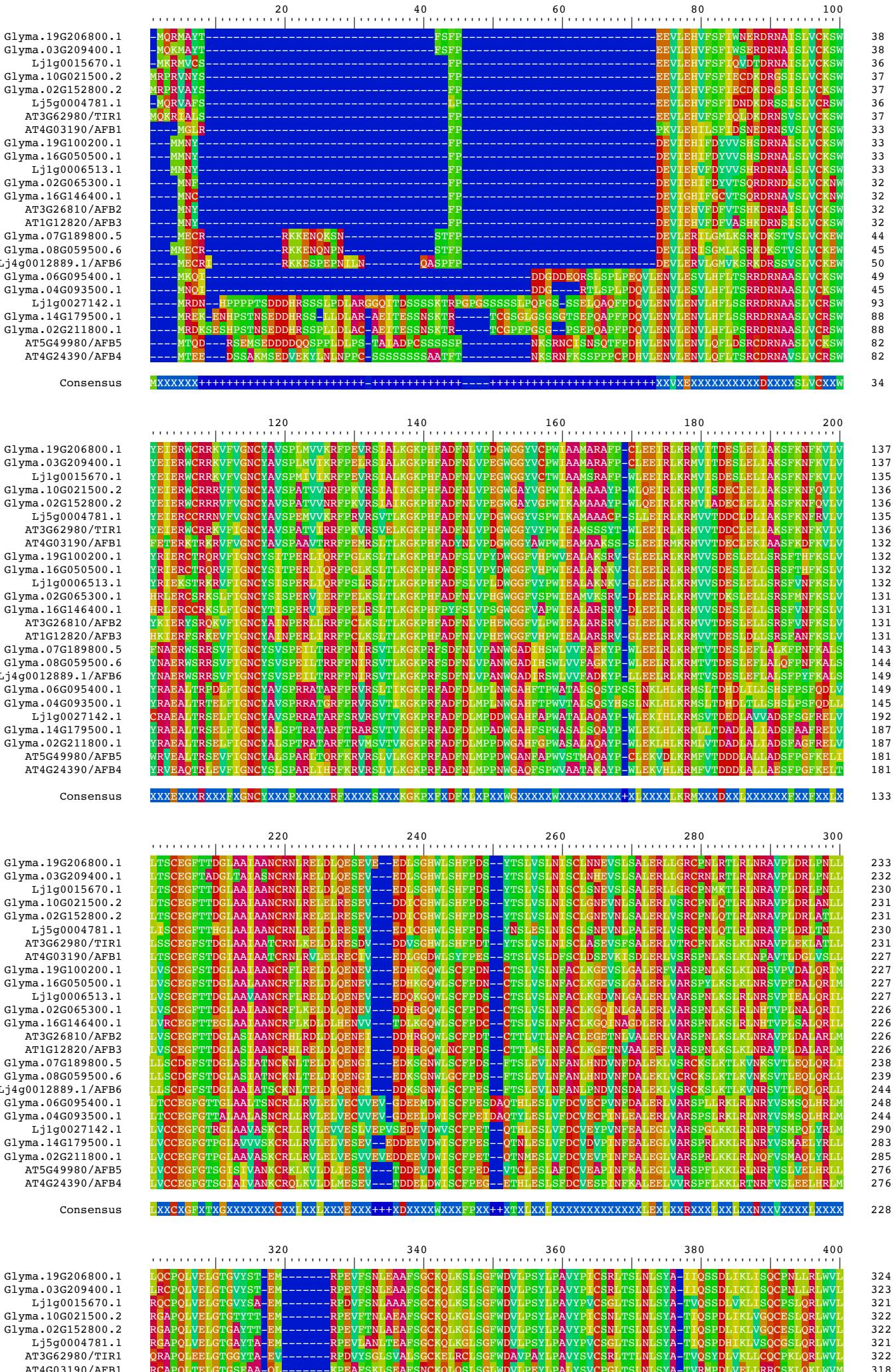


## Appendix A

### Amino Acid Alignment of Auxin SCF<sup>TIR1/AFB</sup>

This appendix presents the full alignment of the F-box proteins of TIR1 and AFBs from *Glycine max* with those from both *Arabidopsis thaliana* and *Lotus japonicus*. The inclusion of the latter is due to its representation as a legume and the absence of the AFB6 member in *A. thaliana*.



Glyma.19G100200.1	MRAPOQLSDLIGIGSLVH-DF-----ESEAYIKLKNTILKCKSITSLSGFLEAVPHCLAAIYPICPNLTSLSYAAIGIQGSALVKLJHHCVKLQRWIM	319
Glyma.16G050500.1	MRAPOQLSDLIGIGSFVH-DF-----ESEAYIKLKNTILKCKSITSLSGFLEAVPHCLAAIYPICPNLTSLSYAAIGQGSDLKLJHHCVKLQRWIM	319
Lj1g0006513.1	MQAPQQLADLGIGGSFVH-NP-----ESDAFSKLKNNTILKKSHTSLSGFLEVGPFPCAMPYICRNLTALNSYAAIGIHNELKLJHCCGKLQRWIM	319
Glyma.02G065300.1	RRAPQQLADLGIGGSFVHP-DF-----NSNWF1KLMTNTIECKSITSLSGFVFPTPRCLPAIYPVCVMNLTTAMNLNSYAAIGOSRELKLJCRGKLQRWIM	318
Glyma.16G146400.1	MQAPQQLADLGIGGSFVH-DF-----RSEVYNNNMKAALIKCMSTSLSGFVWVPHCLSALYPVCVMNLTTLNLRFAAGIQNTTELKLJCCCCGKLQRWIM	318
AT3G26810/AFB2	ACAPQQLVDLGIGSYEN-DF-----DSESYKLMLAIVKKCISLSLGSFLEAAPHCLSAHFPICHNLTSLSNLYAAEIGHSHL1KLJHCKKLQRWIL	318
AT1G12820/AFB3	SCAPQQLVDLGIGSYEN-EP-----DPEPSFKALMATAKKYTSLSLGSFLEAVPLCPAPYPICONLISLSYAAEIQGNHLLKLJOLCKLJLQRWIL	318
Glyma.07G189800.5	VHVPQLGELGTGGSFSQ-EL-----TSQQCSDLESALKNCNKNLTLTSLGIWWATAAQYLPVLYSACTNLTFLNFSYA-PLDSDGTLKLLVHCPKLRWVV	329
Glyma.08G059500.6	VHVPQLGELGTGGSFSQ-EL-----TAQQCSDLESAFKNCNRNLFTLTSGLIWWATAAQYLPVLYSACTNLTFLNFSYA-PLDSDGTLKLLVHCPKLRWVV	330
Lj4g0012889.1/AFB6	VRAPQQLCELGGSFSFSEDDL-----TAQQYSEIESAFNNCNKNCNKNLTLTSLGIWWATAAEQYLPLLYPACTNLTFLNFSYA-PLDGDDLAKLJLVRHCPKLRWVV	336
Glyma.06G095400.1	HRAPQQLTHLGTGGSFSASEL-----DOELDFASAFASACKSLSVCLSGFREFWDALP1AIPYACANLISLSNFSY-DISADQLSV1RHCHKLQFWVL	338
Glyma.04G093500.1	HRAPQQLTHLGTGGSFSASEL-----DOELDFASAFAAACKSLSVCLSGFREIWPDLPAIYPACANLISLSNFSY-DISADQLSV1RHCHKLQFWVL	334
Lj1g0027142.1	LRAPQQLTHLGTGGSFSDEA-----LEQEPDFAASAFACRSLSVCLSGFREIWNANLP1AIPVCANLISLSNFSY-DVNADQLSV1CHCRKLQFWVL	381
Glyma.14G179500.1	LRAPQQLTHLGTGGSFSATEAGA-----VGQEPDFAAFAACRSLSVCLSGFREIWAFLPAIYPVCANLISLSNFSY-DVNADQLSV1RHCHKLQFWVL	382
Glyma.02G211800.1	LRAPQQLTHLGTGGSFSATEAGVVG-----DQEPPDFAAAFAACRSLSVCLSGFREIWAFLPAIYPVCANLISLSNFSY-DINTDQLSV1RHCHKLQFWVL	379
AT5G49980/AFB5	LGAPQQLTSLGTSFSHDEE-----POQEQQDFAAAFRACKSVVCLSGFRELMPPEYLPAIIPVCANLISLSNFSY-NISPDMFKP1IILNCHKLQFWVL	369
AT4G24390/AFB4	VRAPQQLTSLGTSFSFPDNV-----POGEQQDFAAAFRACKSVVCLSGFREFRPEYLLAASSVCANLISLSNFSY-NISPDMFKP1IISNCNCFNIRFWVL	369

Consensus XXXPQXXXXLGCGXXXX+XX++++--++XXXXXXXXXXXXXXXXXXXXXXXLSGXXXXXXXXLXXXXXXCXXLXXXXNSXA+XXXXXXXXXXXXXXCXXLXXXXXX 317

	420	440	460	480	500
Glyma.19G206800.1	DYIEDAGLYAIAASCKDLRELRVFPSPDPFGL--EPNVALTEQQLVSSEGCPKLSQVLIFYCQOMSNAAALHTIARNRINLTRFLCIIEIPRTPDYLTHEPLD				
Glyma.03G209400.1	DYIEDAGLYAIAASCKDLRELRVFPSEPFGL--EPNVNSLTEOQLVSSEGCPKLSQVLIFYCQOMSNAALEHTIARNRPNLTERFLCIIEIPRTPDYLTHEPLD				
Lj1g0015670.1	DYIEDAGLDVIAIAASCKDLRELRVFPSPDPFGF--EPNVNLTEREQLVSSEGCPKLSQVLIFYCQOMTNAAALHTIARNRNPTCFHRLCIIEPQADPYLTQLPLD				
Glyma.10G021500.2	DYIEDAGLEVIAIAASCKDLRELRVFPSPDPFGL--EPNVALTEQQLVSSEGCTKLQSVLIFYCQOMTNAAALHTIARNRNPTMTRFLCIIEPOAPDHBLHQPLD				
Glyma.02G152800.2	DYIEDAGLEVIAIAASCKDLRELRVFPSPDPFGL--EPNVALTEQQLVSSEGCTKLQSVLIFYCQOMSNAAALHTIARNRSPNMTRFLCIIEPRAPDYLTHQLPLD				
Lj5g0004781.1	DYIEDAGLDVIAIAASCKDLRELRVFPSPDPFGL--EPNVNLTEEGLISVSEGCPKLSQVLIFYCQOMSNAALEHTIARNRPNMTRFLCIIEIPRTPDYLTHQLPLD				
AT3G62980/TIR1	DYIEDAGLEVIAIASTCKDLRELRVFPSEPFVM--EPNVALTEQQLVSSEGCPKLSQVLIFYCQOMTNAAALHTIARNRNPTMTRFLCIIEPKAPDYLTLFPLD				
AT4G03190/AFB1	DLIEDKGLEAVASYCKELRELRVFPSEPDID--ATNIPLTEQQLVFVSKGCRKLESVLYFCVOFTNAALHTIARKRPNLKCFCRLCVIEPFAPDYPKTNEPLD				
Glyma.19G100200.1	DCIGDGKGLGVVATTCKDLQELRVPSPVPG---DPAAVTEKGLVAISMCPCPKLHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLDATKPPDPDTMQPLD				
Glyma.16G050500.1	DCIGDGKGLDVATTCKDLQELRVPSPVPG---NPAATTEKGLVAISMCPCPKLHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLDATKPPDPDTMQPLD				
Lj1g0006513.1	DCIGDGKGLGVATTCKDLQELRVPSPVPG---NPAATTEKGLVAISACGCRKLHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLDATKPPDPDTMQPLD				
Glyma.02G065300.1	DCIGDGFLHVAVASTCKDLQELRVPSPVVRGR--NDPAGVTEKGLVAISMCPCPKLHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLILDPTKPDPTDVQPLD				
Glyma.16G146400.1	DSIGDGNGLVVAAATCKDLQELRVPSPVSDLLG--GGANTTATEEGLVAISACGCPKLSHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLILEPDKPDTMQPLN				
AT3G26810/AFB2	DSIGDGKGLLEVATTCKELQELRVPSPDLLG--GGANTTATEEGLVAISACGCPKLSHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLILEPDKPDTMQPLD				
AT1G12820/AFB3	DSIGDGKLAVVAAATCKELQELRVPSPDVHGEEDDNNASVTEVGLVAISACGCPKLSHSLLYFCQOMTNAALEHTITVAKNCNPFIERFLCLILEPHKPDHITFQSMD				
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Glyma.08G059500.6	DTVEDKGLEAVGSHCPLEELRVPADPFDE--GTVHGVTESGFIAISQCPRLHYLVLIFYCQOMTNAAVTVVONCPDFTHFLRCIMHPGQDYLTVQESMD				
Lj4g0012889.1/AFB6	DTVEDKGLEAVGSHCPLEELRVPADPFDE--GTVHGVTESGFIAISQCPRLHYLVLIFYCQOMTNAAVTVVONCPDFTHFLRCIMHPGQDYLTVQESMD				
Glyma.06G095400.1	DTICDEGLQAVAAETCKDLRELRVFPVNTR--EIEGPVSEGVFEIAISRGCRKLSQSLILFFCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
Glyma.04G093500.1	DTICDEGLQAVAAETCKDLRELRVFPVNTR--EIEGPVSEGVFEIAISRGCRKLSQSLILFFCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
Lj1g0027142.1	DSIGDEGLQAVATTCKDLRELRVFPVDARE--ESEGPVSEGVFEIAISGCRKLESILFFCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
Glyma.14G179500.1	DSIRDEGLQAVAAETCKDLRELRVFPVDARE--ETDGPVSEGVFEIAISQCPRLHYLVLIFYCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
Glyma.02G211800.1	DSIRDEGLQAVAAETCKDLRELRVFPVDARE--ETDGPVSEGVFEIAISQCPRLHYLVLIFYCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
AT5G49980/AFB5	DSICDEGLQAVAAATCKELRELRVFPVDARE--DSEGPVSEGVFEIAISGCRKLESILLYFCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				
AT4G24390/AFB4	DSIRDEGLQAVAAATCKELRELRVFPVDARE--DSEGPVSEGVFEIAISGCRKLESILLYFCQOMTNAAVAMMSNCPDLVVFRLCIIIGYRPRDPVTLEPM				

**Consensus** DXXXXDXXXXGXXXXXXCXXXLXLRFXXXXPXXXX+++XXXXXXExGXXXXXsXGCXXXLXXXLXFXXXXXNxNxAXXXXXXFXXXXXFRCLCXXXXXPDXGGTXXXXD 414

	520	540	560	580	600
Glyma.19G206800.1	SGFGA1VEQCKDLQRSLISGLLTDRVFYEYIGTCGKKLEMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				523
Glyma.03G209400.1	SGFGA1VEQCKDLQRSLISGLLTDRVFYEYIGTYAKKLEMMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				522
Lj1g0015670.1	SGFGA1VEHCKGLQRSLISGLLTDRVFYEYIGTYGKKEMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				520
Glyma.10G021500.2	AGFGA1VEHCKDLQRSLISGLLTDRVFYEYIGTYGKKEMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				521
Glyma.02G152800.2	AGFGA1VEHCKDLQRSLISGLLTDRVFYEYIGTYGKKEMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				521
Lj5g0004781.1	AGFGA1V0HCKCNLQRSLISGLLTDRVFYEYIGTYAKKLEMMLSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCPFGDKALLANAEKLETMRSLWMSCSVSYG				520
AT3G62980/TIR1	IGFGA1VEHCKDLRRLSLSGSGLLTDRVFYEYIGTYAKKLEMMLSVAFAGDSDLGMHHVLSGCDNLRKLEIRDCPFGDKALLANASKELETMRSLWMSCSVFSFG				521
AT4G03190/AFB1	KGFKTA1EFGCRDLRRLSLSGSGLTSDRAFKYIYGKHKVRLMMLSVAFAGDSDLMLHHHLSGCESLKMLEIRDCPFGDTALLEAKLETMRSLWMSCSVFSFG				517
Glyma.19G100200.1	EGFGA1VQSCRRRLSLSGSGLTSDQVFPLYIGMYAAELEMMLSVAFAGDGDKGMLYVNLNCKKLRKLEIRDCPFGDMALLTDVGKYETMRSLWMSSECVTVG				516
Glyma.16G050500.1	EGFGA1VQSCRRRLSLSGSGLTSDQVFPLYIGMYAAELEMMLSVAFAGDGDKGMLYVNLNCKKLRKLEIRDCPFGDMALLTDVGKYETMRSLWMSSECVTVG				516
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j4g0012889.1/AFB6	EAFGA1VVKCTSKQLQRLVAVSGYLTDLTFEYIGKVKANLTLISVAFASSWDGMRCVLDCPKLRLKELEVRDCPFGNAALLSERVESMRSLWMSDCNLTMN				536
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Glyma.04G093500.1	EGFGA1VMNCKKLTRLAVSGLLTDRAFPSYIYGTYGKLRITLISVAFAGDTDLGLQYVQLCGPNLQKLEIRDSPFGDGAHLHSLHHFYNMRLFWMSCKLTRQ				532
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Glyma.02G211800.1	EGFGA1VMNCKKLTRLAVSGLLTDRAFPSYIYGTYGKLRITLISVAFAGDTDVGLKLYVLECPNPQLQKLEIRDSPFGDGAHLRSLHHFYNMRLFWMSTCKLTLQ				577
AT5G49980/AFB5	EGFGA1VKNCKKLTRLAVSGLLTDRAFPSYIYGTYGKLRITLISVAFAGDSMDALRHLVLECPGPRLQKLEIRDSPFGDVAIRSGMHRYNNRMFWMSVACLSIKG				567
AT4G24390/AFB4	DGFGA1VKNCKKLTRLAVSGLLTDEAFSYIYGTYGKLRITLISVAFAGNSKALRIVLECPGPRLQKLEIRDSPFGDVLGRSMGHRYNNRMFWMSVACLSIKG				567

**Consensus** XXFGAXVXXCXXLXRLXXXSGXLTDXXXFXXIGXXXXXXXXLSXAFAGXXDXXXXXXXXXVLIXGCXXXXKLEXRDXPFGXXAIXXXXXXXXXXXXXXMRXXWMXSXCXXXXX 514

	620	640	660	680	700
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Glyma.03G209400.1	ACKLLGQKMPRLNVEVIDERG-----PPDSRSPDCPVEKLYIYRTTAGPRLDMPGFVWT				ME
Lj1g0015670.1	ACKLLGQKMPKLNLNEVIDERG-----PPDSRSPDCPVEKLYIYRTTAGPRLDMPGFVWT				ME
Glyma.10G021500.2	ACKLLGQKLPRLNVEVIDERG-----PPDSRSPSSPVEKLYIYRTVSGPRLDMPGYVWR				MQ
Glyma.02G152800.2	ACKLLGQKMPRLNVEVIDERG-----PPDSRSPSSPVEKLYIYRTVSGPRLDMPGYVWR				MQ
Lj5g0004781.1	ACKLLGQKMPRLNVEVIDERG-----PPDSRSPSSPVEKLYIYRTVSGPRLDMPGYVWR				MQ
AT3G2980/TIR1	ACKLLGQKMPKLNLNEVIDERG-----APDSRSPESCPVERVFIYRTTAGPRLDMPGFVWN				MD
AT4G03190/AFB1	ACKLKSQKMPRLNVEVIDEHE-----PFESRSPSSPVERIYIYRTVAGPRLDMPFVWT				IHKNP
Glyma.19G100200.1	ACKLAKKMPRLNVEIFNFNE-----QEDCSLEDGQKVEMYLRYTLAGKRKDAPFYVWT				I*
Glyma.16G050500.1	ACKLLAKKMPRLNVEIFNFNE-----QEDCSLEDGQKVEMYLRYTLAGKRKDAPFYVWT				I*
Lj1g0006513.1	ACKELAEKKMPRLNVEIFNFNE-----QECCSLEDEQSVEKMYLYRTLAGKRKDAPFYVCT				I*
Glyma.02G065300.1	ACKALAKKMPGLNVEIFNGNE-----KVDRDVDDGGQKVETKYLRYTLVGRRKDAPEHFWWT				I*
Glyma.16G146400.1	ACKALAEKKMPRLNVEIFNFNEK-----KVDRDVDDGGQKVEMYLRYTLAGKRKDAPFYVWT				I*
AT3G26810/AFB2	GCKRLAEPKAQPLNVEIIINENDNNRMEEENGHEGPKVDKLYIYRTVVGTRRDAPPFWI				I*
AT1G12820/AFB3	GCKRLAQNPSRLNVEIIINENNNGMNEQNEEDEREVKDLYIYRTVVGTRRDAPPFWI				I*
Glyma.07G178980.5	GVRLLAQEMPRLNVEVIKEEES-----YETHQAKKVVYVRSVAGPRRDAPPFWI				I*
Glyma.08G059500.6	GVRLLAKEMPRLNVEVIKEEET-----YETHQAKKVVYVRSVAGPRRDAPPFWI				I*
j4g0012889.1/AFB6	GCRLLAQEMPRLNVEVIKEEG-----CYGEPAQRVVYVRSVAGPRRDAPPFWI				I*
Glyma.06C095400.1	ACCEVAQTCPHIEEVINSEEF-----DKACTFTIYMPSTDPGPRRDAPPFWI				C

Sequence alignment of Glyma proteins:

Protein ID	Sequence	Length
Glyma.04G093500.1	ACREVARMLPHLVLEVINSEE-----DKADDIELLYMYRSLLDRPRDDAPKVVTI	583
Lj1g0027142.1	ACQDVARALPVLVEVINKED-----EAAVDIELLYMYRSLLDGPRRDAPOCVVTI	631
Glyma.14G179500.1	ACQEVARALPVLVEVINKED-----EAAVDIELLYMYRSLLDGPRRDAPOCVVTI	640
Glyma.02G211800.1	ACQEVARAVLPNLVFEVINNNSE-----ENAGDEVEFLYMYRSLLDGPRRDAPOFVVTI	630
AT5G49980/AFB5	CCKDIARAMPNLVVEVIGSDDD-----D-----DDNRDYYVETLYMYRSLLDGPRRDAPKFVVTI	619
AT4G24390/AFB4	GCRGVSHALPNVVVEVFGADGDDDED----TVTGDYVETLYLYRSLLDGPRRDAPKFVVTI	623
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Phylogenetic tree of Glyma proteins:

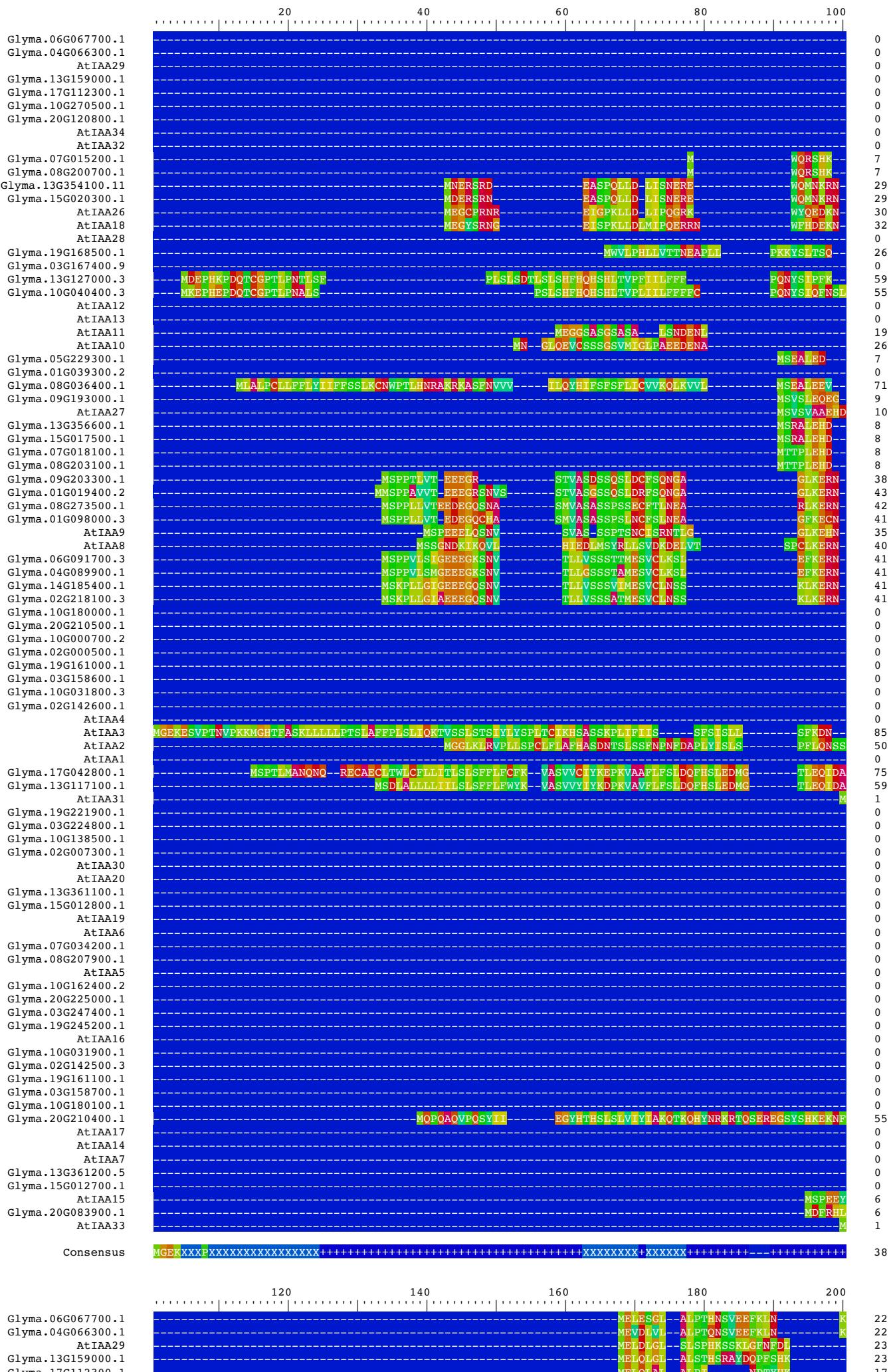
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```

## **Appendix B**

### **Amino Acid Alignment of Auxin Aux/IAA**

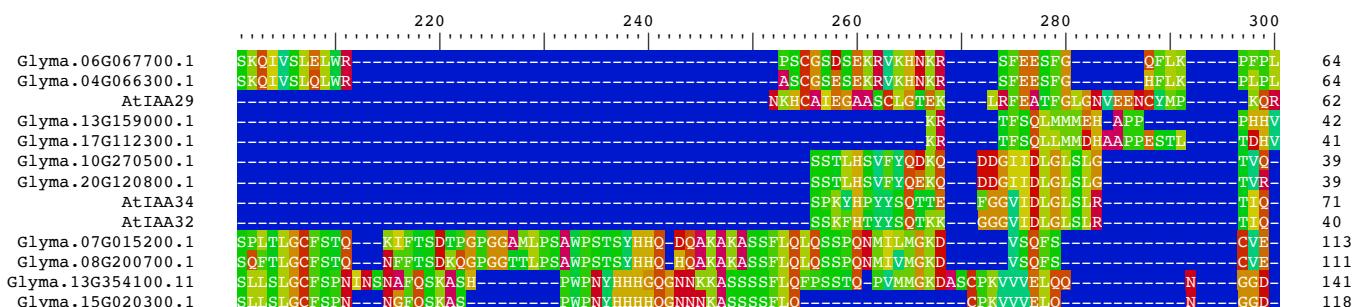
This appendix presents the full alignment of the Aux/IAA repressor proteins *Glycine max* with those from both *Arabidopsis thaliana*.

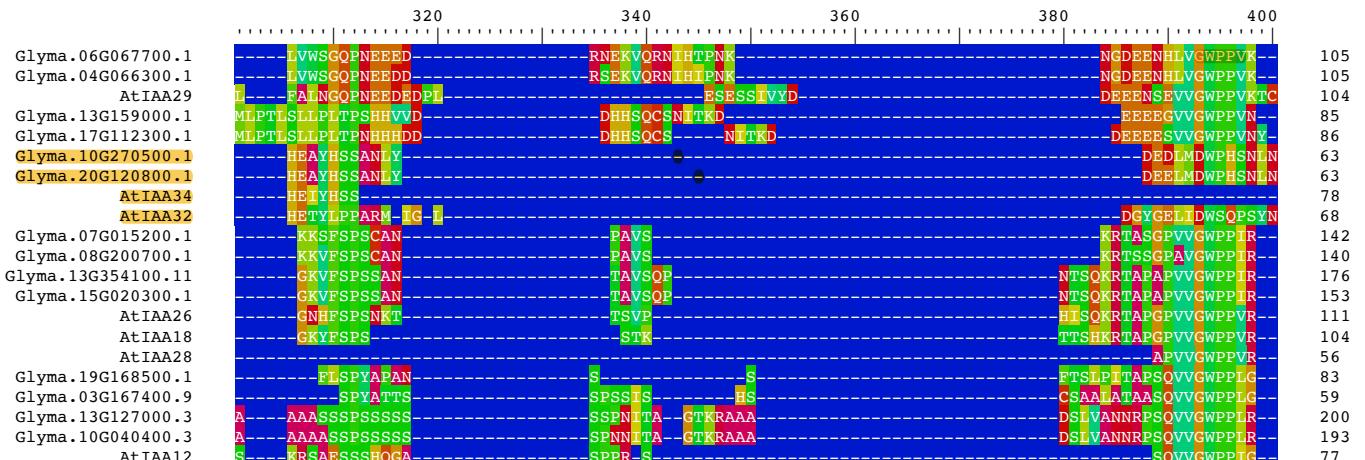
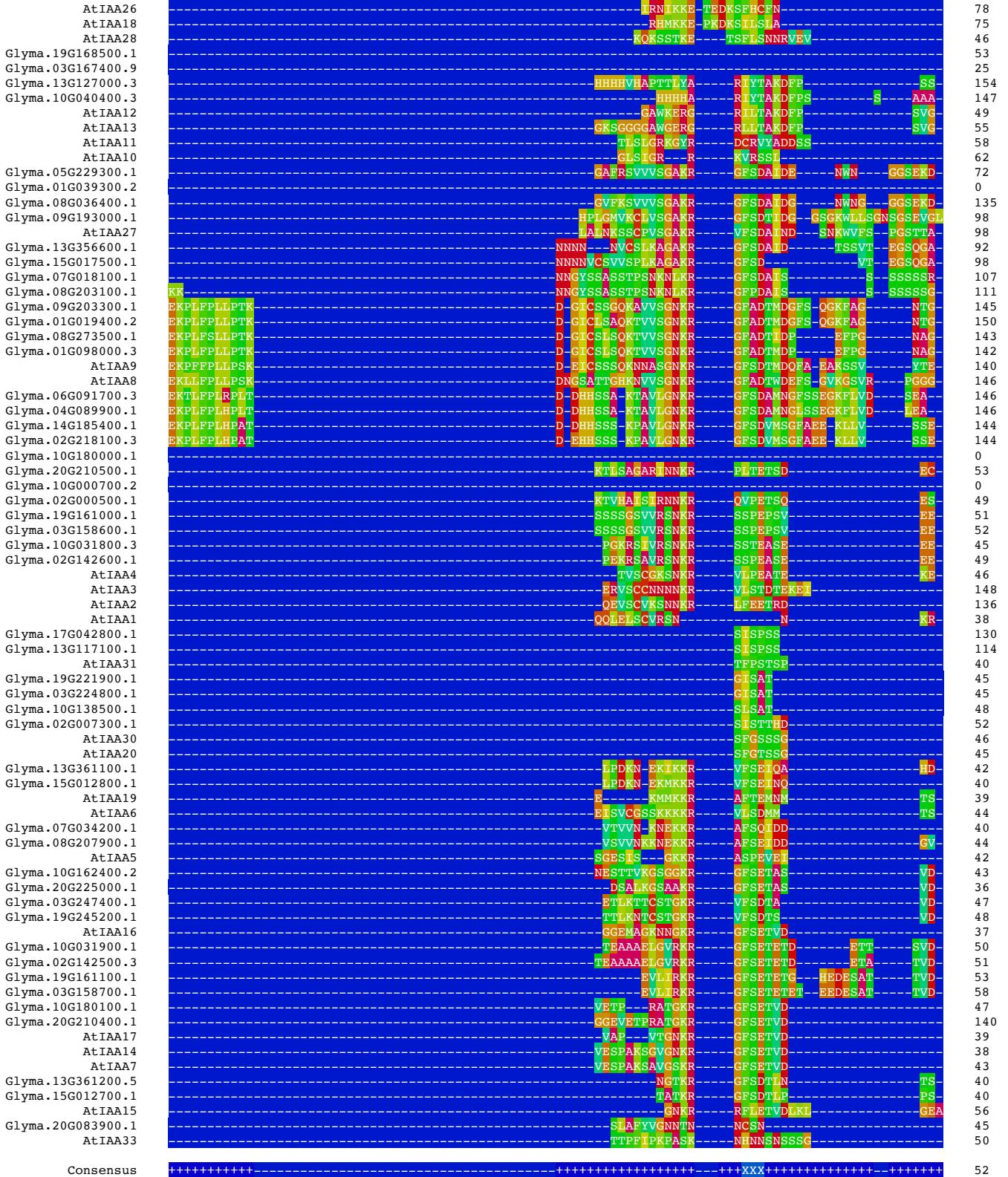


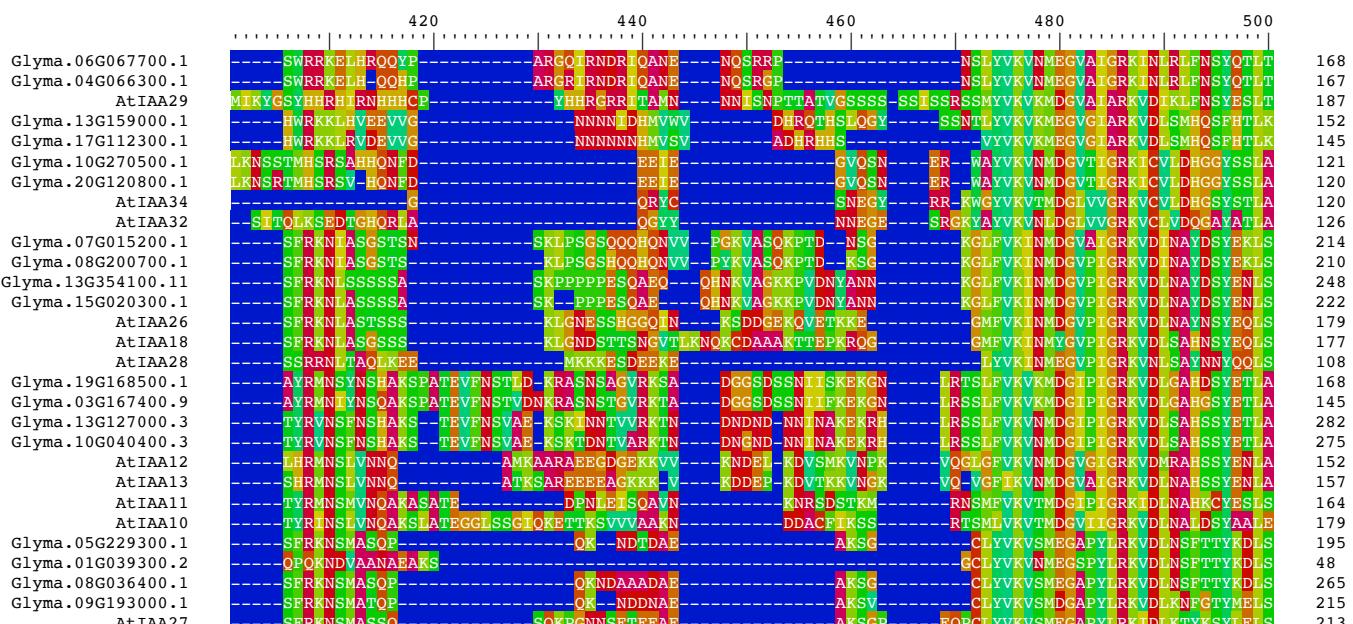
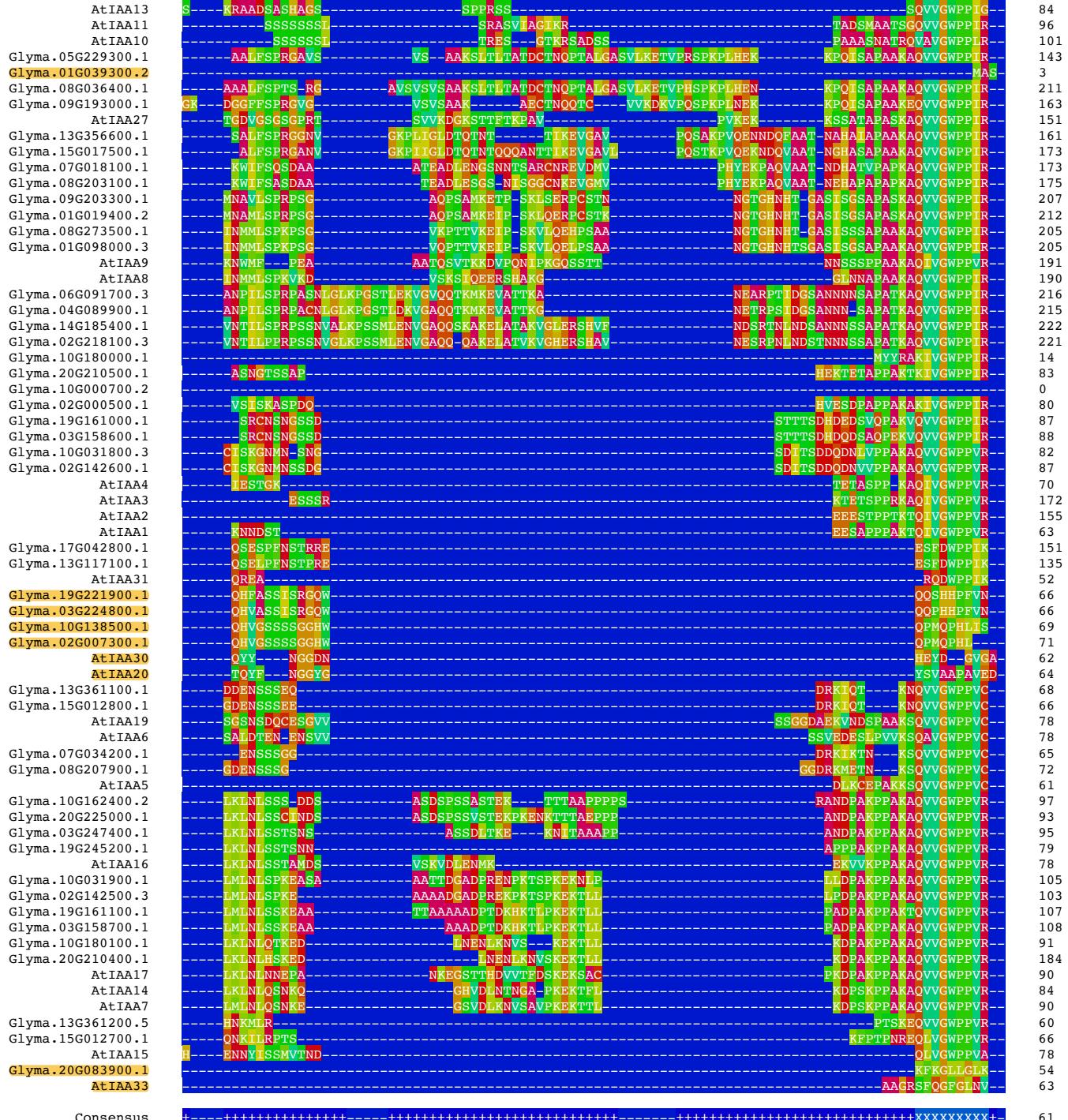


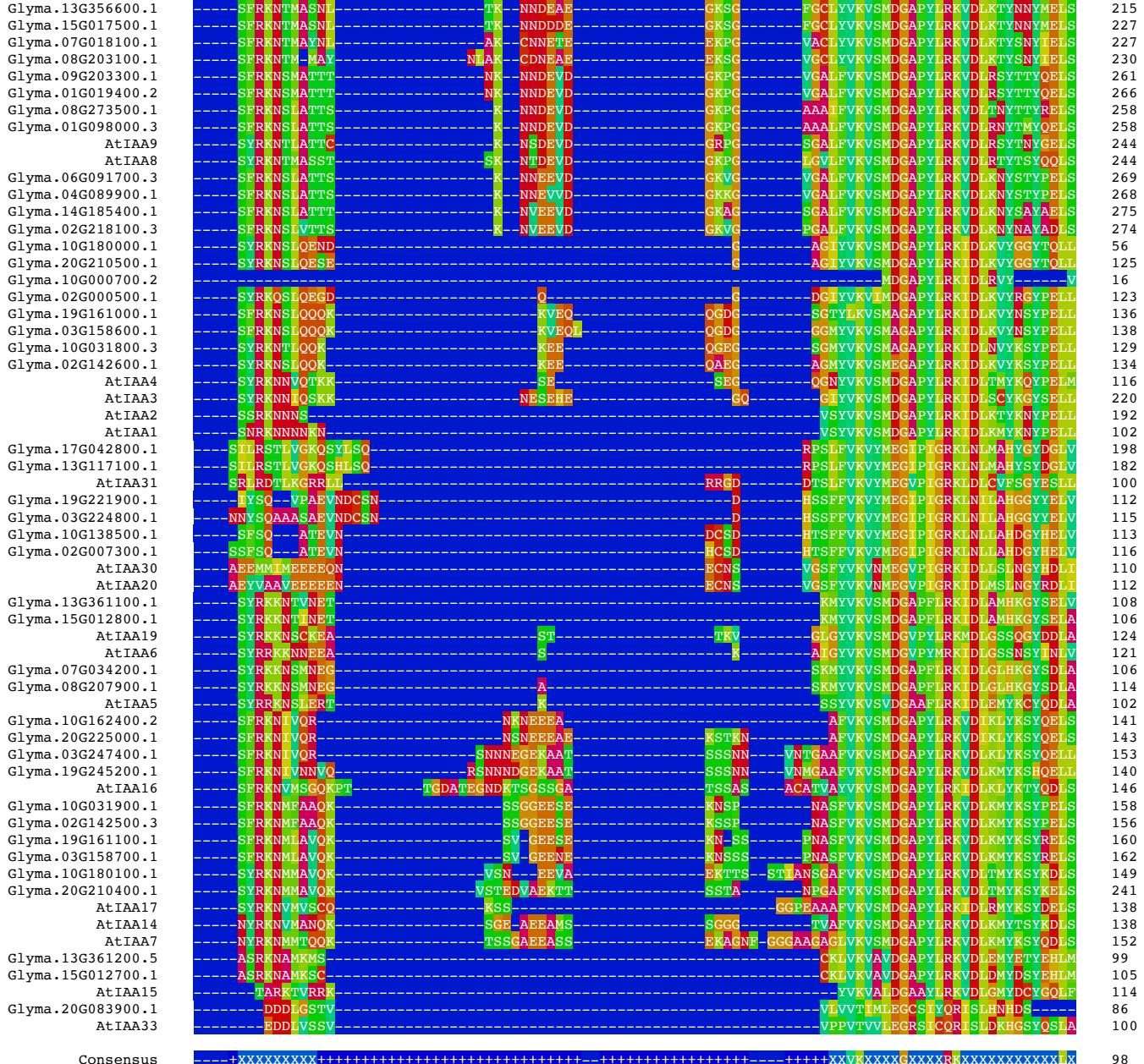
Consensus

49









AtIAA9	SALEKMF	FTLGQCGSNGAAGKDM1SETKLKD1LLNG	-NDYVLTYEDKDGDWMLVGDVPWEMFIDVCKKLKIMKGCDAA	-IGLA	325	
AtIAA8	SALEKMF	FTLGQCGLHQAGRERMRSEI1KLKD1LLHG	-SEFVLTYEDKDGDWMLVGDVPWE1FTFCQKLRLIMKGSDA	-IGLA	325	
Glyma.06G091700.3	SALEKMF	FTMSKCGSH1GLGREM1NETKLKD1LLHG	-SEYVLTYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKSSDA	-IGLA	350	
Glyma.04G089900.1	SALENMF	FTTISKCGSH1GLGREM1NETKLKD1LLHG	-SEYVLTYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKSSDA	-IGLA	349	
Glyma.14G185400.1	SALENMF	FTIGSCGSNHLNLGEV1NETKLKD1LLHG	-SEYVLTYKDKDGDWMLVGDVPWEMF1TCCKRLRLIMKSSDA	-IGLA	356	
Glyma.02G218100.3	SALENMF	FTIGSCGSNHLNLGEV1NETKLKD1LLHG	-SEYVLTYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKSSDA	-IGLA	355	
Glyma.10G180000.1	KALEMF	TIG	-EYSEKEGYKG--SDYAPTYEDKDGDWMLVGDVPWDMFVTCKRLRLIMKGSEA	-RGLG	122	
Glyma.20G210500.1	KALEMF	TIG	-EHSEKEGYKG--SDYAPTYEDKDGDWMLVGDVPWDMFVTCKRLRLIMKGSEA	-RGLG	191	
Glyma.10G000700.2	QALETMF	TIVVSS	-CEYSKREGYKG--SEYAPTYEDKDGDWMLVGDVPWDMFVTCKRLRLIMKGSEA	-RGLG	77	
Glyma.02G000500.1	KALETMF	TIG	-EYSEREGYKG--SEYAPTYEDKDGDWMLVGDVPWDMFVTCKRLRLIMKGSEA	-RGLG	189	
Glyma.19G161000.1	MALONLF	TFG	-EYSEREGYKG--SEYAPTYEDKDGDWMLVGDVPWDMFVTCKRLRLIMKGSEA	-KGLG	202	
Glyma.03G158600.1	AALQLSFTC	TFG	-EYSEREGYNG--SEYAPTYEDKDGDWMLVGDVPWNMFVSSCKRLKIIKGSEA	-KGLG	204	
Glyma.10G031800.3	KALGNMF	TFG	-EYSEREGYNG--SEYAPTYEDKDGDWMLVGDVPWNMFVSSCKRLKIIKGSEA	-KGLG	195	
Glyma.02G142600.1	KALEMF	TFG	-QYSEREGYNG--SEYAPTYEDKDGDWMLVGDVPWNMFVSSCKRLKIIKGSEA	-KGLG	200	
AtIAA4	KALEMF	SVG	-EYFREGYKG--SDFVPTYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKGSEA	-KGLG	182	
AtIAA3	KALEVMF	SVG	-SVGEYFERDYGKG--SDFVPTYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKGSEA	-KGLG	286	
AtIAA2	KALEMF	TVG	-MIGEYCEREGYKG--SGFVPTYEDKDGDWMLVGDVPWDMFSSCKRLKIIKGSDA	-PALD	258	
AtIAA1	KALEMF	TVG	-EYSEREGYKG--SGFVPTYEDKDGDWMLVGDVPWDMFSSCKRLKIIKGSDA	-PT	166	
Glyma.17G042800.1	KT1LGHMFRT	NIIC	-PNSQPLNSGNFH1VLTYEDQECGDWMMVGDVPWEMFLNSVKRLK1TRADRC	-	260	
Glyma.13G117100.1	KT1LGHMFRT	NIIC	-PNSQPLNSRNHFH1VLTYEDQECGDWMMVGDVPWEMFLNSVKRLK1TRADRC	-	244	
AtIAA31	EN1LGMFDT	SIIIC	-NRDKHHV1LYEDKDGDWMMVGDIPWDMFLETVRRLK1TRPERY	-	158	
Glyma.19G221900.1	RT1LEHMFDT	TILWG	-TEMNGVQPERCHV1LYTEDEEGDLVVMVGDPWEMFLSTVKRRLK1TRVDTF	-	175	
Glyma.03G224800.1	RT1LEHMFDT	TILWG	-TEMNGVQPERCHV1LYTEDEEGDLVVMVGDPWEMFLSTVKRRLK1TRVDTF	-	178	
Glyma.10G138500.1	KT1LEQMFDT	TILWG	-TEMDGVQPERCHV1LYTEDEGGDLMVVGDPWEMFLSTVKRRLK1TRVEAF	-	176	
Glyma.02G007300.1	KT1LEQMFDT	TILWG	-TEMDGVQPERCHV1LYTEDEGGDLMVVGDPWEMFLSTVKRRLK1TRVETF	-	179	
AtIAA30	TT1DYMFMNA	SILW	-AEEEDMCSEKS1HV1LYTAKEGDWWMMVGDPWEMFLSTVRRRLK1SRAYHY	-	172	
AtIAA20	RT1DFMFMNA	SILW	-AEEEDMCNEKS1HV1LYTAKEGDWWMMVGDPWEMFLSTVRRRLK1SRAN-Y	-	173	
Glyma.13G361100.1	LALEKFFGC	Y	-GIRREALKDAEN-AEHVPI1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-KGFD	173	
Glyma.15G012800.1	LALEKFFGC	Y	-CIGSALKDEN-VEQVPI1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-KGFD	171	
AtIAA19	FALDKLGF	R	-SIGVALKDGDN-CEYVTI1YEDKDGDWMLVGDVPWGMFLESCKRLIMKGSDA	-TGFG	189	
AtIAA6	TV1LENLFGC	Y	-CIGVA-KECKK-CEY1I1YEDKDGDWMLVGDVPWOMFKESCKRL1RVRSRSDA	-TGFG	185	
Glyma.07G034200.1	LALDKL1FGS	Y	-GMVEALKNADN-SHEVPI1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-KGFG	171	
Glyma.08G207900.1	LALDKL1FGC	Y	-GMVEALKNADN-SHEVPI1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-KGFG	179	
AtIAA5	SALQILFGC	Y	-INF1-DTLKE-SECVP1YEDKDGDWMLVGDVPWEMFLGSCCKRLIMKGSDA	-RG	163	
Glyma.10G162400.2	DALAKMFSS	FT1IEKCGSGQM	-KDFMNETKL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	220
Glyma.20G225000.1	DALAKMFSS	FT1IEKCGSGQM	-KDFMNETKL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	216
Glyma.03G247400.1	DALAKMFSS	FT1IDKCGSGQM	-KDFMNESSL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	232
Glyma.19G245200.1	DALAKMFSS	FT1IDKCGSSQGM	-KDFMNEGL1D1LLNG	-SDYVPTC1EDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	219
AtIAA16	NALSKMFSS	FT1GN1GPQGM	-KDFMNESSL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	225
Glyma.10G031900.1	DALGKMFSS	FT1GN1CESQGF	-KDFMNESSL1D1LLNG	-SDYVPTYEDRDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	237
Glyma.02G142500.3	DALGKMFSS	FT1GN1CESQGF	-KDFMNESSL1D1LLNG	-SDYVPTYEDRDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	235
Glyma.19G161100.1	DSLGKMFSS	FT1GN1CESQGM	-KDFMNESSL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLG	239
Glyma.03G158700.1	DSLGKMFSS	FT1GN1CESQGM	-KDFMNESSL1D1LLNG	-SDYVPTYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLG	241
Glyma.10G180100.1	DALAKMFSS	FTMGNYGAQM	-1DFMNESSL1D1LLNG	-SEYVPSYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	228
Glyma.20G210400.1	DALAKMFSS	FTMGNYGAQM	-1DFMNESSL1D1LLNG	-SEYVPSYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLA	320
AtIAA17	NALSNMFSS	FTMGKHGG	-EEGM1DFMNERKLMD1LLNG	-WDYVPSYEDKDGDWMLVGDVPWEMF1TCCKRLRLIMKGSDA	-IGLA	218
AtIAA14	DALAKMFSS	FTMGSYGAQM	-1DFMNESSL1D1LLNG	-SEYVPSYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-IGLG	217
AtIAA7	DALAKMFSS	FTMGNYGAQM	-1DFMNESSL1D1LLNG	-SEYVPSYEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-VGLG	231
Glyma.13G361200.5	RELETMF	LAI1RN	-HLMNERKL1MESGNG	-IEYMP1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-VGLG	171
Glyma.15G012700.1	RELETMF	LAI1RN	-HLMNERKL1MDPONG	-IEYMP1YEDKDGDWMLVGDVPWEMF1ESCKRLIMKGSDA	-VGLG	177
AtIAA15	TALENMFQG	LITICK*	-TSDDDLDRHSNA1LGH1IA1YEDMENNLL1AGD1	-LIKRD1DPIRGN	-	130
Glyma.20G083900.1	SARQMFVD	SAD1RQMFVD	-GAD1STDDDLDSNA1PGLH1IA1YEDMENNLL1AGD1	-TWKDFVRAK1R1RIPVKG	-	130
AtIAA33	SARQMFVD	SAD1RQMFVD	-GAD1STDDDLDSNA1PGLH1IA1YEDMENNLL1AGD1	-TWKDFVRAK1R1RIPVKG	-	163

This figure displays a sequence alignment of Glyma and AtIAA proteins across the amino acid range of 620 to 700. The alignment is color-coded by residue type: Red for Amino acids (R), Green for Glutamic acid (E), Blue for Aspartic acid (D), Orange for Tyrosine (Y), Yellow for Phenylalanine (F), and Purple for Histidine (H). The alignment shows significant conservation of the YIFR motif at positions 620-640, followed by a highly conserved C-terminal domain from position 660 to 700.

Protein	620	640	660	680	700	Length
Glyma.06G067700.1						228
Glyma.04G066300.1						227
AtIAA29	A	YIFR	CIF			252
Glyma.13G159000.1	R			*		207
Glyma.17G112300.1	R			*		200
Glyma.10G270500.1	SR		Y	T		192
Glyma.20G120800.1	SR		C	T		191
AtIAA34				*		186
AtIAA32				*		192
Glyma.07G015200.1	SK	QD			*	318
Glyma.08G200700.1	SK	QD			*	314
Glyma.13G354100.11	SK	QDK	IPLDS	AMK		347
Glyma.15G020300.1	SK	QDK	IPLDS	AMK		321
AtIAA26	CS	KC	EK	MFR		270
AtIAA18	NG	KO	EK	MRR		268
AtIAA28	PR			HGKE		176
Glyma.19G168500.1	PR	I	EEKNRRSNTSSYR*			270
Glyma.03G167400.9	LIOLLIICSPK		EGKEQKIEQMGAHQIDNVIVCT	FTCARIH	TYELKCTTRILEGT	282
Glyma.13G127000.3	PR	I	EEN		JKQRCKP	381
Glyma.10G040400.3	PR	I	EEN		JKQRCKP	374
AtIAA12	PR	R	QEQ		ADRQRNNPV	240
AtIAA13	AR	N	QEP		NERQRKQPV	248
AtIAA11	D		MKO		IIIIYEPPFMFEAVITRQITDQRE	269
AtIAA10	K*					262
Glyma.05G229300.1	PR	A	MEK	C	KSRN*	288
Glyma.01G039300.2						113
Glyma.08G036400.1	PR	A	MEK	C	KSRY*	358
Glyma.09G193000.1	PR	A	MEK	C	KSRN*	308
AtIAA27	PR	V	MEK	C	RSRN*	306
Glyma.13G356600.1	PR	A	MEK	S	RSON*	308
Glyma.15G017500.1	PR	A	MEK	S	RSON*	320
Glyma.07G018100.1	PR	G	MEK	C	RSQF*	320
Glyma.08G203100.1	PR	G	MEK	C	RSQY*	323
Glyma.09G203300.1	PR	A	MEK	S	KSRJ*	355
Glyma.01G019400.2	PR	A	MEK	S	KSR*	360
Glyma.08G273500.1	PR	A	MEK	S	RSRC*	351
Glyma.01G098000.3	PR	A	MEK	S	RSRC*	351
AtIAA9	AAB	RA	MEK	S	KMRA*	339
AtIAA8	PG	A	VEK	SK	NKERV*	339
Glyma.06G091700.3	PR	A	VEK	C	KSR*	362
Glyma.04G089900.1	PR	A	VEK	S	KSR*	361
Glyma.14G185400.1	PR	A	VEK	S	KRKN*	368
Glyma.02G218100.3	PR	A	VEK	S	KSRN*	367
Glyma.10G180000.1	C			A*		126
Glyma.20G210500.1	C			A*		195

	720
Glyma.06G067700.1	22
Glyma.04G066300.1	22
AtIAA29	25
Glyma.13G159000.1	20
Glyma.17G112300.1	20
Glyma.10G270500.1	19
Glyma.20G120800.1	19
AtIAA34	18
AtIAA32	19
Glyma.07G015200.1	31
Glyma.08G200700.1	31
Glyma.13G354100.11	34
Glyma.15G020300.1	32
AtIAA26	27
AtIAA18	26
AtIAA28	17
Glyma.19G168500.1	27
Glyma.03G167400.9	28
Glyma.13G127000.3	38
Glyma.10G040400.3	37
AtIAA12	24
AtIAA13	24
AtIAA11	DKNIVRSFFFFSPLYSFFFGSATFLIVSYMFSL*
AtIAA10	30
Glyma.05G229300.1	26
Glyma.01G039300.2	28
Glyma.08G036400.1	11
Glyma.09G193000.1	35
AtIAA27	30
Glyma.13G356600.1	30
Glyma.15G017500.1	32
Glyma.07G018100.1	32
Glyma.08G203100.1	32
Glyma.09G203300.1	35
Glyma.01G019400.2	36
Glyma.08G273500.1	35
Glyma.01G098000.3	35
AtIAA9	33
AtIAA8	33
Glyma.06G091700.3	36
Glyma.04G089900.1	36
Glyma.14G185400.1	36
Glyma.02G218100.3	36
Glyma.10G180000.1	12
Glyma.20G210500.1	19
Glyma.10G000700.2	78
Glyma.02G000500.1	19
Glyma.19G161000.1	20
Glyma.03G158600.1	20
Glyma.10G031800.3	19
Glyma.02G142600.1	20
AtIAA4	18
AtIAA3	29

AtIAA2	262
AtIAA1	169
Glyma.17G042800.1	261
Glyma.13G117100.1	245
AtIAA31	159
Glyma.19G221900.1	178
Glyma.03G224800.1	181
Glyma.10G138500.1	178
Glyma.02G007300.1	181
AtIAA30	173
AtIAA20	176
Glyma.13G361100.1	190
Glyma.15G012800.1	188
AtIAA19	198
AtIAA6	190
Glyma.07G034200.1	188
Glyma.08G207900.1	196
AtIAA5	164
Glyma.10G162400.2	232
Glyma.20G225000.1	228
Glyma.03G247400.1	244
Glyma.19G245200.1	231
AtIAA16	237
Glyma.10G031900.1	249
Glyma.02G142500.3	247
Glyma.19G161100.1	253
Glyma.03G158700.1	255
Glyma.10G180100.1	240
Glyma.20G210400.1	332
AtIAA17	230
AtIAA14	235
AtIAA7	244
Glyma.13G361200.5	218
Glyma.15G012700.1	190
AtIAA15	130
Glyma.20G083900.1	141
AtIAA33	172
Consensus	189

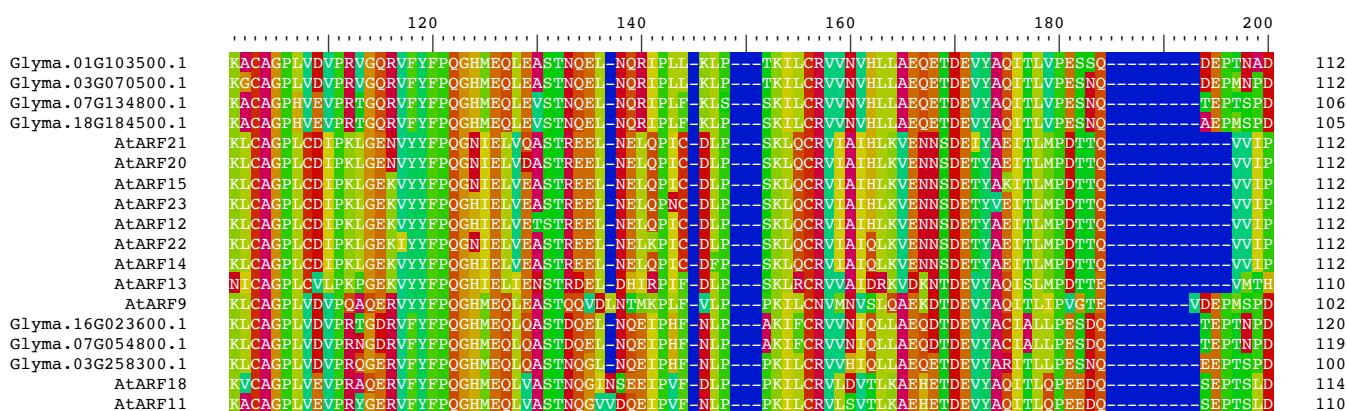
## **Appendix C**

### **Amino Acid Alignment of Auxin ARF**

This appendix presents the full alignment of the ARF transcription factor proteins *Glycine max* with those from both *Arabidopsis thaliana*.



Consensus 35



Glyma.12G164100.1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	104
Glyma.16G000300.1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	104
Glyma.07G272800.1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	137
AtARF1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	110
Glyma.06G164900.3	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVQLKAEPDTEDEVFAQVTLPEPQNQ-----DENAVEKE	128
Glyma.04G200600.1	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVQLKAEPDTEDEVFAQVTLPEPQNQ-----DENAVEKE	128
Glyma.05G200800.4	HACAGPLVTVPREGERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVMIKAEPDTEDEVFAQVTLPEPQNQ-----DENAVEKE	146
Glyma.08G008100.3	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVMIKAEPDTEDEVFAQVTLPEPQNQ-----DENAVEKE	142
AtARF2	HACAGPLVTVPQRDDRVFYFPQGHIEQEVEASTNQAA--QOMPLY-DLP--SKLCLCRINVNLKABADTDEVYAQITLLPEANQ-----DENAIEKE	150
Glyma.03G208800.1	MNVELKAEAYASDEVEYAQTVTLPEVVKQDNICF-----EEEVNID	38
Glyma.07G202200.1	HACAGPLISLPKKGSVVVYFPQGHLEQ-----HLH--DFPLPASANIP--SHVFCRVLVDVLKHAEEGSDEVHCQVLLVPETEQVH--QR-LREGEEFDAD	117
Glyma.13G174000.1	HACAGPMISLPKKGSVVVYFPQGHLEQ-----HLH--DFPLPASANIP--SHVFCRVLVDVLKHAEEGSDEVYCQVLLVPESEQVH--QR-LREGEEFDAD	122
Glyma.13G234200.1	HACAGPLISLPKKGSVVVYLPQGHFE-----HQV--DFPVTAIY-DLP--PHVFCRVLVDVLKHAEEGSDEVYCQVLLVPESEQVH--QS-LREGEEIVAD	140
Glyma.15G078800.1	HACAGPLISLPKKGSVVVYLPQGHFE-----HVO--DFPVNAF-DLP--PHVFCRVLVDVLKHAEEGSDEVYCQVLLVPESEQVH--HS-LREGEEIVAD	131
AtARF3	HACAGPLISLPKKGSVVVYLPQGHFE-----QAF--DFSAAIY-GLP--PHVFCRVLVDVLKHAEEGSDEVYCQVLLVPESEDIF--RN-VREGIIVD	141
Glyma.12G071000.1	HACAGPLTSLLCKGNVVVYFPQGHLEQAVASFSPFT--PLEIPTY-DLQ--POQIFCRVNVNVLQLLANKENDEVYTQVTLPPQAELEG--MY-SEGKEEEL	147
Glyma.11G154632.1	HACAGPLTSLPKKGNNVVVYFPQGHLEQAVASFSPFT--PLEIPTY-DLQ--POQIFCRVNVNVLQLLANKENDEVYTQVTLPPQAELEG--MY-LEGKEEEL	146
Glyma.12G171000.1	HACAGPLTSLPKKGNNVVVYFPQGHLEQAVASFSPFT--PMEMPTY-DLQ--POQIFCRVNVNVLQLLANKENDEVYTQVTLPPQAELEG--MY-MEGKEEKL	143
AtARF4	HACAGPLTCPLKKGNVVVYFPQGHLEQADAMVSYSX--PLEIPKF-DLN--PQTVCRVNVNVLQLLANKDTDEVYTQVTLPLQEFSN--IN-SEGKEEKL	158
Glyma.08G100100.3	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNREV--DGHIPNPYPSLP--PQLICQLHNLTMHADTETDEVYAQMTLQPLNPCQ-----QEKGAY-LP	116
Glyma.05G143800.2	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNREV--DGHIPNPYPSLP--PQLICQLHNLTMHADTETDEVYAQMTLQPLNPOE-----QEKGAY-LP	113
Glyma.13G221400.1	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNKEV--DAHIPNPYPSLP--PQLICQLHNMTMHADAETDEVYAQMTLQPLNPOE-----QEKGAY-LP	113
Glyma.15G091000.1	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNKEV--DAHIPNPYPSLP--PQLICQLHNMTMHADAETDEVYAQMTLQPLNPOE-----QEKGAY-LP	113
AtARF6	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNKEV--DAHIPNPYPSLP--PQLICQLHNMTMHADAETDEVYAQMTLQPLNPOE-----QEKGAY-LP	113
Glyma.02G281700.1	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVAATNREV--DAHIPNPYPNLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLSPOE-----QEKVYLLP	115
Glyma.14G032700.1	HACAGPLVSIPLVGSRVVVYFPQGHSEQEVAATNREV--DAHIPNPYPNLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLSPOE-----QEKVYLLP	115
Glyma.11G204200.1	HACAGPLVSIPLVGSRVVVYFPQGHSEQEVAATNREV--DGHIPNPYPSLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLTPOE-----QEKTTP-LP	114
Glyma.18G046800.1	HACAGPLVSIPLVGSRVVVYFPQGHSEQEVAATNREV--DGHIPNPYPSLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLTPOE-----QEKTTP-LS	114
Glyma.02G239600.1	HACAGPLVSIPLVGSRVVVYFPQGHSEQEVAATNREV--DGHIPNPYPSLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLTPOE-----QEKTTP-LP	114
Glyma.14G208500.1	HACAGPLVSIPLVGSRVVVYFPQGHSEQEVAATNREV--DGHIPNPYPSLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLTPOE-----QEKTTP-LP	114
AtARF8	HACAGPLVSIPSSGSRVVVYFPQGHSEQEVAATNKEV--DGHIPNPYPSLP--PQLICQLHNVTMHADAETDEVYAQMTLQPLTPEE-----QEKTTP-VP	112
Glyma.09G072200.1	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----DKEAI-LA	111
Glyma.15G181000.1	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----DKEAI-LA	111
Glyma.17G047100.1	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----EKEAI-LA	111
Glyma.13G112600.1	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----EKEAI-LA	111
AtARF7	HACAGPLISLPAPGSVVVYFPQGHSEQEVAASMQQT--DF-IPSYPNLP--SKLICMLHNVTLNADPETDEVYAQMTLQPLVNKY-----DRDAI-LA	112
AtARF19	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMQQT--DF-IPSYPNLP--SKLICMLHNVTLNADPETDEVYAQMTLQPLVNKY-----DRDAI-LA	111
Glyma.07G130400.1	QACAGPLVNLLPPSGTHVYFPQGHSEQEVAASLNNDP--HSQIPNPYPNLP--SKLLCCLLHNLTLLADPETDEVYAQITLQPVPSF-----DKDAL-LR	114
Glyma.01G002100.1	HACAGPLVKLPPSGTHVYFPQGHSEQEVAASLRDV--HSQIPNPYPNLP--SKLLCCLLHTLTLLADPODITQVYAOITLQPLPSF-----DKDAL-LR	99
Glyma.05G221300.1	QACAGPLLNLLPSPGTHVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----DKDAL-LR	117
Glyma.08G027800.1	QACAGPLLNLLPSPGTHVYFPQGHSEQEVAASMKREA--DF-IPSYPNLP--SKLICMLCHNLVHALHPETDEVYAQMTLQPLVNKY-----DKDAL-LR	117
Glyma.14G217700.1	HACAGPLVSIPQVGSLSVYFPQGHSEQEVAASRTTA--TSQIPNPYPNLP--YQLLCQVQNVNTLHADKETDEIYAOMLTQPLNSE-----REVPI	133
Glyma.17G256500.1	HACAGPLVSIPQVGSLSVYFPQGHSEQEVAASRTTA--TSQIPNPYPNLP--SQLLCQVQNVNTLHADKETDEIYAOMLTQPLNSE-----REVPI	136
AtARF5	HACAGPLVCIPQVGSLSVYFPQGHSEQEVAASRTTA--TSQIPNPYPNLP--SQLLCQVQNVNTLHADKETDEIYAOMLTQPLNSE-----REVPI	136
Glyma.12G174100.1	HACAGGMVQMPPVNSKVFVFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCVCAAVFKLADPETDEVFARLRLVPLRNSE-----LD-YEDSDGNG	99
Glyma.13G325200.1	HACAGGMVQMPPVNSKVFVFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCVCAAVFKLADPETDEVFARLRLVPLRNSE-----LD-YEDSDANGE	100
Glyma.12G076200.1	HACAGGMVQMPPVNSKVFVFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCVCAAVFKMNPANTEDEVFARLRLVPLRNSE-----LG-ADSDGAGGD	95
Glyma.11G145500.1	HACAGGMVQMPPVNSKVFVFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCVCAAVFKMNPANTEDEVFARLRLVPLRNSE-----LG-PDSDAAGD	95
AtARF16	HACAGGMVRMPMPNSKVFVFPQGHAENAYDCVDFG--NLI--PIP--PMVLCRVLAIKYMADAESDEVFAKRLRIPLKDDE-----Y--VDHEYGDGE	105
AtARF10	HACAGSMVQIPSLINSTVYFPQFAOGTHEAHAPPD--HAPRVP--PILLCRVLVSVSKFLADEFADTDEVFKAITLQPLPGND-----LD-LENDAVIGL	97
Glyma.10G210600.1	HACAGAMVQMPPLNKTFVYFPQGHAEHAKGVYFGF--KHNQTRVP--PLIPCRISAMKYMDPDTDEVYKMRUPLTPIREHEI-----LD-SQDDCFGLN	107
Glyma.20G180000.1	HACAGAMVQMPPLNKTFVYFPQGHAEHAKGRVDFP--KHNQTRVP--PLIPCRISAMKYMDPDTDEVYKMRUPLTPIREHEI-----LD-SQDDCFGLN	106
Glyma.10G053500.1	HACAGGIVQMPPAVNSKVFVYFPQGHAEHACGPVNEF--TCPKVP--PFVPCRVTAFKYRADPETDEVYAKLKLIPLWNAND-----VD-YDRVVVGGA	109
Glyma.13G140600.1	HACAGGMVQMPTVNTKVFVYFPQGHAEHACGPVNFK--TCPKVP--PFVPCRVTAFKYRADPETDEVYAKLKLIPLWNAND-----VD-YDHVIDGAE	109
Glyma.19G181900.2	GACAGGMVQMPPVNAKVFVYFPQGHAEHACGPVDFR--VYPKP--PFICQCKVAKIRYMDPETDEVYVYKLRVPLTRNE-----GD-FEDDAVGGI	119
Glyma.13G084700.1	RACAGAAVQIPKLSRHSRVVYFPQGHMERA--SPSHYL--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAKFLLTPLSQSQQQPFO-----NDTKEARND	103
Glyma.14G166500.1	RACAGAAVQIPKLSRHSRVVYFPQGHMERA--SPSHYL--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAKFLLTPLSQSQQQPFO-----NDTKEARND	100
Glyma.04G254200.1	IVCAGTTVFPITLHSRHSRVVYFPQGHMERA--SPSHYL--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAKFLLTPLSQSQQQPFO-----NDTKEARND	107
AtARF17	RACAGASVQIPVLSRHSRVVYFPQGHMERA--SPSHYL--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAKFLLTPLSQSQQQPFO-----NDTKEARND	103
Consensus	XXCAGXXXXXPXXXXXVXYFPQGXEX+++++XX++-+++++X+++XXX--XXXXCXXXXXXXXXXXXDEXXXXXLXPFXXXX+-+----+X+XX	104

	220	240	260	280	300
Glyma.01G103500.1	PC-----TAEPPRAPVHSFSKVLTAASDTSTHGGFSVLRKHATECLPVLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	205			
Glyma.03G070500.1	PC-----TAEPPRAPVHSFSKVLTAASDTSTHGGFSVLRKHATECLPVLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	205			
Glyma.07G134800.1	PC-----PAELPLPRVHSFSKVLTAASDTSTHGGFSVLRKHATECLPVLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	199			
Glyma.18G184500.1	PC-----PAELPLPRVHSFSKVLTAASDTSTHGGFSVLRKHATECLPVLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSNFTSKRLV	198			
AtARF21	TQ-----SENFRPLVNSFTKVLTAASDTSTAYGGFSVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNEFTSKKLV	205			
AtARF20	TQ-----SENQFRPLVNSFTKVLTAASDTSTAYGGFSVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNEFTSKKLV	205			
AtARF15	TQ-----NENQFRPLVNSFTKVLTAASDTISANGGVFSVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNEFTSKKLV	205			
AtARF23	TB-----NENQFRPLVNSFTKVLTAASDTSAQGEFSVPCKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNAFTTSKKLV	202			
AtARF12	TQ-----NENQFRPLVNSFTKVLTAASDTSAHGGFFVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNAFTTSKKLV	205			
AtARF22	TQ-----NENQFRPLVNSFTKVLTAASDTSGGFFVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNAFTTSKKLV	203			
AtARF14	TQ-----NONQFRPLVNSFTKVLTAASDTSVHGGEFSVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNAFTTSKKLV	205			
AtARF13	NT-----TMDTRRPVYFFSKILTAASDVSLSLGGIIPPKQYAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNAFTTSKKLV	205			
AtARF9	PS-----PPELQRPKVFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	195			
Glyma.16G023600.1	PN-----ISEPPKQKFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	213			
Glyma.07G054800.1	PN-----VSEAPKQKFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	212			
Glyma.03G258300.1	PS-----PPFTQKQVFHTFSKILTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWNEFTSKKLV	193			
AtARF18	PF-----IVGPTKQEFHSFSKILTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	207			
AtARF11	PF-----LVEPAKPTDVSFKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	203			
Glyma.12G164100.1	DP-----LPESPRTCTVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSVFSSSKKLV	197			
Glyma.16G000300.1	DP-----LPESPRTCTVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSVFSSSKKLV	197			
Glyma.07G272800.1	DP-----LPESPRTCTVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSVFSSSKKLV	230			
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Glyma.06G164900.3	PP-----PPPPRPFHVFHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLQS-----GWSVFSSSKKLV	221			
Glyma.04G200600.1	PP-----PPPPRPFHVFHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLQS-----GWSVFSSSKKLV	221			
Glyma.05G200800.4	GP-----PAPPFRHFVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLQS-----GWSVFSSSKKLV	239			
Glyma.08G008100.3	GP-----PAPPFRHFVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLQS-----GWSVFSSSKKLV	235			
AtARF2	AB-----LPPPRPFHVFHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLQS-----GWSVFSSSKKLV	243			
Glyma.03G208800.1	QI-----PSRNAAYSFSKILTPSDTSTHGGFSVPKKHAECLPPLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSLFLVNAKKLV	128			
Glyma.07G202200.1	GEEEED-AEAVMKSTTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSAFVNNKKLV	214			
Glyma.13G174000.1	GEEEED-AEAVMKSTTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSAFVNNKKLV	219			
Glyma.13G234200.1	GEEEED-TEAVLKSTTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSAFVNNKKLV	237			
Glyma.15G078800.1	GEEEED-TGATVKSTTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSAFVNNKKLV	228			
AtARF3	GGEEDD-YEVILKRSNTPHMFCCTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSAFVNNKKLV	238			
Glyma.12G071000.1	GAEEDGDERSPKTPSTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSIFVSKQNLV	245			
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Glyma.12G171000.1	GADEEGNETTPKTPSTPHMFCKTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSIFVSKQNLV	241			
AtARF4	GGEEEERNGSSSVKTPHMFCCTLTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSIFVSKQNLV	256			
Glyma.08G100100.3	AE-----LGT-PSKQPTNPFCKLILTAASDTSTHGGFSVPKRYAAECDFCPPLDLYSQRPSQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSVFSAKRLV	209			
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Glyma.13G221400.1	AE--LGT-PSKOPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHGNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	206
Glyma.15G091000.1	AB--LGT-ASKOPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHGNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	206
AtARF6	AE--LCV-PSRQPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELMARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	206
Glyma.02G281700.1	AE--LGT-PSKOPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	208
Glyma.14G032700.1	AE--LGT-PGKOPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	208
Glyma.11G204200.1	ME--LGI-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSIFVSAKRLV	207
Glyma.18G046800.1	ME--LGI-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSIFVSAKRLV	207
Glyma.02G239600.1	ME--LGV-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	207
Glyma.14G208500.1	ME--LGV-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELIARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	207
AtARF8	IE--LGI-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDYLOPPAQELIARDLHDVEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	205
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Glyma.13G112600.1	SD--MGLKQNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTRHIFRGQPKRHLTT--GWSVFVSTKRLF	205
AtARF7	SD--MGLKLNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTRHIFRGQPKRHLTT--GWSVFVSTKRLF	206
AtARF19	SD--MGLKLNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTRHIFRGQPKRHLTT--GWSVFVSTKRLF	205
Glyma.07G130400.1	SD--LALKSKPQDPDFCKQLTASDTSTHGGFSVPRAAADKIFFPPLDYSMQOPPAQELVARDLHDNTWTRHIFRGQPKRHLTT--GWSLFVSGKRLL	208
Glyma.01G002100.1	SD--LALESTKPPPDDFKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTRHIFRGQPKRHLTT--GWSLFVSGKRLL	193
Glyma.05G221300.1	SD--IFLRSKPQPEFFCKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSVOPPAQELVARDLHDNDVNVRFRHIFRGQPKRHLTT--GWSLFFIGKRLL	211
Glyma.08G027800.1	SD--ISLKLSKPQPEFFCKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSLSQSPVQELVARDLHDNDVNVRFRHIFRGQPKRHLTT--GWSLFISGKRLL	211
Glyma.14G217700.1	SD--FGHKHSKHPSEFFCKTLTASDTSTHGGFSVPRAAEAKLFPPLDVTIQPPTQELVVVRDLHDNTWTRHIFRGQPKRHLTT--GWSLFVGSKRLL	227
Glyma.17G256500.1	SD--FGLKHSHKHPSEFFCKTLTASDTSTHGGFSVPRAAEAKLFPPLDVTIQPPTQELVVVRDLHDNTWTRHIFRGQPKRHLTT--GWSLFVGSKRLL	230
AtARF5	PD--FGMLRSKHPTEFFCKTLTASDTSTHGGFSVPRAAEKLFPLPPLDYSOAOPPTQELVVVRDLHDNTWTRHIFRGQPKRHLTT--GWSLFVGSKRLL	237
Glyma.12G174100.1	-----AEGSEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKFRRHIFRGTPRHLTT--GWSFVNQKKLV	188
Glyma.13G325200.1	-----AEGSEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKFRRHIFRGTPRHLTT--GWSFVNQKKLV	189
Glyma.12G076200.1	DV--AEPSCCEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKFRRHIFRGTPRHLTT--GWSFVNQKKLV	188
Glyma.11G145500.1	DA--AEPSSCEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDCTAEPPVQTVAVNDVGETWFRHIFRGTPRHLTT--GWSFVNQKKLV	188
AtARF16	DS--NGFESENSEKTP-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDVAEAPPVQTIIAKDNDVGETWFRHIFRGTPRHLTT--GWSNFVNQKKLV	199
AtARF10	TPPSSDGNNGKERPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDVAEAPPVQTIIAKDNDVGETWFRHIFRGTPRHLTT--GWSTFVNQKKLV	194
Glyma.10G210600.1	JN--S-GGVEVNEKEPPTSFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIIAKDMGOCWKFRHIFRGTPRHLTT--GWSTFVNQKKLV	202
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Glyma.13G140600.1	-----TRDKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSADPPVQNIILAKDNDVGETWFRHIFRGTPRHLTT--GWSTFVNQKKLV	196
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Glyma.14G166500.1	EE--NRDR--NCGVV-SFSKVLITA-SANNGGGFSVPRFCADSIFPPLNQADPPVQNLIVTDVHGFWVFRHIFRGTPRHLTT--GWSKFVNQKKLV	191
Glyma.04G254200.1	AA--SASAQTCENNQVV-SFSKVLITA-SANNGGGFSVPRFCADSIFPPLNQADPPVQNLIVTDVHGFWVFRHIFRGTPRHLTT--GWSKFVNQKKLV	202
AtARF17	GR--FDGDVDDNNNKVT-TFAKILTPSDANNGGGFSVPRFCADSVFPLNFQIDPPVQKLYVIDHGAWDFRHIFRGTPRHLTT--GWSKFVNQKKLV	198
Consensus	+X+XXXXXX+XFXXKLTxDXXXXXGGFXVXXXXAXXXPxLDXXXXXPQXXXXDXXXXXWXFXHXXRGXPXRXXXX--GWXXFXXXKXLX	192

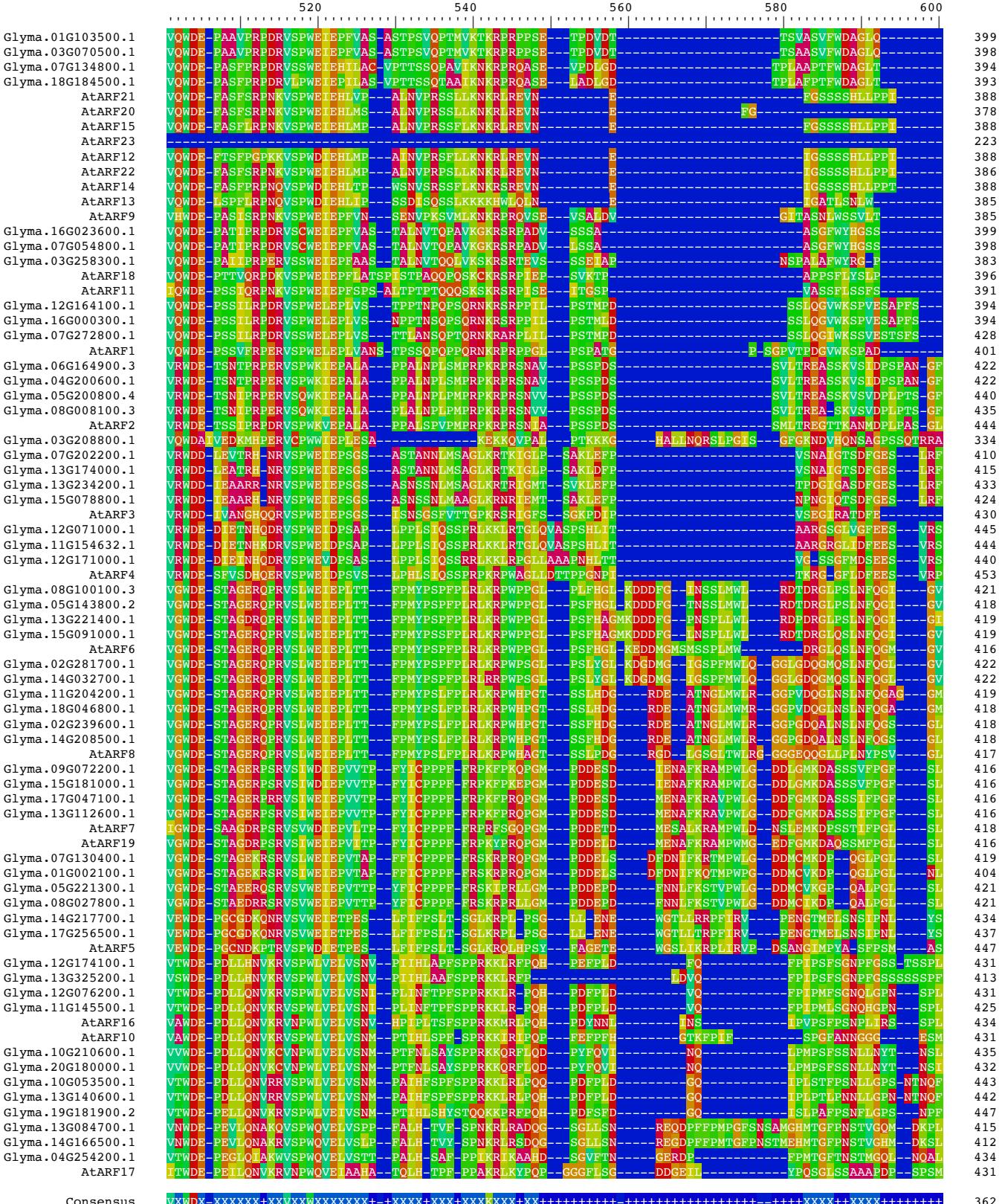
	320	340	360	380	400	
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Glyma.03G070500.1	AGDTFVFLRGDNGELRVGVRRLARQASSMP-----SSVISSQS					243
Glyma.07G134800.1	AGDTFVFLRGDNGELRVGVRRLAPLOSSMP-----SSVISSQS					237
Glyma.18G184500.1	AGDTFVFLRGDNGELRVGVRRLAPVQSSMP-----SSVISSQS					236
AtARF21	KGDVIVFVFRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF20	KGDVIVFVFRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF15	KGDVIVFVFRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF23	VGDVIVFARGETGELRVGIR*					223
AtARF12	AGDVIIVFVFRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF22	AGDVIIVFVFRGETGELRVGIRRAGHQQGNIP-----SSIISIES					241
AtARF14	EGDVIIVFVFRGETGELRVGIRRAGHQQGNIP-----SSIISIES					243
AtARF13	VGDIFVLLRGENGEELRFGIRRRAHQQGHIP-----SSVISANC					243
AtARF9	AGDIFVFLRGENGELRVGVRRLAQQNSMP-----SSVISSHHS					233
Glyma.16G023600.1	AGDAFVFLRGFHGQIRVGVRRLARQSPMP-----SSVISSQS					251
Glyma.07G054800.1	AGDAFVFLRGEHGQIRVGVRRLARQSPMP-----SSVISSQS					250
Glyma.03G258300.1	AGDAFVFLRGENGELRVGVRVARQSPMP-----SSVISSQS					231
AtARF18	AGDAFVFLRGENGDLRVGVRRLARQSTMP-----TSVISSQS					245
AtARF11	AGDAFVFLRGETGDLRVGVRRLAKQSTMP-----AVSISSQS					241
Glyma.12G164100.1	AGDAFIIFLRGENGEELRVGVRRLMRQQSNMP-----SSVISSHS					235
Glyma.16G000300.1	AGDAFIIFLRGENGEELRVGVRRLMRQNSNMP-----SSVISSHS					235
Glyma.07G272800.1	AGDAFIIFLRGENGEELRVGVRVRMQQSNVP-----SSVISSHS					268
AtARF1	AGDAFIIFLRGENEELRVGVRHRMRQQTNP-----SSVISSHS					241
Glyma.06G164900.3	AGDAFIIFLRGENEELRVGVRAMRQQGNVP-----SSVISSHS					259
Glyma.04G20600.1	AGDAFIIFLRGENEELRVGVRAMRQQGNVP-----SSVISSHS					259
Glyma.05G200800.4	AGDAFIIFLRGENEELRVGVRAMRQQGNVP-----SSVISSHS					277
Glyma.08G008100.3	AGDAFIIFLRGENEELRVGVRAMRQQGNVP-----SSVISSHS					273
AtARF2	AGDAFIIFLRGENEELRVGVRAMRQQGNVP-----SSVISSHS					281
Glyma.03G208800.1	AGDSC1IFVFRGESGELRVGIRRANEINSNIQS-----SSLISGHS	S				168
Glyma.07G202200.1	SGDAVFLFLRGEDGELRLGIRRRAOLKSGST-----FSAISGQO					252
Glyma.13G174000.1	SGDAVFLFLRGEDGELRLGIRRRAOLKSGST-----FSAISGQO					257
Glyma.13G234200.1	SGDAVFLFLRGDGLRLGIRRRAOLKSAGS-----FAPVSGQO					275
Glyma.15G078800.1	SGDAVFLFLRNDGELRLGIRRRAOLKWAGS-----FAVPSGQO					266
AtARF3	SGDAVFLFLRGDDGKRLGICRAQSLQEGTAA-----LSAQYNQN					276
Glyma.12G071000.1	SGDAVFLFLRGENGELRLGIRRRAVPRNDLP-----ESVIGSQN					283
Glyma.11G154632.1	SGDAVFLFLRGENGELRLGIRRRAVPRNDLP-----ESVIGSQN					282
Glyma.12G171000.1	SGDAVFLFLRGENGELRLGIRRRAARPRNGLP-----ESIVGQS					279
AtARF4	SGDAVFLFLRDGGELRLGIRRRAARPRNGLP-----DSIEKNS					294
Glyma.08G100100.3	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					247
Glyma.05G143800.2	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					244
Glyma.13G221400.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					244
Glyma.15G091000.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					244
AtARF6	AGDSVLFIWNDKNQNLGGIRRAQPNQVMP-----SSVLISSDS					244
Glyma.02G281700.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					246
Glyma.14G032700.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					246
Glyma.11G204200.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					245
Glyma.18G046800.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					245
Glyma.02G239600.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					245
Glyma.14G208500.1	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					245
AtARF8	AGDSVLFIWNEKNQNLGGIRRAQPNQVMP-----SSVLISSDS					243
Glyma.09G072200.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					243
Glyma.15G181000.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					243
Glyma.17G047100.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					243
Glyma.13G112600.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					243
AtARF7	AGDSVLFIIRDGKAQLLLGGIRRAQPNQVMP-----SSVLISSDS					244
AtARF19	AGDSVLFIIRDEKSQMLGGIRRAQPNQVMP-----SSVLISSDS					243
Glyma.07G130400.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					246
Glyma.01G002100.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					231
Glyma.05G221300.1	AGDSVLFIIRDEKQQLLGGIRRAQPNQVMP-----SSVLISSDS					249
Glyma.08G027800.1	AGDSVLFIIRDEKSQMLGGIRRAQPNQVMP-----SSVLISSDS					249
Glyma.14G217700.1	AGDSVLFIIRDEKSQMLGGIRRAQPNQVMP-----SSVLISSDS					265

Multiple sequence alignment of Glyma.17G256500.1 and its orthologs. The alignment highlights conservation of amino acid residues across the proteins. A color scale at the bottom indicates conservation levels: black (highly conserved), green, yellow, orange, red, purple, blue, and cyan (least conserved).

Consensus XGDX XXXFXXXXXXXXXXGXRXXXXXXX ++++++---+-----+-----+XXXXXX XX -+++++-----+---++

	420	440	460	480	500
Glyma.01G103500.1	----MHLGVILATASHAVATQTLFVYYYYKPR-T-	-SQFIIGVNKYLEAM--DKKPSVGNRFKMRFEQDDSAETD	KRFSCTIVGVEDI-SPHWVNSKWRSLK		
Glyma.03G070500.1	----MHLGVILATASHAVATQTLFVYYYYKPR-T-	-SQFIISVNKYLEAM--NRFSVGMRLKMRFEQDDSAETD	KRFSCTIVGVEDI-SPHWVNSKWRSLK		
Glyma.07G134800.1	----MHLGVILATASHAVATQTLFVYYYYKPR-T-	-SQFIISVNKYLEAI-NQKNCVNGRFKMRFEQDESPEND	KRFSCTILGVEDI-SPHWVNSNWRSLK		
Glyma.18G184500.1	----MHLGVILATASHAVATQTLFVYYYYKPR-A-	-SQFIISVNKYLEAI-NQKNCVNGRFKMRFEQDDPENY	KRFSCTIVGVEDI-SPHWVNSNWRSLK		
AtARF21	MRHGVIASAKAHFDNQCFLIVVVYKPR-----	--SSQFIVSYDKFLDAV--NNKFNVGSRTFMREFGDDFSE	--RRYFGTIIGVSDF-SPHWKCSEWRSL		
AtARF20	MRHGVIASAKAHFDNQCFLIVVVYKPR-----	--SSQFIVSYDKFLDAV--NNKFNVGSRTFMREFGDDFSE	--RRYFGTIIGVNF-SPHWKCSEWRSL		
AtARF15	MRHGVIASAKAHFDNQCFLIVVVYKPR-----	--SSQFIVSYDKFLDAV--NNKFNVGSRTFMREFGDDFSE	--RRYFGTIIGVSNF-SPHWKCSEWRSL		
AtARF23					
AtARF12	MRHGVVASAKAHFDNQCFLIVVVYKPR-----	--SSKFIIVSYDKFLDAV--NNKFNVGSRTFMREFGDDFSE	--RRCFGTIIGVSDF-SPHWKCSEWRSL		
AtARF22	MRHGVIASAKAHFDNQCFLIVVVYKPR-----	--SSQFIVSYDKFLDAV--NNKFNVGSRTFMREFGDDFSE	--RRYFGTIIGVSDF-SPHWKCSEWRNL		
AtARF14	MRHGVIASAKAHFDNQCFLIVVVYKPR-----	--SSQFIVSYDKFLDVV--NNKFNVGSRTFMREFGDDFSE	--RRSFGTIIIGVSDF-SPHWKCSEWRSL		
AtARF13					
AtARF9	MHLGVILATARHATQTKTMFIVVVYKPR-T-	-SQFIISLNKYLEAM-SNKFSVGNRFKMRFEQEDSPE	--RRYSGTIVGVKD-SPHWKDSKWRCL		
Glyma.16G023600.1	----MHLGVILATASHAVMTRTMFLVYVYKPR-T-	-SQFIVGLNVKLYEAV--NNKFNSLGNRFKMRFEQDDDFSE	--RRFSGTIVGVGDV-SAGWSNSQWRSLK		
Glyma.07G054800.1	----MHLGVILATASHAVMTRTMFLVYVYKPR-T-	-SQFIVGLNVKLYEAV--NNKFNSLGNRFKMRFEQDDDFSE	--RRFSGTIVGVGDV-SAGWSNSQWRSLK		
Glyma.03G258300.1	----MHLGVILATASHAFLITSTMFVYYYYKPR-T-	-SQFIIGVNKYLEAE--NNKFSVGNRFKMRFEVEDSPE	--RRFSCTIVGVGDV-SPGWNSNSQWRSLK		
AtARF18	MHLGVILATASHAFLITSTMFVYYYYKPR-T--	-SQFIVGVNKYMEAI-KHGFSLGTRFRMRFEGEESPE	--RIFTGTIVGSDL-SSQWPASKWRSLQ		
AtARF11	MRLGVILATASHAVRTTTFIVVVYKPR-I--	-SQFIVGVNKYMEAI-KHGFSLGTRFRMRFEGEESPE	--RIFTGTIVGSDL-SSQWPASKWRSLQ		
Glyma.12G164100.1	----MHLGVILATASHAFLATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLEAR-SHLKLSVGMRFKMRFEQEDVPE	--RRFSGTIVGVGDNK-SVVWADSEWRSLK		
Glyma.16G000300.1	----MHLGVILATASHAFLATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLEAR-SHLKLSVGMRFKMRFEQEDVPE	--RRFSGTIVGVGDNK-SVVWADSEWRSLK		
Glyma.07G272800.1	----MHLGVILATASHAFLATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLEAR-SHLKLSVGMRFKMRFEQEDVPE	--RRFSGTIVGVGDNK-SVVWADSEWRSLK		
AtARF1					
Glyma.06G164900.3	MHLGVILATAHAIIATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLREAK-TOKLSQLGMRFKMRFEQEEAPE	--KRFSCTIVGVQENK-SVVWADSEWRSLK		
Glyma.04G2200600.1	MHLGVILATAHAIIATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLREAK-TOKLSQLGMRFKMRFEQEEAPE	--KRFSCTIVGVQENK-SVVWADSEWRSLK		
Glyma.05G200800.4	MHLGVILATAHAIIATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLREAK-TOKLSQLGMRFKMRFEQEEAPE	--KRFSCTIVGVQENK-SVVWADSEWRSLK		
Glyma.08G008100.3					
AtARF2	MHLGVILATAHAIIATGTLFSVFKYKPR-T-	-TSRSEFIVSVNKYLREAK-TOKLSQLGMRFKMRFEQEEAPE	--KRFSCTIVGVQENK-SVVWADSEWRSLK		
Glyma.03G208800.1	MQLGILNTNA\$NAVGNTRMFLVYVYRP-TNPFEEVHLQTYLKST-LQDYPIEGTRVQMOHEEESR--	--RIFTGTIVGIEED-SIRWPWSAQRWLK			
Glyma.07G202200.1	LSPTSLMDVNVNALSARCAFSIHYNP-VSTSEFIIPIHFLKSLI-DYSYSAGMRFRMRFFTEDAAER-R-FTGLIVGIAVD-PVRWPWSQRCLM				
Glyma.13G174000.1	GSPTSLMDVNVNALSARCAFSIHYNP-VSSSEFIIPIHFLKSLI-DYSYSAGMRFRMRFFTEDAAER-R-FTGLIVGIAVD-PVRWPWSQRCLM				
Glyma.13G234200.1	LNPATLKGVVNVNALSTRCAFSVCYCNPR-FSSSEFIIPIVHKFLKSLI-DCSYSVGNRMRFRMRFFTEDAAER-R-CTGLIAGISDWD-PVRWLGSKWRCLL				
Glyma.15G078800.1	LNPATLKGVVNVNALSTRCAFSVCYCNPR-FSSSEFIIPIVHKFLKSLI-DCSYSVGNRMRFRMRFFTEDAAER-R-FTGLIAGISDWD-PVRWLGSKWRCLL				
AtARF3	MNHINNPSEVA\$BAI\$THVSFSI\$Y\$PN-AWSWNF\$PA\$PKFLKV-D\$PC\$IGMRFRKA\$VE\$SER-R-SPGI\$CISLDL-PIRWPWSQRCLL				
Glyma.12G071000.1	CYSNVLSSVANA\$IA\$TSK\$KFHVFSYSPR-A\$HADFVPPYQ\$Y\$V\$K\$-KNPVSIGTRFKMRFE\$DE\$QER-RCSSGTLI\$AT\$DLD-PYRWAKSKWRCLM				
Glyma.11G154632.1	CYPNVLSSVANA\$IA\$TSK\$KFHVFSYSPR-A\$O\$AD\$FVPPYQ\$Y\$V\$K\$-KNPVSIGTRFKMRFE\$DE\$QER-RCCS\$GMLI\$GT\$DLD-PYRWAKSKWRCLM				
Glyma.12G171000.1	YYPN\$FLSSVANA\$IA\$KSM\$HFHVFSYSPR-A\$HADFVPPYQ\$Y\$K\$-KNPVTIGTRFKMRFE\$EE\$P\$R-RCTSGIVT\$GMS\$DLD-PYRWAKSKWRCLM				
AtARF4	CS-NIL\$NLSVANAV\$TA\$TSK\$MFHVFSYSPR-A\$HAEFVPPYQ\$Y\$K\$-TSR\$V\$CIGTRFKMRFE\$MD\$P\$R-CAGVVTG\$CDLD-PYRWNSKWRCLL				
Glyma.08G100100.3	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.05G143800.2	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.13G221400.1	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$D\$D\$-PVRWPNSHWR\$SVK				
Glyma.15G091000.1	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$D\$D\$-PVRWPNSHWR\$SVK				
AtARF6					
Glyma.02G281700.1	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-PVRWPNSHWR\$SVK				
Glyma.14G032700.1	MHGLLIAAAA\$AAA\$TNSRFTI\$Y\$FN\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-PVRWPNSHWR\$SVK				
Glyma.11G204200.1	MHGLLIAAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.18G046800.1	MHGLLIAAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.02G239600.1	MHGLLIAAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-PVRWPNSHWR\$SVK				
Glyma.14G208500.1	MHGLLIAAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-PVRWPNSHWR\$SVK				
AtARF8					
Glyma.09G072200.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$Q\$SE\$FV\$IO\$LS\$K\$Y\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.15G181000.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.17G047100.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.13G126000.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
AtARF7					
Glyma.07G130400.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$Q\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.01G02100.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$H\$PR-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.05G221300.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.08G027800.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.14G217700.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
Glyma.17G256500.1	MHIGILAAA\$AAA\$TNSC\$T\$V\$F\$Y\$NP\$-A\$P\$SE\$FV\$IP\$PL\$AK\$Y\$V\$K\$AV\$Y\$H\$TR\$V\$S\$G\$M\$R\$F\$R\$ML\$F\$TE\$E\$S\$V\$-RRYMGTIT\$G\$S\$D\$-SIRWPNSHWR\$SVK				
AtARF5					
Glyma.12G174100.1	GRPKVSGESVREA\$T\$LA\$AS\$NO\$PE\$FV\$V\$Y\$PR-A\$T\$PE\$F\$C\$IR\$T\$A\$V\$R\$G\$A\$M\$-R\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$IA\$S\$V\$Q\$V\$D\$-P\$IR\$W\$P\$N\$P\$W\$R\$R\$L\$Q				
Glyma.13G25200.1	GRAKVSGESVREA\$T\$LA\$AS\$NO\$PE\$FV\$V\$Y\$PR-A\$T\$PE\$F\$C\$IR\$T\$A\$V\$R\$G\$A\$M\$-R\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$IA\$S\$V\$Q\$V\$D\$-P\$IR\$W\$P\$N\$P\$W\$R\$R\$L\$Q				
Glyma.12G076200.1	GRVKVRAED\$V\$EA\$V\$T\$LA\$AS\$N\$K\$A\$F\$E\$V\$Y\$Y\$PR-A\$T\$PE\$F\$C\$V\$K\$A\$S\$V\$G\$A\$M\$-R\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$IA\$S\$V\$Q\$V\$D\$-P\$IC\$W\$P\$N\$P\$W\$R\$R\$L\$Q				
Glyma.11G145500.1	GRVKVRAED\$V\$EA\$V\$T\$LA\$AS\$N\$K\$A\$F\$E\$V\$Y\$Y\$PR-A\$T\$PE\$F\$C\$V\$K\$A\$S\$V\$G\$A\$M\$-R\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$IA\$S\$V\$Q\$V\$D\$-P\$IC\$W\$P\$N\$P\$W\$R\$R\$L\$Q				
AtARF16	RKCKVTAES\$V\$EA\$A\$T\$LA\$AS\$G\$R\$F\$F\$E\$V\$Y\$Y\$PR-A\$T\$SE\$F\$C\$V\$K\$A\$D\$A\$R\$A\$-R\$IP\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$V\$A\$N\$V\$D\$-P\$IR\$W\$P\$N\$P\$W\$R\$R\$L\$Q				
AtARF10	AT\$G\$R\$V\$A\$E\$V\$A\$A\$R\$A\$A\$C\$Q\$G\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$S\$V\$K\$A\$M\$-Q\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$S\$V\$Q\$V\$D\$-P\$IL\$W\$D\$P\$S\$P\$W\$R\$R\$L\$Q				
Glyma.10G210600.1	I\$V\$G\$R\$V\$A\$E\$V\$A\$A\$R\$A\$A\$C\$Q\$G\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$S\$V\$K\$A\$M\$-Q\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$S\$V\$Q\$V\$D\$-P\$IL\$W\$D\$P\$S\$P\$W\$R\$R\$L\$Q				
Glyma.20G180000.1	I\$V\$G\$R\$V\$A\$E\$V\$A\$A\$R\$A\$A\$C\$Q\$G\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$S\$V\$K\$A\$M\$-Q\$IO\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$S\$V\$Q\$V\$D\$-P\$IL\$W\$D\$P\$S\$P\$W\$R\$R\$L\$Q				
Glyma.10G053500.1	G\$K\$G\$K\$V\$R\$P\$E\$A\$V\$E\$A\$S\$N\$LA\$A\$N\$K\$K\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$S\$V\$K\$A\$M\$-Q\$IR\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$S\$V\$Q\$V\$D\$-P\$IL\$W\$D\$P\$S\$P\$W\$R\$R\$L\$Q				
Glyma.13G140600.1	G\$K\$G\$K\$V\$R\$P\$E\$A\$V\$E\$A\$S\$N\$LA\$A\$N\$K\$K\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$S\$V\$K\$A\$M\$-Q\$IR\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$S\$V\$Q\$V\$D\$-P\$IL\$W\$D\$P\$S\$P\$W\$R\$R\$L\$Q				
Glyma.19G181900.2	A\$K\$G\$K\$V\$R\$P\$E\$A\$V\$E\$A\$S\$A\$R\$A\$N\$A\$F\$F\$E\$V\$Y\$Y\$PR-A\$S\$P\$E\$F\$C\$V\$K\$A\$N\$L\$V\$R\$A\$A\$-Q\$VR\$W\$C\$G\$M\$R\$F\$K\$M\$F\$E\$T\$D\$S\$R\$I-SWF\$M\$G\$T\$T\$V\$S\$V\$N\$F\$A\$D\$-P\$RW\$P\$N\$P\$W\$R\$R\$L\$Q				
Glyma.13G084700.1	T\$T\$G\$R\$V\$T\$E\$A\$A\$A\$A\$A\$S\$A\$R\$A\$N\$A\$F\$F\$E\$V\$Y\$Y\$PR-T\$G\$F\$A\$D\$F\$V\$V\$S\$A\$E\$V\$V\$E\$E\$M\$-K\$C\$A\$W\$V\$G\$G\$M\$R\$V\$K\$1\$S\$M\$E\$T\$D\$S\$R\$M\$-T\$W\$Y\$Q\$T\$V\$S\$S\$A\$C\$A\$E\$-N\$G\$P\$W\$R\$M\$L\$Q				
Glyma.14G166500.1	A\$T\$G\$R\$V\$T\$E\$A\$A\$A\$A\$A\$S\$A\$R\$A\$N\$A\$F\$F\$E\$V\$Y\$Y\$PR-T\$G\$F\$A\$D\$F\$V\$V\$S\$A\$E\$V\$V\$E\$E\$M\$-K\$C\$A\$W\$V\$G\$G\$M\$R\$V\$K\$1\$A\$M\$E\$T\$D\$S\$R\$M\$-T\$W\$F\$O\$G\$T\$V\$S\$A\$C\$A\$E\$-N\$G\$P\$W\$R\$M\$L\$Q				
Glyma.04G254200.1	G\$R\$G\$K\$L\$K\$S\$A\$V\$V\$A\$A\$E\$A\$A\$L\$A\$N\$R\$M\$P\$F\$F\$E\$V\$Y\$Y\$PR-E\$R\$W\$E\$F\$V\$V\$K\$T\$E\$A\$N\$A\$M\$-K\$V\$A\$N\$P\$G\$R\$V\$K\$1\$A\$E\$T\$D\$S\$R\$V\$-S\$W\$C\$Q\$T\$V\$S\$S\$V\$A\$L\$H\$G\$-N\$G\$Q\$W\$R\$G\$S\$L\$W\$R\$M\$Q				
AtARF17	G\$N\$G\$K\$L\$T\$E\$A\$V\$D\$A\$N\$R\$A\$Q\$G\$L\$P\$F\$F\$E\$V\$Y\$Y\$PR-A\$G\$W\$E\$F\$V\$V\$R\$A\$E\$D\$V\$E\$S\$M\$-S\$M\$Y\$W\$P\$G\$T\$V\$R\$K\$N\$A\$M\$E\$T\$D\$S\$R\$I-T\$W\$F\$Q\$G\$V\$S\$S\$T\$Y\$-Q\$E-P\$G\$P\$W\$R\$G\$S\$P\$W\$K\$Q\$O\$				

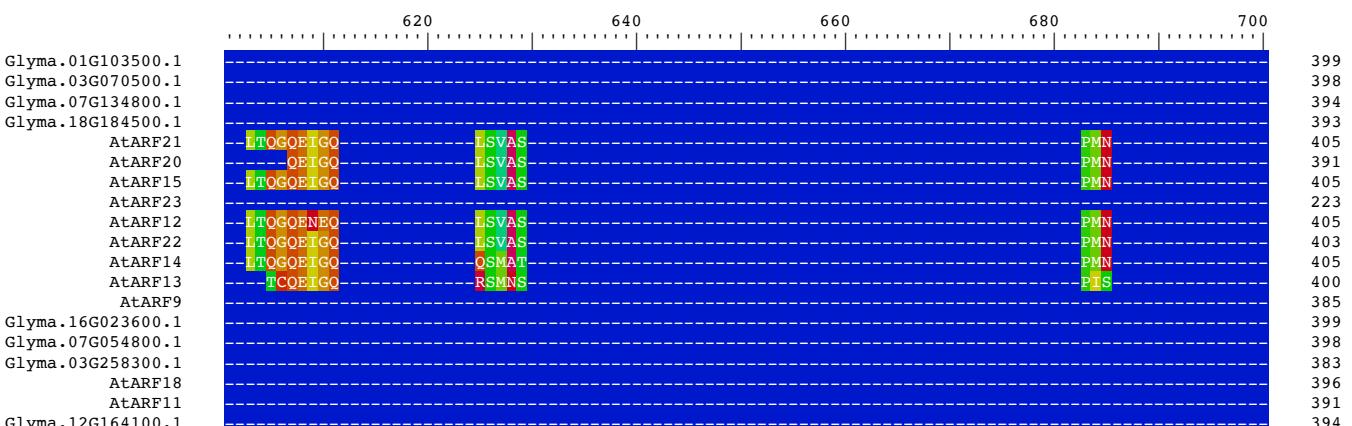
**Consensus** +++++XXXXXXXXXXXXXXXXXXXXFXXXXYXPX-+---XXFXXXXXXX+XXXXXXGXRXXXXXEXXXXXXXX+-+X+XXGXXXXXXXX+-XXXWXXSXWRXXX

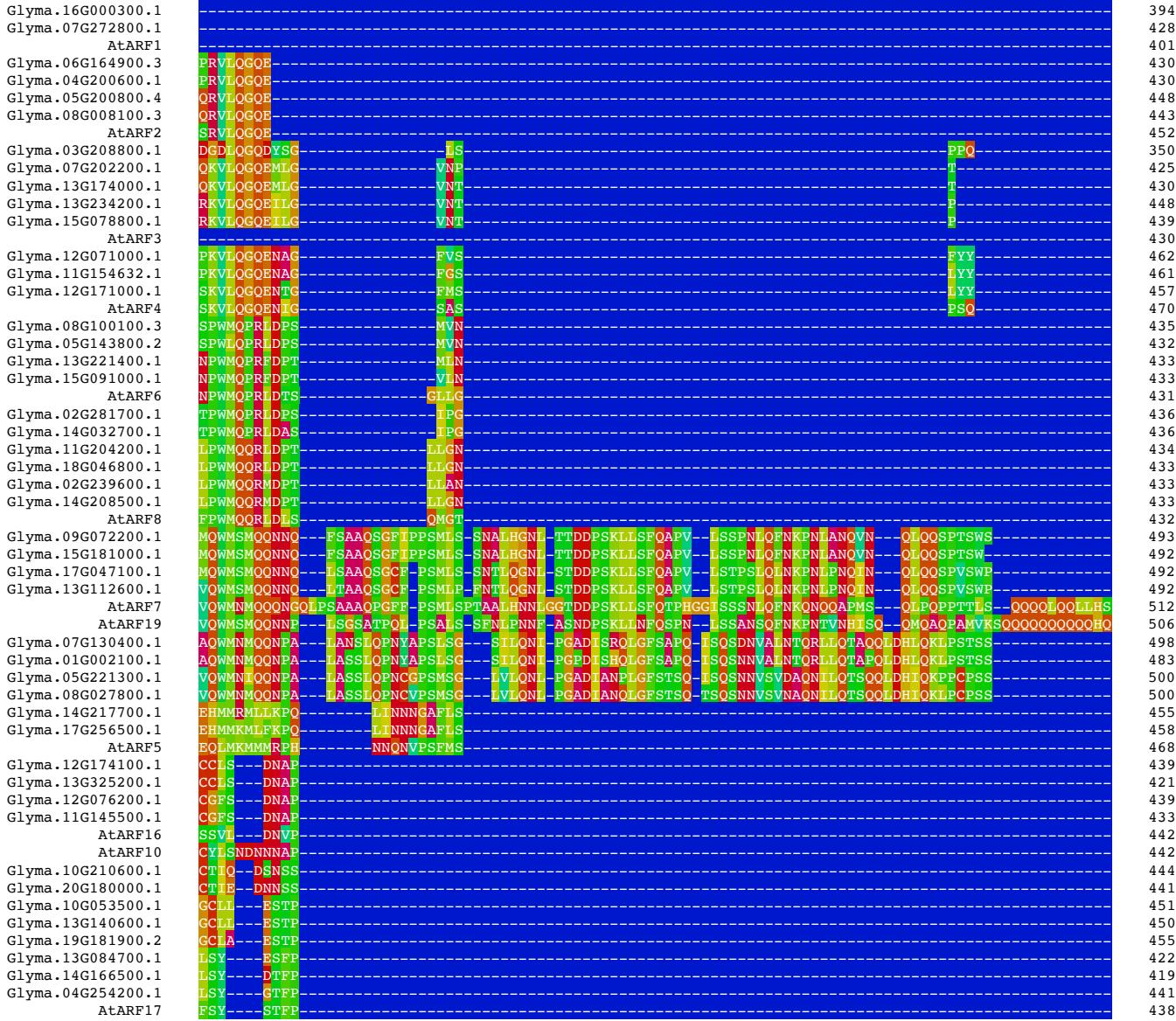


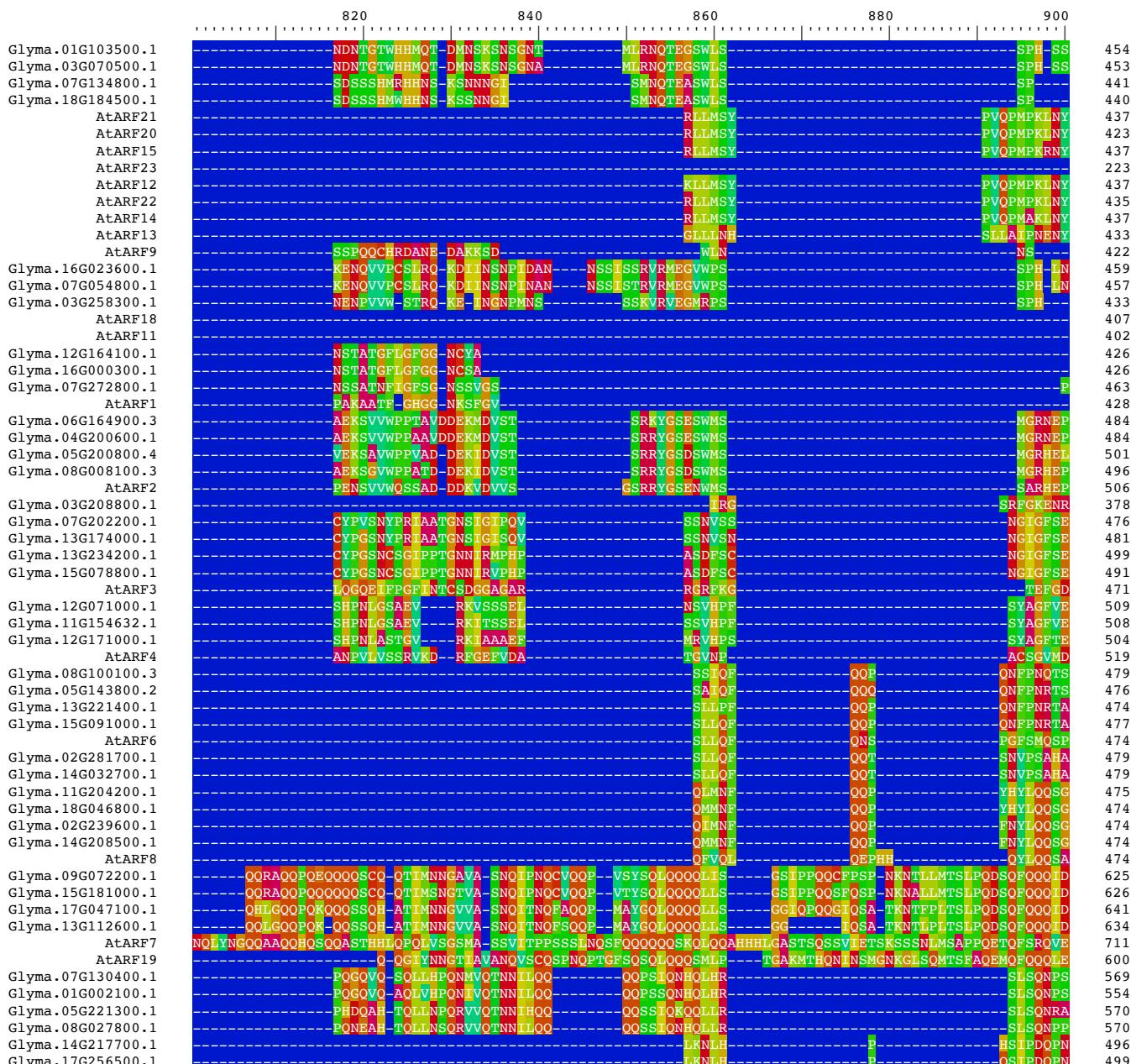
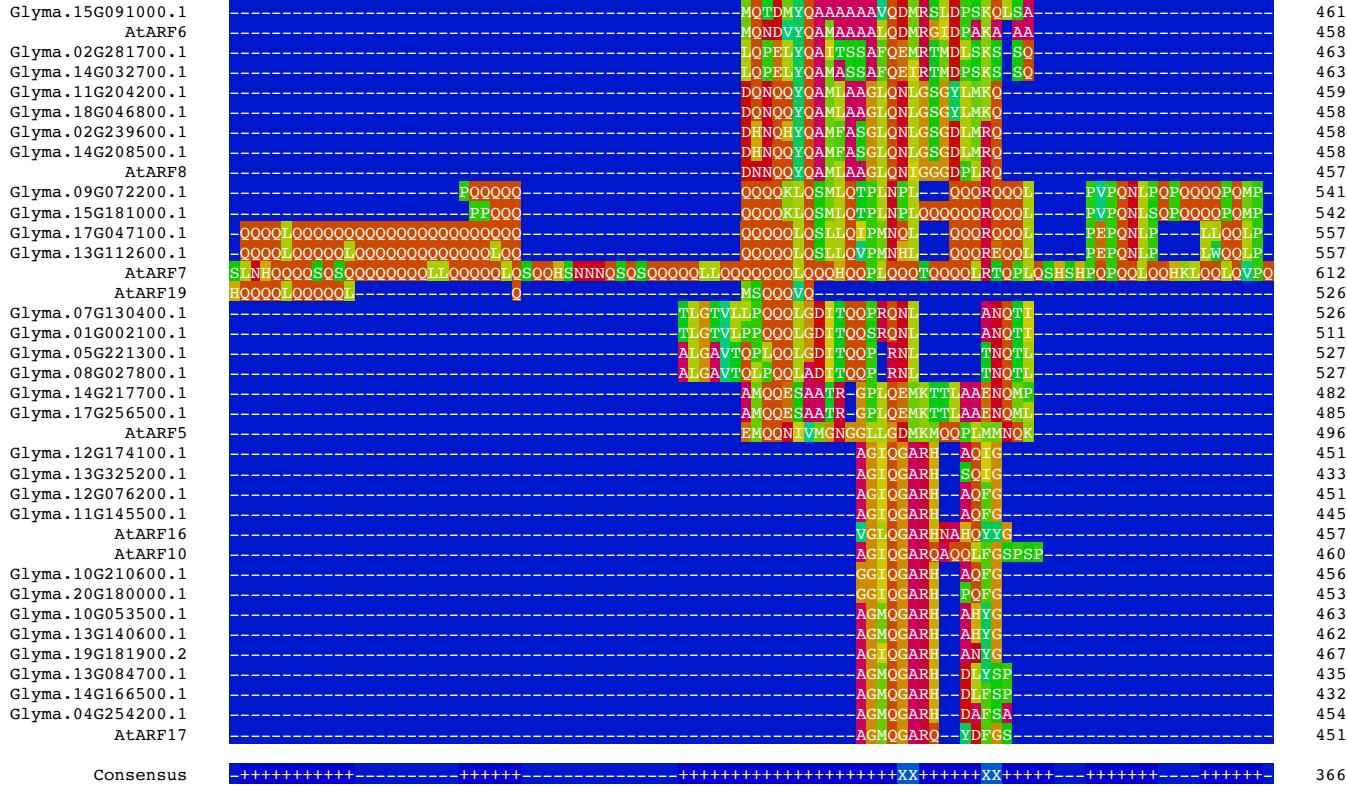
## Consensus

VXWDX-XXXXXX+XXVXXWXXXXXXX+-+XXXX+XXX+XXX~~XXXX~~+XX+++++++-+-----+XXXX+-+XXX+-----+

362



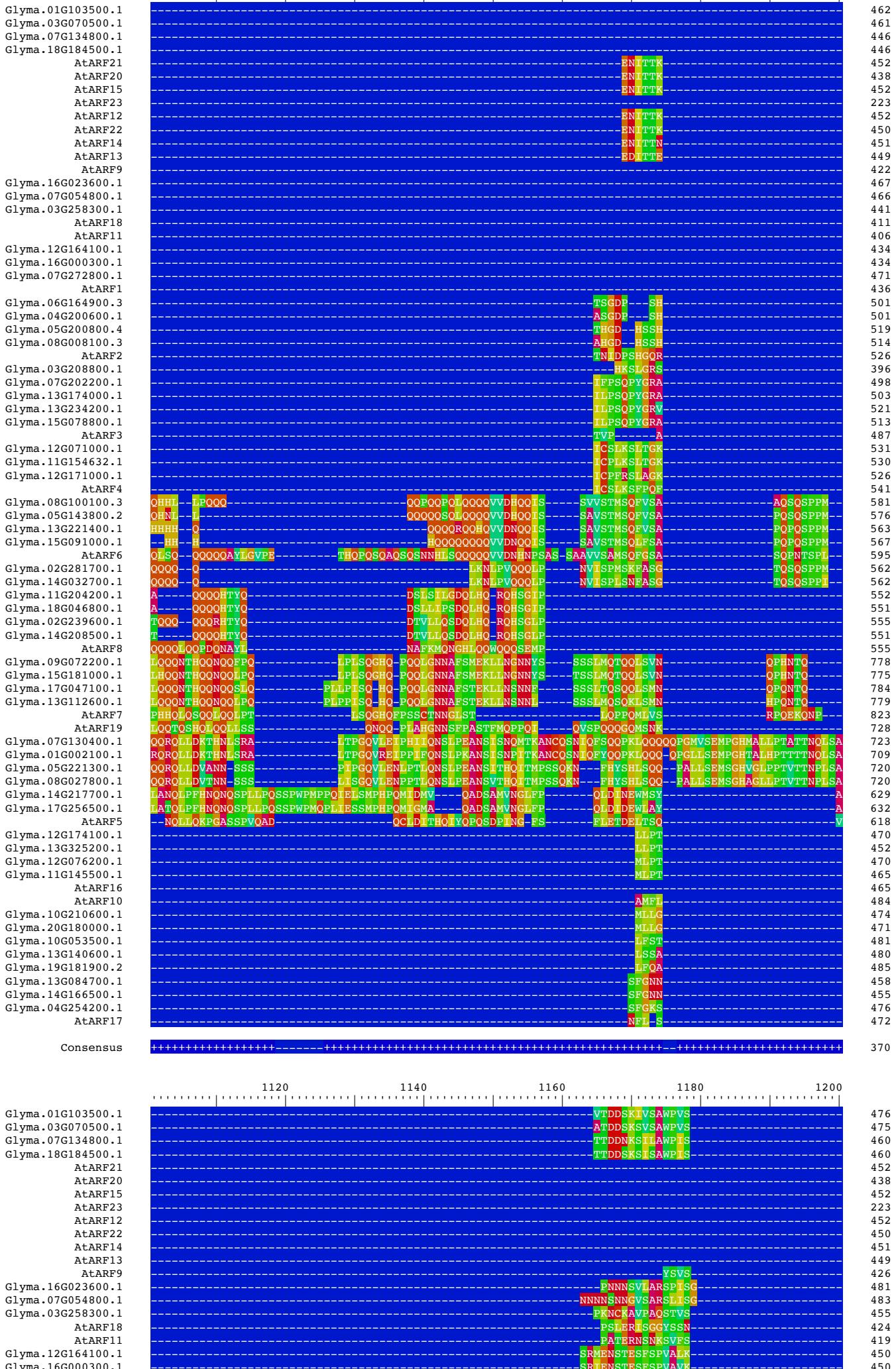




	SEVQ	PQN	KLTVNPS	511
Glyma.12G174100.1	ISL	SDLHN	SDLHN	460
Glyma.13G325200.1	ISL	SDLHN	SDLHN	442
Glyma.12G076200.1	KSL	SDLHLN	SDLHLN	460
Glyma.11G145500.1	KSL	SDLHLNN	SDLHLNN	455
AtARF5				
AtARF16	LSS	SDLH	SDLH	465
AtARF10	SLL	SDLNLSSY	SDLNLSSY	471
Glyma.10G210600.1	LSP	SDFPF	SDFPF	464
Glyma.20G180000.1	LSP	SDFPF	SDFPF	461
Glyma.10G053500.1	LSL	SDLHL	SDLHL	471
Glyma.13G140600.1	LSL	SDLHL	SDLHL	470
Glyma.19G181900.2	ISL	SNLHP	SNLHP	475
Glyma.13G084700.1	LSF	SNFLNDN	SNFLNDN	445
Glyma.14G166500.1	SSF	SNFLNDK	SNFLNDK	442
Glyma.04G254200.1	SRF	CNYPTDM	CNYPTDM	464
AtARF17	FNP	TGFITGGN	TGFITGGN	461

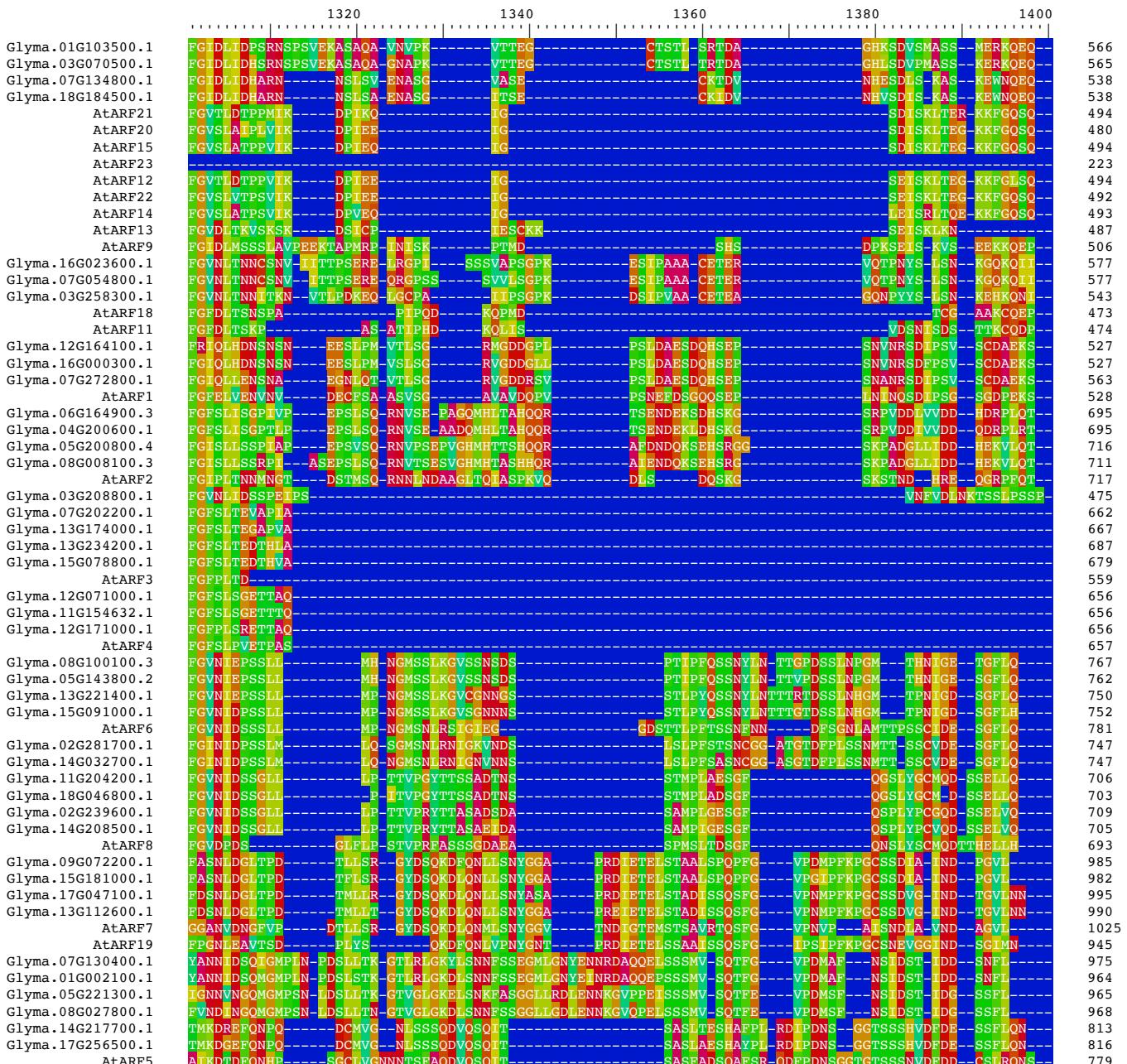
Sequence logo showing the conservation of amino acids across a set of Glyma and AtARF proteins. The x-axis represents positions 920, 940, 960, 980, and 1000. The y-axis lists protein accessions. The legend indicates the following color scheme: C (blue), P (green), S (yellow), T (orange), A (red), D (purple), G (pink), F (light blue), I (light green), V (light orange), H (light pink), K (light purple), and N (light blue).

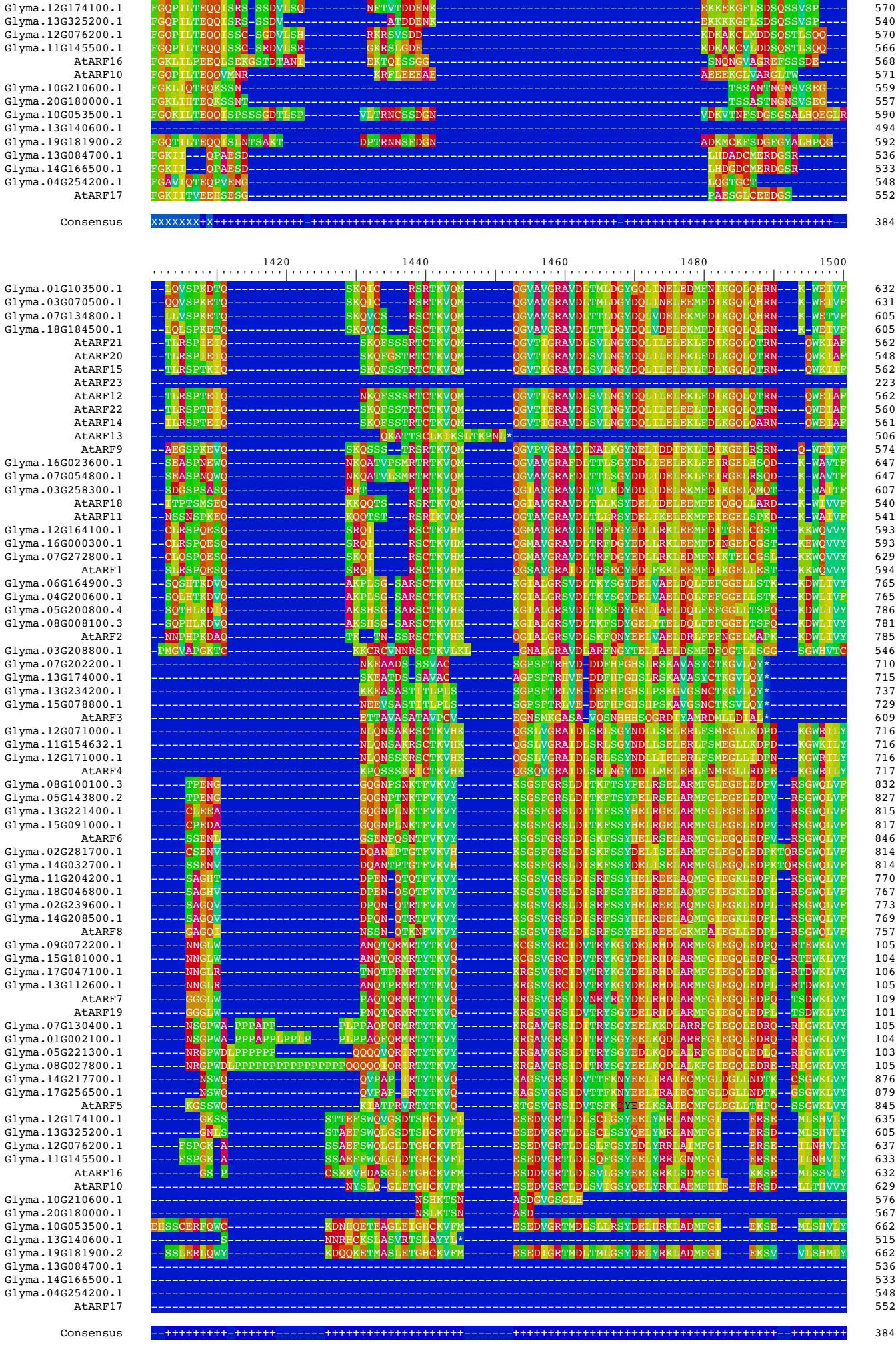
Position	920	940	960	980	1000
Glyma.01G103500.1	CP	SHLFQD			
Glyma.03G070500.1	CP	SHLFQD			
Glyma.07G134800.1		QLYQD			
Glyma.18G184500.1		SQLYHD			
AtARF21	N	NOMVTOIE			
AtARF20	N	NOMVTOIE			
AtARF15	N	NOMVTOIE			
AtARF23					
AtARF12	N	NOMVTEME			
AtARF22	N	NOMVTOIE			
AtARF14	N	N-VVTPPIE			
AtARF13	NS	DOMIQPRK			
AtARF9					
Glyma.16G023600.1	VT	PNLFSID			
Glyma.07G054800.1	AT	PNLFSDE			
Glyma.03G258300.1	SK	PNLFMD			
AtARF18		LFQD			
AtARF11		LFQD			
Glyma.12G164100.1	SN	KSIYWS			
Glyma.16G000300.1	SN	KSIYWS			
Glyma.07G272800.1	SN	KSIYWS			
AtARF1	SI	GSAFWP			
Glyma.06G164900.3	TY	SDLLSGFC			
Glyma.04G200600.1	TY	SDLLSGFC			
Glyma.05G200800.4	TY	PDLISGFC			
Glyma.08G008100.3	TY	PDLISGFC			
AtARF2	TY	TDLISGFC			
Glyma.03G208800.1	NO	HPFLKQDEL			
Glyma.07G202200.1	SFRF	QKVLOGQE			
Glyma.13G174000.1	SFRF	QKVLOGQE			
Glyma.13G234200.1	SFRF	QKVLOGQE			
Glyma.15G078800.1	SFRF	QKVLOGQE			
AtARF3	SYGF	HKVLOGQE			
Glyma.12G071000.1	TNRE	PRVLQGQE			
Glyma.11G154632.1	TNRF	PRVLQGQE			
Glyma.12G171000.1	TNMF	PRVLQGQE			
AtARF4	LDRE	PRVLQGQE			
Glyma.08G100100.3	PLM	OTOLIQQSPF	SQQAFFNSQENPHP	SPSQOSQAOTQTHFQOHLQHQHSF	NNQN
Glyma.05G143800.2	ALM	OTOMIQQSPF	PQQAFFNSQENPHSP	SPSQOSQAOTQTHFQOHLQHQHSF	NTQN
Glyma.13G221400.1	ALM	OAOMLQQSO	PQQIFGNTQENQHS	POSQAHLQOHLQHQHSF	NSQH
Glyma.15G091000.1	ALM	OAOMLQKSQ	PQQIFCENNQENQHS	OSQFQOTQAHLQOHLQHQHSF	NSQ
AtARF6	SLV	OPQMLQQOI	SQQQQQLSQQQQQQQ	OLSQQQQQLSQQQQQLSQ	QQQQ
Glyma.02G281700.1	SEV	ORQLPPOSQ	LONTLLHNPOENQVP	AOSOLLOQCLERYHPY	SDQO
Glyma.14G032700.1	SEV	ORQLPPOSQ	PONTLLHNYPENOVP	AOSOLLOQCLERYHPY	SDPR
Glyma.11G204200.1	NSN	SPLQLQQQQ	PIQQSVSS-NMLQPO	TNVLTENLSQHLLQPKHNN	QFVO
Glyma.18G046800.1	NSN	SPLQLQQQQ	PIQQSVSS-NMLQPO	AVHLTENLSQHLLQPKHNN	QFVO
Glyma.02G239600.1	NPN	PPQLQPO	AIQQSVSNNLQPO	AQVMAENLSQHLLQKSHNN	REDQ
Glyma.14G208500.1	NPN	PPQLQPO	AIQQSVSNNLQPO	AQVLAENLSQHLLQKSHNN	REDQ
AtARF8	SHN	SDMLMQQQQ	QQQASR-HLMHQ	TQJMSENLPQDNMROEVSN	OPAG
Glyma.09G072200.1	QQ	ASLLQRQQQQQQQQ	TOLOSSPLQLQQSLSORA	QQQKPLISTSSPLQLSQL	715
Glyma.15G181000.1	QQ	ASLLQRQQ	QQOTOLOSSPLQLQQSLSORA	QQQPMOTMCQQNSSEQOPQLLQQ	712
Glyma.17G047100.1	QQ	ASLLQRQQ	QQOTOLLOSSPLQLQQNLPQRALQOPPATQMLQNPSEQQLHILQLLQKLOQQQQ	QLLILSTSTPLQLSQL	721
Glyma.13G112600.1	QQ	ASLLQRQQ	QQOTOLLOSSPLQLQQNLPQRALQOPPATQMLQNPSEQQLHILQLLQKLOQQQQ	QLLILSTSTPLQLSQL	716
AtARF7	QQCOPPGINGQNQQTLLQKA	HQAAQOQIFQOSLLEO	PHIQFOLLRLQKQOOQFTS	POSQL	773
AtARF19	MHN	SSQLLRNQQ	EGSSLHSLQQLNLSQN	SIAPPVSSSLQPQISA	676
Glyma.07G130400.1	QQ	QTIGQNO	PQNLQISPMEDHV-QQLQMS	DNQIQOLQLLQKQOTLLAQ	635
Glyma.01G021000.1	QQO	QOTIGQNO	HQNLQISPMEDHV-QQLQMS	DDQIQOLQLLQKQOTLLAQ	622
Glyma.05G221300.1	OKH	QOTTGLNE	ROIIVFQSPMPDHFNQOLMS	DNQVRFOLLLQKQOQNTLLAQ	638
Glyma.08G027800.1	OKD	QOTTFQGNE	RQNVFQSPMPDHFNQOLMS	DNQVRFOLLLQKQOQNTLLAQ	638
Glyma.14G177000.1	ALN	MQSLLKNKDQ	PEKLHPLGKIDNHISSGIVI	DKPKSESEVLPDVIVDYPSEMGCIERVAANP-VNQG	565
Glyma.17G256500.1	ALN	MQSLLKNKDQ	PEKFHPLAKIDNHIPSGIVI	DKPKLECEVLPDRVIVDYPSEMGCNNEKVAVNP-VNQG	568
AtARF5	ASN	TSGQEON-I	SOSMSAPAKENSTLSCSS	GRVQHGLEQSMEQAOASQTTSTVCNEEKV	570
Glyma.12G174100.1		NKLQLG			466
Glyma.13G325200.1		NKLQLG			448
Glyma.12G076200.1		NKLQLG			466
Glyma.11G145500.1		NKLQLG			461
AtARF16					465
AtARF10	TGN	NKLHSP			480
Glyma.10G210600.1		NKLPLAD			470
Glyma.20G180000.1		NKLPLAD			467
Glyma.10G053500.1		SKLQSG			477
Glyma.13G140600.1		SKLQSG			476
Glyma.19G181900.2		NKLQSG			481
Glyma.13G084700.1		SYLYMGSG			453
Glyma.14G166500.1		SYLYMGSG			450
Glyma.04G254200.1		SRLCMGN			471
AtARF17		PPQLFTN			468



Consensus		370
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Sequence logo showing the conservation of amino acids across 1300 positions for various Glyma genes. The x-axis represents positions 1220 to 1300. The y-axis lists Glyma genes. Each position has four bars representing A, T, C, and G. The height of each bar indicates the frequency of that nucleotide at that position.





1520 1540 1560 1580 1600

Glyma.01G103500.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SVEDG-----	TVISSL-----	TTET-----	692
Glyma.03G070500.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SVEDG-----	TVISSL-----	TTET-----	691
Glyma.07G134800.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SMGE-----	IVISLN-----	TTET-----	664
Glyma.18G184500.1	TDDEGDMMVLVGDDPWL-----	EFCNMVRRIFIYSSQDVKKMCGS-----	KLPIS-----	SMEE-----	IVTSID-----	TTET-----	664
AtARF21	TDSGDEMVLVGDDPWP-----	EFCNMVKKLIYSSKEEVKNL-----	SSK-----			SLSS-----	606
AtARF20	TDSGDEMVLVGDDPWP-----	EFCNMVKKLIYSSKEEVKNL-----	SSK-----			SLSS-----	592
AtARF15	TGSDEDEMLVGDDPWP-----	EFCNMVKRIFYIQKR-----			R-----		593
AtARF23							223
AtARF12	TDSDEDKMLVGDDPWP-----	EFCNMVKKIFIQKR-----			R-----		593
AtARF22	TDSDDDMLVGDDPWP-----	EFCNMVKKILIFKRG-----	GOK-----		LEVO-----		598
AtARF14	TNNNEEDKMLGEDPWP-----	EFCNMVKKIFIYSSKEEVKNL-----	SRK-----		SLSS-----		605
AtARF13							506
AtARF9	TDDEGDMMVLVGDDPWP-----	EFCNMVKRIFIWSKEEVKKMTPGN-----	QLRMLLR-----	EVEITL-----	TTTSKID-----	NHSN-----	638
Glyma.16G023600.1	TDDENDMMVLVGDDPWP-----	EFCNMVKRIFIICSRIDLKKMKC-----	CKLPAS-----	SSEVE-----	VILLSPDSQRND-----	ETQOSHMP-----	716
Glyma.07G054800.1	TDDENDMMVLAGDDPWP-----	EFCNMVKRIFIICSRIDLKKMKC-----	CKLPAS-----	SSEVE-----	EILLSPDSQRND-----	ETQOSHMP-----	716
Glyma.03G258300.1	TDDGNDMMVLVGDDPWP-----	EFCFTVKRIFIICSRIDLKKMK-----	KHSSS-----	SSVGE-----	ETLLSD-----		662
AtARF18	TDDEGDMMLAGDDPWN-----	EFCKMAKKIFIYSSDEVKKM-----	KLKIS-----	SSLEN-----	EEYGNESE-----	NRSRG-----	602
AtARF11	TDDEGDRMLVGDDPWN-----	EFCKMAKKIFIYSSDEVKKMRS-----	KSLLG-----	D-RG-----	TIVNLESDO-----	RTVHV-----	601
Glyma.12G164100.1	TDNEDEDDMMVGDDPWL-----	EFCSEVRKIFIYTAEEEVKSLSPK-----	GLPIS-----	EEVKPSKNDSEA VAN PED OSS-----	VPGC-----		665
Glyma.16G000300.1	TDNEDEDDMMVGDDPWL-----	EFCSEVRKIFIYTAEEEVKSLSPK-----	GLPIS-----	EEVKPSKNDSEA VNPDQD OSS-----	LGPCC-----		665
Glyma.07G272800.1	TDNEDEDDMMVGDDPWD-----	EFCGMRVRKIFIYTAEEEVKSLSPK-----	RPLMN-----	EKVNPSCQDSEAI VNPFDQD OSS-----	MGpsc-----		701
AtARF1	TDDEDDMMVGDDPWN-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	KLAVN-----	ARMQ-LKADAENGNT EGRSS-----	MAGRS-----		665
Glyma.06G164900.3	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSVMASDGA DADAKVVKCOPHQKF-----	NSENGLDA-----			843
Glyma.04G200600.1	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	HSVTASEGADTKDVKCOPHQKF-----	NSENGLDA-----			843
Glyma.05G200800.4	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSASEG-ATDT QEI KCOLNN-----	SASDT-----			858
Glyma.08G008100.3	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSASEG-A ADAQEIECOLNP-----	SSSDT-----			853
AtARF2	TDEENDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	AVVGE-----	SDADAKSASN PSL-----	SS-----AGNS-----		859
Glyma.03G208800.1	TDDEGDMMQLGDYWPQ-----	DFLGVVQRMIIICPKEGTDNLKPGS-----				SANP-----	590
Glyma.07G202200.1							710
Glyma.13G174000.1							715
Glyma.13G234200.1							737
Glyma.15G078800.1							729
AtARF3							609
Glyma.12G071000.1	TDSENDIMVVGDDPWH-----	EFCDVVSCHKIHIYTQEEVEKMTIG-----	MISDDTHS-----	CLEEAPVIMEASKSSSVGQPDYSPATAV-----			792
Glyma.11G154632.1	TDSENDIMVVGDDPWH-----	EFCDVVSCHKIHIYTQEEVEKMTIE-----	MISDDTHS-----	CLEEAPVIMEASKSSSVGQPDYSPATAV-----			792
Glyma.12G171000.1	TDSENDIMVVGDDFWHPFLFV-----	EFCDVVSCHKIHIYTQEEVEKMTIG-----	MISDDTHS-----	CLEOAPVMVEASKSSSVGQPDSSPTVVRM-----			799
AtARF4	TDSENDIMMVVGDDPWH-----	DFCNVWVKIHIYTKEEVENA-----	NDDNKS-----	CLEOAAALMMEASKSSSVGQPDSSPTVVRM-----			788
Glyma.08G100100.3	VDQENDVLLLGDPWP-----	EFCNVSVGCIKIILSPQEVQQMG-----	IQR-----	SNGVC-----	EDPRNLSTGTITV-----	GSLNY-----	907
Glyma.05G143800.2	VDOENDVLLLGDPWP-----	EFCNVSVGCIKIILSPQEVQQMG-----	IQR-----	SNGVCDDYAGREDPRNLSTGTITV-----	GSLNY-----		908
Glyma.13G221400.1	VDRENDVLLLGDPWP-----	EFCNVSVCWIKIILSPQEVQQMG-----	IQR-----	SNGICDDYVSQDPRNLGTCTV-----	GSDLY-----		896
Glyma.15G091000.1	VDRENDVLLLGDPWP-----	EFCNVSVCWIKIILSPQEVQQMG-----	NQR-----	SNGICDDYVSQDPRNLGTCTV-----	GSDLY-----		898
AtARF6	VDRENDVLLLGDDPWE-----	EFVSSVVCWKIILSPQEVQQMG-----	VDKLP-----	SNCNCDFGNRSDFPRNLNGNLASVG-----			933
Glyma.02G281700.1	VDRENDVLLLGDDPWO-----	EFVNNVWVYIKILSPLEPVQKLS-----	GDKL-----	SGNQDNGNAWRQYEDNS-----			896
Glyma.14G032700.1	VDRENDVLLLGDDPWO-----	EFVNNVWVYIKILSPLEPVQKLS-----	GDKL-----	SGNQDNGNAWRQYEDNS-----			896
Glyma.11G204200.1	VDRENDVLLLGDDPWE-----	EFVNNVWVYIKILSPEDIQKMG-----	GKLS-----	SGNQDNGNAWRQYEDNS-----			844
Glyma.18G046800.1	VDRENDVLLLGDDPWE-----	EFVNNVWVYIKILSPEDIQKMG-----	GKLS-----	SGNQDNGNAWRQYEDNS-----			841
Glyma.02G239600.1	VDRENDVLLLGDDPWE-----	EFVNNVWVYIKILSPEDIHKM-----	SGRIN-----	SGRIN-----			847
Glyma.14G208500.1	VDRENDVLLLGDDPWE-----	EFVNNVWVYIKILSPEDIHKM-----	SGRIN-----	SGRIN-----			843
AtARF8	VDKENDILLLGDDPWE-----	EFVNNVWVYIKILSPEDVHQMG-----	HCEGSGGLFPQNP-----		THL-----		811
Glyma.09G072200.1	VDHENDILLVGDDPWE-----	EFVNCVQSIKIILSSSEVQQMS-----	NQACSGT-----	DNGNAWRQYEDNS-----	ASFNR-----		1125
Glyma.15G181000.1	VDHENDILLVGDDPWE-----	EFVNCVQSIKIILSSSEVQQMS-----	NQACSGT-----	DNGNAWRQYEDNS-----	ASFNR-----		1122
Glyma.17G047100.1	VDHENDILLVGDDPWE-----	EFVNCVQSIKIILSSSEVQQMS-----	PNQACSGT-----	DNGNAWRQYEDNS-----	ASFNR-----		1136
Glyma.13G112600.1	VDHENDILLVGDDPWE-----	EFVNCVQSIKIILSSSEVQQMS-----	PNQACSGT-----	DNGNAWRQYEDNS-----	ASFNR-----		1131
AtARF7	VDHENDILLVGDDPWE-----	EFVNCVQSIKIILSSSEVQQMS-----	PNOAYSGT-----	DNGNAWRQYEDNS-----	TSFNR-----		1165
AtARF19	TDHENDILLVGDDPWE-----	EFVNCVQNIKIILSSSEVQQMS-----	NQACSGG-----	DNGNAWRQYEDNS-----	ASFNR-----		1086
Glyma.07G130400.1	VDHESDVLLVGDDPWE-----	EFVNCVRCIKIILSPQEVQQMS-----	NQACSSS-----		GGNT-----		1110
Glyma.01G002100.1	VDHESDVLLVGDDPWE-----	EFVNCVRCIKIILSPQEVQQMS-----	NQACSSS-----		GGDT-----		1104
Glyma.05G221300.1	VDHENNDVLLVGDDPWE-----	EFVNCVRCIKIILSPQEVQQMS-----	VPAGSSSD-----		GGNA-----		1099
Glyma.08G027800.1	VDHENNDVLLVGDDPWE-----	EFVNCVRCIKIILSPQEVQQMS-----	VPAGSSSD-----		GGNA-----		1113
Glyma.14G217700.1	VYQESDVLLVGDDPWE-----	EFVGCVCRCIRILSPSEVQOMS-----	LOGM-----		NV-----		930
Glyma.17G256500.1	VYQESDVLLVGDDPWE-----	EFVGCVCRCIRILSPSEVQOMS-----	LOGM-----		NV-----		933
AtARF5	VYQESDVLLVGDDPWE-----	EFVGCVCRCIRILSPTEVQOMS-----	INDLK-----		TSVS-----		902
Glyma.12G174100.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----	HGLDT-----		GIFA-----		700
Glyma.13G325200.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----	HGLDAA-----		SIFIA-----		670
Glyma.12G076200.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----	HGLDAA-----		SIFIA-----		701
Glyma.11G145500.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSGSKNIKRAF-----	HGLD-----		SIFIA-----		697
AtARF16	RDASGAIKYAGNEPFS-----	EFLKTARRITII TEQSE-----	HGLD-----		SVVV-----		670
AtARF10	RDANGVIKRIGDEPFS-----	DFMKATKRITII KMDIGGDN-----	NGID-----		ASTKTPGL-----		693
Glyma.10G210600.1	--QGSPINNSDGGS-----	PWYKDQHKSDLGTDN-----	I-----		CAIA-----		612
Glyma.20G180000.1	--QGSPINNSDGGS-----	PWYKDQHKSDLGDN-----	I-----		CAIA-----		593
Glyma.10G053500.1	RDSTGAVKRSDESFS-----	DFTRTAKRILTILMDSGSN-----			NVGV-----		700
Glyma.13G140600.1							515
Glyma.19G181900.2	RDITGAVKHIGDEAFS-----	EFTKTAARRITIILMDNS-----			GRGI-----		700
Glyma.13G084700.1	--GS-----	NKLKTVEAICYFSK-----					551
Glyma.14G166500.1	--GS-----	NKLKTVEAICYFSK-----					548
Glyma.04G254200.1	--CTGDECQCOR-----				AINS-----		562
AtARF17		KESSDNETQLSLSHAPPSPFK-----			HSNSNAGS-----		585
Consensus	+++++-----XX-----	XXXXXXXXXXXXJXXX-----	-----	-----	-----		401

Glyma.01G103500.1 \* 693  
Glyma.03G070500.1 \* 692  
Glyma.07G134800.1 \* 665  
Glyma.18G184500.1 \* 665  
AtARF21 \* 607  
AtARF20 \* 593  
AtARF15 \* 594  
AtARF23 \* 223  
AtARF12 \* 594  
AtARF22 \* 599  
AtARF14 \* 606  
AtARF13 \* 506  
AtARF9 \* 639  
Glyma.16G023600.1 \* 717  
Glyma.07G054800.1 \* 717  
Glyma.03G258300.1 \* 663  
AtARF18 \* 603  
AtARF11 \* 602  
Glyma.12G164100.1 \* 666  
Glyma.16G000300.1 \* 666  
Glyma.07G272800.1 \* 702

AtARF1	*	666
Glyma.06G164900.3	*	844
Glyma.04G200600.1	*	844
Glyma.05G200800.4	*	859
Glyma.08G008100.3	*	854
AtARF2	*	860
Glyma.03G208800.1	*	591
Glyma.07G202200.1	-	710
Glyma.13G174000.1	-	715
Glyma.13G234200.1	-	737
Glyma.15G078800.1	-	729
AtARF3	-	609
Glyma.12G071000.1	*	793
Glyma.11G154632.1	*	793
Glyma.12G171000.1	*	800
AtARF4	*	789
Glyma.08G100100.3	*	908
Glyma.05G143800.2	*	909
Glyma.13G221400.1	*	897
Glyma.15G091000.1	*	899
AtARF6	*	934
Glyma.02G281700.1	*	897
Glyma.14G032700.1	*	897
Glyma.11G204200.1	*	845
Glyma.18G046800.1	*	842
Glyma.02G239600.1	*	848
Glyma.14G208500.1	*	844
AtARF8	*	812
Glyma.09G072200.1	*	1126
Glyma.15G181000.1	*	1123
Glyma.17G047100.1	*	1137
Glyma.13G112600.1	*	1132
AtARF7	*	1166
AtARF19	*	1087
Glyma.07G130400.1	*	1111
Glyma.01G002100.1	*	1105
Glyma.05G221300.1	*	1100
Glyma.08G027800.1	*	1114
Glyma.14G217700.1	*	931
Glyma.17G256500.1	*	934
AtARF5	*	903
Glyma.12G174100.1	*	701
Glyma.13G325200.1	*	671
Glyma.12G076200.1	*	702
Glyma.11G145500.1	*	698
AtARF16	*	671
AtARF10	*	694
Glyma.10G210600.1	*	613
Glyma.20G180000.1	*	594
Glyma.10G053500.1	*	701
Glyma.13G140600.1	-	515
Glyma.19G181900.2	*	701
Glyma.13G084700.1	*	552
Glyma.14G166500.1	*	549
Glyma.04G254200.1	*	563
AtARF17	*	586
Consensus	*	402