




	10	20	30	40	50	60	70	80	
Glyma.01G180400	MGACASSPSAKTTAASVNKGGGGGAPASESFRPSSIMV.....				M	DMLGRINEYKQPIPARNVLSENPHFYLCNSETVHIGTCMPRPVDE			86
Glyma.02G060800MVHGA.....				L	FLLAAVATFH.....VSSEAE.....			22
Glyma.16G143300MVHGA.....				L	FLLAAVATLH.....VSSEAAA.....			23
Glyma.10G047000MTYTMRPFLFSI.....				L	FTFLATVFAQ.....PLQPSSTPTSFPIDSNAPQRSSPQTPP			50
Glyma.13G252600MMSPCNVI.....				L	SIFFLVCTRT.....PLLSLAQ.....			26
Glyma.15G062300MMSPSHVI.....				L	SIFFLVCTTT.....PPLSLAQ.....			26
Glyma.07G186400MQKIGEGKLLSFSSKHQPSSNINFSTNRNGVTQGS				I	LYLLLCLGPS.....HSGHAH.....			52
Glyma.07G186300MG...SAKFAL.....				I	LTIIVIISMCS.....ISLAQ.....			24
Glyma.07G186200MG...SHKVSFFV.....				F	FFFLVLAFQPH.....VGHAQ.....			26
Glyma.15G062700MGS.GIKVSFSV.....				L	CLLGLVIVGD.....HAAYAQ.....			28
Glyma.15G062500MG.LYKISLCL.....				L	CVLGLVIVGD.....HVAYAQ.....			27
Glyma.15G062900MLKIQH.....								6
Glyma.13G252400MGYMCIKISFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.13G252300MGYMCIKISFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.13G251700MGYMCIKISFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.13G252000MGYMCIKISFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.13G251600MGYMCIKISFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.15G062800MGYLCIKVSFCV.....				M	CVLGLVIVGD.....VAYAQ.....			28
Glyma.13G252500MG.LCKVSFSV.....				L	CVLGLVIVSH.....VAYAL.....			26
Glyma.15G062400MG.LCKVSFPV.....				L	CVLGLVMIVS.....HVANAQ.....			27
Glyma.13G094200MKHCISKHFLSCF.....				A	LFLLLVATTYA.....TVVPTTTQ.....			33
Glyma.17G066000MRHCL.....				A	MFLFLVTTTYA.....NTVVPPTTTQ.....			26
Glyma.17G066100MRQYIEYQSSY.....								19
Glyma.13G094100MKAHLV.....				L	FLLMILVTFTSNVNTLSINPKSNSSIPQLTQ.....			38
consensus					*				

	90	100	110	120	130	
Glyma.01G180400	EELLPGRIYFLVPLSHSDSP.....		L	SLPLLCDLAVKAGSALPNPNNNS	Y	NGCIMWF 138
Glyma.02G060800APP.....		L	APELSAEAR.....	E 37
Glyma.16G143300APP.....		P	ATALSAAAR.....	E 38
Glyma.10G047000	ATSFPADSNAPQQPSPQTPPATSFADSNAPNLPSPSSENRLQGVGRHKGGHSGRRKRVNTRKYFGYVPQTNDTSFTNQTALAQEF.....					138
Glyma.13G252600NTP.....		Q		D 32
Glyma.15G062300NTP.....		Q		D 32
Glyma.07G186400DSQ.....		A		N 58
Glyma.07G186300NSP.....		K		D 30
Glyma.07G186200CSQ.....		E		D 32
Glyma.15G062700DSP.....		T		D 34
Glyma.15G062500DSP.....		T		D 33
Glyma.15G062900					6
Glyma.13G252400DSA.....		E		D 34
Glyma.13G252300DSA.....		E		D 34
Glyma.13G251700DSA.....		E		D 34
Glyma.13G252000DSA.....		E		D 34
Glyma.13G251600DSA.....		E		D 34
Glyma.15G062800DSA.....		Q		D 34
Glyma.13G252500DSP.....		S		D 32
Glyma.15G062400DSP.....		A		D 33
Glyma.13G094200KPP.....		R	SFAN.....	Q 43
Glyma.17G066000KPP.....		R	SFAN.....	Q 36
Glyma.17G066100				W 21
Glyma.13G094100QKRP.....		D	NETIYRVSKQLCWGCIAESL	E 65
consensus					*	

 non conserved
 similar
 $\geq 80\%$ conserved