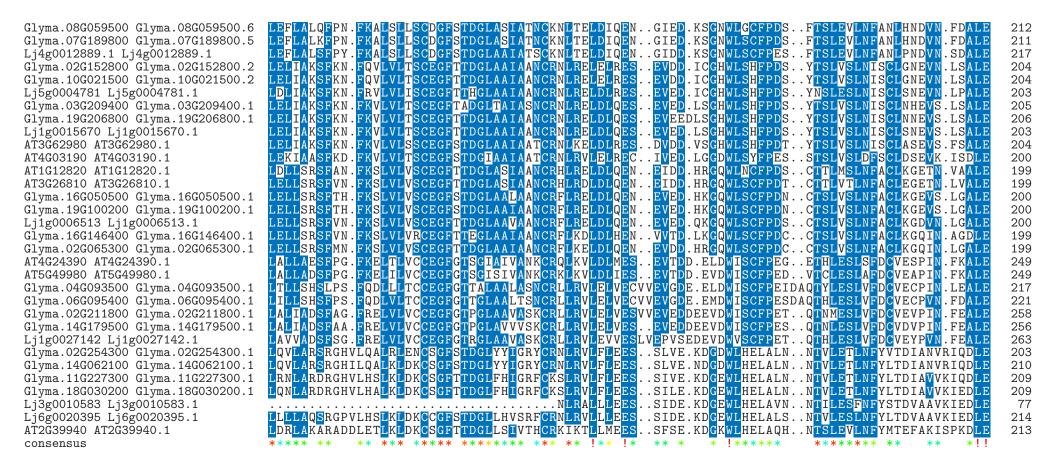
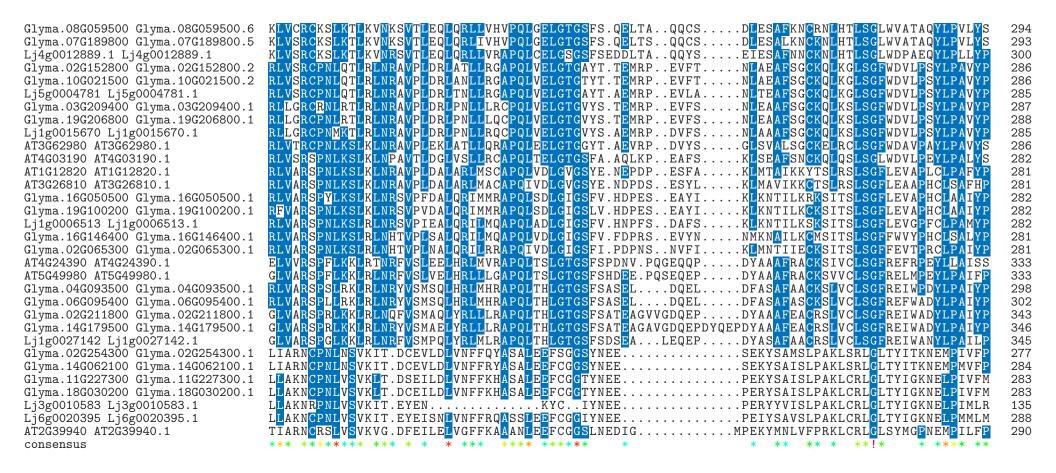
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Glyma.08G059500 Glyma.08G059500.6	MMECR.RKKENQNPNMLKSRKDKSTVSL	40
Glyma.07G189800 Glyma.07G189800.5		39
Lj4g0012889.1 Lj4g0012889.1	ASP <mark>FPDEVLE</mark> R <mark>V</mark> LG <u>M</u> VK <mark>S</mark> RKDRSSV <mark>SL</mark>	45
Glyma.02G152800 Glyma.02G152800.2	S <mark>fpeevleh</mark> vfs <mark>f</mark> ieCd <mark>kdr</mark> gsi <mark>sl</mark>	32
Glyma.10G021500 Glyma.10G021500.2	<mark>M</mark> RPRVNY <mark>F</mark> IECD <mark>KDR</mark> GSI <mark>SL</mark>	32
Lj5g0004781 Lj5g0004781.1	S <mark>lpeevle</mark> hvfs <mark>f</mark> idnd <mark>kdr</mark> ssi <mark>sl</mark>	31
Glyma.03G209400 Glyma.03G209400.1	S <mark>FPEEVLE</mark> HVFS <mark>F</mark> IW <mark>SERDRNA</mark> I <mark>SL</mark>	33
Glyma.19G206800 Glyma.19G206800.1	S <mark>FPEEVLE</mark> HVFS <mark>F</mark> IWNERDRNA <mark>ISL</mark>	33
Lj1g0015670 Lj1g0015670.1	SFPEEVLEHVFSFIQVDTDRNAISL	31
AT3G62980 AT3G62980.1	SFPEEVLEHVFSFIQLDKDRNSVSL	32
AT4G03190 AT4G03190.1		28
AT1G12820 AT1G12820.1		27
AT3G26810 AT3G26810.1		27
Glyma.16G050500 Glyma.16G050500.1		28
Glyma.19G100200 Glyma.19G100200.1		28
Lj1g0006513 Lj1g0006513.1	MMNYYVVSHRDRNALSL	28
Glyma.16G146400 Glyma.16G146400.1		27
Glyma.02G065300 Glyma.02G065300.1		27
AT4G24390 AT4G24390.1	MTEEDSSAKMSEDVEKYLNLNPPCSSSSSSSSAATFTNKSRNFKSSPPPCPDHVLENVLENVLENVLQFLTSRCDRNAVSL	77
AT5G49980 AT5G49980.1	MTQDRSE <mark>M</mark> SEDDDDQQSPPLDLPSTAIADPCSSSSSPNKSRNCISNSQT <mark>FPD</mark> H <mark>VLE</mark> NVLENVLQ <mark>F</mark> LD <mark>S</mark> RCDRNA <mark>ASL</mark>	77
Glyma.04G093500 Glyma.04G093500.1	RTLSPLPDQVLENVLESVLHFLTSRRDRNAASL	40
Glyma.06G095400 Glyma.06G095400.1		44
Glyma.02G211800 Glyma.02G211800.1	MRDKSESHPSTNSEDDHRSSPLLDLAC.AEITESSNSKTRTCGPFPGSGPSEPQAP <mark>FPD</mark> QVLENVLENVLHFLPSRRDRNAASL	83
Glyma.14G179500 Glyma.14G179500.1	MREK.ENHPSTNSEDDHRSS.LLDLAR.AEITESSNSKTRTCGSGLGSGSGTSEPQAP <mark>FPD</mark> QVLENVLENVLHFLS <mark>S</mark> RRDRNAA <mark>SL</mark>	83
Lj1g0027142 Lj1g0027142.1	MRDNHPPPPTSDDDHRSSSLPDLARGGQITDSSSSKTRPGPGSSSSSLPQPGSSSELQAQ <mark>FPD</mark> Q <mark>VLENV</mark> LENVLH <mark>F</mark> LS <mark>S</mark> RRDRNAA <mark>SL</mark>	88
Glyma.02G254300 Glyma.02G254300.1	RRLSDVVLDCVMPYIHDSKDRDAVSQ	29
Glyma.14G062100 Glyma.14G062100.1	MEDRDAKRMAYIHDS <mark>KDRDA</mark> V <mark>S</mark> Q	36
Glyma.11G227300 Glyma.11G227300.1	TRVVDLVLDCVIPYIDDPKDRDAVSQ	35
Glyma.18G030200 Glyma.18G030200.1	MTEERNVRKYIDDPKDRDAVSQ	35
Lj3g0010583 Lj3g0010583.1		28
Lj6g0020395 Lj6g0020395.1	Maaaaatedrsarryiddp <mark>kdrdavS</mark> Q	40
AT2Ğ39940 AT2Ğ39940.1	MEDPDIKRCKLSCYITDPKDRDSASI	39

Glyma.08G059500 Glyma.08G059500.6 Glyma.07G189800 Glyma.07G189800.5	VCKEWYNAERWSRRSVFIGNCYSVSPEILTRRFPNIRSVTLKGKPRFSDFNLVPANWGADIHSWLVVFAGKYP.WLEELRLKRMTVTDES VCKEWFNAERWSRRSVFIGNCYSVSPEILTRRFPNIRSVTLKGKPRFSDFNLVPANWGADIHSWLVVFAEKYP.WLEELRLKRMTVTDES	129 128
Lj4g0012889.1 Lj4g0012889.1	VCK <mark>EWYNA</mark> ERWSRRSVFIGNCYSVSPEILTRRFPNIRSVTLKGKPRFSDFNLVPANWGADIRSWLVVFADKYP.LLEELRLKRMTVSDES	134
Glyma.02G152800 Glyma.02G152800.2	VCKSWYEIERWCRRRVFVGNCYAVSPATVVNRFPKVRSIAIKGKPHFADFNLVPEGWGAYVGPWIKAMAAAYP.WLQEIRLKRMVIADEC	121
Glyma.10G021500 Glyma.10G021500.2	VCKSWYEIERWCRRRVFVGNCYAVSPATVVNRFPKVRSIAIKGKPHFADFNLVPEGWGAYVGPWIKAMAAAYP.WLQEIRLKRMVISDEC	121
Lj5g0004781 Lj5g0004781.1	VCRSWYEIERCCRRNVFVGNCYAVSPEMVVKRFPRVRSVTLKGKPHFADFNLVPDGWGGYVSPWIKAMAAACP.SLLEIRLKRMVVTDDC	120
Glyma.03G209400 Glyma.03G209400.1	VCKSWYEIERWCRRKVFVGNCYAVSPLMVIKRFPELRSIALKGKPHFADFNLVPEGWGGYVCPWIAAMARAFP.CLEEIRLKRMVITDES	122
Glyma.19G206800 Glyma.19G206800.1	VCKSWYEIERWCRRKVFVGNCYAVSPLMVVKRFPEVRSIALKGKPHFADFNLVPDGWGGYVCPWIAAMARAFP.CLEEIRLKRMVITDES	122
Lj1g0015670 Lj1g0015670.1	VCKSWYEIERWCRRKVFVGNCYAVSPMIVIKRFPEVRSIALKGKPHFADFNLVPEGWGGYVCTWIAAMSRAFP.WLEEIRLKRMVISDES	120
AT3G62980 AT3G62980.1	VCKSWYEIERWCRRKVFIGNCYAVSPATVIRRFPKVRS <mark>VE</mark> LKGKPHFADFNLVPDGWGGYVYPWIEAMSSSYT.WLEEIRLKRM <mark>V</mark> VTDDC	121
AT4G03190 AT4G03190.1	VCKSWFETERKTRKRVFVGNCYAVSPAAVTRRFPEMRSLTLKGKPHFADYNLVPDGWGGYAWPWIEAMAAKSS.SLEEIRMKRMVVTDEC	117
AT1G12820 AT1G12820.1	VCKSWHKIERFSRKEVFIGNCYAINPERLIRRFPCLKSLTLKGKPHFADFNLVPHEWGGFVHPWIEALARSRV.GLEELRLKRMVVTDES	116
AT3G26810 AT3G26810.1	VCKSWYKIERYSRQKVFIGNCYAINPERLLRRFPCLKSLTLKGKPHFADFNLVPHEWGGFVLPWIEALARSRV.GLEELRLKRMVVTDES	116
Glyma.16G050500 Glyma.16G050500.1	VCKSWYRIER <mark>CTRQR</mark> VFIGNCY <mark>S</mark> ITPERLIQRFPGLKSLTLKGKPHFADF <mark>S</mark> LVPYDWGGFVHPWIEALAKNKV.GLEELRLKRM <mark>V</mark> VSDES	117
Glyma.19G100200 Glyma.19G100200.1	VCKSWYRIER <mark>C</mark> TRQRVFIGNCYSITPERLIQRFPGLKSLTLKGKPHFADFSLVPYDWGGFVHPWVEALAKSRV.GLEELRLKRM <mark>V</mark> VSDES	117
Lj1g0006513 Lj1g0006513.1	VCKSWYRIEKSTRKRVFIGNCYSISPERLIQRFPSLRSLTLKGKPHFADFSLVPLDWGGFVYPWIEALAKNKV.GLEELRLKRMVVSDES	117
Glyma.16G146400 Glyma.16G146400.1	VCK <mark>NWHRLERCCRKSL</mark> FIGNCYTISPERVIËRFPELRSLTLKGKPHFPYFSLVPSGWGGFVAPWIEALARSRV.DLEELRLKRMVVSDES	116
Glyma.02G065300 Glyma.02G065300.1	VCK <mark>NWHRLERCSRKSL</mark> FIGNCYSISPERVIERFPELKSLTLKGKP <mark>HFADFNLVPHGWGGFVS</mark> PWIEAMVKSRV.DLEELRLKRM <mark>V</mark> VTDKS	116
AT4G24390 AT4G24390.1	VCRSWYRVEAQTRLEVFIGNCYSLSPARLIHRFKRVRSLVLKGKPRFADFNLMPPNWGAQFSPWVAATAKAYP.WLEKVHLKRMFVTDDD	166
AT5G49980 AT5G49980.1	VCKSWWRVEALTRSEVFIGNCYALSPARLTQRFKRVRSLVLKGKPRFADFNLMPPDWGANFAPWVSTMAQAYP.CLEKVDLKRMFVTDDD	166
Glyma.04G093500 Glyma.04G093500.1	VCKSWYRAEALTRTELFIGNCYA <mark>VSPRRATG</mark> RFPRVRS <mark>VTI</mark> KGKPRFADFDLMPLNWGAHFTPWVTALSQSYHSSLNKLHLKRMSLTDHD	130
Glyma.06G095400 Glyma.06G095400.1	VCKSWYRAEALTRPDLFIGNCYA <mark>VSPRRATARFPRVRSLTI</mark> KGKPRFADFDLMPLNWGAHFTPWATALSQSYPSS <mark>LNKL</mark> HLKRMSLTDHD	134
Glyma.02G211800 Glyma.02G211800.1	VCRSWYRAEALTRSELFIGNCYALSPTRATARFTRVMSVTVKGKPRFADFDLMPPDWGAHFGPWASALAQAYP.WLEKLHLKRMLVTDAD	172
Glyma.14G179500 Glyma.14G179500.1	VCRSWYRAEALTRSELFIGNCYALSPTRATARFTRARSVTVKGKPRFADFDLMPADWGAHFSPWASALSQAYP.WLEKLHLKRMLLTDAD	172
Lj1g0027142 Lj1g0027142.1	VCRSWCRAEALTRSELFIGNCYAVSPRRATARFSRVRSVTVKGKPRFADFDLMPDDWGAHFAPWATALAQAYP.WLEKIHLKRMSVTDED	177
Glyma.02G254300 Glyma.02G254300.1	VCRRWYELDSLTRKHVTIALCYTTTPDRLRRRFPHLESLKLKGKPRAAMFNLIPEDWGGFVTPWVRVISQYFD.CLKSLHFRRMIVRDSD	118
Glyma.14G062100 Glyma.14G062100.1	VCRRLYELDSLTRKHVTIALCYTTTPDRLRRRFPHLESLNLKGKPRAAMFNLIPEDWGGFVTPWVREISQYFD.CLKSLHFRRMIVRDSD	125
Glyma.11G227300 Glyma.11G227300.1	VCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFD.CLKSLHFRRMIVKDSD	124
Glyma.18G030200 Glyma.18G030200.1	VCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFD.CLKSLHFRRMIVKDSD	124
Lj3g0010583 Lj3g0010583.1		28
Lj6g0020395 Lj6g0020395.1	VCKCWYELDSLTRKHVTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNLIPEDWGGHVTPWVLEINQYFD.CLKSLHFRRMIVKDND	129
AT2G39940 AT2G39940.1	VCRRWFKIDSETREHVTMALCYTATPDRLSRRFPNLRSLKLKGKPRAAMFNLIPENWGGYVTPWVTEISNNLR.QLKSVHFRRMIVSDLD	128
consensus	***** ** ** ****** ** ** ** ** *** *****	





ACTNLTFLNFSYAP.LDSDGLAKLLVHCPKLQRIWVVDTVEDKGLEAVGSHCPLLEELRVFPADPFD..EGIVHGVTESGFIAVSQGCPRACTNLTFLNFSYAP.LDSDGLTKLLVHCPKLQRLWVVDTVEDKGLEAVGSHCPLLEELRVFPADPFD..EGIVHGVTESGFIAVSQGCPR 381 Glyma.08G059500 Glyma.08G059500.6 Glyma.07G189800 Glyma.07G189800.5 380 ACTNLTFFNLSYAP.LDGDDLAKLLVHCPNLRRLWVVDTVEDKGLEAVGSHCPLLEELRVFPADPFED.EAIGHGVTESGFVALSRGCPR Lj4g0012889.1 Lj4g0012889.1 388 ICSNLTSLNLSYAT.IQSPDLIKLVGQCESLQRLWVLDYIEDAGLEVIAASCKDLRELRVFPSDPFG..LEPNVALTEQGLVSVSEGCTK Glyma.02G152800 Glyma.02G152800.2 373 ICSNLTSLNLSYAT.IQSPDLIKLVGQCESLQRLWVLDYIEDAGLEVIAASCKDLRELRVFPSDPFG..LEPNVALTEQGLVSVSEGCTK VCSGLTSLNLSYAT.IQSPDHIKLVSQCGSLQRLWVLDYIEDAGLDVLAASCKDLRELRVFPSDPFG..LEPNVALTEEGLISVSEGCPK 373 Glyma.10G021500 Glyma.10G021500.2 Lj5g0004781 Lj5g0004781.1 372 ICSRLTSLNLSYAI.IQSSDLIKLTSQCPNLLRLWVLDYIEDAGLYALAASCKDLRELRVFPSEPFG..LEPNVSLTEQGLVSVSEGCPP Glyma.03G209400 Glyma.03G209400.1 374 ICSRLTSLNLSYAI.IQSSDLIKLISQCPNLLRLWVLDYIEDAGLYALAASCKDLRELRVFPSDPFG..LEPNVALTEQGLVSVSEGCP 375 Glyma.19G206800 Glyma.19G206800.1 VCSGLTSLNLSYAT.VQSSDLVKLISQCPSLQRLWVLDFIEDAGLDVLAASCKDLRELRVFPSDPFG..FEPNVALTERGLVSVSEGCPF Lj1g0015670 Lj1g0015670.1 372 VCSRLTTLNLSYAT.VQSYDLVKLLCQCPKLQRLWVLDYIEDAGLEVLASTCKDLRELRVFPSEPFV..MEPNVALTEQGLVSVSMGCPK VCPGLTSLNLSYAT.VRMPDLVELLRRCSKLQKLWVMDLIEDKGLEAVASYCKELRELRVFPSEPDL..DATNIPLTEQGLVFVSKGCRK AT3G62980 AT3G62980.1 373 AT4G03190 AT4G03190.1 369 CQNL<mark>I</mark>SLNLSYAAEIQGNHLIKLIQLCKRLQRLWILDSIGDKGLAVVAATCKELQELRVFPSDVHGE.EDNNASVTE**V**GLVAISAGCPK CHNLTSLNLSYAAEIHGSHLIKLIQHCKKLQRLWILDSIGDKGLEVVASTCKELQELRVFPSDLLG...GGNTAVTEEGLVAISAGCPK 370 AT1G12820 AT1G12820.1 368 AT3G26810 AT3G26810.1 ICPNLTSLNLSYAAGIQGSDLIKLIRHCVKLQRLLIMDCIGDKGLDVVATSCKDLQELRVFPSVPFG....NPAAVTEKGLVAISMGCPK
ICPNLTSLNLSYAAGIQGSALVKLIHHCVKLQRLWIMDCIGDKGLGVVATTCKDLQELRVFPSVPFG....DPAAVTEKGLVAISMGCPK
ICRNLTALNLSYAAGIHGNELIKLIYHCGKLQRLWIMDCIGDKGLGIVASTCKELQELRVFPSAPFG....NPAAVTEKGLVAISAGCRK Glyma.16G050500 Glyma.16G050500.1 368 368 Glyma.19G100200 Glyma.19G100200.1 368 Lj1g0006513 Lj1g0006513.1 VCMNLTTLNLRFAAGIQNTELIKLICCCGKLQRLSIMDCIGDNGLGVVAATCKDLQELRVFPVVRVGG..NGPTRVTEKGLVAISMGCPE VCMNLTAMNLSYAAGIQSRELIKLICRCGKLQRLWIMDCIGDFGLHVVASTCKDLQELRVFPSVRVGR..NDPAGVTEKGLVAISMGCPK Glyma.16G146400 Glyma.16G146400.1 369 Glyma.02G065300 Glyma.02G065300.1 369 VCANLTSLNFSYAN.ISPHMLKPIISNCHNIRVFWALDSIRDEGLQAVAATCKELRELRIFPFDPRE...DSEGPVSGVGLQAISEGCRK VCANLTSLNFSYAN.ISPDMFKPIILNCHKLQVFWALDSICDEGLQAVAATCKELRELRIFPFDPRE...DSEGPVSELGLQAISEGCRK ACANLISLNFSYAD.ISADQLISVIRHCHKLQTFWVLDTICDEGLQAVAETCKDLRELRVFPVNTRE...EIEGPVSEVGFEAISRGCRK AT4G24390 AT4G24390.1 419 AT5G49980 AT5G49980.1 419 Glyma.04G093500 Glyma.04G093500.1 384 ACANLISLNFSFAD. ISADQLKSVIRHCHKLQTFWVLDTICDEGLQAVAETCKDLRELRVFPVNTRE. . . EIEGPVSEVGFEAISRGCR 388 Glyma.06G095400 Glyma.06G095400.1 VCANLTSLNLSYAD.INTDQLKSVICHCHKLQIFWVLDSIRDEGLQAVAATCKDLRELRVFPMDARE...ETDGPVSEVGFEAISQGCRK VCTNLTSLNLSYAD.VNTDQLKSVIRHCHKLQIFWVLDSIRDEGLQAVAATCKDLRELRVFPVDARE...ETDGPVSEVGFEAISQGCRK Glyma.02G211800 Glyma.02G211800.1 429 Glyma.14G179500 Glyma.14G179500.1 432 VCANLTSLNLSYAD.VNADQLRSVICHCRKLQILWALDSIGDEGLQAVATTCHDLRELRVFPVDARE...ESEGPVSEVGFEAISKGCRK
YAALLKKLDLLYAM.LDTEDHCTLIQRCPNLEVLESRNVIGDRGLEVLARCCRRLKRIRIERGDDDQGMEDEEGVVSQRGLIALSHGCPE
YAALLKKLDLLYAM.LDTEDHCTLIQRCPNLEVLESRNVIGDRGLEVLARCCRRLKRLRIERGDDDQGMEDEEGVVSQRGLIALSHGCPE Lj1g0027142 Lj1g0027142.1 431 Glyma.02G254300 Glyma.02G254300.1 366 Glyma.14G062100 Glyma.14G062100.1 373 FAAVLKKLDLLYAM.LDTEDHCMLIQKCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQGCSE Glyma.11G227300 Glyma.11G227300.1 372 FAAVLKKLDLLYAM.LDTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRIERGEDDDQGMEDEEGTVSHRGLIALSQGCSE Glyma.18G030200 Glyma.18G030200.1 372 FAAALTKLDLLYAL.LDTDDH......DRGLEVLGSCCKRLKRLRIECGDDDQGMEDEGGTVCHRGLIALSE.... Lj3g0010583 Lj3g0010583.1 200 FAAALTKLDLLYAL.LDTDDHCMLIQKCPNLEVLETRNVIGDRGLEVLGSCCKRLKRLRIERGDD.....EGETVSHRGLIALSEGCSE Lj6g0020395 Lj6g0020395.1 371 FAAQIRKLDLLYAL.LETEDHCTLIQKCPNLEVLETRNVIGDRGLEVLAQYCKQLKRLRIERGADEQGMEDEEGLVSQRGLIALAQGCQE 379 AT2G39940 AT2G39940.1 consensus

Glyma.08G059500 Glyma.08G059500.6	LHYVLYFCRQMTNAAVATVVQNCPDFTHFRLCIMHPGQPDYLTQESMDEAFGAVVKTCTKLQRLAVSGYLTDLTFEYIGKYAKNLET	468
Glyma.07G189800 Glyma.07G189800.5	LHYVLYFCRQMTNAAVATVVQNCPDFTHFRLCIMHPGQLDYLTQESMDEAFGAVVKTCTKLQRLAVSGYLTDLTFEYIGKYAKNLET	467
Lj4g0012889.1 Lj4g0012889.1	LHYVLYFCRQMTNAAVATVVQNCPDFTHFRLCIMNPGQPDYLTHEPMDEAFGAVVKTCSKLQRLAVSGLLTDLTFEYIGKYAKNLET	475
Glyma.02G152800 Glyma.02G152800.2	LQSVLYFCRQMSNAALDTIARSRPNMTRFRLCIIEPRAPDYLTHQPLDAGFGAIVEHCKDLQRLSLSGLLTDRVFEYIGTYGKKLEM	460
Glyma.10G021500 Glyma.10G021500.2	LQSVLYFCRQMTNSALDTIARNRPNMTRFRLCIIEPQAPDHLTHQPLDAGFGAIVEHCKDLQRLSLSGLLTDRVFEYIGTYGKKLEM	460
Lj5g0004781 Lj5g0004781.1	LQSVLYFCRQMSNAALNTIAQNRPNMTRFRLCIIEPRTPDYLTHQPLDAGFGAIVQHCKNLQRLSLSGLLTDRVFEYIGTYAKKLEM	459
Glyma.03G209400 Glyma.03G209400.1	LQSVLYFCRQMSNAALHTIARNRPNLTRFRLCIIEPRTPDYLTLEPLDSGFGAIVEQCKDLQRLSLSGLLTDRVFEYIGTYAKKLEM	461
Glyma.19G206800 Glyma.19G206800.1	LQSVLYFCRQMSNAALHTIARNRTNLTRFRLCIIEPRTPDYLTHEPLDSGFGAIVEQCKDLQRLSLSGLLTDRVFEYIGTCGKKLEM	462
Lj1g0015670 Lj1g0015670.1	LQSVLYFCRQMSNAALHTIARNRPNFTCFRLCIIEPQAPDYLTLQPLDSGFGAIVEHCKGLQRLSLSGLLTDRVFEYIGTYGKKLEM	459
AT3G62980 AT3G62980.1	LESVLYFCRQMTNAALITIARNRPNMTRFRLCIIEPKAPDYLTLEPLDIGFGAIVEHCKDLRRLSLSGLLTDKVFEYIGTYAKKMEM	460
AT4G03190 AT4G03190.1	LESVLYFCVQFTNAALFTIARKRPNLKCFRLCVIEPFAPDYKTNEPLDKGFKAIAEGCRDLRRLSVSGLLSDKAFKYIGKHAKKVRM	456
AT1G12820 AT1G12820.1	LHSILYFCKQMTNAALIAVAKNCPNFIRFRLCILEPHKPDHITFQSLDEGFGAIVQACKGLRRLSVSGLLTDQVFLYIGMYAEQLEM	457
AT3G26810 AT3G26810.1	LHSILYFCQQMTNAALVTVAKNCPNFIRFRLCILEPNKPDHVTSQPLDEGFGAIVKACKSLRRLSLSGLLTDQVFLYIGMYANQLEM	455
Glyma.16G050500 Glyma.16G050500.1	LHSLLYFCHQMTNAALITVAKNCPNFIRFRLCILDATKPDPDTMQPLDEGFGAIVQSCRRLRRLSLSGQLTDQVFLYIGMYAEKLEM	455
Glyma.19G100200 Glyma.19G100200.1	LHSLLYFCHQMTNAALITVAKNCPNFIRFRLCILDATKPDPDTMQPLDEGFGAIVQSCRRLRRLSLSGKLTDQVFLYIGMYAEKLEM	455
Lj1g0006513 Lj1g0006513.1	LHSLLYFCHQMTNAALITVAKNCPNFIRFRLCILDATKPDPDTMQPLDEGFGAIVQSCKRLRRLSLSGQLTDQVFLYIGMYAEQLEM	455
Glyma.16G146400 Glyma.16G146400.1	LHSLLYFCQQMTNAALITVAKNCPNFIRFRLCILDPTKPDPDTMQPLNEGFGAIVQSCKQLRRLSLSGQLTDQVFLYIGMYAEQLEM	456
Glyma.02G065300 Glyma.02G065300.1	LHSLLYFCQQMTNAALITVAKNCPNFIRFRLCILDPTKPDPDTVQPLDEGFGAIVQSCKQLRRLSLSGQLTDQVFLYIGVYAEQLEM	456
AT4G24390 AT4G24390.1	LESILYFCQNMTNGAVTAMSENCPQLTVFRLCIMGRHRPDHVTGKPMDDGFGAIVKNCKKLTRLAVSGLLTDEAFSYIGEYGKLIRT	506
AT5G49980 AT5G49980.1	LESILYFCQRMTNAAVIAMSENCPELTVFRLCIMGRHRPDHVTGKPMDEGFGAIVKNCKKLTRLAVSGLLTDQAFRYMGEYGKLVRT	506
Glyma.04G093500 Glyma.04G093500.1	LQSILFFCQRMTNAAVVAMSNNCPDLVVFRLCIIGRYRPDPETLEPMDEGFGAIVMNCKKLTRLAVSGLLTDRAFNYIGTYGKLIRT	471
Glyma.06G095400 Glyma.06G095400.1	LQSILFFCQRMTNAAVVAMSNNCPDLVVFRLCIIGQYRPDPVTLEPMDEGFGAIVMNCKKLTRLAVSGLLTDRAFSYIGTYGKLIRT	475
Glyma.02G211800 Glyma.02G211800.1	LESILFLCQRMTNAAVVAMSKNCPDLVVFRLCIIGRYRPDPVTQEPMDEGFGAIVMNCKKLTRLAVSGLLTDRAFEYIGTYGKLVRT	516
Glyma.14G179500 Glyma.14G179500.1	LESILFFTQRMTNAAVVAMSKNCPDLVVFRLCIIGRYRPDPVTEEPMDEGFGAIVMNCKKLTRLAMSGLLTDRVFEYIGMYGKLVRT	519
Lj1g0027142 Lj1g0027142.1	LESILFFCQRMTNAAVVAMSKNCPDLLVFRLCIIGRYRPDAVTQEPMDEGFGAIVMNCRKLTRLAVSGLLTDRAFEYIGRYGKLVRT	518
Glyma.02G254300 Glyma.02G254300.1	LEYLAVYVŠDITNASLEHIGTHLKNLCDFRLVLLDREEKITDLPLDNGVRALLRGCDKLRRFALYLRPGGLTDVGLGYVGQYSPNVRW	454
Glyma.14G062100 Glyma.14G062100.1	LEYLAVYVSDI <mark>TNASLEHIGTHLKNLCDFRL</mark> VLLDREEKI <mark>T</mark> DLPLDNGVRALLRGCDKLRRFALYLRPGGLTDVGLGYIGQYSPNVRW LEYMAVYVSDITNA <mark>S</mark> LEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCNKLRRFALYLRRGGLTDVGLGYIGQYSPNVRW	461
Glyma.11G227300 Glyma.11G227300.1	LEYMAYYVSDITNASLEHIGIHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCNKLRRFALYLRRGGLTDVGLGYIGQYSPNVRW	460
Glyma.18G030200 Glyma.18G030200.1	LEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRW	460
Lj3g0010583 Lj3g0010583.1	VYLPLDRGVRALLRGCDKLKRFALYLRRRGLTDVGLGYIG.YPP	243
Lj6g0020395 Lj6g0020395.1	LEYLAVYVSDITNASLEHMGTHLRNLCDFRLVLLDQEEKITDLPLDRGVQALLRGCDKLKRFALYLRRGGLTDVGLSYIGQYSQNVRW	459
AT2G39940 AT2G39940.1	LEYMAVYVSDITNESLESIGTYLKNLCDFRLVLLDREERITDLPLDNGVRSLLIGCKKLRRFAFYLRQGGLTDLGLSYIGQYSPNVRW	467
consensus	* * * * * * * * * * * * * * * * * * * *	

Glyma.08G059500 Glyma.08G059500.6	LSVAFAGSSDWGMRCVLDGCPKLRKLEVRDCP.FGNGALLSGLGKYESMRSLWMSDCNLTMNGVRLLAKEMPRLNVEVIKEETYLSVAFAGSSDWGMRCVLDGCPKLRKLEVRDCP.FGNGALLSGLGKYESMRSLWMSDCNLTMNGVRLLAQEMPRLNVEVIKEESY	. 551 . 550
Glyma.07G189800 Glyma.07G189800.5	LSVAFAGSSDWGMECVLDGGFKLRKLEVRDGF.FGNGALLSGLGRIESMRSLWMSDCNLIMNGVRLLAGEMFRLNVEVIKEESI LSVAFAGSSDWGMECVLRGCPKLRKLEIRDCP.FGNGALLSGLERYESMRSLWMSDCKLTMNGCRLLAKEMPRLNVEVIKEEGC	
Lj4g0012889.1 Lj4g0012889.1	LSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCP.FGNAALLSGLERIESHRSLWMSDCKLIMNGGRELAKEMPRENVEVIRDEGCP	. 556 D 545
Glyma.02G152800 Glyma.02G152800.2		D 545 D 545
Glyma.10G021500 Glyma.10G021500.2		
Lj5g0004781 Lj5g0004781.1	LSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCP.FGDKALLANAAKLETMRSLWMSSCLVSYGACKLLGQKMPRLNVEVIDERGPP	
Glyma.03G209400 Glyma.03G209400.1	LSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCP.FGDKALLANAEKLETMRSLWMSSCSVSYGACKLLGQKMPRLNVEVIDERGPP	
Glyma.19G206800 Glyma.19G206800.1	LSVAFAGDSDLGLHHVLSGCDNLRKLEIRDCP.FGDKALLANAEKLETMRSLWMSSCSVSYGACKLLGQKMPRLNVEVIDERGPP	D 547
Lj1g0015670 Lj1g0015670.1	LSLAFAGDSDLGLHHVLSGCDNLKKLEIRDCP.FGDKALLANAAKLETMRSLWMSSCSVSYGACKLLGLKMPKLNVEVIDERGPP	D 544
AT3G62980 AT3G62980.1	LSVAFAGDSDLGMHHVLSGCDSLRKLEIRDCP.FGDKALLANASKLETMRSLWMSSCSVSFGACKLLGQKMPKLNVEVIDERGAP	D 545
AT4G03190 AT4G03190.1	LSIAFAGDSD <mark>LM</mark> LHHLLSGCESLKKLEIRDCP.FGDTALLEHAAKLETMRSLWMSSCFVSFGACKLLSQKMPRLNVEVIDEH.PP	E 540
AT1G12820 AT1G12820.1	LSIAFAGDTDKGMLYVLNGCKKMRKLEIRDSP.FGNAALLADVGRYETMRSLWMSSCEVTLGGCKRLAQNSPRLNVEIINENENNGMEQ	N 546
AT3G26810 AT3G26810.1	LSIAFAGDTDKGMLYVLNGCKKMKKLEIRDSP.FGDTALLADVSKYETMRSLWMSSCEVTLSGCKRLAEKAPWLNVEIINENDNNRMEE	N 544
Glyma.16G050500 Glyma.16G050500.1	LSIAFAGESDKGMLYVLNGCKKLRKLEIRDCP.FGNVALLTDVGKYETMRSLWMSSCEVTVGACKLLAKKMPRLNVEIFNENEQED	C 541
Glyma.19G100200 Glyma.19G100200.1	LSIAFAGDGDKGMLYVLNGCKKLRKLEIRDCP.FGDMALLTDVGKYETMRSLWMSSCEVTVGACKLLAKKMPRLNVEIFNENEQED	C 541
Lj1g0006513 Lj1g0006513.1	LS <mark>I</mark> AFAG <mark>ESDKGMQYVLNGCKKLR</mark> KLEIRDCP.FG <mark>N</mark> MALLADIGKYETMRSLWMSSCEVTVGACKELAEKMPRLNVEIFNENEQEE	C 541
Glyma.16G146400 Glyma.16G146400.1	LSVAFAGESDKAMLYVLNGCKKIHKLAIRGSP.FGDSALLMDVGKYETMQFLWMTSCNVTVGACKALAEKMPRLNVEIFNENKKVD	R 542
Glyma.02G065300 Glyma.02G065300.1	LSIAFAGESDKAMLYVLNGCKKLRKLEIRDSP.FGDSALLMDVGKYETMRSLWMSSCDVTIGACKALAKKMPGLNVEIFNGNEKVD	R 542
AT4G24390 AT4G24390.1	LSVAFAGNSDKALRYVLEGCPKLQKLEIRDSP.FGDVGLRSGMHRYSNMRFVWLSSCLISRGGCRGVSHALPNVVVEVFGADGDDDEDT	V 595
AT5G49980 AT5G49980.1	LSVAFAGDSDMALRHVLEGCPRLQKLEIRDSP.FGDVALRSGMHRYYNMRFVWMSACSLSKGCCKDIARAMPNLVVEVIGSDDDDD	. 591
Glyma.04G093500 Glyma.04G093500.1	LSVAFAGDTDLGLQYVLEGCPNLQKLEIRDSP.FGDGALRSGLHHFYNMRFLWMSSCKLTRQACREVARMLPHLVLEVINSEEDKADD.	. 558
Glyma.06G095400 Glyma.06G095400.1	LSVAFAGDTDLGLQYVLQGCPNLQKLEIRDSP.FGDGALHSGLHHFYNMRFLWMSSCKLTRQACQEVAQTLPHLVLEVINSEEDKADG.	. 562
Glyma.02G211800 Glyma.02G211800.1	LSVAFAGDTDVGLKYVLKGCPNLQKLEIRDSP.FGDGALRSGLHHYYNMRFLWMSTCKLTLQACQEVARVLPNLVFEVINNNSEENAG.	. 603
Glyma.14G179500 Glyma.14G179500.1	LSVAFAGDTDVGLKYVLEGCPNLQKLEIRDSP.FGDGALRSGLHHYYNMRFLWMSSCKLTRQACQEVARALPNLVLEVINNNNEENAGD	E 608
Ljľg0027142 Lj1g0027142.1	LSVAFNGDTDLALKYVLEGCPNMOKLEIRDCP.FGDAALRSGLHHYYNMRFLWMSNCKLTROACODVARALPHLVVEVINKEDEAAVD.	. 605
Glyma.02G254300 Glyma.02G254300.1	MLLGYVGETDAGLLEFSKGCPSLQKLEMRGCSFFSEYALAIAATQLNSLRYLWVQGYSASASGRDLLAMARPYWNIELIPSRSVVVSNQ	Q 544
Glyma.14G062100 Glyma.14G062100.1	MLLGYVGETDAGLLEFSKGCPSLQKLEMRGCSFFSEYALAIAATQLNSLRYLWVQGYGASPSGRDLLAMARPYWNIELIPSRRVVVSNQ	Q 551
Glyma.11G227300 Glyma.11G227300.1	MLLGYV <mark>GESDAGL</mark> LEFSK <mark>GCPSLQKLEMRGCSFF</mark> SER <mark>ALAVAATQLTSLRYLWVQGYGVS</mark> PSGRDLLAMARPFWNIELIPSRKVAMNTN	S 550
Glyma.18G030200 Glyma.18G030200.1	MLLGYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVATNTN	P 550
Lj3g0010583 Lj3g0010583.1	VIELIPSRRVVTKNN	M 300
Lj6g0020395 Lj6g0020395.1	MLLGAVGETDEGLLEFAKGCPNLQKLEMRGCSFFSEHALAVAATQLTSLRYLWVQGYGASPTGRDLLAMARPFWNIELIPSRRVVVNNN	M 549
AT2G39940 AT2G39940.1	MLLGYVGESDEGLMEFSRGCPNLQKLEMRGCC.FSERATAAAVTKLPSLRYLWVQGYRASMTGQDLMQMARPYWNIELIPSRRVPEVNQ	Q 556
consensus	******* ** ** ** ** ** ** ** ** ** ** *	7 000
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Glyma.08G059500 Glyma.08G059500.6	ET HOAKKVYVYBSVAGPERDAPPFWI.TL	579
Glyma.07G189800 Glyma.07G189800.5	ETHQAKKVYVYRSVAGPRRDAPPFVLTL	578
Lj4g0012889.1 Lj4g0012889.1	YEGPAQRVYVYRSVAGPRRDAPSFVLAHCGPHNARGSGKGSTTWSIVCTMQPYLVCYMRGYFQNL.	623
Glyma.02G152800 Glyma.02G152800.2	SRPESSPVEKLYIYRTVSGPRLDMPGYVWRMQDDSALRIS	585
Glyma.10G021500 Glyma.10G021500.2	SRPES SPVEKLVMYRTVSGPRLDMPGYVWRMODD SALRIS	585
Lj5g0004781 Lj5g0004781.1	TRPESSPVEKLYIYRTISGPRVDMPGYVWTMEDDSAYLK	583
Glyma.03G209400 Glyma.03G209400.1	SRPDDCPVEKLYIYRTVAGPRLDMPGFVWTMEDDSSLRLE	586
Glyma.19G206800 Glyma.19G206800.1	SRPDDCPVEKLYIYRTIAGPRLDMPGFVWTMEDDSSLRLE	587
Lj1g0015670 Lj1g0015670.1	SRPDSCPVEKLYIYRTIAGPRMDMPGFVYRMEDDDSALRLE	585
AT3G62980 AT3G62980.1	SRPESCPVERVFIYRTVAGPRFDMPGFVWNMDQDSTMRFSRQIITTNGL	594
AT4G03190 AT4G03190.1	SRPESSPVERIYIYRTVAGPRMDTPEFVWTIHKNPENGVSHLAIK	585
AT1G12820 AT1G12820.1	EEDEREKVDKLYLYRTVVGTRKDAPPYVRIL	577
AT3G26810 AT3G26810.1	GHEGRQKVDKLYLYRTVVGTRMDAPPFVWIL	575
Glyma.16G050500 Glyma.16G050500.1	SLEDGQK <mark>VE</mark> KM <mark>YLYRTLAG</mark> KRKDAPEY <mark>V</mark> WTL	572
Glyma.19G100200 Glyma.19G100200.1	SLEDGQK <mark>VE</mark> KMYLYR <mark>T</mark> LAGK <mark>R</mark> KDAPEYVWTL	572
Lj1g0006513 Lj1g0006513.1	SLEDEQSVEKMYLYRTLAGKRNDAPEYVCTL	572
Glyma.16G146400 Glyma.16G146400.1	DVDDGQK <mark>VE</mark> KM <mark>YLYRTLAGRR</mark> KDAPEL <mark>VWTL</mark>	573
Glyma.02G065300 Glyma.02G065300.1	DVDDGQK <mark>VEKTYLYRTLVGRRKDAPEHVWTL</mark>	573
AT4G24390 AT4G24390.1	TGDYVETLYLYRSLDGPRKDAPKFVTIL	623
AT5G49980 AT5G49980.1	NRDY <mark>VE</mark> TL <mark>YMYRSL</mark> DGPRNDAPKFVTIL	619
Glyma.04G093500 Glyma.04G093500.1	IEILYMYRSLDRPRDDAPKVVTILC	583
Glyma.06G095400 Glyma.06G095400.1	<u>l</u> eilymyrsl <mark>dgpr</mark> ddapkvvti <mark>l</mark> c	587
Glyma.02G211800 Glyma.02G211800.1	DE <mark>VETLYMYRSL</mark> DGPR <mark>DDAP</mark> RF <mark>V</mark> TI <mark>L</mark> Q	630
Glyma.14G179500 Glyma.14G179500.1	EENAGDE <mark>VETLYMYRSL</mark> DGPRDDAPRFVTI <mark>L</mark> Q	640
Lj1g0027142 Lj1g0027142.1	DIELLYMYRSLDGPRDDAPQVVTILH	631
Glyma.02G254300 Glyma.02G254300.1	EDPVV.VEHLAHILA <mark>YYSLAGPR</mark> TDFPDTVIPLDPGTYVDT	584
Glyma.14G062100 Glyma.14G062100.1	EEPVV.VEHPAHILAYY <mark>SLAGPRT</mark> DFPDTVIPLDPATYVDT	591
Glyma.11G227300 Glyma.11G227300.1	DETVV.VEHPAHILA <mark>YYSLAGQRS</mark> DFPDTVVPLDTATCVDT	590
Glyma.18G030200 Glyma.18G030200.1	DETVV.VEHPAHILAYYSLAGQRSDFPDTVVPLDTATCVDT	590
Lj3g0010583 Lj3g0010583.1	DEPVVAAHIFAYYSLAG	317
Lj6g0020395 Lj6g0020395.1	DGPVVSVHHPAHILAYYSLAGQRSDFPDTVVPLDPATFVEP	590
AT2G39940 AT2G39940.1	GEIRE.MEHPAHILA <mark>Y</mark> Y <mark>SLAGQRTDCP</mark> TT <mark>V</mark> RV <mark>L</mark> KEPI	592
consensus	** * ! ***** * * *	

 $\overline{X}$  non-conserved  $\overline{X}$   $\geq 50\%$  conserved