

$1/3$

Glyma.19G100200.1	MRAPQLSDLGIGSLVH-DP-----ESEAYIKLKNLTILKCKSITSLSGFLVAPHCIAATYPCPNLTSNLNSYAAGIQGSALVKLIHHCVKLQRLWIM	319
Glyma.16G050500.1	MRAPQLSDLGIGSFFVH-DP-----ESEAYIKLKNLTILKCKSITSLSGFLVAPHCIAATYPCPNLTSNLNSYAAGIQGSALVKLIHHCVKLQRLWIM	319
Lj1g0006513.1	MOAPQLADLGIGSFFVH-NP-----ESDAFSKLKNLTILKCKSITSLSGFLVAPHCIAATYPCPNLTSNLNSYAAGIQGSALVKLIHHCVKLQRLWIM	319
Glyma.02G065300.1	RRAPQIVDLGIGSFTIP-DP-----NSNVFIKLMNTIIECKSITSLSGFFVETPRCLPATYPCVMNLTAMNLSYAAGIQSRELKIKICRCGKQLQRLWIM	318
Glyma.16G146400.1	MAAPQLVLDLGIGSFFV-DP-----RSEVYNNMKNAIKLCKMSITSLSGFFVWYVPHCLSAIYPCVMNLTITNLRFAGIQNTLICKLICCCKGKQLQRLWIM	318
AT3G26810/AFB2	ACAPQIVDLGIGSFFVH-DP-----DSEYLYKLMAVKKCTSRSLSGFLVAPHCIAATYPCPNLTSNLNSYAAGIQGSALVKLIHHCVKLQRLWIM	318
AT1G12820/AFB3	SCAPQLVLDLGIGSFFVH-DP-----DPEFAKLMTAIIKKYTSIRSLSGFLVAPHCIAATYPCPNLTSNLNSYAAGIQGSALVKLIHHCVKLQRLWIM	318
Glyma.07G189800.5	VHVPQLGELGTGSFSQ-EL-----TSQOCSDLSEALKNCKNLHLSGLWVATAQYLPVLVSACTNLTFLNFSYA-PLDSDGLTKLIVHCPKQLQRLWIM	329
Glyma.08G059500.6	VHVPQLGELGTGSFSQ-EL-----TAQOCSDLSEALKNCKNLHLSGLWVATAQYLPVLVSACTNLTFLNFSYA-PLDSDGLTKLIVHCPKQLQRLWIM	330
Lj4g0012889.1/AFB6	VRAPOCELGLGSFSFSEDDL-----TAQOYSEIASFANNCKNLHLSGLWVATAQYLPVLVSACTNLTFLNFSYA-PLDSDGLTKLIVHCPKQLQRLWIM	336
Glyma.06G095400.1	HRAPQITHLGTGSFSASEL-----DOELDFASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-DISADQLSVIRHCHKLQTFWVL	338
Glyma.04G093500.1	HRAPQITHLGTGSFSASEL-----DOELDFASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-DISADQLSVIRHCHKLQTFWVL	334
Lj1g0027142.1	LRAPQITHLGTGSFSASEL-----LEQEPDYASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-DVNADQLSVIRHCHKLQTFWVL	381
Glyma.14G179500.1	LRAPQITHLGTGSFSASEL-----LEQEPDYASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-DVNADQLSVIRHCHKLQTFWVL	382
Glyma.02G211800.1	LRAPQITHLGTGSFSASEL-----DOEPDYASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-DINTDQLSVIRHCHKLQTFWVL	379
AT5G49980/AFB5	LGAPQITSLGTGSFSHDEE-----POSEQEPDYASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-NISPDMPKPIILNCHKLQTFWVL	369
AT4G24390/AFB4	VRAPOITSLGTGSFSFDPNV-----POGEQPDYASAFACKSLVCLSGFREFWADYLPATYPCANLISLNFSA-NISPDMPKPIILNCHKLQTFWVL	369

Consensus XXXXQXXXLXGXXXXXX+++++---+XXXXXXXXXXXXXXXXXXXXLXGXXXXXXXXXXLXXXXXXCXXLXXXXXSA+XXXXXXXXXXXXXXXXXXCXXLXXXXXX 317

	420	440	460	480	500	
Glyma.19G206800.1	DYIEDAGLYALAASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMSNAALHTIARNRNLTRFRLCIIEPRTPDYLTHEPLD	423			
Glyma.03G209400.1	DYIEDAGLYALAASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMSNAALHTIARNRNLTRFRLCIIEPRTPDYLTHEPLD	422			
Lj1g0015670.1	DFIEDAGLVLAASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMSNAALHTIARNRNLTRFRLCIIEPRTPDYLTHEPLD	420			
Glyma.10G021500.2	DYIEDAGLEVIASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMTNSALDTIARNRNLTRFRLCIIEPRTPDYLTHEPLD	421			
Glyma.02G152800.2	DYIEDAGLEVIASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMSNAALDTIARSRPNMTRFRLCIIEPRAPDYLTHQPLD	421			
Lj5g0004781.1	DYIEDAGLVLAASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSEGCCKLQSVLYFCROMSNAALHTIARNRNLTRFRLCIIEPRTPDYLTHEPLD	420			
AT3G62980/TR1	DYIEDAGLEVIASCKDLRELRFVPSDPFGL	EPNVALTEOGLVSVSMGCKPCLSVLYFCROMTNAALHTIARNRNLTRFRLCIIEPKAPDYLTHEPLD	421			
AT4G03190/AFB1	DLIEDKGLBAVASCKDLRELRFVPSDPFGL	ATNIPITLTOGLVSVSGKGRKLESVLYFCVQFTNAALFTIARKRPNLKCFLRCVIEPPAPDYKTNELD	417			
Glyma.19G100200.1	DCIGDKGLGVVATCKDLRELRFVPSDPFGL	DPAAVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILDATKPDPTDTPQLD	416			
Glyma.16G050500.1	DCIGDKGLGVVATCKDLRELRFVPSDPFGL	DPAAVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILDATKPDPTDTPQLD	416			
Lj1g0006513.1	DCIGDKGLGVVATCKDLRELRFVPSDPFGL	DPAAVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILDATKPDPTDTPQLD	416			
Glyma.02G065300.1	DCIGDKGLGVVATCKDLRELRFVPSDPFGL	NDPAGVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILDPTKPDPTDTPQLD	417			
Glyma.16G146400.1	DCIGDKGLGVVATCKDLRELRFVPSDPFGL	NDPAGVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILDPTKPDPTDTPQLD	417			
AT3G26810/AFB2	DSIGDKGLGVVATCKDLRELRFVPSDPFGL	GGNATVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	416			
AT1G12820/AFB3	DSIGDKGLGVVATCKDLRELRFVPSDPFGL	GGNATVTEKGLVAISMGCCKLHSLYLYFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	418			
Glyma.07G189800.5	DTVEDKGLBAVASCKDLRELRFVPSDPFGL	GIVHGVTESGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	428			
Glyma.08G059500.6	DTVEDKGLBAVASCKDLRELRFVPSDPFGL	GIVHGVTESGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	429			
Lj4g0012889.1/AFB6	DTVEDKGLBAVASCKDLRELRFVPSDPFGL	GIVHGVTESGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	436			
Glyma.06G095400.1	DTVEDKGLBAVASCKDLRELRFVPSDPFGL	GIVHGVTESGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	436			
Glyma.04G093500.1	DTVEDKGLBAVASCKDLRELRFVPSDPFGL	GIVHGVTESGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	432			
Lj1g0027142.1	DSIGDEGLQAVATCKDLRELRFVPSDPFGL	ESEGPVSEVGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	479			
Glyma.14G179500.1	DSIRDEGLQAVATCKDLRELRFVPSDPFGL	ETDGPVSEVGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	480			
Glyma.02G211800.1	DSIRDEGLQAVATCKDLRELRFVPSDPFGL	ETDGPVSEVGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	477			
AT5G49980/AFB5	DSICDEGLQAVATCKDLRELRFVPSDPFGL	DSEGPVSEVGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	467			
AT4G24390/AFB4	DSIRDEGLQAVATCKDLRELRFVPSDPFGL	DSEGPVSEVGFEAISGCKRKLESILFFCQOMTNAALITVAKNCPNTRFRLCILEPNKPDHVTQSPLD	467			

Consensus DXXXDXGLXXXXXXCXXLXELRXFPXXXXX++XXXXXXXEXGXXXXXSGCXXLXXXLFCXXXMXAXXXXXXXXXXXPXXXXFRLCIXXXXXDXXTXXXXX 414

	520	540	560	580	600	
Glyma.19G206800.1	SGFGAIVEQCKDLQRLSLSGLLTDRVFEYIGTCGKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCSVSYG					523
Glyma.03G209400.1	SGFGAIVEQCKDLQRLSLSGLLTDRVFEYIGTYAKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCSVSYG					522
Lj1g0015670.1	SGFGAIVEQCKDLQRLSLSGLLTDRVFEYIGTYGKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCSVSYG					520
Glyma.10G021500.2	AGFGAIVEHCKDLQRLSLSGLLTDRVFEYIGTYGKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCLVSYG					521
Glyma.02G152800.2	AGFGAIVEHCKDLQRLSLSGLLTDRVFEYIGTYGKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCLVSYG					521
Lj5g0004781.1	AGFGAIVQCKNLRQRLSLSGLLTDRVFEYIGTYAKKLEMLSVAFAGSDSLGLHHVLSGCDNLRKLETRDCPPFGDKALLANAQKLEMTMSRLWMSSCLVSYG					520
AT3G62980/TIR1	IGFGAIVEHCKDLRRLSLSGLLTDKVFPEYIGTYAKKMEMLSVAFAGSDSLGMLHHVLSGCDLSRKLETRDCPPFGDKALLANASKLEMTMSRLWMSSCSVSYG					521
AT4G03190/AFB1	KGFGAIAEGCDLRRLSVSGLLTDKFAFYIGKHAKKVRMLSTAFAGSDSLGMLHLLHSGCESLKKLETRDCPPFGDTALLEHAQKLEMTMSRLWMSSCSVSYG					517
Glyma.19G100200.1	EGFGAIVQSCRRRLRLSLSGLLTDOVFLYIGMYAEKLEMLSTAFAGSDGKMLYVINGCKKLRKLETRDCPPGDMALLTDVGKYETMSRLWMSSCEVTVG					516
Glyma.16G050500.1	EGFGAIVQSCRRRLRLSLSGLLTDOVFLYIGMYAEKLEMLSTAFAGSDGKMLYVINGCKKLRKLETRDCPPGNVALLTDVGKYETMSRLWMSSCEVTVG					516
Lj1g0006513.1	EGFGAIVQSCRRRLRLSLSGLLTDOVFLYIGMYAEQLEMLSTAFAGESDKGMYYVINGCKKLRKLETRDCPPGNALLADIKGYETMSRLWMSSCEVTVG					516
Glyma.02G065300.1	EGFGAIVQSCRRRLRLSLSGLLTDOVFLYIGMYAEQLEMLSTAFAGSDKAMLYVINGCKKLRKLETRDSPFGDALLMDVGKYETMSRLWMSSCEVTIG					517
Glyma.16G146400.1	EGFGAIVQSCRRRLRLSLSGLLTDOVFLYIGMYAEQLEMLSTAFAGSDKAMLYVINGCKKILHKLARSPFGDALLMDVGKYETMQFLWMTSCNVTVG					517
AT3G26810/AFB2	EGFGAIVQCKSLRLSLSGLLTDOVFLYIGMYANQLEMLSTAFAGDTDKGMLYVINGCKKMKLETRDSPFGDTALLADVSKYETMSRLWMSSCEVTLS					516
AT1G12820/AFB3	EGFGAIVQACKGLRRLSVSGLLTDVFLYIGMYAEQLEMLSTAFAGDTDKGMLYVINGCKKMKLETRDSPFGNAALLADVGRYETMSRLWMSSCEVTLG					518
Glyma.07G189800.5	EAFGAVVKTCTKLQRLAVSGYLTLTDFEYIGTYAKNLETLSTAFAGSSDWGMCRLVDGCPKLRKLETRDCPPGNAALLSGLGKYESMRSLWMSSDCNLTMM					528
Glyma.08G059500.6	EAFGAVVKTCTKLQRLAVSGYLTLTDFEYIGTYAKNLETLSTAFAGSSDWGMCRLVDGCPKLRKLETRDCPPGNAALLSGLGKYESMRSLWMSSDCNLTMM					529
Lj4g0012889.1/AFB6	EAFGAVVKTCSKLQRLAVSGLLTLTDFEYIGTYAKNLETLSTAFAGSSDWGMCBLVRCGPKLRKLETRDCPPGNAALLSGLERYESMRSLWMSSDCKLTMM					536
Glyma.06G095400.1	EGFGAIVMCKKRLRLAVSGLLTDRAFSYIGTYGKLRTLSVAFAGSDTLGLQYVLGGCPNLQKLETRDSPFGDGLRSGLHHFYNNMRFLWMSSCKLTRQ					532
Glyma.04G093500.1	EGFGAIVMCKKRLRLAVSGLLTDRAFNIGTYGKLRTLSVAFAGSDTLGLQYVLGGCPNLQKLETRDSPFGDGLRSGLHHFYNNMRFLWMSSCKLTRQ					536
Lj1g0027142.1	EGFGAIVMCKKRLRLAVSGLLTDRAFSYIGTYGKLVRTLSVAFAGSDTLALKYVLGGCPNLQKLETRDCPPGDAALRSGLHHFYNNMRFLWMSSCKLTRQ					579
Glyma.14G179500.1	EGFGAIVMCKKRLRLAVSGLLTDRVFEYIGRYGKLVRTLSVAFAGSDTVGLKYVLGGCPNLQKLETRDSPFGDGLRSGLHHFYNNMRFLWMSSCKLTRQ					580
Glyma.02G211800.1	EGFGAIVMCKKRLRLAVSGLLTDRAFSYIGTYGKLVRTLSVAFAGSDTVGLKYVLGGCPNLQKLETRDSPFGDGLRSGLHHFYNNMRFLWMSSCKLTRQ					577
AT5G49980/AFB5	EGFGAIVMCKKRLRLAVSGLLTDQAFRYMGYEGKLVRTLSVAFAGSDMAIRHVLGGCPNLQKLETRDSPFGDVALRSGMHRYNNRFLWMSSACSLSKG					567
AT4G24390/AFB4	DGFGAIVMCKKRLRLAVSGLLTDEAFSYIGYEGKLVRTLSVAFAGSDMAIRYVLGGCPNLQKLETRDSPFGDVALRSGMHRYNNRFLWMSSACSLISRG					567

Consensus XXFGAXVXXCXXLXRLXXSGXLTDXFXFYIGXXXXXXXXXXLSXAFAGXDXDXXXXXVLXGXXXXXLEXRDXPFGXALXXXXXXXXXXMRXXWMSXCCCCXX 514

	620	640	660	680	700	
Glyma.19G206800.1	ACKLLGQKMPRLNVEVIDERG	PPDSRPDDCPVEKLYIYRTIAGPRIDMPCFVWT			ME	579
Glyma.03G209400.1	ACKLLGQKMPRLNVEVIDERG	PPDSRPDDCPVEKLYIYRTVAGPRIDMPCFVWT			ME	578
Lj1g0015670.1	ACKLLGLKMPRLNVEVIDERG	PPDSRPDSCPVEKLYIYRTIAGPRIDMPCFVYR			MED	577
Glyma.10G021500.2	ACKLLGQKLPRLNVEVIDERG	PPDSRPESSPVEKLYMYRTVSGPRIDMPCGYVWR			MQ	577
Glyma.02G152800.2	ACKLLGQKMPRLNVEVIDERG	PPDSRPESSPVEKLYIYRTVSGPRIDMPCGYVWR			MQ	577
Lj5g0004781.1	ACKLLGQKMPRLNVEVIDERG	PPDTRPESSPVEKLYIYRTISGPRVDMPCGYVWT			ME	576
AT3G62980/TIR1	ACKLLGQKMPRLNVEVIDERG	APDSRPESCVERVFIYRTVAGPRIDMPCFVWN			MD	577
AT4G03190/AFB1	ACKLLSQKMPRLNVEVIDEH	PPESRPESSPVERIYIYRTVAGPRMDTPEFVWT			THKNP	575
Glyma.19G100200.1	ACKLLAKKMPRLNVEIFNENE	QEDCSLEDGQKVEKMYLYRTLAKKRDAPYVWT			L *	573
Glyma.16G050500.1	ACKLLAKKMPRLNVEIFNENE	QEDCSLEDGQKVEKMYLYRTLAKKRDAPYVWT			L *	573
Lj1g0006513.1	ACKELAEMKMPRLNVEIFNENE	QECCSLEDEQSVKEMLYLYRTLAKKRDAPYVCT			L *	573
Glyma.02G065300.1	ACKALAKKMPGLNVEIFNGNE	KVDRDVDDGQKVEKTYLYRTLVGRRKDAPEHVWT			L *	574
Glyma.16G146400.1	ACKALAEMKMPRLNVEIFNENK	KVDRDVDDGQKVEKMYLYRTLAKGRRKDAPELVWT			L *	574
AT3G26810/AFB2	GCKRLAEKAPLWNLVEIINENDNNRMEENGHEGRQKVDKLYLYRTVVGTRMDAPPFWIT				L *	576
AT1G12820/AFB3	GCKRLAQSRLNVEIITINENNNGMQNEEDEREKVDKLYLYRTVVGTRKDAPPVYVIT				L *	578
Glyma.07G189800.5	GVRLLAQEMPRLNVEIVIKES	YETHQAQKVYVYRSVAGPRRDAPPFVLT			L *	579
Glyma.08G059500.6	GVRLLAKEMPRLNVEIVIKET	YETHQAQKVYVYRSVAGPRRDAPPFVLT			L *	580
Lj4g0012889.1/AFB6	GCKRLAEKMPRLNVEIVKEEG	CXEGEPAQRVYVYRSVAGPRRDAPSFVLAHCCGPHNARGSGKGSTTWSIVCTMQPYLVICYMRGYFONL				624
Glyma.06G095400.1	ACQEVQATLPHLVLEVINSEB	KDAGDIEILYMYRSLDGRDDAPKVVIT			LC	587

Glyma.04G093500.1	ACREVARMLPHLVLEVINSEE-----DKADDIELLYMYRSLDRPRDDAPKVVTI-----LC	583
Ljl1g0027142.1	ACQDVARALPHLVVEVINKED-----EAAVDDIELLYMYRSLDGPRDDAPQVVTI-----LH	631
Glyma.14G179500.1	ACQEVARALPNLVLEVINNNNEENAGDEEENAGDEVETLYMYRSLDGPRDDAPRFVTI-----LQ	640
Glyma.02G211800.1	ACQEVARVLPNLVFEVINNNNSE-----ENAGDEVETLYMYRSLDGPRDDAPRFVTI-----LQ	630
AT5G49980/AFB5	CKKDIAAMPNLLVVEVIGSDD---D---DDNRDYYVETLYMYRSLDGPRNDAPKFVTI-----L	619
AT4G24390/AFB4	GCRGVSHALPNVVVEVFGADGDDDED---TVTGDYVETLYLYRSLDGPRKDAPKFVTI-----L	623
Consensus	XXXXXXXXXXPXLXXEXXXXXXXX+++++++XXXXXXXXXXYXRXRXGXRXDXPXXVXX-----X++++	564
720		
Glyma.19G206800.1	---DDSSLRL*-----	588
Glyma.03G209400.1	---DDSSLRL*-----	587
Ljl1g0015670.1	---DDSLRL*-----	586
Glyma.10G021500.2	---DDSLRL*-----	586
Glyma.02G152800.2	---DDSLRL*-----	586
Lj5g0004781.1	---DDSLRL*-----	584
AT3G62980/TIR1	---QDSTMRFSSQITITNGL*-----	595
AT4G03190/AFB1	ENGVSHLAK*-----	586
Glyma.19G100200.1	-----	573
Glyma.16G050500.1	-----	573
Ljl1g0006513.1	-----	573
Glyma.02G065300.1	-----	574
Glyma.16G146400.1	-----	574
AT3G26810/AFB2	-----	576
AT1G12820/AFB3	-----	578
Glyma.07G189800.5	-----	579
Glyma.08G059500.6	-----	580
Lj4g0012889.1/AFB6	-----	624
Glyma.06G095400.1	-----*	588
Glyma.04G093500.1	-----*	584
Ljl1g0027142.1	-----*	632
Glyma.14G179500.1	-----*	641
Glyma.02G211800.1	-----*	631
AT5G49980/AFB5	-----*	620
AT4G24390/AFB4	-----*	624
Consensus	+++++++XQITITNGL*	574