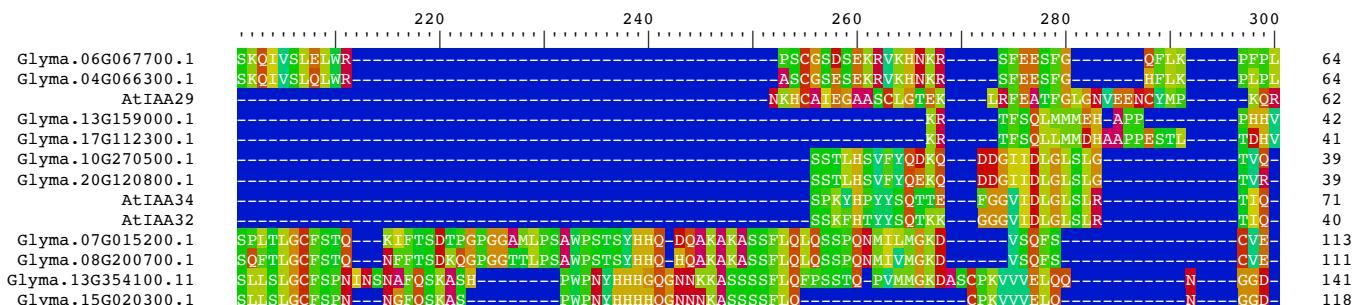


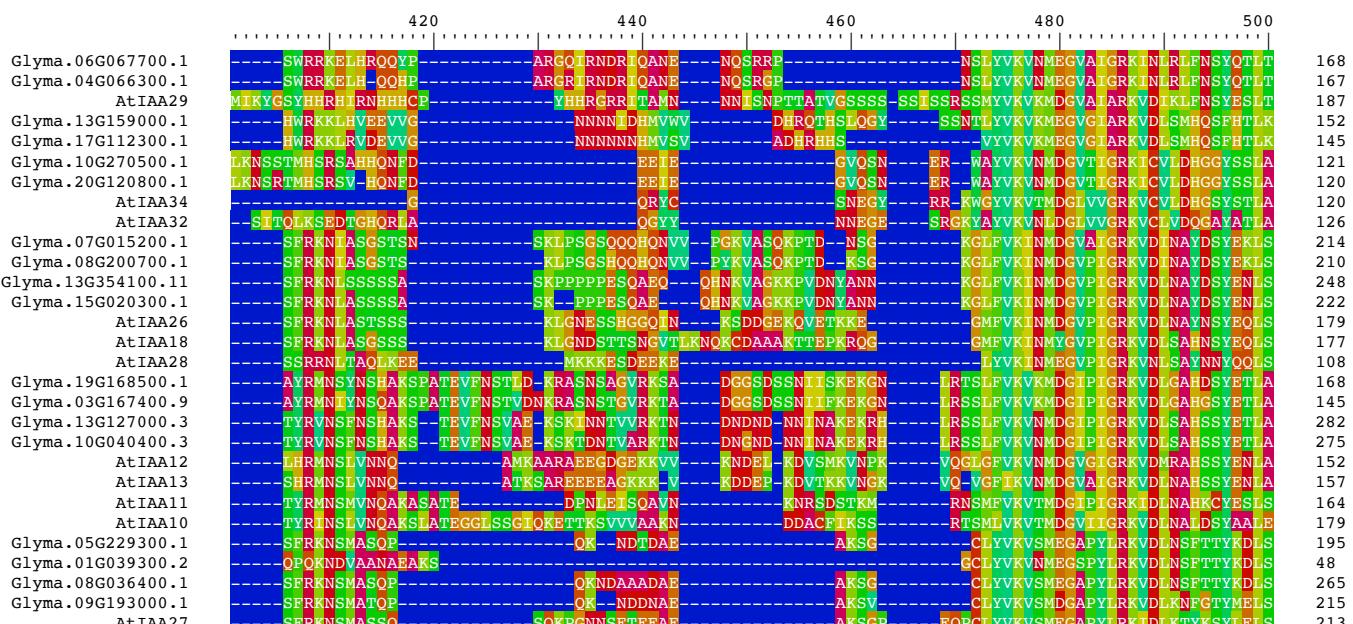
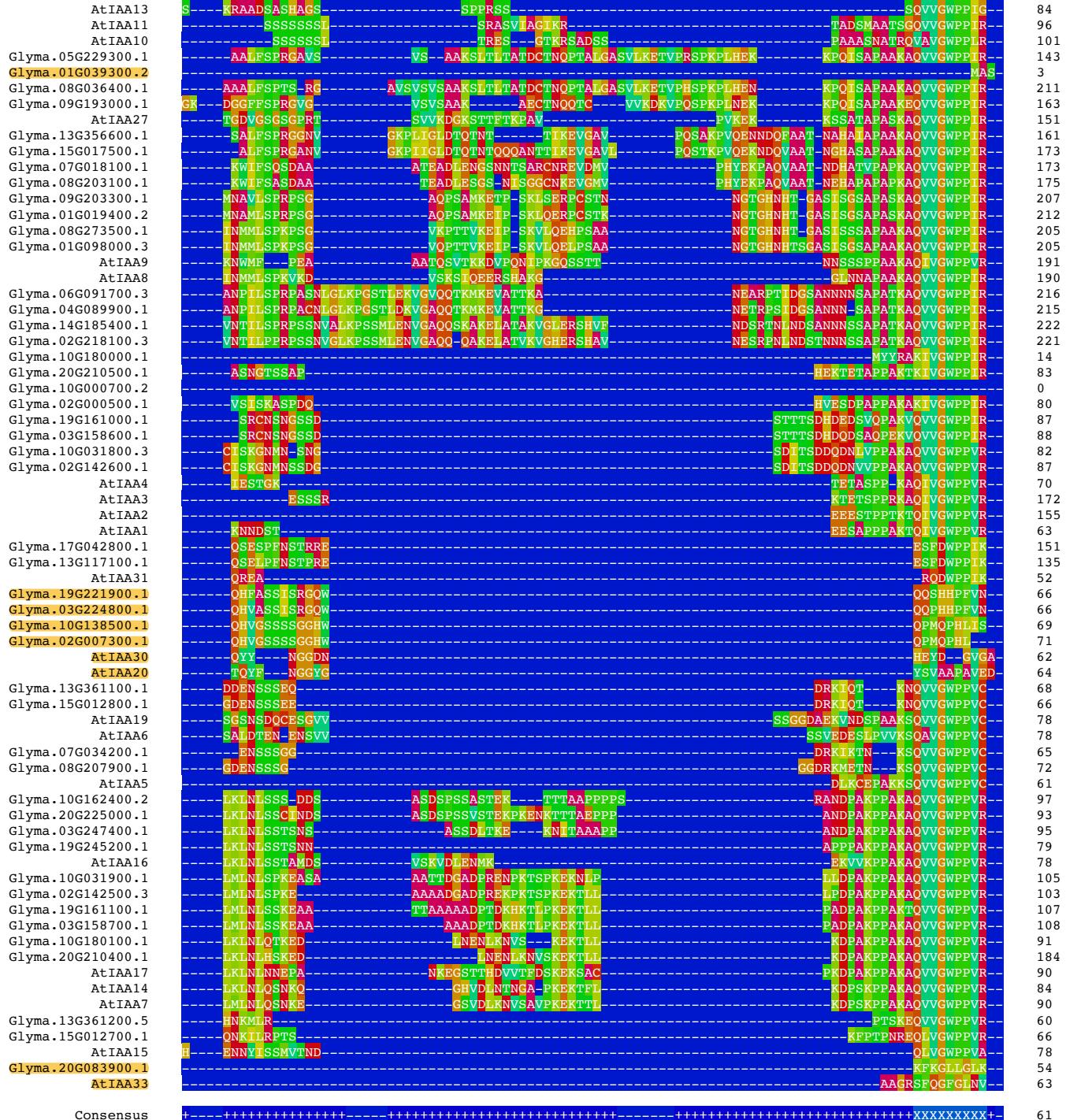


Consensus

49



Sequence logo showing the conservation of amino acids across 100 Glyma orthologs. The x-axis represents positions 1 to 100, and the y-axis lists 100 orthologs. Each position has four bars representing A, T, C, and G. The height of each bar indicates the probability of that amino acid at that position. The sequence logo is color-coded: A (green), T (red), C (blue), and G (yellow).



Glyma.13G356600.1	SFRKNTMASNL	TK	NNDEAE	GKSG	FCCLYVKVNSNDGAPYLRKVLKDLKTYYNNYMELS	215
Glyma.15G017500.1	SFRKNTMASNL	T'K	NNDDDE	GKSG	FGCLYVKVNSNDGAPYLRKVLKDLKTYYNNYMELS	227
Glyma.07G018100.1	SFRKNTMAYNL	N'AK	CNNEAE	EKPG	VACLYVKVNSNDGAPYLRKVLKDLKTYSNYIELS	227
Glyma.08G203100.1	SFRKNTMAY	NIAK	CDNEAE	EKSG	VGCLYVKVNSNDGAPYLRKVLKDLKTYSNYIELS	230
Glyma.09G203300.1	SFRKNSMATT	-NK	NNDEV	GKPG	VGALFVKVNSNDGAPYLRKVLKDLRSYTYYQELS	261
Glyma.01G019400.2	SFRKNSMATT	NK	NNDEV	GKPG	VGALFVKVNSNDGAPYLRKVLKDLRSYTYYQELS	266
Glyma.08G273500.1	SFRKNSMATT	K	NNDEV	GKPG	AAAIFVKVNSNDGAPYLRKVLTLTNYTTYRELS	258
Glyma.01G098000.3	SFRKNSMATT	K	NNDEV	GKPG	AAALFVKVNSNDGAPYLRKVLTLRNTYTMQELS	258
AtIAA9	SYRKNTPLATC	K	NSDEV	GRPG	SGALFVKVNSNDGAPYLRKVLTLRNTYTMQELS	244
AtIAA8	SYRKNTPLATC	SK	NTDEV	GKPG	LGVLFVKVNSNDGAPYLRKVLTLRTYTSYQOLS	244
Glyma.06G091700.3	SFRKNSMATT	K	NNEEVD	GKVG	VGALFVKVNSNDGAPYLRKVLKNYSTPELS	269
Glyma.04G089900.1	SFRKNSMATT	K	NNEEVD	GKKG	VGALFVKVNSNDGAPYLRKVLKNYSTPELS	268
Glyma.14G185400.1	SFRKNSMATT	K	NVEEV	GKAG	SGALFVKVNSNDGAPYLRKVLKNYSAYAELS	275
Glyma.02G218100.3	SFRKNSMATT	K	NVEEV	GKVG	P GALFVKVNSNDGAPYLRKVLKNYNAYADLS	274
Glyma.10G180000.1	SYRKNSLQEND	G		AGIY	AGIYVKVNSNDGAPYLRKIDLKVYGGYTOLL	56
Glyma.20G210500.1	SYRKNSLQESE	G		AGIY	AGIYVKVNSNDGAPYLRKIDLKVYGGYTOLL	125
Glyma.10G000700.2				MGAPYL	RKIDLVRYV-----V	16
Glyma.02G000500.1	SYRKQSLOEGD	Q		DGIY	VKVIINDGAPYLRKIDLKVYRGYPPELL	123
Glyma.19G161000.1	SFRKNSLQQOK	KVEQ	OQDG	SGTY	LKVSMAGAPYLRKIDLKVYNSYPELL	136
Glyma.03G158600.1	SFRKNSLQQOK	KVEQ	OQDG	GGMY	VKSMAGAPYLRKIDLKVYNSYPELL	138
Glyma.10G031800.3	SFRKNTLOOK	KEE	OQEG	SGMY	VKSMAGAPYLRKIDLNVYNSYPELL	129
Glyma.02G142600.1	SFRKNSLLOOK	KEE	OQEG	AGMY	VKVSMEGAPYLRKIDLKVYNSYPELL	134
AtIAA4	SYRKNNVQITKK	SE	SEG	OGNY	VKVSNDGAPYLRKIDLTMYQYPELM	116
AtIAA3	SYRKNNIOSKK	NESHE	GO	GIY	VKVSNDGAPYLRKIDLSCYKGYSSELL	220
AtIAA2	SSRKNNNS			VSV	VKVSNDGAPYLRKIDLTKYKNYPPELL	192
AtIAA1	SNRKNNNNNN			VSV	VKVSNDGAPYLRKIDLKLYKNYPPELL	102
Glyma.17G042800.1	SILRSTLVKGQSYLE			RPSL	FVKVYMEGIPIGRKLNLMAHYGYDGLV	198
Glyma.13G171100.1	SILRSTLVKGQSILSQ			RPSL	FVKVYMEGIPIGRKLNLMAHYGYDGLV	182
AtIAA31	SRLRDITLKGRRLI			DTSL	FVKVYMEGIPIGRKLDLQLCVFSGYESLL	100
Glyma.19G221900.1	HYSQ-VPAEVNDCSN			D	HSSFFVKVYMEGIPIGRKLNLLAHGGYYELV	112
Glyma.03G224800.1	NNYSQAAASAFVNDCSN			D	HSSFFVKVYMEGIPIGRKLNLLAHGGYYELV	115
Glyma.10G138500.1	SFSQ-ATEVN			DCSD	HTSFFVKVYMEGIPIGRKLNLLAHGDYHELV	113
Glyma.02G007300.1	SSFSO-ATEVN			HCSD	HTSFFVKVYMEGIPIGRKLNLLAHGDYHELV	116
AtIAA30	AEEMMIEEEEQN			ECNS	VGSFYVKVNNMEGVPIGRKLIDLMSLNGYHDLI	110
AtIAA20	AEYVAEEEEEQN			ECNS	VGSFYVKVNNMEGVPIGRKLIDLMSLNGYHDLI	112
Glyma.13G361100.1	SYRKNTVNET				KMYVKVNSNDGAPFLRKIDLAMHKGYSELV	108
Glyma.15G012800.1	SYRKNTINET				KMYVKVNSNDGAPFLRKIDLAMHKGYSELV	106
AtIAA19	SYRKNSCKEA	ST	TKV	GLGY	VKVSNDGVPYLRKIDLMLGDSQYDDLA	124
AtIAA6	SYRRKNNNEEA	S	K	AIGY	VKVSNDGVPMRKIDLGSNSYINV	121
Glyma.07G034200.1	SYRKNSMNEG			SKMV	VKVSNDGAPFLRKIDLGLHGKYSQDLA	106
Glyma.08G207900.1	SYRKNSMNEG	A		SKMV	VKVSNDGAPFLRKIDLGLHGKYSQDLA	114
AtIAA5	SYRRKNSLERT	K		SSVY	VKVSNDGAPFLRKIDLLEMYCYQDLA	102
Glyma.10G162400.2	SFRKNIVQR	NKNEEEA		AFV	VKVSNDGAPYLRKIDLKLYKSYQELS	141
Glyma.20G225000.1	SFRKNIVQR	-NSNEEEAE		AFV	VKVSNDGAPYLRKIDLKLYKSYQELS	143
Glyma.03G247400.1	SFRKNIVQR	GNNEGEKAAT		KSTK	VNTGAAFVKVNSNDGAPYLRKIDLKLYKTYQDLS	153
Glyma.19G245200.1	SFRKNIVNNVQ	RSNNNDGEKAAT		SSNN	VNMGAFFVKVNSNDGAPYLRKIDLKMYKSQELL	140
AtIAA16	SFRKNIVMSQKPT	TGDATEGNDKTSGSSGA		TSSA	ACATVAYVKVNSNDGAPYLRKIDLKLYKTYQDLS	146
Glyma.10G031900.1	SFRKNMFAQK			SSGGE	SSGGE	158
Glyma.02G142500.3	SFRKNMFAQK			KNSP	NASFVKVNSNDGAPYLRKIDLKMYKSYPELS	156
Glyma.19G161100.1	SFRKNMLAVOK	SV-GESE		KSSP	NASFVKVNSNDGAPYLRKIDLKMYKSYPELS	160
Glyma.03G158700.1	SFRKNMLAVOK	-SV-GEEN		KNSS	PNAFVKVNSNDGAPYLRKIDLKMYKSYRELS	162
Glyma.10G180100.1	SFRKNMMAVOK	VSN--EEVA		EKTT	STIANSGAFVKVNSNDGAPYLRKIDLTMYKSYDLS	149
Glyma.20G210400.1	SFRKNMMAVOK	VSTEDVAEKTT		SSTA	NPGAFVKVNSNDGAPYLRKIDLTMYKSYKELS	241
AtIAA17	SYRKNMVSCQ	KSS			GGPEAAAFVKVNSNDGAPYLRKIDLKMYKSYDELS	138
AtIAA14	NYRKNMANQK	SGE-AEEAMS		SGGG	TVAFVKVNSNDGAPYLRKIDLKMYKSYDELS	138
AtIAA7	NYRKNMTOOK			ERAGNF	GGGAAGAGLKVNSNDGAPYLRKIDLKMYKSYQDLS	152
Glyma.13G361200.5	ASRKNAMEKNS				CKLVKVAVGAPYLRKIDLKMYKSYDELS	99
Glyma.15G012700.1	ASRKNAMEKNS				CKLVKVAVGAPYLRKIDLKMYDMDYSYEHLM	105
AtIAA15	TARKTVRK				YVKAVGAPYLRKIDLGMYDCYOLF	114
Glyma.20G083900.1	DDLGSTV				VLVVTIMLEGCSIYQRISLHNHD-----	86
AtIAA33	EDDLVSSV				VPPVTVLEGRSICORISLKDGHGSYQSLA	100

Sequence logo showing the conservation of amino acids at each position of the IAA29 gene across various Glyma species. The x-axis represents positions 520, 540, 560, 580, and 600. The y-axis lists species from Glyma.06G067700.1 to Glyma.01G098000.3. Each position is represented by a stack of colored bars (A, T, C, G) indicating their relative frequency. A color scale from blue (low) to red (high) is provided on the right.

AtIAA9	SALEKMF	FTLGQCGSNGAAGKDM1SETKLKD1LLNG	RDVYLTYEDKDGDWMLVGDVPWEMFIDVCKKLKIMKGCDAA	IGLA	325
AtIAA8	SALEKMF	FTLGQCGLHQAGQRRERMSEI1KLKD1LLHG	SEFVFLTYEDKDGDWMLVGDVPWEIPTFCQKRLRIMKGSDAA	IGLA	325
Glyma.06G091700.3	SALEKMF	FTMSKCGSH1LGRERMLNETKLKD1LLHG	SEYVFLTYEDKDGDWMLVGDVPWEMFIPCTCKRLRIMKSSDA	IGLA	350
Glyma.04G089900.1	SALENMF	FTISKCGSH1LGRERMLNETKLKD1LLHG	SEYVFLTYEDKDGDWMLVGDVPWEMFIPCTCKRLRIMKSSDA	IGLA	349
Glyma.14G185400.1	SALENMF	FTIGSCGSHGNLGGEVNLTKLKD1LLHG	SEYVFLTYEDKDGDWMLVGDVPWEMFIPCTCKRLRIMKSSDA	IGLA	356
Glyma.02G218100.3	SALENMF	FTIGSCGSHGNLGGEVNLTKLKD1LLHG	SEYVFLTYEDKDGDWMLVGDVPWEMFIPCTCKRLRIMKSSDA	IGLA	355
Glyma.10G180000.1	KALENMF	TIG	EYSEREGYKG-SDYAPTYEDKDGDWMLVGDVPWDMFTSCKRLRIMKGSEA	RGLG	122
Glyma.20G210500.1	KSENLMFK	TIG	EHSEREGYKG-SDYAPTYEDKDGDWMLVGDVPWDMFTSCKRLRIMKGSEA	RGLG	191
Glyma.10G000700.2	QALETMF	TIVVSS	CEYSEREGYKG-SEYAPTYEDKDGDWMLVGDVPWDMFTSCKRLRIMKGSEA	RGLG	77
Glyma.02G000500.1	KALETMF	TIG	EYSEREGYKG-SEYAPTYEDKDGDWMLVGDVPWDMFTSCKRLRIMKGSEA	RGLG	189
Glyma.19G161000.1	MALQNLFK	TFG	EYSEREGYNG-SEYAPTYEDKDGDWMLVGDVPWNFMVSSCKRLT1IKGSEA	KGLG	202
Glyma.03G158600.1	AALQSLETC	TFG	EYSEREGYNG-SEYAPTYEDKDGDWMLVGDVPWNFMVSSCKRLT1IKGSEA	KGLG	204
Glyma.10G031800.3	KALGNMF	TFG	EYSEREGYNG-SEYAPTYEDKDGDWMLVGDVPWNFMVSSCKRLT1IKGSEA	KGLG	195
Glyma.02G142600.1	KALENMF	TFG	QYSEREGYNG-SEYAPTYEDKDGDWMLVGDVPWNFMVSSCKRLT1IKGSEA	KGLG	200
AtIAA4	KSENLMFK	SVG	EYFVEREGYKG-SDFVPVTYEDKDGDWMLVGDVPWEMFSSCKRLRIMKGSE	V	182
AtIAA3	KALEVNMFK		SVGEREGYDYGKG-SDFVPVTYEDKDGDWMLVGDVPWEMFIC1CTCKRLRIMKGSEA	V	286
AtIAA2	KALENMF		MIGYCYEREGYKG-SGFVPVTYEDKDGDWMLVGDVPWDMFTSSCKRLRIMKGSEA	PAID	258
AtIAA1	KALENMF	TVG	EYSEREGYKG-SGFVPVTYEDKDGDWMLVGDVPWDMFTSSCKRLRIMKGSEA	PT	166
Glyma.17G042800.1	KT1LGHMFR	NIIC	PNSOPLINSNFHVLTYEDQECWMMVMGDVPWEMFLNSVKRLK1ITRADRC		260
Glyma.13G117100.1	KT1LGHMFR	NIIC	PNSOPLINSNFHVLTYEDQECWMMVMGDVPWEMFLNSVKRLK1ITRADRC		244
AtIAA31	ENLISHMFD	S11CG	-NRDRKKHVTYEDKDGDWMMVMD1LPWDFLTVRRLK1ITRPERY		158
Glyma.19G221900.1	RTLEHMEDT	TILWG	-TEMNGVOPERCVHLTYDEECDLVMVGDPWEMFLSTVKRRLK1ITRVDTF		175
Glyma.03G224800.1	RTLEHMFD	TILWG	-TEMNGVOPERCVHLTYDEECDLVMVGDPWEMFLSTVKRRLK1ITRVDTF		178
Glyma.10G138500.1	KT1LEQMFD	TILWG	-TEMGVQOPERCVHLTYDEGECIDLIMVGDPWEMFLSAVKRRLK1TRVEAF		176
Glyma.02G007300.1	KT1LEQMFD	TILWG	-TEMGVQPDRCVHLTYDEGEGDLIMVGDPWEMFLSAVKRRLK1TRVEAF		179
AtIAA30	TT1DYMFMNA	SILW	-AEEEDMCSEKS1HVLTYADKEGDWMMVMGDVPWEMFLSSVRRLK1ISRAYH		172
AtIAA20	RT1DYMFMNA	SILW	-AEEEDMCNEKS1HVLTYADKEGDWMMVMGDVPWEMFLSTVRRLK1ISAYH		173
Glyma.13G361100.1	LALEKFFGC	Y	CIREALKDAEN-AEHVPIYEDKDGDWMLVGDVPWEMFIBSCKRLRIMKRSDA		173
Glyma.15G012800.1	LALEKFFGC	Y	CIGSALKDEEN-VEQVPIYEDKDGDWMLVGDVPWEMFIISCKRLRIMKRSDA		171
AtIAA19	FALDKLIFGF	R	CIGVALKDGD-CYEVTIYEDKDGDWMLVGDVPWGMFSCSKRLRIMKRSDA		189
AtIAA6	TV1LENLF	GC	CIGVA-KECKC-CYEVIIYEDKDGDWMLVGDVPWEMFLKSCKRLRIMKRSDA		185
Glyma.07G034200.1	LALDKLIFGS	Y	CMVEALKNADN-SEHVP1YEDKDGDWMLVGDVPWEMFSCSKRLRIMKRSDA		171
Glyma.08G207900.1	LALDKLIFGS	Y	CMVEALKNADN-SEHVP1YEDKDGDWMLVGDVPWEMFSCSKRLRIMKRSDA		179
AtIAA5	SALQILEFGC	Y	INF1-DT1KE-SECVP1YEDKDGDWMLVAGDVPWEMFLGSCSKRLRIMKRSNA		163
Glyma.10G162400.2	DALAKMF	FT1IEKCGSQM	KDFMNETKL1D1LLNG-SDVVPYTDKGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		163
Glyma.20G225000.1	DALAKMF	FT1IEKCGSQM	KDFMNET--NG-SDVVPYTDKGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		216
Glyma.03G247400.1	DALAKMF	FT1DKCGSQM	KDFMNESKL1D1LLNG-SDVVPYTDKGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		232
Glyma.19G245200.1	DALAKMF	FT1DKCGSSQ	KDFMNEKL1D1LLNG-SDVVPCTEDKDGDWMLVGDVPWELVSBSCQRLRIMKGSEA		219
AtIAA16	NALSKMF	FT1GNVGPQGM	KDFMNESKL1D1LLNG-SDVVPYTDKGDWMLVGDVPWEMFDSCKRLRIMKGSEA		225
Glyma.10G031900.1	DALAKMF	FT1GNCESQF	KDFMNESKLMD1LLNS-SDVVPYTDKGDWMLVGDVPWEMFBSCQRLRIMKGSEA		237
Glyma.02G142500.3	DALAKMF	FT1GNCESQF	KDFMNESKLMD1LLNS-SDVVPYTDKGDWMLVGDVPWEMFBSCQRLRIMKGSEA		235
Glyma.19G161100.1	DLSLGKMF	FT1FGNCESQGM	KDFMNESKLND1LLNS-SDVVPYTDKGDWMLVGDVPWEMFVBSCQRLRIMKGKEA		191
Glyma.03G158700.1	DLSLGKMF	FT1FGNCESQGM	KDFMNESKLND1LLNS-SDVVPYTDKGDWMLVGDVPWEMFVBSCQRLRIMKGKEA		241
Glyma.10G180100.1	DALAKMF	FTMGNVGAQGM	KDFMNESKLMD1LLNS-SEYVPSYEDKDGDWMLVGDVPWEMFVGSCSKRLRIMKGSEA		228
Glyma.20G210400.1	DALAKMF	FTMGNVGAQGM	KDFMNESKLMD1LLNS-SEYVPSYEDKDGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		320
AtIAA17	NALSNMESS	FTMGKHG	EEGM1DFMNERKLMD1LVS-WDYVPSYEDKDGDWMLVGDVPWPMPF1TCRRLRIMKGSDA		218
AtIAA14	DALAKMF	FTMGSYGAQGM	1DFMNESKVMD1LLNS-SEYVPSYEDKDGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		217
AtIAA7	DALAKMF	FTMGNVGAQGM	1DFMNESKLMLNNS-SEYVPSYEDKDGDWMLVGDVPWEMFVBSCQRLRIMKGSEA		231
Glyma.13G361200.5	RELETMFCG	LAIRN	HLMNERKLMEGNG-IEYMPYTEDKDGDWMLVGDVPWKMVFVBSCQRLRIMMISSEA		171
Glyma.15G012700.1	RELETMFCG	LAIRN	HLMNERKLMDPNCN-IEYMPYTEDKDGDWMLVGDVPWKMVFVBSCQRLRIMMISSEA		177
AtIAA15	TALENMFQ	LITICK*	TSDDDLHD1SNA1LGH1IAYEDMENNLL1AGD-LIKR1DILPIRCN		130
Glyma.20G083900.1	TALENMFQ	LITICK*	GADSTDDLD1SNA1FGH1IAYEDMENNLL1AGD-LIKR1DILPIRCN		130
AtIAA33	SARQMFVD		GADSTDDLD1SNA1FGH1IAYEDMENNLL1AGD-TWKDFVRVAKR1R1ILPVKG		163

Sequence logo showing the conservation of amino acids at positions 620-700 across various Glyma and AtIAA proteins. The x-axis represents position 620 to 700. The y-axis lists protein accessions. Positions 620, 640, 660, 680, and 700 are marked with vertical dashed lines. The sequence logo uses four colors: red, green, blue, and orange. Amino acids are represented by bars of these colors, with height indicating frequency. Asterisks indicate positions where all or most sequences have the same amino acid.

Position	620	640	660	680	700	Accession
						Glyma.06G067700.1
						Glyma.04G066300.1
AtIAA29	A	YTR	CLE			
Glyma.13G159000.1	R					
Glyma.17G112300.1	R					
Glyma.10G270500.1	SR		Y	T		
Glyma.20G120800.1	SR		C	I		
AtIAA34						
AtIAA32						
Glyma.07G015200.1	SK	QD				
Glyma.08G200700.1	SK	QD				
Glyma.13G354100.11	SK	QDK	IPLDS			
Glyma.15G020300.1	SK	QDK	IPLDS			
AtIAA26	CS	KQ	EK			
AtIAA18	NG	KQ	EK			
AtIAA28	PR					
Glyma.19G168500.1	P	I	EEKNRRSNTSSYR*			
Glyma.03G167400.9	LLOLTLCSPKI		EGKEQKIEQM QA HIDN VIVCT	FTCARIHK	TYELKCTTTRIEGT*	
Glyma.13G127000.3	P	I	EEN			
Glyma.10G040400.3	PR		EEN			
AtIAA12	PR		QEQ			
AtIAA13	AR	N	QEP			
AtIAA11	D		MKQ			
AtIAA10	K					
Glyma.05G229300.1	PR	A	MEK	C		
Glyma.01G039300.2						
Glyma.08G036400.1	PR	A	MEK	C		
Glyma.09G193000.1	PR	A	MEK	C		
AtIAA27	PR	V	MEK	C		
Glyma.13G356600.1	PR	A	MEK	S		
Glyma.15G017500.1	PR	A	MEK	S		
Glyma.07G018100.1	PR	G	MEK	C		
Glyma.08G203100.1	PR	G	MEK	H		
Glyma.09G203300.1	PR	A	MEK	S		
Glyma.01G019400.2	PR	A	MEK	S		
Glyma.08G273500.1	PR	A	MEK	S		
Glyma.01G098000.3	PR	A	MEK	S		
AtIAA9	AAAP	RA	MEK	S		
AtIAA8	PG	A	VEK	SK		
Glyma.06G091700.3	PR	A	VEK	C		
Glyma.04G089900.1	PR	A	VEK	S		
Glyma.14G185400.1	PR	A	VEK	S		
Glyma.02G218100.3	PR	A	VEK	S		
Glyma.10G180000.1	C					
Glyma.30G210500.1	C					

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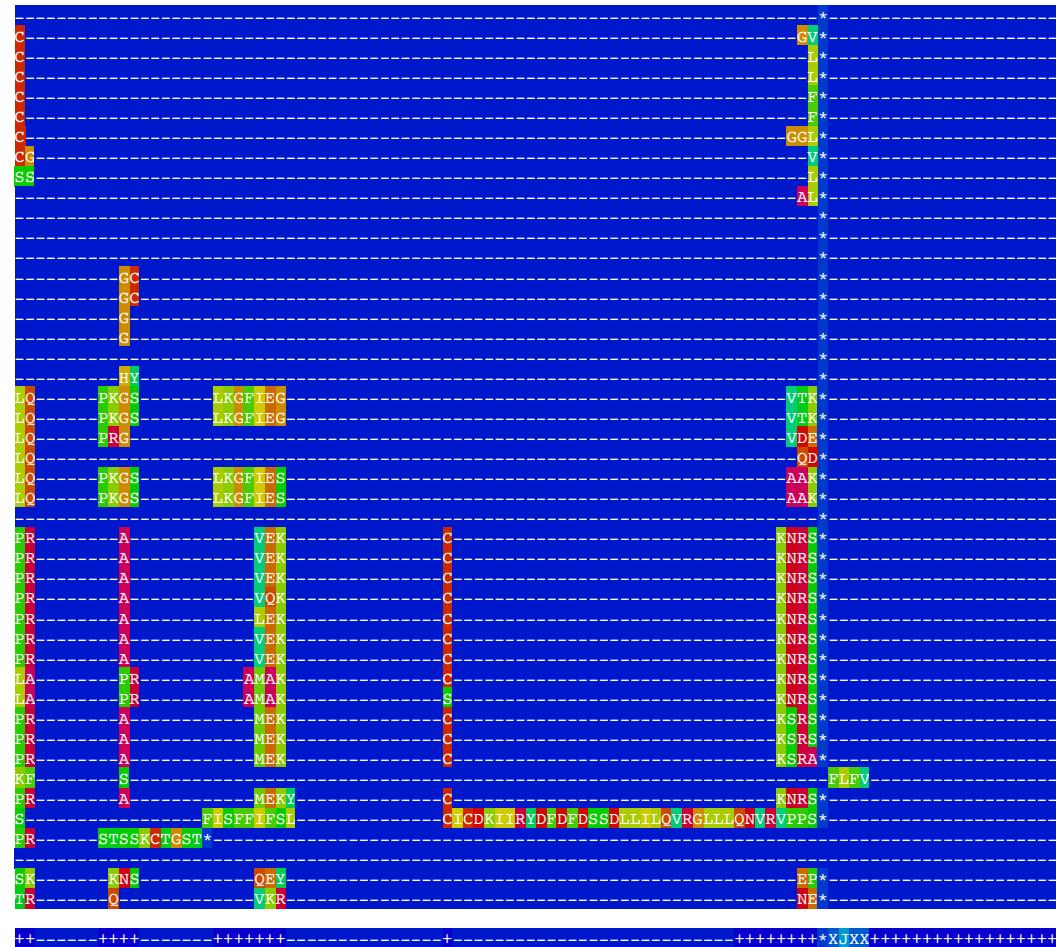
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AtIAA11

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AtIAA4

AtIAA3

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