

Table S1. Characters of the GmMATE proteins.

Gene name	JGI ID	Protein length (aa)	Molecular weight(Da)	Isoelectric point
GmMATE1	Glyma.01G007100	343	36805.41	7.48
GmMATE2	Glyma.01G025200	491	54297.15	5.93
GmMATE3	Glyma.01G026200	518	56511.29	5.77
GmMATE4	Glyma.01G132200	538	58666.11	6.96
GmMATE5	Glyma.01G213000	511	55508.20	8.23
GmMATE6	Glyma.01G216600	541	58998.70	8.06
GmMATE7	Glyma.02G038600	507	55501.60	6.73
GmMATE8	Glyma.02G039500	492	54733.67	7.57
GmMATE9	Glyma.02G075300	507	54832.32	8.50
GmMATE10	Glyma.02G089900	476	51784.54	7.01
GmMATE11	Glyma.02G090000	482	52143.68	5.59
GmMATE12	Glyma.02G090100	475	51329.79	8.98
GmMATE13	Glyma.02G181800	500	53538.18	7.72
GmMATE14	Glyma.02G218400	527	56999.57	8.62
GmMATE15	Glyma.02G310800	526	56643.60	9.70
GmMATE16	Glyma.03G005200	488	53896.75	8.03
GmMATE17	Glyma.03G005300	487	53908.84	6.45
GmMATE18	Glyma.03G005400	487	53628.32	5.40
GmMATE19	Glyma.03G005500	429	47141.11	8.87
GmMATE20	Glyma.03G005600	490	54084.85	6.90
GmMATE21	Glyma.03G005800	494	54597.63	7.50
GmMATE22	Glyma.03G036200	539	58602.06	7.43
GmMATE23	Glyma.04G089000	537	58756.28	8.80
GmMATE24	Glyma.04G097700	524	57266.61	8.01
GmMATE25	Glyma.04G097900	503	55390.87	5.29
GmMATE26	Glyma.04G102100	199	22101.34	8.42
GmMATE27	Glyma.05G001700	486	52789.16	6.55
GmMATE28	Glyma.05G049700	531	57947.35	7.44
GmMATE29	Glyma.05G054000	525	57134.66	8.93
GmMATE30	Glyma.05G054100	315	34689.82	9.43
GmMATE31	Glyma.05G226400	480	51863.58	8.14
GmMATE32	Glyma.06G091100	548	59505.15	7.51
GmMATE33	Glyma.06G103400	480	52566.46	7.86
GmMATE34	Glyma.06G305200	517	56027.78	6.19
GmMATE35	Glyma.06G318700	480	51993.42	9.03
GmMATE36	Glyma.07G099900	469	51260.00	9.27
GmMATE37	Glyma.07G100000	467	50905.44	9.15
GmMATE38	Glyma.07G100100	422	45942.72	8.46
GmMATE39	Glyma.07G124600	497	53882.29	6.59
GmMATE40	Glyma.07G156100	539	57276.57	6.24

GmMATE41	Glyma.07G246100	506	55485.71	8.64
GmMATE42	Glyma.08G033200	494	53145.83	6.59
GmMATE43	Glyma.08G050500	498	54695.73	8.59
GmMATE44	Glyma.08G050700	475	52207.37	9.32
GmMATE45	Glyma.08G244400	173	19261.97	7.58
GmMATE46	Glyma.09G042700	528	57747.13	8.76
GmMATE47	Glyma.09G102800	556	59867.47	9.43
GmMATE48	Glyma.09G134000	522	57574.19	6.98
GmMATE49	Glyma.09G134100	488	54083.16	8.22
GmMATE50	Glyma.09G134200	488	54192.10	7.91
GmMATE51	Glyma.09G146800	572	62436.51	8.64
GmMATE52	Glyma.09G178700	323	35443.88	9.31
GmMATE53	Glyma.09G178800	444	48774.14	9.16
GmMATE54	Glyma.09G178900	474	51503.57	9.23
GmMATE55	Glyma.09G179000	489	53142.64	8.41
GmMATE56	Glyma.09G257400	510	55533.58	5.36
GmMATE57	Glyma.09G276100	542	59162.51	7.85
GmMATE58	Glyma.10G099900	501	53844.53	6.23
GmMATE59	Glyma.10G231800	80	8712.35	6.50
GmMATE60	Glyma.10G232200	494	54060.18	5.65
GmMATE61	Glyma.10G239000	530	57916.80	8.21
GmMATE62	Glyma.10G267300	478	52266.96	6.32
GmMATE63	Glyma.10G267400	477	52176.96	6.65
GmMATE64	Glyma.10G267600	146	16023.96	8.57
GmMATE65	Glyma.10G267700	475	51702.26	7.49
GmMATE66	Glyma.10G267800	459	49978.14	7.07
GmMATE67	Glyma.11G026300	534	58040.87	8.68
GmMATE68	Glyma.11G028900	467	50963.91	8.15
GmMATE69	Glyma.11G112100	548	59820.58	8.90
GmMATE70	Glyma.11G112200	546	59513.21	9.18
GmMATE71	Glyma.12G099300	441	48129.84	6.65
GmMATE72	Glyma.12G194000	504	54372.93	5.90
GmMATE73	Glyma.12G225600	287	31508.89	9.07
GmMATE74	Glyma.12G237400	549	69698.46	9.40
GmMATE75	Glyma.13G203000	428	46528.63	9.36
GmMATE76	Glyma.13G275400	504	55564.59	8.28
GmMATE77	Glyma.13G275500	500	55105.07	7.16
GmMATE78	Glyma.13G275600	536	59475.90	6.17
GmMATE79	Glyma.13G339800	555	59390.55	6.76
GmMATE80	Glyma.14G002000	559	60438.80	9.60
GmMATE81	Glyma.14G032400	505	55204.03	8.10
GmMATE82	Glyma.14G078000	483	52446.27	8.10
GmMATE83	Glyma.14G158100	129	14551.38	8.18
GmMATE84	Glyma.15G034600	554	59382.86	7.66

GmMATE85	Glyma.15G107100	505	54762.52	7.09
GmMATE86	Glyma.15G150300	516	56369.59	8.62
GmMATE87	Glyma.15G274600	553	59165.46	9.46
GmMATE88	Glyma.16G149100	261	29192.42	7.91
GmMATE89	Glyma.16G157300	505	54515.81	8.39
GmMATE90	Glyma.16G180000	477	52924.83	5.98
GmMATE91	Glyma.16G180200	488	54132.13	6.64
GmMATE92	Glyma.16G198700	562	60875.93	8.63
GmMATE93	Glyma.17G027900	507	55484.66	8.39
GmMATE94	Glyma.17G131700	511	55550.12	8.48
GmMATE95	Glyma.17G136400	505	55034.06	8.91
GmMATE96	Glyma.17G136500	507	55266.87	9.26
GmMATE97	Glyma.17G175100	355	38042.08	9.12
GmMATE98	Glyma.17G247400	483	52470.19	6.62
GmMATE99	Glyma.18G110800	112	12473.05	5.38
GmMATE100	Glyma.18G143700	509	55625.41	6.30
GmMATE101	Glyma.18G206500	593	64280.52	5.83
GmMATE102	Glyma.18G214800	505	55348.60	8.52
GmMATE103	Glyma.18G235200	505	55266.15	5.60
GmMATE104	Glyma.18G293100	480	51993.52	9.07
GmMATE105	Glyma.18G293200	406	43894.12	6.04
GmMATE106	Glyma.18G293300	288	41861.79	8.04
GmMATE107	Glyma.19G001600	498	53804.16	6.32
GmMATE108	Glyma.19G120200	495	54624.36	7.60
GmMATE109	Glyma.19G120300	496	54692.57	8.04
GmMATE110	Glyma.19G120700	400	44084.40	6.72
GmMATE111	Glyma.19G120900	491	54183.95	6.16
GmMATE112	Glyma.19G244000	273	29530.09	9.27
GmMATE113	Glyma.20G123300	555	60571.17	7.40
GmMATE114	Glyma.20G123400	409	44326.97	5.13
GmMATE115	Glyma.20G123500	476	52024.51	6.65
GmMATE116	Glyma.20G155500	550	60448.62	8.30
GmMATE117	Glyma.20G162000	494	54051.22	5.78
GmMATE118	Glyma.05G243100	373	41788.58	9.42
GmMATE119	Glyma.06G099600	102	11263.01	7.74
GmMATE120	Glyma.08G282600	351	38073.32	5.96
GmMATE121	Glyma.11G133900	125	13457.96	6.00
GmMATE122	Glyma.12G122000	208	22412.43	9.15
GmMATE123	Glyma.16G180100	235	26168.82	8.62
GmMATE124	Glyma.18G097600	494	54051.22	5.78

Table S2. Conserved sequence detected in GmMATE.

Motif number	Amino acid sequence
1	TLCGQAYGAKZYHMLGVYLQR

2	AJPSAVMVCLEWWYFEILVLLAGLLPNPK
3	JWJFMEPILLLLQDPEIAEVAGLYAJWLIPALFAYAV
4	GVARGSGWQKJGAYVNLGCYY
5	SAAASTRVSNELGAGNPKA
6	YLLSVISTAFVGHLELELAA
7	FPLQRFLQTQSITLP
8	KKTWTGFSFEAFKJWEFFKL
9	AISFANVTGFSVLSGLAGGLE
10	LRHVWGYIFTNDKEVVD

Table S3. MATE protein sequence used in constructing the phylogenetic tree.

ID	Sequence
AT1G1 1670	MGSEATTAVNNLQQPLLESTKSEADFRMESVLTDTHLSTYFRRRIYLASLIEMKYLF HLAAPAIFVYVINNGMSMLTRIFAGRLGSMQLAAASLGNSGFNMFTLGLMLG MGSAVETLCGQAHGAHRYDMLGVYLQRSTIVLVITGLPMTLLFIFSKPLLISLGE PADVASVASVFVYGMIPMIFAYAVNFPIQKFLQSQSIVTPSAYISAATLVIHLILS WLSVFKFGWGLLGLSVVHSLSWWIIVLAQIIYIKISPRCRRTWDGFSWKAFDGL WDFQQLSAAASAVMLCLESWYSQILVLLAGLLKDPELALDSLAIKMSISAMSFMV SVGFNAAAASVRVSNELGAGNPRSAAFSTAVTTGVSFLLSLFEAIVILSWRHVISYI FTDSPAVAEVAELSPFLAITIVLNGVQPVLSGVAVGCGWQAYVAYVNIGCYII VGIPIGYVLGFTYDMGARGIWTGMIGGTLMQTIILVIVTFRTDWDKEVEKASRRL DQWEDTSPLLKQ
AT1G1 2950	MEKDNDFKDPFLASTEELDPATQKALMEYLGVGSRASSLVSFSSTAVDIPPIS GVGDFVREFRIESRKLWKLGAFTTMSQYSLGAVTQVFAGHISTLALAAVSIE NSVIAGFSFGIMLGMGSALETLCGQAFGAGKVSMLGVYLQRSWVILSVTALFLS LIYIFAAPILTFIGQTAASAMAGIFSIYMIPQIFAYAINFPTAKFLQSQSKIMVMA GISGVVLVIHSSFTWLMSRLHWGLPGLALVLNTSWWVIVVAQLVYIFNCTCG EAWSGFTWEAFHNLWGFVKLSLASAAMLCLEIWYFMALVLFAGYLKNAEVS AALSICMNILGWAAMVAFGTNAASVRVSNELGASHPRTAKFSLVAVILSTAI GMFIAAGLLFFRNEYPVLFVEDEEVNRNVRELTPMLAFCIVINNVPVLSGVAV GAGWQAVVAYVNIACYLFGVFPGLLLGFKLEYGVMGIWWGMVTGTFVQSIV LTWMICKTNWEKEASMAERIKEWGGVPAEKETLLN
AT1G1 5150	MQDAERTTNDPVDRIEKVTWRDLQDGSFTAELKRLICFAAPMAAVVIIQFMIQI ISMVMVGHLGRLSLASASFAVSFCNVTGFSFIIGLSCALDTLSGQAYGAKLYRKL GVQAYTAMFCLTLVCLPLSLLWFNMGKLIVILGQDPAIAHEAGRYAAWLIPGL FAYAVLQPLIRYFKNQSLITPLLVTSSVVFCHVPLCWLLVYKSGLGHIGGALALS LSYWLYAIFLGSMYYSSACSETRAPLTMEIFEGVREFIKYALPSAAMLCLEWWS YELIILLSGLLPNPQLETSVLSICFETLSITYSIPLAIAAASTRISNELGAGNSRAA HIVVYAAMSLAVMDALMVMSLLAGRHVFGHVFSDDKKTIEYVAKMAPLVVIS IILDSLQGVLSGVASGCGWQHIGAYINFGAFYLVGPIAASLAFWVHLKGVGL WIGILAGAVLQTLALLVTGCTNWKTQAREARERMAVAHESELTESELP
AT1G1 5160	MEDAESTTKDPVDRVEKVTWRDLQDGSFTAELKKLICFAAPMAAVVITQSMLQ IITMVIVGHLGRLSLASASFAISFCNVTGFSFIMGLSCALDTLSGQAYGAKLYRKL GVQAYTAMFCLTLVCLPLSLLWFNMGKLLVILGQDPSIAHEAGRFAAWLIPGL

	FAYAVLQPLTRYFKNQSLITPLLITSCVVFCLHVPLCWLLVYKSGLDHIGGALAL SLSYWLYAIFLGSMYFSSACSETRAPLTMEIFEGVREFIKYALPSAAMLCLEWW SYELIILLSGLLPNPQLETSVLSVCLQTLSTMTYSIPLAIAAAASTRISNELGAGNSR AAHIVVYAAMSLAVVDALMVGTSLLAGKNLLGQVFSSDKNTIDYVAKMAPLV SISLILDSLQGVLSGVASGCGWQHIGAYINFGAFYLVGPIAASLAFWVHLKGV GLWIGIAGAVLQTLLLALVTGCINWENQAREARKRMAVAHESELTESELPF MGDAESTKDRLLLPVERVENVTWSDLRDGSFTVELKRLIFFAAPMAAVVIAQF MLQIVSMMMVGHLGNLSLASASSFCNVTGFSFIIGLSCALDTLSGQAYGAK LYRKLGVQTYTAMFCLALVCLPLSLIWFNMEKLLLILGQDPSIAHEAGKYATWL IPGLFAYAVLQPLTRYFQNNQSLITPLLITSYVVFCHVPLCWFLVYNSGLGNLGG ALAISLSNWLYAIFLGSMYSSACSETRAPLSMEIFDGIGEFFKYALPSAAMICL EWWSYELIILLSGLLPNPQLETSVLSVCLQTISTMYSIPLAIAAAASTRISNELGAG NSRAAHIVVYAAMSLAVIDALIVSMSLLIGRNLFGHIFSSDKETIDYVAKMAPLV SISLMLDALQGVLSGIARGCGWQHIGAYINLGAFLYLVGPIAASLAFWIHLKGV GLWIGIQAGAVLQTLLLALVTGCTNWESQADKARNRMALAYGT MGDAESTSKTSLLPVERVENVTWRDLRDGLFTAELKRLICFAAPMAAVVIAQF MLQIISMVMVGHLGNLSLASASSFCNVTGFSFIVGLSCALDTLSGQAYGAK LYRKVGQTYTAMFCLALVCLPLTLIWLNMETLLVFLGQDPSIAHEAGRYAAC LIPGLFAYAVLQPLTRYFQNNQSMITPLLITSCFVFCLHVPLCWLLVYKSGLGNLGG GALALSFSNCLYTIILGSLMCFSSACSETRAPLSMEIFDGIGEFFRYALPSAAMICL EWWSYELIILLSGLLPNPQLETSVLSVCLQTTATVYSIHLAIAAAASTRISNELGA GNSRAANIVVYAAMSLAVVEILILSTSLLVGRNVFGHVFSDDKETIDYVAKMAP LVSISLILDGLQGVLSGIARGCGWQHIGAYINLGAFLYLVGPIAASLAFWIHLKGV VGLWIGIQAGAVLQTLLLTLVTGCTNWESQADKARNRMALAYGT METLNVDHEDTISSEQEHRAHTKSDTDMPPISGGRDFIRQFAAESKKLWWLAG PAIFTSFCQYSLGAVTQILAGHVNTLALAAVSIQNSVISGFSVGIMLGMGSALAT LCGQAYGAGQLEMMGIYLQRSWIILNSCALLLCLFYVFATPLLSLLGQSPEISKA AGKFSLWMIPQLFAYAVNFATAKFLQAQSKVIAMAVIAATVLLQHTLLSWLL MLKLRWGMAGGAVVLNMSWWLIDVTQIVYICGSSGRAWSGLSWMAFKNL RGFARLSLASAVMVCLEVWYFMALILFAGYLKNPQVSVAALSICMNILGWPIM VAFGFNAAVSVRESNELGAEHPRRAKFLIVAMITSVIGIVISVTLIVLRDKYPA MFSDDEEVRVLVKQLTPLLALTIVINNIQPVLSGVAVGAGWQGIVAYVNIGCY LCGIPIGLVLGYKMELGVKGIWTGMLTGTVVQTSVLLFIYRTNWKKEASLAEA RIKKWGDQSNKREEIDLCEEDENNSNGENNNHRK MARREGEVTETLLKKSTENRGEDRDGLGMKEKVVWRESKKLWVWAGPAIFTRFS TSGLSLISQAFIHLGSTELAAYSITLTVLLRFSNGILLGMSALETLGQAYGAK QYHMLGIYLQRSWIVLTGCTICLMPYIFAGPILLALGQEERLVRVARIIALWVIGI NISFVPSFTCQMFLQAQSKNKIIAYVAASVLSGVHVFSLWLLVVHFDGFIAGAMT SSLVAHWLPNIAQVLFVTCGGCTETWRGFSWLAFKDLWPVFKLSVSSGGMICL ELWYNSILILLTGNLKNAEVALNALAICININALEMMVAFGFMAAASVRVSNEI GSGNSNGAKFATMVVVSTLSIGIIFFIFLFLRERSYIFTTSEAVATQVADLSPLL AFSILLNSIQPVLSGVAVGAGWQKYVTVVNLACYLVGIPSGFLGYVVGLQVK GVWLGMIFGIFVQTCVLTVMTMRTDWDQVSSSLKRLNRWVEPESPSRNQTL QNE
AT1G1 5170	
AT1G1 5180	
AT1G2 3300	
AT1G3 3080	

		MAGEGGELTAALLKKTENGGEENDELGLKEKVVIESKKLWVVAAPSIFTKFS TYGVSLVTQGFVGHIGPTELAAYSITFTVLLRFSNGILLGMASALGTLCCQAYGA KQYHMLGIHLQRSWIVLTGCTICIMPIFIFSGPILLALGQEDHIVRVARVIALWLI AINFTFVPAFTCQIFLQSQSKNKIIAYVSAVTLGLHVFFSWLLVVHFNFGITGAM
AT1G3	3090	TSTLVAFWMPNIVQLLYVTSGGCKDTWRGFTMLAFKDLWPVFKLSLSSGGMV CLELWYNSILVLLTGNLKNAEVAIDALAICINVNALQMMIALGFLAAVSVRVS NELGRGNPEGAKFATIVAVFTSLSIGLVFFVFLFLRGRISYIFTTSEAVAAEVADL SPLLAFSILLNSVQPVLSGVAVGAGWQGYVAYINLACYLLGIPVGLVLGYVVG LQVKGVWIGMLFGIFVQTCVLTIMTLRTDWDQVSTSLKNINRWVVPESRDAN QISSEE
AT1G3	3100	MAGRGGELTEALVKKTGREEEDELGMKEKVVIESKKLWVVAAPAIFFTRYSTFG VSMVTQAFIGHLGPTELAAYSITFTILLRFSNGILLGMAGALGTLCCQAYGAKQ YQMLGIYLQRSWIVLTGGTICLMPVFIFAGPILLALGQEERIVRVARVLALWVIGI NFSFVPSFTCQMFLQAQSKNKIISYVTAVSLGLHVFFSWLLVAHFNFGITGAMTS MLIAFWLPIIVQLLYVTCGGCKDTWRGFSMLAFKDLWPVLKLSLSSGGMCLCEL WYNSVLVLLTGNLKNAEVALDALAICISINALEMMIALGFLAAVSVRVSNELGS GNPKGAKFATLIAVFTSLSIGIVLFFVFLFLRGRISYIFTTSEAVAAEVADLSPLLA SILLNSVQPVLSGVAIGAGWQGYVAYVNLACYLVGIPIGVILGYVVGLQVKGV WIGMLFGIFVQTCVLTVMTLRTDWDQVSTSLRNINRWVVPESRDANQISSEE MAGGGGELTAALLKKTAEENGEEKDELGLKQKVVIESKKLWIVAAPAIFFTRFS TFGVSIISQSFIGHLGPIELAAYSITFTVLLRFSNGILLGMASALETLCCQAYGAKQ NHMLGIYLQRSWIVLTGCTICLTPVYIFSGPILLALGQEERIVRVARIIALWVIGIN FSFVPSFTCQMFLQAQSKNKIIAYVAASVSLGVHVFLSWLLMVHFNFGITGAMTS
AT1G3	3110	TLVAFWLPNIAQLLFVTCGGCKDTWRGFSMMAFKDLWPVFKLSMSSGGMCLCL ELWYNSILVLLTGNLKNAEVALDALAICLNINGLEMMIALGFLAAASVRVSNE LGSGNPKGAKFATLTAVFTSLSLGIVLFFVFLFLRGRVSYIFTTSEAVAAEVADLS PLLAFSILMNSVQPVLSGVAVGAGWQGYVTYVNLACYLVGIPIGIILGYVVGL QVKGVWIGMLFGIFVQTCVLTVMTLRTDWDQVSTSLRRLNRWVVPESRDVN QVSSEE
AT1G4	7530	MGKDKTLPLDPREPPELTGTKSASKVWAKEFGEESKRLWELAGPAIFTAISQYS LGALTQTFSGRLGELELAASVSVENSISGLAFGVMLGMGSALETLCGQAYGAG QIRMMGIYMQRSWVILFTTALFLLPVYIWAPPILSFFGEAPHISKAAGKFALWMI PQLFAYAANFPIQKFLQSQRKVLVMAWISGVVLVIHAVFSWLFILYFKWGLVG AAITLNTSWWLIVIGQLLYILITKSDGAWTGFSMLAFRDLYGFVKLSLASALMLC LEFWYLMVLVVVTGLLPNPLIPVDAISICMNIEGWTAMISIGFNAAISVRVSNEL GAGNAALAKFSVIVVSITSTLIGIVCMIVVLATKDSFPYLFTSSEAVAAETTRIAVL LGFTVLLNSLQPVLSGVAVGAGWQALVAYVNIACYIIGLPAGLVLGFTLDLGV QGIWGGMVAGICLQTLILIGIYFTNWNKEAEQAESRVQRWGGTAQE MMSEDGYNTDFPRNPLYIFFSDFRSVLKFDELGLEIARIALPAALALTADPIASLV DTAFIGQIGPVELAAVGVSIALFNQVSRIAIFPLVSITTSFVAEEDACSSQQDTRV
AT1G5	1340	DHKECIEIGINNPTEETIELIPEKHKDSLDEFKTSIFSISKPPAKKRNPSSASSALI IGGVLGLFQAVFLISAAKPLLSFMGVKHDSPMMRPSQRYLSLRSLGAPAVLLSL AAQGVFRGFKDTTTPLFATVIGDVTNIILDPIFIFVRLGVTGAATAHVISQYLMC GILLWKLMGQVDIFNMSTKHLQFCRFMKNGFLLLMRVIAVTFCVTLASLAAR

	EGTSMAAFQVCLQVWLATSLLADGYAVAGQAILASAFKKDYKRAAATASR VLQLGLVLGFVLAVILGAGLHFGARVFTKDDKVLHLISIGLPFVAGTQPINALAF VFDGVNFGASDFGYAAASLVMVAIVSILCLLFLSSTHGFGLWFGLTIYMSLRAA VGFWRIGHTGPWSFLRS MCNSKPSSASSSLLSCKDKTHISKLETCDTDNPHYSEFRDTSLDLKRWPSFLEG LEEYKAIGKISGPTAMTGLLMYSRAMISMLFLGYLGELELAGGSLSIGFANITGYS VISGLSMGMEPICQAYGAKQMKLLGLTLQRTVLLLLSCSVPIFSWLNMRILL WCGQDEEISSVAQQFLFAIPDLFLLSLLHPLRIYLRTQNITLPVITYSTAVSVLLH AT1G5 VPLNYLLVVKLEMGVAGVAIAMVLTNLNLVLLSSFVYFTSVHSDTWVPITIDS 8340 LKGWSALLSLAIPTCVSVCLEWWWYEFMIILCGLLANPRATVASMGIQTAL VYVFPSSSLGVSTRISNELGAKRPAKARVSMIISLFCIALGLMAMVFAVLVRH HWGRLFTTDAEILQLTSIALPIVGLCELGNCPQTTGCGVLRGCARPTLGANINL GSFYFVGMPVAILFGFVFKQGFPGLWFGLLAAQATCASMLCALLRTDQWVQ AERAEELTSQTPGKSPPLLPIASSKSRSTSGTEDMMRTMLV MNSELENLHRPLIESSKSFVDYRLETVLTDRPEYFRRIYLAMMIEMKFLFHLA APAIFVYVINNGMSILTRIFAGHVGSFELAAASLGNSGFNMFTYGLLLGMGSAV ETLCGQAHGAHRYEMLGVYLQRSTVVLILTCLPMSFLFLSPNILTALGEPEQVA TLASVFVYGMIPVIFAYAVNFPIQKFLQSQSIVTPSAYISAATLVIHLILSWIAVYR AT1G6 LGYGLLALSLIHSFSWWIIVVAQIVYIKMSPRCRRTWEGFSWKAPEGLWDFFRLS 1890 AASAVMLCLESWYSQILVLLAGLLKNPELALDSLAIKMSISAIKFMVSVGFNA ASVRVSNELGAGNPRAAAFSTVTTGVSFLLSVFEAIVVLSWRHVISAFTDSPA VAEAVADLSPFLAITIVLNGIQPVLSGVAVGCGWQAFVAYVNIGCYVVGIPVG FVLGFTYDMGAKGIWTGMIGGTLMQTIILVIVTLRTDWDKEVEKASSRLDQWE ESREPLLKQ METDFSLVRKEEEEEEDNRNGMSYLSMEMMKKVSSMAAPMVAVSVSQFLLQV ISMVMAGHLDELSLSAVAIATSLTNVTGFSLVGFAGALDTLCGQAFGAEQFGK IGAYTYSSMLCLLVFCFSISIVWFFMDKLEIFHQDPLISQLACRYSIWLIPALFGFT LLQPMTRYFQSQGITLPLFVSSLGALCFHIPFCWLLVYKLFKFGIVGAALSIGFSYW AT1G6 LNVFLLWIFMRYALHREMKNLGLQELISSMKQFIALAIPSAMMICLEWWSFEIL 4820 LLMSGLLPNSKLETSVISICLTTSVHFVLVNAIGASASTHVSNELGAGNHRAAR AAVNSAIFLGGVGALITTITLYSRKSWGYVFSNEREVVRYATQITPILCLSIFVNS FLAVLSGVARGSGWQRIGGYASLGSYYLVGIPLGWFLCFVMKLRGKGLWIGILI ASTIQIVFALVTFFTNWEQEATKARDRVFEMTPQVKGNQKTQIIVEEDTQVLL NHIAETV MKKSIETPLLLNTKQSQDEDEKIRWEKMKKVASMAAPMVAVNMSQYLLQAT STMIVGHRSELALAGIALGSSFANVTGFGVLFGLSGSLETLCGQAYGAKQYHKL GSYTFTSIVFLLIISVPISILWMFMNQILLLLHQDPQIAELAGVYCLWLVPALFGYS VLESIVRYFQSQSLIYPMVLSSLAALSFHVPLCWLMVHKFDFGAKGAAASIGISY AT1G6 WLNVAFLWVYMKRSSRCVETRIYMSKDVVHTNIFFQFAIPSAMMCLEWLAF 6760 EVITLLSGLLPNSKLETSVISICLTSSSLHYNLVNGIGDAASTNVANELGAGNPRG ARDSAAAIIIAAVESVIVSSSLFLRSVWPYAYSNEVEVISYVTDITPILCISILMDS FLTVLSGIVRGTGWQKIGAYVNITSYYVIGIPVGLLLCFHLHFNGKGLWAGLVT GSTLQTLILFLVIGFTNWSKEAIKARERIGDEKVWRHDSLLN AT1G6 MENGFSLVPKEEEEEEDYSNEKSEDQTSYYLSTEMMKKVSFMAAPMVAVAASQ
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6780	YLLQVISIVMAGHLDELSLSAVAIATSLTNVTGFSLIFGLAGALETLCGQAFGAG QFRNISAYTYGSMCLLLVCFPISLLWVFMDKLLELFHQDPLISQLACRYSIWLIP ALFGYSVLQSMTRFFQSQGLVLPFLSSLGALFFHVPFSWLLVYKLRFGIVGAAL SIGFSYWLNVGLLWAFMRDSALYRKNWNLRAQEIFLSMKQFITLAIPTAMMTC LEWWSFELLILMSGLLPNSKLETSVLSICLTMSSLHYVIVNAIGAAASTHVSNKL GAGNPKAARSAANSAIFLGMIDAAIVSISLYSYRRNWAYIFSNESEVADYVTQIT PFLCLSIGVDSFLAVLSGVARGTGWQHIGAYANIGSYLVGIPVGSILCFVVKLR GKGLWIGILVGSTLQTIVLALVTFFTNWEQEVAKARDRVIEMIPQEII MDSAEEKGLLVVSDREEVNKKDGFRETCKLSYIAGPMIAVNSSMYVLQVISIMM VGHLGELFLSSTAIAVSFCSVTGFSVVFGLASALETLCGQANGAKQYEKLGVHT YTGIVSLFLVCIPLSLLWTYIGDILSLIGQDAMVAQEAGKFATWLIPALFGYATLQ PLVRFFQAQSLILPLVMSSVSSLCIHIVLCWSLVFKFGLGSLGAAIAIGVSYWLNV TVLGLYMTFSSSSCSKSRATISMSLFEGMGFFRFGIPSASMICLEWWSFEFLVLLSG ILPNPKLEASVLSVCLSTQSSLYQIPESLGAAASTRVANELGAGNPKQARMNAVY TAMVITGVESIMVGAIVFGARNVFGYLFSSSETEVVVDYVKSMAPLLSLSVIFDALH AALSGVARGSGRQDIGAYVNLAAYYLFGIPTAILLAFGFKMRGRGLWIGITVGS CVQAVLLGLIVILTNNWKKQARKARERVMGDEYEEKESEEEHEEYIS MEDKIQSDDFTSHKNPTLPQVIEELKELWAMVLPITAMNCLVYVRVAVSVLFL GRLGSLELAGGALSIGFTNITGYSVMVGLASGLEPVCQAYGSKNWDLLTSLH RMVVILLMASLPISLLWINLGPIMLFMCQNPEITATAAEYCLYALPDLLTNTLLQ PLRVYLRQRVTKPMMWCTLA AVAFHVPLNYWLV MVKHWGVPGVAIASVVT NLIMVVLLVGYVWVSGMLQKRVSGDGDGGSTTMVAVVAQSSSMELVGGLG PLMRVAVPSCLGICLEWVWYIEIVVMGGYLENPKLAVAATGILIQTSTLMYTVP MALAGCVSARVGNELGAGRPYKARLAANVALACAFVVGALNVAWTVILKER WAGLFTGYEPLKVLVASVMPIVGLCELGNCPQTTGCGILRGTGRPAVGAHVNL GSFYFVGTPVAVGLAFWLKIGFSGLWFGLLSAQAAACVVSILYAVLARTDWEGE AVKAMRLTSLEMRKVGQDEESSLLLLDDEKLGDVL MEDGVTPLLLITEKDTTMIRVKEEVKKQLWLSAPLIGVSLLQYSLQVISVMFVGH LGSLPLSAASIATSFASVTGFTFLLGTASALETLCGQAYGAKLYGKLGIQMORA MFVLLILSVPLSIIWANTEQILVLVHQDKSIASVAGSYAKYMIPSLFAYGLLQCIN RFLQAQNNVFPVFVCSGITTC LHLLLCWLFVLKTGLGYRGAAL AISVSYWFNVI LLSCYVKFSPSCSHSWTGFSKEAFQELYDFSKIAFPSAVMVCELWSFELLVLASG LLPNPVLETSVLSICLNTSLTIWQISVGLGGAASIRVSNELGAGNPQVAKLAVYV IVGIAVAEGIVVTVLLSIRKILGHAFSSDPKIIAYAASMIPIVACGNFLDGLQCVL SGVARGCGWQKIGACVNLGSYLVGVPLGLLGFHFHIGGRGLWLGIVTALSV QVLCLSLVTIFTNWDKEAKKATNRVGSSDDKDGDVQ MEEPFLLRDELLVPSQVTWHTNPLTVELKRVSRLAAPMATVTIAQYLLPVISVM VAGHNDELQLSGVALANSFTNVTGFSIMCGLVGALETLCGQAYGAKQYEKIGT YAYSAIASNIPICFLISILWLYIEKILISLGQDPEISRIAGSYAFWLIPALFGQAIVIP SRFLLTQGLVIPLLF TAVTTLLFHVLCWTLVFLFGLGCNGPAMATSVSFWFYA VILSCYVRFSSSCEKTRGFVSRDFVSSIKQFFQYGIPSAAMICLEWWLFEILILCSGL LPNPKLETSVLSICLTIETLHYVISAGVAAAVSTRVSNNLGAGNPQVARVSVLAG LCLWIVESAFFSILLFTCRNIIGYAFSNSKEVLDYVADLTPLLCLSFILDGFTA VLN GVARGSGWQHIGAWNNTVSYYLVGAPVGIYLAFSRELNGKGLWCGVVVGSTV
AT1G7 1140	
AT1G7 1870	
AT1G7 3700	
AT2G0 4040	

AT2G0 4050	<p>QATILAIVTASINWKEQAEKARKRIVSTENRLA</p> <p>MEEPFLQDEHLVPCKDTWKSGQVTVELKKVSSLAAPMAAVTIAQYLLPVISV</p> <p>MVAGHNGELQLSGVALATSFTNVSGFSILFGLAGALETLCGQAYGAKQYEKIG</p> <p>TYTYSATASNIPICVLISVLWIYIEKLLISLGQDPDISRVAGSYALWLIPALFAHAFF</p> <p>IPLTRFLLAQGLVLPALLYCTLTTLLFHIPVCWAFVYAFGLGSNGAAMASVSFWF</p> <p>YVILSCYVRYSSCDKTRVSVSSDFVSCIKQFFHFGVPSAAMVCLEWWLFELLIL</p> <p>CSGLLPNPKLETSVLSICLTATSLHYVIPGGVAAAVSTRVSNKLGAGIPQVARVS</p> <p>VLGLCLWLVESAFFSTLLFTCRNIIGYAFSNSKEVVDYVANLTPLLCLSFILDGF</p> <p>TAVLNGVARGSGWQHIGALNNVVAYYLVGAPVGVYLA FNRELNGKGLWCG</p> <p>VVVGSAVQAII LAFTASINWKEQAEKARKRMVSSSENRLA</p>
AT2G0 4070	<p>MEEPFLPQDEQIVPCKATWKSGQLNVELKKVSRLAVPMATVTIAQYLLPVISM</p> <p>VAGHNGELQLSGVALATSFTNVSGFSIMFGLVGSLETLSGQAYGAKQYKMG</p> <p>YTSAISSNIPICVLISILWIYMEKLLISLGQDPDISRVAGSYALRLIPTLFAHAIVLP</p> <p>LTRFLLAQGLVLPALLYFALTLLFHIAVCWTLVSALGLGSNGAALASVSFWFFA</p> <p>MTLSCYVRFSSSCEKTRRFVSQDFLSSVKQFFRYGVPSAAMLCLEWWLFELLILC</p> <p>SGLLQNPKLETSVLSICLTATLHYVIPVGVAAAVSTRVSNKLGAGIPQVARVSV</p> <p>LAGLCLWLVESSFFSILLFAFRNIIGYAFSNSKEVVDYVADLSPLLCLSFVLDGFT</p> <p>AVLNGVARGCGWQHIGALNNVVAYYLVGAPVGIYLA FSCELNGKGLWCGVV</p> <p>VGSAVQAII LAIVTASMNWKEQAKKARKRLISSENGLA</p>
AT2G0 4080	<p>MEEPFLPRDEQLVSCSTWQSGQVTVELKKVSRLAAPMATVTIAQYLLPVISM</p> <p>VAGHIGELELAGVALATSFTNVSGFSIMFGLVGALETLCGQAYGAEQYEKIGTY</p> <p>TYSAMASNIPICFIISILWIYIEKLLITLGQEPDISRVAGSYSLWLVPALFAHAIFLPL</p> <p>TRFLLAQGLVISLLYSAMTTLLFHIAVCWTLVFALGLGSNGAAIAISLSFWFYAVI</p> <p>LSCHVRFFSSCEKTRGFVSNDFMSSIKQYFQYGVPSAGLICLEWWLFELLILCSGL</p> <p>LPNPKLETSVLSICLTIGTLHYVIPSGVAAAVSTRVSNKLGAGNPQVARVSVLAG</p> <p>LCLWLVESAFFSTLLFTCRNIIGYTFSNSKEVVDYVADISPLLCLSFILDGLTAVLN</p> <p>GVARGCGWQHIGALINVVAYYLVGAPVGVYLA FSREWNGKGLWCGVMVGS</p> <p>AVQATLLAIVTASMNWKEQAEKARKRIISTENGLV</p>
AT2G0 4090	<p>MEDPLLLGDDQLITRNLKSTPTWWMNFTAELKNVSSMAAPMATVTVSQYLLP</p> <p>VISMVAGHCGELQLSGVTLATAFANVSGFGIMYGLVGALETLCGQAYGAKQ</p> <p>YTKIGTYTFSIAVSNVPIVVLISILWFYMDKLFVSLGQDPDISKVAGSYAVCLIPAL</p> <p>LAQAVQQPLTRFLQTQGLVLPALLYCAITTTLLFHIPVCLILVYAFGLGSNGAALAI</p> <p>GLSYWFNVLILALYVRFSSACEKTRGFVSDDFVLSVKQFFQYGIPSAAMTTIEWS</p> <p>LFELLILSSGLLPNPKLETSVLSICLTSSSLHCVIPMGIGAAGSTRISNELGAGNPE</p> <p>VARLAVFAGIFLWFLEATICSTLLFTCKNIFGYAFSNSKEVVDYVTELSLLCLSF</p> <p>MVDGFSSVLDGVARGSGWQNGAWANVVAYYLLGAPVGGFLGFWGHMNGK</p> <p>GLWIGVIVGSTAQGI LAIVTACLSWEEQAAKARERIVGRTLE</p>
AT2G0 4100	<p>MEDPLLLGDNQIITGSLKPTPTWRMNFTAELKNLSRMALPMATVTVQAQYLLPV</p> <p>ISMVAGHRSELQLSGVALATSFTNVSGFSVMFGLAGALETLCGQAYGAKQYA</p> <p>KIGTYTFSIAVSNVPIVVLISILWFYMDKLFVSLGQDPDISKVAGSYAVCLIPALLA</p> <p>QAVQQPLTRFLQTQGLVLPALLYCAITTTLLFHIPVCLILVYAFGLGSNGAALAI</p> <p>GLSYWFNVLILALYVRFSSSCEKTRGFVSDDFVLSVKQFFQYGIPSAAMTTIEWSLFE</p> <p>FLILSSGLLPNPKLETSVLSICLTSSSLHYVIPMGIGAAGSIRVSNELGAGNPEVAR</p> <p>LAVFAGIFLWFLEATICSTLLFICRDIFGYAFSNSKEVVDYVTELSPLLCLSFVLDGF</p>

AT2G2 1340	<p>SAVLGGVARGSGWQHIGAWANVVAYYLLGAPVGLFLGFWCHMNGKGLWIG VVVGSTAQGIILAIVTACMSWNEQAAKARQRIVVRTSSFGNGLA MQIQCKTLTFTVSSIPCNPKLPFPSSLTLRSWNPSFSPFRSSAVSGPKSSLKLNRF RNCASNQELVVDGETGNNGSISELQGDAANGSISPVEVEAEVEEVKVDLATQ SIWGQMKEIVMFTGPAAGLWLCGPLMSLIDTAVIGQGSSLELAALGPATVICDY LCYTFMFLSVATSNLVATSLARQDKDEVQHQSILLFIGLACGVTMMVLTRLFGS WALTAFTGVKNADIVPAANKYVQIRGLAWPAVLIGWVAQSASLGMKDSWGP LKALAVASAINGVGDVVLCTFLGYGIAGAAWATMVSQVVAAYMMMDALNK KGYSAFSFCVPSPSELLTIFGLAAPVFITMMSKVLFYTLLVYFATSMGTNIIAAHQ VMLQIYTMSTVWGEPLSQTAAQSFMPPELLFGINRNLPKARVLLKSLVIIATLGI VGTIGTAVPWLFPGIFTRDKVVTSEMCHKVIIPYFLALSITPSTHSLEGTLLAGRDL RYISLSMTGCLAVAGLLMLLSNGGFGLRGCWYALVGFWARFSLSLFRLLSRD GVLYSEDTSRYAEKVKAA</p>
AT2G3 4360	<p>MREEREDMLSWPLIGEKEKRSRFVKEEVEKQLLLSGPLIAVSLLQFCLQIISVMFV GHLGSLPLSAASIATSFASVTGFTFLMGTASAMDTVCGQSYGAKMYGMLGIQM QRAMLVLTLLSVPLSIVWANTEHFLVFFGQDKSIAHLSGSYARFMIPSIFAYGLL QCLNRFLQAQNNVIPVVICSGVTTSLHVIICWVLVLKSGLGFRGAAVANAISYW LNVILLSCYVKFSPSCSLTWTGFSKEARRDIIPFMKLVIPSAFMVCSLEMWSFELL VLSSGLLPNPVLETSCPRTVWMIPFGLSGAASTRVSNELGSGNPKGAKLAVRVV LSFSIVESILVGTVLILIRKIWGFAYSSDPEVVSHVASMLPILALGHSLDSFQTVLSC VARGCGWQKIGAFVNLGSYYLVGVPFGLLLGFHFHVGGRLWLGIICALIVQG VCLSLITFFTNDWDEEVKKATSRAKSSSEVKEFAVDNGSILV</p>
AT2G3 8330	<p>MAAVATSFCFSPHRSPSRFGNPNSSIRRTIVCKSSPRDESPAVSTSSQRPEKQQNP LTSQNKPDHDKPDGIGKIGMEIMSIALPAALALAADPITSLVDTAFAVGHIGS AELAAVGVSVSFNLVSKLFNVPLLNVTTSFVAEEQAIKDDNDNDIETSKKVL PSVSTSLVLAAGVGIAEAIASLGSDFLMDVMAIPFDSPMRIPAEQFLRLRAYGA PPIVVALAAQGAFRGFKDTTTPLYAVVAGNVLNAVLDPILIFVLGFGISGAAAA TVISEYLIAFILLWKLNNENVLLSPQIKVGRANQYLKSGGLLIGRTVALLVPFTLA TSLAAQNGPTQMAGHQIVLEIWLAVSLLTDALAIQAQSLATTYSQGEYKQAR EVLFGLVQVGLATGTGLAAVLFITFEFSSSLFTTDSEVLKIALSGTLFVAGSQPVN ALAFVLDGLYYGVSDFGFAAYSMVIVGFISSLFMLVAAPTFLAGIWTGLFLFM ALRLVAGAWRLGTRTGPKWMLWSAPEKPE</p>
AT2G3 8510	<p>MQVGEEMASLTKIACPIVMTSLLIFSRSIISMWFLSHLGKVELAGGALAMGFGNI TGVSVLKGLSVGMDPICGQAFGAKRWTVLSTHTFQKMFCLLIVSVPIAVTWLNI EPIFLRLGQDPDITKVAKTYMLFFVPELLAQAMLHPLRTFLRTQGLTSPLTISAIV SILLHPLFNYVFVVRMRLGVKGVAIAMAFNTMNIDVGLLVYTCFSDSLIKPWEG LALRSLFRGWWPILLSLAAPSAISVCLEYWWYEIMLFLCGLLGNPKASVAAMGIL IQTGILYVVPFAISSAIATRVGHALGGGQPTRAQCTTVIGLILAVAYGLAAAVF VTALRSVWGKMFTDEPEILGLISAALPILGLCEIGNSPQTAACGVLGTARPKDG ARVNLCAFYIVGLPVAVTTTTFGFKVGFRGLWFGLLSAQMTCLVMMLYTLIRTD WSHQVKRAEELTSAADKSHSEDETVAEVDQDDDDVSSNDLEIGLLQNTN</p>
AT3G0 3620	<p>MSTQEEMEERLLREGSDAEGQSNNRESIYLRTKVWSEVNKMWRIALPSSLFRMT SFGSIIVAQAFIGHSELGLAAYALLQSTFIRFLYGLMGGMSSATETLCGQAYGA EQYHTMGIYLRQSWIVDMAVTTTLFPLFIVLAGPILRLLGQNVEITKTVDIYPWM</p>

IPYVYSLIFTMTIQMYLQAQMRNAIVGVLSTLSLALDLVVTWVCVSMGMGIG
 GALLGLNVGSWAMVLAEFVYIFGGWCPFTWTGFSIAAFVDLIPMLKLSISSGFM
 ICLEYWYMSILVLMAGYTKDAKIAISAFSICQYIYTWELNICLGFLGAACVRVAN
 ELGKGAHAHVRFSIKVILTISTLMGVIFSALCLAFCGRISYLFNSNSDEVSDAVNDL
 SVILAVSILLNSIQPILSGVAVGAGMQSIVAVVNLASYYAIGIPLGLILTYVFHLGV
 KGLWSGMLAGIAIQTIILCYIYKTDWELEVKRTCERMKVWSLKPSNEESNPIIRE
 ESRSK
 MTETGDDLATVKKPIPFVLVIFKDLRHVFSRDTTGREILGIAFPAALALAADPIASL
 IDTAFVGRLGAVQLAAVGVSAIFNQASRITIFPLVSLTTSFVAEEDTMEKMKEE
 ANKANLVHAETILVQDSLEKGISSPTSNDTNQPQQPPAPDTKSNSGNKSNKKE
 KRTIRTASTAMILGLILGLVQAIFLIFSKLLLGVMGVKPNPMLSPAHKYLSIRA
 AT3G0 LGAPALLLSLAMQGIFRGFKDTKTPLFATVVADVINVLDPIFIFVLRGLIIGAAIA
 8040 HVISQYFMTLILFVFLAKKVNLIPPNFGDLQFGRFLKNGLLLLARTIAVTFCQTL
 AAAMAARLGTTTPMAAFQICLQVWLTSLLNDGLAVAGQAILACSFAEKDYNK
 VTAVASRVLQMGFVLGLGLSVFVGLGLYFGAGVFSKDPAVIHLMAIGIPFIAAT
 QPINSALFVL DGVNFGASDFAYTAYSMVGVA AISIAAVIYMAKTNGFIGIWIALT
 IYMALRAITGIARMATGTGPWRFLRGRSSSSSS
 MDSSPNDGVHQPLLHPQSPSPPESTNGELETVLSDVETPLFLRLRKATIIESKLL
 FNLAAPAVIVYMINYLMSMSTQIFSGHLGNLELAAASLGNTGIQVFAYGLMLG
 MGSAVETLCCQAYGGRKYEMLGYYLQRSTVLLTLTGLLLTLIYVFSEPIILLFLGE
 SPAIASAASLFVYGLIPQIFAYAANFPIQKFLQSQSIVAPSAYISTATLFVHLLLSW
 AT3G2 LAVYKLGMLLGASLVLSLWWIIVVAQFVYIVTSECRETWRGFSVQAFSGLW
 1690 SFFKLSAASAVMLCLETWYFQILVLLAGLLENPELALDSLICMTISGWVFMISV
 GFNAAISVRVSNELGAGNPKSAAFSVIIVNIYSLITCVILAIVILACRDVLSYAFTE
 GKEVSDAVSDLCPLLAVTLVLNGIQPVLSGVAVGCGWQTFVAKVNVGCYYIIGI
 PLGALFGFYFNFGAKGIWTGMIGGTVIQTFILAWVTFRTDWTKEVEEASKRLDK
 WSNKKQEVVPE
 MADPTSKDDHDGEGGRDKSSTFVQKLIDVEEAKTQIIYSLPMIFTNLFYYCIPLTS
 VMFASQLGQLELAGATLANSWATVTGFAFMTGLSGALETLCGQGFGAKSYRM
 LGIHLQSSCIVSLVFTILITILWFFTESVFLLLRQDPSISKQAALYMKYLAPGLLAY
 AT3G2 GFLQNILRFCQTQCIVTPLVLFSFLPLVINIGTTYALVHLAGLGFIGAPIATSISLWI
 3550 AFVSLGFYVICSDKFKETWTGFSMESFHHVVLNLTLSIPSAAMVCLEYWAFEILV
 FLAGLMRNPEITTSLSVAICVNTEISYMLTCGLSAATSTRVSNELGAGNVKGAK
 KATSVSVKLSLVLALGVVAILVGHDAWVGLFSNSHVIKEGFASLRFFLAASITL
 DSIQGVLSGVARGCGWQRLATVINLGTFFYLIGMPISVLCGFKLKLHAKGLWIGL
 ICGMFCQSASLLMTIFRKWTKLTAATV
 MADPATSSPLDDHVGGEDERGRRSRSSTLVQKVIDVEEAKAQMIYSLPMILT
 NLFYYCIPITSVMFASHLGQLELAGATLANSWATVSGFAFMVGLSGSLETLCGQG
 FGAKRYRMLGVHLQSSCIVSLVFSILITIFWFFTESIFGLLRQDPSISKQAALYMKY
 AT3G2 QAPGLLAYGFLQNILRFCQTQSIIAPLVFSFVPLVINIATAYVLVYVAGLGFIGAP
 3560 IATSISLWIAFLSLGTYVMCSEKFKETWTGFSLESFRYIVINLTLSLPSAAMVCLEY
 WAFEILVFLAGVMPNPEINTSLVAICVNTEAISYMLTYGLSAAASTRVSNELGA
 GNVKGAKKATSVSVKLSLVLALGVVIVLLVGHDWVGLFSDSYVIKEEFASLRF
 FLAASITLDSIQGVLSGVARGCGWQRLVTVINLATFYLIGMPIAAFCGFKLKFYA

	KGLWIGLICGIFCQSSSLLMTIFRKWTKLNVATV
	MAKDKDITETLLTAAEERSDLPFLSVDDIPPITTVGGFVREFNVETKKLWYLAGP
	AIFTSVNQYSLGAITQVFAGHISTIALAAVSVENSVVAGFSFGIMLGMGSALETL
	CGQAFGAGKLSMLGVYLQRSWVILNVTALILSLLYIFAAPILASIGQTAAISSAA
	GIFSIYMIPQIFAYAINFPTAKFLQSQSKIMVMAVISAVALVIHVPLTWVIVKLQ
AT3G2	WGMPGLAVVLNASWCFIDMAQLVYIFSGTCGEAWSGFSWEAFHNLWSFVRLS
6590	LASAVMLCLEVWYFMAIILFAGYLKNAEISVAALSICMNLGWTAMIAIGMNT
	AVSVRVSNELGANHPRTAKFSLLVAVITSTLIGFIVSMILLIFRDQYPSLFVKDEK
	VILVKELTPILALSIVINNVPVLSGVAVGAGWQAVVAYVNIACYVVFQIPFGL
	LLGYKLNYGVMGIWCGMLTGTVVQTVLVTWMICKTNWDTEASMAEDRIREW
	GGEVSEIKQLIN
	MSSTETYEPLLTRLHSDSQITERSSPEIEEFLRRRGSTVTPRWWLKLAVWESKLLW
	TLGSASIVSVLNYMLSFTVMFTGHLGSLQLAGASIATVGIQGLAYGIMLGMA
	SAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVFLTFLYWYSGPILKTMGQ
	SVAIAHEGQIFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTL
AT3G5	LTWLVTNVLDFGLLGAALILSFSWWLLVAVNGMYILMSPNCKETWTGFSTRAF
9030	RGIWPFYFKLTVASAVMLCLEIWYNQGLVIISGLLSNPTISLDAISICMYLNDWM
	QFMLGLSAAISVRVSNELGAGNPRVAMLSVVVVNITTVLISVLCVIVLVFRVGL
	SKAFTSDAEVIAAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTY
	YVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTLTLIVLTLKTNWTSEVENAA
	QRVKTSATENQEMANAGV
	MEIPVREERRSSSSSAGPLQQTISLAADDAIDSGPSSPLVVKVSVFETEHETTKLIH
	APSTLLGETTGDADFPPIQSFRDAKLVCVNETSKLWEIAAPIAFNILCNYGVNSF
	TSIFVGHIGDLELSAVAIALSVVSNFSFGFLGMASALETLCGQAFGAGQMDML
	GVYMQRSWLILLGTSVCLLPYIYATPLLLLLGQEPEIAEISGKFTTQIIPQMFALAI
AT4G0	NFPTQKFLQSQSKVGIMAWIGFFALT LHIFILYLFINVFKWGLNGAAA AFDVSA
0350	WGIAIAQVYVVGWCKDGWKGLSWLAFQDVWPFLKLSFASAVMLCLEIWYF
	MTIIVLTGHLEDPVIAVGSLICMNINGWEGMLFIGINAAISVRVSNELGSGHPR
	AAKYSVIVTVIESLVIGVVCAIVILITRDDFAVIFTESEEMRKAVADLAYLLGITMI
	LNSLQPVISGVAVGGGWQAPVAYINLFCYYAFGLPLGFLGKYKTS LGVQGIWIG
	MICGTSLQTLILLYMIYITNWNKEVEQASERMKQWGAGYEKLEKIAT
	MNGSNETVERRIELRRPLVDTEKKLPLEVGLESVLTESSLPYRRRVYLGMCIELKL
	LLRLALPAILVYLINGGMGISARIFAGHLGSTQLAAASIGNSSFSVLVYALMLGMG
	SAVETLCGQAYGAHRYEMLGIYLQRATIVLALVGFPMTILYTFSYPILLLLGEPKT
	VSYMGSLYIAGLIPQIFAYAVYFTAQKFLQAQSVVAPSAYISAAALVLQISLTWIT
AT4G2	VYAMGQGLMGIAVYVLTISWWFIVGAQTFYVITSVRFKDTWTGFSWKS LHGLWS
1903	FFKLSAGSAVMICLELWYTQILVLLAGLLKDPALSLDSLCSISALSFMVSVGF
	NAAVSVRTSNELGAGNPKSALFSTWTATFVSFVISVVEALVVIASRDNVSYIFTS
	DADVAKAVSDLCPLAVTHILNGIQPVLSGVAVGCGWQTYVAYVNIGCYIYVGI
	PIGCILGFTFNFQAKGIWTGMIGGTLMQTLILLYVITYQADWDKEVMLHEIKLKK
	RESDWICGTTKSLSRISNFVMK
AT4G2	MEVPSETTNLADLRRPLVVPVVSERKPPADVGLGLESVLTERSLPYRRRVYLGA
1910	CIEMKLLFRLALPAILVYLVNSGMGISARIFAGHLGKNELAAASIGNSCFSLVYG
	LMLGMGSAVETLCGQAYGAHRYEMLGIYLQRATIVLALVGLPMTLLYTFSYPIL

	ILLGEPKTVSYMGSKYIAGLIPQIFAYAVNFTAQKFLQAQSVVAPSAFISAAALIL QILLTWITVYVMDMGFMGIAYYLTISWWVIVGSQCFYIAVSPKFRHTWTGLSW RSLQGLWSFFKLSAGSAVMICLEMWYSQILVLLAGLLENPARSLDSLSICMSISA LSFMVSVGFNAAVSVRTSNELGAGNPKSAWFSTWTATFVSFVISVTEALAVIWF RDYVSYIFTEDADVAKAVSDLCPLAITIILNGIQPVLSGVAVGCGWQTYVAYV NVGCYYVVGIPVGCILGFTFDFQAKGIWTGMIGGTLMQTLILLYVITYRTDWDKE VMLHEIKWKKRGNVWICGTTRRSLSKTSYNKFGGVIDNKEKEISVVCAGDFNV RSFSWLLCLFYGNRTIKIYFCLMDYSLFTKSCS MSETSKSESLDPEVSEGLCSKTLMQSIVHELKLQMRIGLPLVVMNLLWFGKMTT TSVFLGRQGELNLAGGSLGFSFANVTGFSVLYGISAAMEPICGQAFGAKNFKLL HKTLFMAVLLLLLLISVPISFLWLNHVKILTGFQREDISFIAKKYLLYLLPELPILSF LCPLKAYLSSQGVTLPIMFTTAAATSLHIPINIVLSKARGIEGVAMAVWITDFIVV ILLTGYVIVVERMKENKWKQGGWLNQSAQDWLTLIKLSGPCCLTVCLEWWCY EILVLLTGRLPNPVQAVSILIIVFNFYLLYAVMLSLGTCVATRVSNELGANNPK GAYRAAYTTLIVGIISGCIGALVMIAFRGFWGSLYTHHDQLILNGVKKMMLIMA VIEVVNFPLMVCGEIVRGTAKPSLGMYANLSGFYLLALPLGATLAFKAKQGLQ GFLIGLVFGISLCLSILLIFIARIDWEKEAGKAQILTCNTEDEQTSQSGSQDSHS MAAPLLMIKNQTDHRQDPNPNPHTLSSSIQEAKSIKISLPLILTGLLLYSRSMIS MLFLGRLNDLSALSGGSLALGFANITGYSLLSGLSIGMEPICVQAFGAKRFKLLG LALQRTTLLLLLLCSLPISILWLNKILLFFGQDEEISNQAEIFILFSLPDLILQSFLH PIRIYLRQSITLPLTYSAFFAVLLHIPINYLLVSSLGLGLKGVALGAIWTNVNLLG FLIIYIVFSGVYQKTWGGFSMDCKGWRSLMKLAIPSCVSVCLEWWWYEIMILL CGLLLNPQATVASMGIQTTALIIYFSSLSISVSTRVGNELGANQPKARIAAR TGLSLSLGLGLLAMFFALMVRNCWARLFTDEEEIVKLTSMLPIIGLCELGNCP QTTLGVLRGSAKPKLGANINLCCFYFVGMPVAVWLSFFSGFDFKGLWLGLFA AQGSCLISMLVVLARTDWEVEVHRAKELMTRSCDGEDDDGNTPFLLDSLIDIEE NLVF MDPTAPLLTHGGEVEEDYAPARSWTDVKRVLSTESAKLWMIAAPVGFNIICQY GVSSVTNIFVGHIGEVELSAVSISLSVIGTFSFGFLLGMGSALETLCGQAYGAGQV NMLGVYMQRSWIILFVSCFFLLPIYIFATPVLRLLGQAEIIVPAGQFTLLTIPQLF SLAFNFPTSKFLQAQSKVVAIAWIGFVALSLHVIMLWLFIIIEFGWGTNGAALAF NITNWGTAAIAQIVYVIGWCNEGWTGLSWLAFKEIWAFFVRLSIASAVMLCLEIW YMMSIIVLTGRLDNAVIAVDSLICMNINGLEAMLFIGNAAISVRVSNELGLGR PRAAKYSVYVTVFQSLIGLVFMVAIIHARDHFAIIFTSSKVLQRAVSKLAYLLGIT MVLNSVQPVVSGVAVGGGWQGLVAYINLGCYYIFGLPFGYLLGYIANFGVMG LWSGMIAGTALQTTTTLLIVLYKTNWNKEVEETMERMKKWGGSETTSKDILASG WPSGLRRQTQVLVFRGRGFKPHF MCNPSTTTTTTGSSENQESRTGLFLDLFSINSFEPTKRNLRHCCENRGSPMAEAVT EAKSLFTLAFPIAVTALVLYLRSVSMFFLGQLGDLELAAGSLAIAFANITGYSVL SGLALGMEPLCSQAFAHFRKLLSLTLHRTVVFLVCCVPISVLWFNVGKISVYL HQDPDIAKLAQTYLIFSLPDLTNTLLHPIRIYLRAQGIIHPVTLASLSGAVFHLP ANLFLVSYLRLGLTGVAVASSITNIFVVAFLVCYVWASGLHAPTWTDPTRDCFR GWAPLLRLAGPSCVSVCLEWWWYEIMIVLCGLLVNPRSTVAAMGVLIQTTSFL YVFPSSLSFAVSTRVGNELGANRPKTAKLTATVAIVFAAVTGIIAAAFAYSVRNA
AT4G2 2790	
AT4G2 3030	
AT4G2 5640	
AT4G2 9140	

AT4G3 8380	<p>WGRIFTGDKEILQLTAAALPILGLCEIGNCPQTVGCGVVRGTARPSTAANVNLG AFYLVGMPVAVGLGFWAGIGFNGLWVGLLAAQISCAGLMMYVVGTTDWESE AKKAQTLTCAETVENDIIKAVVASTIDGECDEAEPLIRITVLY MESSRVVVGGLPLANRRNSSFAKPKIQQGTFLPLSRINNV SAPQKCSLHTNPN PMFPFVTRRKSQTNPD CGVVKLGEEDDSCSSLDKLPEVNGVHTGVARPVDIKR ELVMSLSLPAIAGQAIDPLTLLMETAYIGRLGSVELGSAGVSMAIFNTISKLFNIPL LSVATSFVAEDIAKIAAQDLASEDSQSDIPSQGLPERKQLSSVSTALVLAIGIGIFE ALALSLASGPFLRLMGIQSMSEMFIPARQFLVLRALGAPAYVVS LALQGIFRGFK DTKTPVYCLGIGNFLAVFLFPLFIYKFRMGVAGAAISSVISQYTVAILMLILLNKR VILLPPKIGSLKFGDYLKSGGFVLGRTLSVLVTMTVATSMAARQGVFAMAAHQI CMQVWLAVSLLTDALASSGQALIASSASKRDFEGVKEVTTFVLKIGVVTGIALAI VLGMSFSSIAGLFSKDPEVLRIVRKGVLVFAATQPITALAFIFDGLHYGMSDFPY AACSM MVVGGISSAFMLYAPAGLGLSGVWVGLSMFMGLRMVAGFSRLMW RK GPWWFMHTSDKRLA MLIKSQRLTLFSPLLSKTRRIPVNSHQTLVAESVITRRTLGAITATPSFHKNPVVIR RRIKLERVTRNCVRIDREIDEEEEEEKERGDLVKQSIWEQMKEIVKFTGPAMG MWICGPLMSLIDTVVIGQGSSI ELAALGPGTVLCDHMSYVFMFLSVATS NMVAT SLAKQDKKEAQHQISVLLFIGLVCGLMMLLLTRLFGPWAVTAFTRGKNIEIVPA</p>
AT4G3 9030	<p>ANKYIQIRGLAWPFILVGLVAQSASLGMKNSWGPKALAAATIINGLGDITLCL FLGQGIAGAAWATTASQIVSAYMMMDSLNKEGYNAYSFAIPSPQELWKISALA APVFISIFS KIAFYSFIIYCATSMGTHVLA AHQVMAQTYRMCNVWGEPLSQT AQ SFMPEMLYGANRNL PKARTLLKSLMIIGATLGLVLGVIGTAVPGLFPGVYTHDK VIISEMHRLLPFFMAL SALTMTVSLEGTLLAGRD LKFVSSVMSSSFIIGCLTLMFV TRSGYGLLG CWFVLVGFQWGRFGLYLRRLSPGGILNSDGPSPYTVEKIKSI MDKKSGGTKAIEEATVPLLECHNAAEEGGGMKREIW IETKKIWIYIVGPSIFTGL ATYSILIITQAFAGHLGDLELAAISIINNFTLG FNYGLLLGMA SALETLCGQAFGA REYYMLGVYMQRYWILFLCCILLP MYLFATPILKFIGQSDDIAELTG TIALWVI PVHFAFAFFFLNRFLQCQLKNKVIAISAGVSLAVHILVCWFFVYGYKLGIIGTM</p>
AT5G1 0420	<p>ASVNVPPWWLNIFILFLYSTRGGCTLTWTGFSSE AFTGLLELTKLSASSGIMLCLE NWYYKILMLMTGNLVNAKIAVDSL SICMSVNGWEMMIPLAFFAGTGVRVANE LGAGNGKGARFATIVSITLSLMIGLFFT VIIIVIFHDQIGSIFSSEAVLNAVDNLSV LLAFTVLLNSVQPVLSGVAVGSGWQSYVAYINLGCYYLIGLPFGLTMGWIFKFG VKGIWAGMIFGGTAIQTLILIIITTRCDWDNEAHKSSVRIKKWLVS DAGN MSGGGGEMEERLLNGSETEQRRESLYLRKKIWSEVRKMWRIALPSTLFRVMSFG CVVVAQAFIGHSSSETGLAAYALLQSTFIRFIYGIMAGMSSATETLCGQAYGAEQ YHMMGIYLRQSWIVDTFIATLFPFIVLAGPILRLLGQNVV ISETVDEIYPWVIPY LYSIVFTMTMQMYLQAQMKNAIIGILSTLALVLDIAATWWCVSVMGMGIHGA</p>
AT5G1 7700	<p>LLGLNISSWSVAIAEFVYVFGGWCPHTWTGFS TAAFLDLIPMLKLSISSGFMLCL EYWYMSIIVLMSGYAKDANIAISAFSICQYIYSWEMNICFGLMGAACVRVANEL GKGDADAVRFSIKVVLVVS AVIGVICSALCLAFGGQISYLFSDSQAVSDAVADLS IVLSISILFNIIQPILSGVAIGAGMQSMVALVNLASYAIGVPLGVLLVYVFNFGIK GLWSGMLAGVG IQTLILCYVIYKTDWELEVKKTNERMKTWTLNLP AVQSTTIST RDEERK</p>
AT5G1	<p>METPNIIISHTNLLSKIDLEKQNPAPIFPTITELKSEARSLFSLAFPTIL AALILYARS</p>

9700	<p> AISMLFLGHIGELELAGGSLAIAFANITGYSVLAGLALGMDPLCSQAFGAGRPK LLSLTLQRTVLFLLTSSVVIVALWLNLGKIMIYLHQDPSISLAQTYILCSIPDLLT NSFLHPLRIYLRAQGITSPLTLATLAGTIFHIPMNFLLVSYLGWGFMGVSMAAA ASNLLVVIFLVAHVWIAGLHQPTWTRPSSECFKDWGPVVTALPISCGVCLEW WWYEIMTVLCGLLIDPSTPVASMGILIQTTSLLYIFPSSLGLAVSTRVGNELGSNR PNKARLSAIVAVSFAGVMGLTASAFAGVSDVWGWIFTNDVAIIKLTAALPI LGLCELGNCPQTVGCGVVRGTARPSMAANINLGAFYLVGTPVAVGLTFWAAY GFCGLWVGLLAAQICCAAMMLYVVATTDWEKEAIRARKLTCTEGVDVVITTT QTNGDLSEPLIYVTVATD MEEDKILTETLLSAAEPPALPFSSVEDIPPITTVGGFVKEFNVEVKKLWYLAGPA IFMSITQYSLGAATQVFAGHISTIALAAVSVENSVIAGFSFGVMLGMGSALETLC GQAFGAGKLSMLGVYLQRSWVILNVTAVILSLLYIFAAPILAFIGQTPAISSATGI FSIYMIPQIFAYAVNYPTAKFLQSQSKIMVMAAISAVALVLHVLLTWVIEGLQ </p>
AT5G3 8030	<p> WGTAGLAVVLNASWWFIVVAQLVYIFSGTCGEAWSGFSWEAFHNLWSFVRLS LASAVMLCLEVWYLMNAVILFAGYLNKAEISVAALSICMNILGWTAMIAIGMNA AVSVRVSNELGAKHPRTAKFSLLVAVITSTVIGLAISIALIFRDKYPSLFVGDEEV IIVVKDLTPILAVSIVINNVPVLSGVAVGAGWQAVVAYVNIVCYVFGIPFGLL LGYKLNFGVMGIWCGMLTGTVVQTIVLTWMICRTNWDTEAAMAEGRIREW GEVSDQLLN MGERDDEAEGILEKAKIPLLDQNVAAEEENGINEIKKEIWLETKKLWRIVGPAIFTR VTNLIFFVITQAFAGHLGELELAASIVNNVHIGFNYSFIGMATALETLCGQAFG AKKYDMFGVYLQRSWIVLFLFSILLPLMYIFATPILKFMGQPDDIAELSGIISVWA IPTHFSFAFFFPINRFLQCQLKNSVIAISSGVSLVVHIFVCWLFVYVLELGVIGTIAT ANVSWWLNVFILFTYTTCCGGCPLTWTGFSMESFTRLWEFTKLSASSGIMVCLEN WYYRMLIVMTGNLEDARIDVDSMSICMSINGLEMMVPLAFFAGTSVRVANELG AGNGKRARFAMIISVTQSLIIGIIISVLIYFLLDQIGWMFSSSETVLKAVNNLSILLS FAILLNSVQPVLSGVAVGSGWQSLVAFINLGCYYFIGLPLGIVMGWMFKFGVK IWAGMIFGGTMVQTLILIFITMRCDWEKEAQNAKVRVNKWSVSDARK MVVEEDSRLINLQHKYNPTMPEVVEELKRIWDISFPVAAMSILNYLKNMTSVVC MGRGSLLELAGGALAIGFTNITGYSVLSGLATGMEPLCGQAIGSKNPSLASLTLK RTIFLLLLASLPISLLWLNLAFLMLMLRQQHDITRVASLYCSFSLPDLLANSFLHP LRIYLRCKGTTWPLMWCTLVSVLLHLPITAFFTFYISLGVPGVAVSSFLT NFISLSL </p>
AT5G4 4050	<p> LLCYIYLENNNNNDKTTSKSLCLDTPLMLYGSRDSENDVWSTLVKFVAVPSCIAV CLEWWWYEFMTVLAGYLPEPKVALAAAIVIQTTSLMYTIPTALSAVSTRVS NELGAGRPEKAKTAATVAVGA AVAVSVFGLVGTTVGREAWGKVFTADKVVL ELTAAVIPVIGACELANCPQTISCGILRGSARPGIGAKINFYAFYVVGAPVAVL AFVWGLGFMGLCYGLLGAQLACAISILTVVYNTDWNKESLKAHDLVGKNVIS PNVDQIIVKCEEGLH MSQSNRVRDEVTLPLLQKTSHLKNHSSVLSVFLNEAISICKISYPLVLTGLFLYVR SFVSLSFLGGLGDATLAGGSLAAAFANITGYSLSGLTMGVESICSQAFGARRYN </p>
AT5G4 9130	<p> YVCASVKRGIILLVTSPLVTLWMNMEKILLILKQDKKLASEAHIFLLYSVPDLV AQSFLHPLRVYLRTQSKTLPLSICTVIASFLHLPITFFLVSYLGIGKIALSGVVS N FNLVAFFLYICFFEDKLSVNEDEKITEETCEDSVREWKKLLCLAIPSCISVCLEW WCYEIMILLCGFLDPKASVASMGIQITSLVYIFPHSLSLGVSTRVGNELGSNQ </p>
AT5G5 2050	<p> AQSFLHPLRVYLRTQSKTLPLSICTVIASFLHLPITFFLVSYLGIGKIALSGVVS N FNLVAFFLYICFFEDKLSVNEDEKITEETCEDSVREWKKLLCLAIPSCISVCLEW WCYEIMILLCGFLDPKASVASMGIQITSLVYIFPHSLSLGVSTRVGNELGSNQ </p>

AT5G5 2450	PKRARRAAIVGLGLSIALGFTAFAFTVSVRNTWAMFFTDDKEIMKLTAMALPIV GLCELGNCPQTTGCGVLRGSARPKIGANINGVAFYAVGIPVGAVLAFWFGFGF KGLWLGMMLAAQITCVIGMMAATCRTDWELEAERAKVLTTAVDCGSSDDDAK EDMEAGMVDK MRDDREREGEDLSWPLIGEKSSEVKEEVKKQLWLSGPLIAVSLLQFCLQVISVMF VGHLGSLPLSAASIATSFASVTGFSFLMGTASALDTLCCQAYGAKKYGMLGIQ MQRAMFVLTLASIPLSIIWANTEHLLVFFGQNKSIATLAGSYAKFMIPSIFAYGLL QCFNRFLQAQNNVFPVVFCSGVTTSLHVLLCWVLVFKSGLGFQGAALANSISY WLVNVLFCYVKFSPSCSLTWTGFSKEALRDILPFLRLAVPSALMVCLEMWSFE LLVLLSGLLPNPVLETSLVLSICLNTSGTMWMIPFGLSGAASTRISNELGAGNPKV AKLAVRVVICIAVAESIVIGSVLILIRNIWGLAYSELEVVSIVASMMPIALGNFL DSLQCVLSGVARGCGWQKIGAIINLGSYYLVGVPSGLLLAFHFHVGGRLWL IICALVVQVFGGLGLVTIFTNWDEEAKKATNRIESSSVKDFAVDDRSVVVF MRGGDGEESERVALLKSPHTAEEDGEGLKDRILVETKKLWQIVGPAIFSRVT TYSMLVITQAFAGHLGDLELAAISIVNNVTGFGNFGLLLGMASALETLCCQAFC AKKYHMLGVYMQRSWIVLFCCVLLLPTYIFTTPVLKFLGQPDIAELSGVVAI WVIPLHFAFTLSFPLQRFLQCQLKNRVTAYAAAVLVHILVCWLFVDGLKLG VVGTVATISISWWVNVLLVYSTCGGCPLTWTGLSSEALTGLWEFLKLSASSGV MLCLENWYYRILIIMTGNLQNAIAVDSLICMAINGWEMMIPLAFFAGTGVR VANELGAGNGKGARFATIVSVTQSLIIGLFFWVLMILLHNQIAWIFSSSAVLDA VNKLSLLLAFTVLLNSVQPVLSGVAVGSGWQSYVAYINLGCYYCIGVPLGLFMG WGFKLGVMGIWGGMIFGGTAVQTMILSFITMRCDWEKEAQKASARINKWSNT IK MAQTYLLFLLPDLLINSFLHPIRVYLRAQNVTHPVTLASLAGTLLHVAFNLALV ERGLGGVAAAAAASSFSILCLLVLYLWISGVHLATWTAPSRECLTCWEPLIRLA APSCVSVCLEWWWYEIMILLCGLLVDPTASVAAMGILIQTTSLIYVFPSSLGLAV STRVGNELGANRGRARRMSAVVAVFFAAVMGFSVVFATAMRRRWGRMFTG DEGILRLTGAALPILGLCELGNCPQTVGCGVVRRGTARPNVAANVNLGAFYLVG MPVAVGLAFWLEVGFCLWLGLLSAQVCCAGLMLYMIGTTDWEYQACRAQL LTALDEGSDGHKQPLIATLDNNNYS* MPSKEDSPLVEAKLPLLEAHPLTDEREQDQSFPRRFWLESKRLWHIVGPSIFSRIA SYSMLVITQAFAGHLGDLELAAISIANNVVVGDFGLLLGMASALETLCCQAFC AKKYHMLGVYMQRSWIVLFICCIFLLPLYLFAFPVLKLLGQPEELAEELSGAVSIW MIPVHFAFAFQFPLQRFLQCQLKTAPIAWVSLVALVVHVFSWLVFVKLQFGV VGAAATINFSWWVLTGLFGYVWVGCPHTWSGFSVEAFSGLWEFLKLSAAA GVMLCLENWYYKILIVMTGNLENAEIAVDALSICMTINSLELMIPLAFFAATGV RVANELGAGNGKGAKFATMVSVVTSVIIIGLFFWMLILHDKFGYIFSNSKAVL DEVNNLSLLAFTILLNSVQPVLSGVAVGSGWQSYVAYINLGCYYIIGVPLGILM GWVFNQGVMIWAGMIFGGTATQTLILSLITIRCDWDKEAERAKLHLTKWTD PKQELN*
AT5G6 5380	
Glyma. 01G007 100.1. Wm82. a2.v1	
Glyma. 01G025 200.1. Wm82. a2.v1	
Glyma. 01G026 200.1. Wm82.	

a2.v1	<p>GMAMVLHPVLSWLLMVKLEWGLVGAADVVLNGSWWFVVVAQLVYVFGGWC WPAWNGFSWEAFRSLWGFFRLSLASAVMLCLETWYFMALILFAGYLKNAQVS VDAFSICMNILGWTIMVSFGMNAATSVRISNELGARHPRTALFSLVVAVITSVLI GVLLAIVLMISRNEYPSSLFSNDTEVQDLVKDLTPFLCFCIVINNVPVLSGVAIG AGWQALVAYVNIACYLFGIPVGLVLGYKLDWGVKGIWLGMMISGTILQTCVLL VLIYKTNWNEEASLAEDRIRTWGGHKKATVNDTENTQET*</p> <p>MCTGAESRGDINGDPVISKVGGDYEDRMRTIELEGGEETACNWGTFVRGLLQG IQHHLTALNLPSSLASELKEELQSLAKVACPIIMTSLMMYSRSASVSMFLGRQGK VELAGGSLALGFANITANSVLKGLTMGMDPICCQAYGAKRWSVLNQTFRLTL CLLLLVAIPISILWLNMEPIQLMLGQDPEVTKVAQVYMFVFSIPELLAQAHNLPLR SFLRTQGLTTPVTIAASCAALLHLPINYFLATYLNLGVKGIALATGLNSINMTLG 200.1. LLLYILFSKKPLKPWQGATLLSAFHGWKPLLSLALPSCISVCLEWWWYEIMFLC Wm82. GLLSNPQATVATMGILIQTGLFLYVFPFSLSIALTTRIGHSLGAGQASKAQSTAI a2.v1 GFLTAFTLGLTAFILLFLVRKSWGKLFNTNETQIVELVTILPILGLCEVSNWPQTV SCGILSGTARPYLGARINLCAFYLVLGPVSVFATFIYKYELVGLWSGMVAAQAS CLCMMVYTLIQTDWEQQCKRAVELAQKTTERENKNDDEESGLLGSDQ*</p> <p>MSATLTCKLGDNNLSLNDKNDQPPSPQPLQKCPANMVSMVSELRIQRGIAL PMVAMNLAWFAKTAITTAFLGRLGELSLAGGALGFTFANVTGFSVLNGLCGA MEPICGQAHGAKNFRLLHKTLLMAISLLLLVSLPITFLWLNVDKILILFGQQQDI Glyma. STVARTYVVSCLIPDLFVASLFCPLKAYLSCQSITLPTMFSSAVALAFHIPINIVLSRT 01G213 MGLRGVSMVWITDLIVVLLAIYVLILENKKESMWKEGGWWDQSIEDWIRLL 000.1. KLCGSCCLNTCLEWWCYEILVLLTGHLTNAKQAVGVLAIVLNFDYLLFSVMLS Wm82. LATCVSTRVSNELGANQAGLAYRSACVSLALGFISGCIGSLVMVAARGIWGPLF a2.v1 SHDMAIIKGVKKTMLLMALVEVFNFPLAVCGGIVRGRTARPWLGMYANLGGFY FLALPLGVVFAFKLCLGLVGLLIGLLTGIVTCLTLLLVFIARLNWVEEAAKAQT TGQEQVKELSKYDAEERIDAHEKDVV*</p> <p>MCQLSSPSTLCESNEGHPNMPPTKIHEEPPDMFVLLIPKPPTTTTTFEQGQNNQK PHKTHFSLALDEVKCIANIALPMVLTGLLLYSRSVISMLFLGRVGELALAGGSLA IGFANITGYSILSGLAMGMEPICGQAFGAKRFKLLGLAMQRTMVLLLLTCVFISF Glyma. LWFMKKILVLCCQQEDATEAQSFILFSIPDLVAQSLLHPLRIYLRQSITLPLTY 01G216 TASLILLHVPINYFLVSVLKLGIKIALGAVWTNFNLFVSLILYIWSGVYKKTW 600.1. PGVSLKGVFSGWKSLLNLAIPSCISVCLEWWWYEIMILLCGLLINPQATVASMG Wm82. VLIQTTALIYFPSSLSFAVSTRVGNELGAENPKKAKLAALVGLCFSYGLGFSALF a2.v1 FAVSVRHVWASMFTSDAEIHALTSMVLPPIGLCELGNCPQTTVCGVLRGTARPKL GANINLGC FYLVGMPVAVRLSFFAGFDKGLWLGLLAAQASCMFTMLIVLART NWEQVQRAKELTSSSDSSEEEEEQDQKCLFSSGATKECSHSDSLV*</p> <p>MPRSRRSNPRLAERVFIAGTPDIAPITSTGDFYREFMVESKKLGYLAGPAIFSFVS KYSLGAFQTQIFAGHVTIDLAADVSVENSLIAGFSYGIMLGMGSALETLCGQAVG Glyma. AGKLDMLGVYMQRSWVLLLSMAFVLWPMYIFAGQVLKFIGQDTQISEAAGTF 02G038 AIWMIPQLFAYALNFPVAKFLQAQVLSWLLMVKLELGLVGAAVLVYVFGGWC 600.1. WPAWNGFSGEAFRNLCGFFRLSLASAVMLCVNNEVFKIDNFSPLVTSLLLLDY Wm82. IVECTALDGFDAKKKQVQGILVGLIPLGNMYFMALILFAGYLKNAQVFVDAF a2.v1 SICMNILGWTIMVSFGMNAATRATLFSLVVAVITSVLIGILLAIVLMILRNEYP FSNDTEGQDLVKNLTPFLCFCIVINNVPVLSGVAIGAGWQALVAYVNIACY</p>
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	LFGIPVGLVLGYKLDWGVKGIWLGMIAGTILQTCVLLVLIYKTNWNEEASLAED RIRTWGGHEKATVKDTKNTKEET*
Glyma. 02G039 500.1. Wm82. a2.v1	MSKMSSDEALALEEVHHPLEDDYCADGEEKEYFVRRVWNESKKLWNISGPAIF NRVATFSMFVITQAFAGHLGDLELAATSIAINVILGLDFGILLGMSSALDTLCGQ AFGAKKYYMLGIYMQRSWVVLSTGVMFLALFLFVTPILKFFGQTSEIAELAGVI SLWLIPTHLAYIFYLPMHFLLQSQLKNNVTTWVSLLGLLVHAYLCWLVVNKFH LGVIALVAFGNIAWLLVLGYFGYVICGGCTLTWTGFSIEAFSGVWEFSKLSTAS GIMICLEVWYDKALMLMTGNLQSAKTITIEALTICLTINIWELMFPLSFYAATAV RVANELGAGNGKGAKFASMVSVVTSHHSIFFWLLIMVFRRLAYLFSSESVIKE VDKLSFPLGVITLLNSVQPVLSGVAVGSGWQKYVAFINLGSYYLIGLPLGYLLGF VFRLGVQGVWAGLIFGGPAIQTLLILAWVTSRCNWDKQAERARLHLTKWDPNQ ELIR*
Glyma. 02G075 300.1. Wm82. a2.v1	MGDNKDRDFFSHKFPTTSQVMEEMKELWGMALPITAMNMLVFVRVSVLFL GRLGSLELAGGALSIGFTNITGYSVLVGLAAGLEPVCSQAYGSKNWDLLSLSLQ RMVLILLMAIVPISLLWLNLERIMLFMCQDSAITGMASLYCFYSLPDLTNTLLQ PLRVFLRSQKVTKPMMYCSLVAVLFHVPLNYLLVVVMGLGVPGVAMASVMT NLNMVVLMAGYVCVCRKREVVVKWGCWGVGGGVVCSGLGQLMGFAVPSC MICLEWWWYEIVTVLAGYLPRLTAVAATGILIQTTSMMYTVPMALAGCVSAR VGNELGAGKPYKAKLAADVVALGCAVIGFINVTWTVILGQRWAGLFTNDEPV KALVASVMPIMGLCELGNCPQTTGCGILRGMARPGIGAHINLGSFYFVGTPVA VGLAFWFKVGFSGLWFGLLSAQVACAVSILYVVLVRTDWEAEALKAELTRIE MGSCNGLRNKENERDEERKGLLVNGNGNKKDDIC*
Glyma. 02G089 900.1. Wm82. a2.v1	MEETLLPKENKRVTLTNSKSSSGFVQELKNVSLMAAPMVVVSVSQFLLQVVSL MMAGHLGELSLAGVALATSFADVTGFSILMGMAGALETQCGQSFGAEQFHLK GNYVFCAILSLILSSVPISIIWIFMDKLLILLGQDHAISLIAGNYCIWLIPALFGYAV LQALVRYFQTQSLIFPMLVTSVVVLVLHIPICWVLVFGGLGLGQNGAAISIGISYW LSVMLLLIYTKYYPSCQKTKIALGSNALRSIKEFFFLAIPSALMICFEWWSFELVVI LAGLLPNPKLETSVLSICLNICTLHYFIPYGTGAADVSTRVSNELGARRPQAAREA VFAVIVLAFTDAVVFSSVLCFRHVLGFASFNEMEVVHYVAKIVPVLCLSFMD GFLGVLCGIVRGSGWQKIGAITNLVAYYAVGIPVSLLFGFGLNFNGKGLWIGILT GSTLQTIILALLTAFTNWEKQASLAIERLSEPDVTF*
Glyma. 02G090 000.1. Wm82. a2.v1	MMGKEEATPLLRKSEVAPLEDDDAFCVELKRVGSMAAPMVAANMCQYLLQV VSLMMVGHLGVLVSFSGVAIATSFAEVTGFCVLMGMAGALETLCGQTYGAEFF SEIGNYTFCAIVTLLLVLCPISMLWIFVDKILLFGQDPEISHVAHEYCIYSIPALY GFAVLQCQIRYFQTQSMIFPMVFSSIAVLCLHVPICWALVFKLALGHVGAAYAI GISYWLNVIGLGIYMNFSPECKTKIVFSFNALLSIPEFCQFAIPSGLMFCFEMWS FELLTLFAGLLPNPQLQTSVLSVCLNTTTLHYIIPYAVGASASTRISNELGAGNPK AAQGIVRVIVIIIGIVDGVIVSIFVCCRHILGYAYSNDKEVVVDYVSDIVPILCSFT ADSLIGALSIGARGGGFQQIGAYVNLGAYYLVGVPLAFLGLFVLHFNAGLWLM GSLTGSVLQVILTVVTVLTDWQKEATKARVRIVEKSIKAHNGSV*
Glyma. 02G090 100.1. Wm82.	MEESSGKKGWGMKREELKKVGTIAAPMAVSSVLQYLLPVVSLVMVGHLNQ LSLSSVAIATSLTNVSGFSVLSGMAGGLETLCGQAFGAGQYEFGLYTYTAHLS LVCFPITILWIFNDKILTLLGQDPTISLEVRKYAIWLIPALFGSAILKPLTRFFQTQS LISPMILTSIALCFHVVTCTWTLVFKLGLGHVGAASFSLCVWFNVIMLLSFVRY

a2.v1	<p>SACEKTRISFSKNALVGVGEFFRFAVPAAVMVCLKWWACEILVLLAGLFPNPKL ETSVLISICTISTLHFTIPYGFGAASTRVSNELGAGNPQAVHVAVSATMFLAVT EGFIVSATLFGCRHILGYAYSDDRMVVHYVAVMIPLLCLSIFTDSLQGVLSGVAR GSGWQHLGAYVNLGAFYLVGIPVGILLGFVAHFRAKGLWIGIVTGSIVQSILLSL ITALTNWKKQAIMARERVFDKPPDVNGSYHMTSA*</p> <p>MMPLLMFLSGIRNAFSSDELGLEILNIALPTTLALAADPIASLIDTAFIGHIGPVEL AAVGVSIAIFNQISKITIIPVSVTTSLVAEEDAADQNQQSEKEMLMKVSNEVDV KLDVHDHIEKAGNPSSANVGRVAKLKHDKSYIPSASSGVVIGGVLGVLQALFLI FTAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKT PLYATVMGDVTNIILDPLLMFVLRGNGAAISHIISQYLISIMLLWSLMQQQVVL IPPSIQDFQFGKILKNGFLLLIKVASVTFCVTLSASLAARKGSTTMAAFQICLQIW MATSLADGLAVAGQAIISAFARNDYKRVIASASRVLQLGLILGLVLSVLLLSL LPFASRLFTNDNNVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSM IMVALVSILSLYTLSSSLGFTGIWIALSIYMTLRIFAGFWRIGTGSGPWSFLKVNNV GL*</p> <p>MEEIKAIGRISCPTAITGLILYSRAMISMIFLGYLGEMELAGGSLSIGFANITGYSVI SGLAMGMEPICGQAYGAKQWKILGLTLQRTVLLLLSTSIPIFMWLNMKRILLW SGQDQEIASVAQTFITFSIPDLFLLSLLHPLRIYLRTQSITLPTYCSAISVLLHVPLN FLLVVLHKMGIAGVATAMVLTNLNLILFISSFVYFSGAYKASWVSPSVDCIKGW SSLLSLAIPTCVSVCLEWWWYEFMIMLCGLLVNPKATIASMGILIQTTSLVYVFP SLSLGVSTRVGNELGAKNPRKARVSMIVSLFCALALGLAAMLFTTLMRHQWGR FFTNDHEILELTSLVLPIAGLCELGNCPQTTGCGVLRGSARPTIGANINLGSFYLV GMPVAILLSFVAKMGFPGLWLGLLAAQASCAGLMFYVLCTTDWNVQVERAK ELTKSSTTTTTAMTATIATTSCSTSPNCNYKLLPTLTKKEANMNKNAHVCLEEIV ITSGGGGDELTKISSVETDPLIIPTTKHTQV*</p> <p>MVMEATHFTTSQYQYHIDGGFTRRPFMRMRKRSHISYGYGPHFLRRSLYVPFIA LGPKAKAKAEAEAEAEASSFSSVDVRRELISLTLPALASQAIDPLAQLMETAYIG RLGTVELASAGVSISIFNIISKLFNIPLLSVATSFVAEDIAKASSTADAKTKQQLSSV STALLALVLGFFEALALYLGSGAFLHLIGVSTQNPTYVPAHFSLSLRAVGAPA VVLSSLQGIFRGFKDTKTVPICLGIGNFSVFLFPLLMYYFRLGVTGAAISTVISQ YIGTMLMIWCLNKRAELLPPKMGDQLQFGSYIKSGGFLGRTL SVLSTMTLGTSM AARHGPVAMAAHQICMQVWLAVSLTDLAASGQALIASSVSRHEYKVAKE VTSVLRLIGLVMGICLTAILGASFGSLATIFTQDTEVLQVIRTLALFVSASQPFNAL AYIFDGLHYGVSDFRYAAFSMMFVGAVSSAFLVFAPPLFGLQGVLGLGLFMA LRAAAGAVRLLSKNGPWWFLHRFTNCRGGLISL*</p> <p>MEGNLKQKLLSREKISEEEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGLSVIS QAFIGHIGSKELAAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG VYLQRSSIVLFLTALCLLPFIFTSPILTLLGQDESIARVARNVSLWSIPILFAYIVSF NCQTFLQSQSKNVIIAFLATLSIIHVLSLSWLFTIQFKYGIPGAMISTILAYWIPNVG QLIFITCGWCPETWKGFSSLAFKDLWPVVKLSLSAGAMLCLELWYNTILILLTG NMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKDAKFSI VVTVLTSFSIGFILFVLFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSIQP VLSGVAVGAGWQSIVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLI QTIVLTIITYKTNWDEQVIIARNRISKWSKVDLDRET VTSDN*</p>
Glyma. 02G181 800.1. Wm82. a2.v1	<p>FTAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKT PLYATVMGDVTNIILDPLLMFVLRGNGAAISHIISQYLISIMLLWSLMQQQVVL IPPSIQDFQFGKILKNGFLLLIKVASVTFCVTLSASLAARKGSTTMAAFQICLQIW MATSLADGLAVAGQAIISAFARNDYKRVIASASRVLQLGLILGLVLSVLLLSL LPFASRLFTNDNNVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSM IMVALVSILSLYTLSSSLGFTGIWIALSIYMTLRIFAGFWRIGTGSGPWSFLKVNNV GL*</p> <p>MEEIKAIGRISCPTAITGLILYSRAMISMIFLGYLGEMELAGGSLSIGFANITGYSVI SGLAMGMEPICGQAYGAKQWKILGLTLQRTVLLLLSTSIPIFMWLNMKRILLW SGQDQEIASVAQTFITFSIPDLFLLSLLHPLRIYLRTQSITLPTYCSAISVLLHVPLN FLLVVLHKMGIAGVATAMVLTNLNLILFISSFVYFSGAYKASWVSPSVDCIKGW SSLLSLAIPTCVSVCLEWWWYEFMIMLCGLLVNPKATIASMGILIQTTSLVYVFP SLSLGVSTRVGNELGAKNPRKARVSMIVSLFCALALGLAAMLFTTLMRHQWGR FFTNDHEILELTSLVLPIAGLCELGNCPQTTGCGVLRGSARPTIGANINLGSFYLV GMPVAILLSFVAKMGFPGLWLGLLAAQASCAGLMFYVLCTTDWNVQVERAK ELTKSSTTTTTAMTATIATTSCSTSPNCNYKLLPTLTKKEANMNKNAHVCLEEIV ITSGGGGDELTKISSVETDPLIIPTTKHTQV*</p> <p>MVMEATHFTTSQYQYHIDGGFTRRPFMRMRKRSHISYGYGPHFLRRSLYVPFIA LGPKAKAKAEAEAEAEASSFSSVDVRRELISLTLPALASQAIDPLAQLMETAYIG RLGTVELASAGVSISIFNIISKLFNIPLLSVATSFVAEDIAKASSTADAKTKQQLSSV STALLALVLGFFEALALYLGSGAFLHLIGVSTQNPTYVPAHFSLSLRAVGAPA VVLSSLQGIFRGFKDTKTVPICLGIGNFSVFLFPLLMYYFRLGVTGAAISTVISQ YIGTMLMIWCLNKRAELLPPKMGDQLQFGSYIKSGGFLGRTL SVLSTMTLGTSM AARHGPVAMAAHQICMQVWLAVSLTDLAASGQALIASSVSRHEYKVAKE VTSVLRLIGLVMGICLTAILGASFGSLATIFTQDTEVLQVIRTLALFVSASQPFNAL AYIFDGLHYGVSDFRYAAFSMMFVGAVSSAFLVFAPPLFGLQGVLGLGLFMA LRAAAGAVRLLSKNGPWWFLHRFTNCRGGLISL*</p> <p>MEGNLKQKLLSREKISEEEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGLSVIS QAFIGHIGSKELAAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG VYLQRSSIVLFLTALCLLPFIFTSPILTLLGQDESIARVARNVSLWSIPILFAYIVSF NCQTFLQSQSKNVIIAFLATLSIIHVLSLSWLFTIQFKYGIPGAMISTILAYWIPNVG QLIFITCGWCPETWKGFSSLAFKDLWPVVKLSLSAGAMLCLELWYNTILILLTG NMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKDAKFSI VVTVLTSFSIGFILFVLFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSIQP VLSGVAVGAGWQSIVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLI QTIVLTIITYKTNWDEQVIIARNRISKWSKVDLDRET VTSDN*</p>
Glyma. 02G218 400.1. Wm82. a2.v1	<p>FTAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKT PLYATVMGDVTNIILDPLLMFVLRGNGAAISHIISQYLISIMLLWSLMQQQVVL IPPSIQDFQFGKILKNGFLLLIKVASVTFCVTLSASLAARKGSTTMAAFQICLQIW MATSLADGLAVAGQAIISAFARNDYKRVIASASRVLQLGLILGLVLSVLLLSL LPFASRLFTNDNNVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSM IMVALVSILSLYTLSSSLGFTGIWIALSIYMTLRIFAGFWRIGTGSGPWSFLKVNNV GL*</p> <p>MEEIKAIGRISCPTAITGLILYSRAMISMIFLGYLGEMELAGGSLSIGFANITGYSVI SGLAMGMEPICGQAYGAKQWKILGLTLQRTVLLLLSTSIPIFMWLNMKRILLW SGQDQEIASVAQTFITFSIPDLFLLSLLHPLRIYLRTQSITLPTYCSAISVLLHVPLN FLLVVLHKMGIAGVATAMVLTNLNLILFISSFVYFSGAYKASWVSPSVDCIKGW SSLLSLAIPTCVSVCLEWWWYEFMIMLCGLLVNPKATIASMGILIQTTSLVYVFP SLSLGVSTRVGNELGAKNPRKARVSMIVSLFCALALGLAAMLFTTLMRHQWGR FFTNDHEILELTSLVLPIAGLCELGNCPQTTGCGVLRGSARPTIGANINLGSFYLV GMPVAILLSFVAKMGFPGLWLGLLAAQASCAGLMFYVLCTTDWNVQVERAK ELTKSSTTTTTAMTATIATTSCSTSPNCNYKLLPTLTKKEANMNKNAHVCLEEIV ITSGGGGDELTKISSVETDPLIIPTTKHTQV*</p> <p>MVMEATHFTTSQYQYHIDGGFTRRPFMRMRKRSHISYGYGPHFLRRSLYVPFIA LGPKAKAKAEAEAEAEASSFSSVDVRRELISLTLPALASQAIDPLAQLMETAYIG RLGTVELASAGVSISIFNIISKLFNIPLLSVATSFVAEDIAKASSTADAKTKQQLSSV STALLALVLGFFEALALYLGSGAFLHLIGVSTQNPTYVPAHFSLSLRAVGAPA VVLSSLQGIFRGFKDTKTVPICLGIGNFSVFLFPLLMYYFRLGVTGAAISTVISQ YIGTMLMIWCLNKRAELLPPKMGDQLQFGSYIKSGGFLGRTL SVLSTMTLGTSM AARHGPVAMAAHQICMQVWLAVSLTDLAASGQALIASSVSRHEYKVAKE VTSVLRLIGLVMGICLTAILGASFGSLATIFTQDTEVLQVIRTLALFVSASQPFNAL AYIFDGLHYGVSDFRYAAFSMMFVGAVSSAFLVFAPPLFGLQGVLGLGLFMA LRAAAGAVRLLSKNGPWWFLHRFTNCRGGLISL*</p> <p>MEGNLKQKLLSREKISEEEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGLSVIS QAFIGHIGSKELAAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG VYLQRSSIVLFLTALCLLPFIFTSPILTLLGQDESIARVARNVSLWSIPILFAYIVSF NCQTFLQSQSKNVIIAFLATLSIIHVLSLSWLFTIQFKYGIPGAMISTILAYWIPNVG QLIFITCGWCPETWKGFSSLAFKDLWPVVKLSLSAGAMLCLELWYNTILILLTG NMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKDAKFSI VVTVLTSFSIGFILFVLFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSIQP VLSGVAVGAGWQSIVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLI QTIVLTIITYKTNWDEQVIIARNRISKWSKVDLDRET VTSDN*</p>
Glyma. 02G310 800.1. Wm82. a2.v1	<p>FTAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKT PLYATVMGDVTNIILDPLLMFVLRGNGAAISHIISQYLISIMLLWSLMQQQVVL IPPSIQDFQFGKILKNGFLLLIKVASVTFCVTLSASLAARKGSTTMAAFQICLQIW MATSLADGLAVAGQAIISAFARNDYKRVIASASRVLQLGLILGLVLSVLLLSL LPFASRLFTNDNNVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSM IMVALVSILSLYTLSSSLGFTGIWIALSIYMTLRIFAGFWRIGTGSGPWSFLKVNNV GL*</p> <p>MEEIKAIGRISCPTAITGLILYSRAMISMIFLGYLGEMELAGGSLSIGFANITGYSVI SGLAMGMEPICGQAYGAKQWKILGLTLQRTVLLLLSTSIPIFMWLNMKRILLW SGQDQEIASVAQTFITFSIPDLFLLSLLHPLRIYLRTQSITLPTYCSAISVLLHVPLN FLLVVLHKMGIAGVATAMVLTNLNLILFISSFVYFSGAYKASWVSPSVDCIKGW SSLLSLAIPTCVSVCLEWWWYEFMIMLCGLLVNPKATIASMGILIQTTSLVYVFP SLSLGVSTRVGNELGAKNPRKARVSMIVSLFCALALGLAAMLFTTLMRHQWGR FFTNDHEILELTSLVLPIAGLCELGNCPQTTGCGVLRGSARPTIGANINLGSFYLV GMPVAILLSFVAKMGFPGLWLGLLAAQASCAGLMFYVLCTTDWNVQVERAK ELTKSSTTTTTAMTATIATTSCSTSPNCNYKLLPTLTKKEANMNKNAHVCLEEIV ITSGGGGDELTKISSVETDPLIIPTTKHTQV*</p> <p>MVMEATHFTTSQYQYHIDGGFTRRPFMRMRKRSHISYGYGPHFLRRSLYVPFIA LGPKAKAKAEAEAEAEASSFSSVDVRRELISLTLPALASQAIDPLAQLMETAYIG RLGTVELASAGVSISIFNIISKLFNIPLLSVATSFVAEDIAKASSTADAKTKQQLSSV STALLALVLGFFEALALYLGSGAFLHLIGVSTQNPTYVPAHFSLSLRAVGAPA VVLSSLQGIFRGFKDTKTVPICLGIGNFSVFLFPLLMYYFRLGVTGAAISTVISQ YIGTMLMIWCLNKRAELLPPKMGDQLQFGSYIKSGGFLGRTL SVLSTMTLGTSM AARHGPVAMAAHQICMQVWLAVSLTDLAASGQALIASSVSRHEYKVAKE VTSVLRLIGLVMGICLTAILGASFGSLATIFTQDTEVLQVIRTLALFVSASQPFNAL AYIFDGLHYGVSDFRYAAFSMMFVGAVSSAFLVFAPPLFGLQGVLGLGLFMA LRAAAGAVRLLSKNGPWWFLHRFTNCRGGLISL*</p> <p>MEGNLKQKLLSREKISEEEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGLSVIS QAFIGHIGSKELAAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG VYLQRSSIVLFLTALCLLPFIFTSPILTLLGQDESIARVARNVSLWSIPILFAYIVSF NCQTFLQSQSKNVIIAFLATLSIIHVLSLSWLFTIQFKYGIPGAMISTILAYWIPNVG QLIFITCGWCPETWKGFSSLAFKDLWPVVKLSLSAGAMLCLELWYNTILILLTG NMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKDAKFSI VVTVLTSFSIGFILFVLFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSIQP VLSGVAVGAGWQSIVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLI QTIVLTIITYKTNWDEQVIIARNRISKWSKVDLDRET VTSDN*</p>
Glyma. 03G005 200.1. Wm82. a2.v1	<p>FTAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKT PLYATVMGDVTNIILDPLLMFVLRGNGAAISHIISQYLISIMLLWSLMQQQVVL IPPSIQDFQFGKILKNGFLLLIKVASVTFCVTLSASLAARKGSTTMAAFQICLQIW MATSLADGLAVAGQAIISAFARNDYKRVIASASRVLQLGLILGLVLSVLLLSL LPFASRLFTNDNNVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSM IMVALVSILSLYTLSSSLGFTGIWIALSIYMTLRIFAGFWRIGTGSGPWSFLKVNNV GL*</p> <p>MEEIKAIGRISCPTAITGLILYSRAMISMIFLGYLGEMELAGGSLSIGFANITGYSVI SGLAMGMEPICGQAYGAKQWKILGLTLQRTVLLLLSTSIPIFMWLNMKRILLW SGQDQEIASVAQTFITFSIPDLFLLSLLHPLRIYLRTQSITLPTYCSAISVLLHVPLN FLLVVLHKMGIAGVATAMVLTNLNLILFISSFVYFSGAYKASWVSPSVDCIKGW SSLLSLAIPTCVSVCLEWWWYEFMIMLCGLLVNPKATIASMGILIQTTSLVYVFP SLSLGVSTRVGNELGAKNPRKARVSMIVSLFCALALGLAAMLFTTLMRHQWGR FFTNDHEILELTSLVLPIAGLCELGNCPQTTGCGVLRGSARPTIGANINLGSFYLV GMPVAILLSFVAKMGFPGLWLGLLAAQASCAGLMFYVLCTTDWNVQVERAK ELTKSSTTTTTAMTATIATTSCSTSPNCNYKLLPTLTKKEANMNKNAHVCLEEIV ITSGGGGDELTKISSVETDPLIIPTTKHTQV*</p> <p>MVMEATHFTTSQYQYHIDGGFTRRPFMRMRKRSHISYGYGPHFLRRSLYVPFIA LGPKAKAKAEAEAEAEASSFSSVDVRRELISLTLPALASQAIDPLAQLMETAYIG RLGTVELASAGVSISIFNIISKLFNIPLLSVATSFVAEDIAKASSTADAKTKQQLSSV STALLALVLGFFEALALYLGSGAFLHLIGVSTQNPTYVPAHFSLSLRAVGAPA VVLSSLQGIFRGFKDTKTVPICLGIGNFSVFLFPLLMYYFRLGVTGAAISTVISQ YIGTMLMIWCLNKRAELLPPKMGDQLQFGSYIKSGGFLGRTL SVLSTMTLGTSM AARHGPVAMAAHQICMQVWLAVSLTDLAASGQALIASSVSRHEYKVAKE VTSVLRLIGLVMGICLTAILGASFGSLATIFTQDTEVLQVIRTLALFVSASQPFNAL AYIFDGLHYGVSDFRYAAFSMMFVGAVSSAFLVFAPPLFGLQGVLGLGLFMA LRAAAGAVRLLSKNGPWWFLHRFTNCRGGLISL*</p> <p>MEGNLKQKLLSREKISEEEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGLSVIS QAFIGHIGSKELAAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG VYLQRSSIVLFLTALCLLPFIFTSPILTLLGQDESIARVARNVSLWSIPILFAYIVSF NCQTFLQSQSKNVIIAFLATLSIIHVLSLSWLFTIQFKYGIPGAMISTILAYWIPNVG QLIFITCGWCPETWKGFSSLAFKDLWPVVKLSLSAGAMLCLELWYNTILILLTG NMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKDAKFSI VVTVLTSFSIGFILFVLFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSIQP VLSGVAVGAGWQSIVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLI QTIVLTIITYKTNWDEQVIIARNRISKWSKVDLDRET VTSDN*</p>

		MEGNLEKKLLSREQKSEENLSLVKRVWEESKVMWIVAAPAIFTRFTTFGISVIS QAFIGHIGSRELAAYALVFTVIIRFANGILLGMASALSTLCGQAYGAKEYDMMG
Glyma.		VYLQRSWIVLFLSAICLLPLFIFTSPILTLLGQDESIAQVARTISIWSIPVLFAIVSN
03G005		SCQTFLQSQSKNVIISYLAALSIIHVLSLWLFMTMQFKYGIPGAMISTILAYWIPNIG
300.1.		QLIFITCGWCPETWKGFSFLAFKDLWPVAKLSISSGAMLCLELWYSTILILLTGN
Wm82.		MKDAEVQIDALSICINISGWEMMIAFGFMAAVSVRVANELGRENSKAAKFSIV
a2.v1		VTVLTSFAIGFILFVLFLILREKVAYLFTSNEDVATAVGDLSPLLALSLLLNSIQPV LSGVAVGAGWQSTVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFGTLIQ TIILIIITYKTNWDEQVIIARDRINKWSKMLVDHETITSDN*
		MEGNLEKKLLSKEEVSEEDNLSLVKRVWEESKEMWIVAAPAIFTRFTTFGINVIS QAFIGHIGSRELAAYALVFTVIIRFANGILLGMSSALSTLCGQAYGAKEYDMMG
Glyma.		VYLQRSSIVLFLTALCLLPVFIFTSPILMLLGQDENIAQVAGTISLWSIPILFAYIVSF
03G005		NCQTFLQSQSKNVVIAFLAALSIIHVFLSWLLTIQFKFGIPGAMISTILAFWIPNIG
400.1.		QLIFITCGWCDETWKGFSFLAFKDLGPVVKLSLSSGAMLCLELWYNTVLILLTG
Wm82.		NMKNAEVEINALSICININGWEMMIALGFMAAAASVRVANELGRGSSQAAKFSI
a2.v1		VVSVLTSFVIGFILFVLFLFLREKIAYLFTSNEDVVTAVGDLSPLLALSLLLNSIQPV LSGVAVGAGWQSTVAYVNIGCYYLIGIPVGIVLGNIIHLEVKGIWIGMLFGTLVQ TIVLTIITYKTNWDEQVTIARNRISKWYKVELDHETSTSDN*
		MWVVAAPAIFTRFSTFGINVITHAFVGHIGSRELAALVFTVLIRFGNSILLGM GTALSTLCGQAYGAKEYGMMGVYIQRSWIVLSLTALCLLPLLIFAIPILTLLDQD
Glyma.		ETIAQVAGTISLWSIPVLFSFIVSFTTQTFLQSQSKNIIIAFLAASFIVIHVFLSWLLT
03G005		MKFKLGIAGAMTSTSLALWIPNIGQLIFITCGWCYDTSKWKGFSFLAFKDLWPV
500.1.		VKLSLSSLPTNGLELWYSTILILLTGNMEDAEVQIDALSICLNINGWELMISLGFM
Wm82.		AAASVRVAKGSSKAAKFSIVVKVLTSAIGFILFFIFLFLKEKLAYIFTSSKDVADA
a2.v1		VGDLSPLLAISILLNSVQPVLSGIPVGVVLGNVHLQVKGIWFGMLFGTFIQTIVL IIITYKTNWDEQVIIARNHINKWSKVDSHHKIIPSEN*
		MQGGVKEKLLIKEKKTSEQEEEEELSLVKRVWNEKVMWVVAAPGIFTRFSTFGI NVISQAFIGHIGSRELAAYALVFTVLIRFANGILLGMASALSTLCGQAYGAKEYV
Glyma.		MMGVHLQRSWIVMSITSLFLLPVFIFTRPILMLLGQDENIAEVAGNISLWSIPMIF
03G005		AFIASFTCQNFLQSQSKNTIISFLAASFIVIHVFLSWLLTIQFKLEIPGAMTSTNLAF
600.1.		WIPNIGQLIFITCGWCSDTWKGFSFLAFKDLWPVVKLSLSSGIMLCLELWYNTIL
Wm82.		VLLTGNMENAEVQIDALSICLNINGWEMMISLGFMAAASVRVANELGKGSSK
a2.v1		AAKFSIVVTVLTSLAIGFVLFLFFLFLRGKLAYIFTSNKDVADAVGDLSPLLAISIL LNSVQPVLSGVAIGAGWQSIVAYVNIGCYIIIGIPVGVVLGNVNLQVKGIWIG MLFGTFIQTIVVLTIVITYKTDWDEQVTKARNRINKWSKVESDHETITSDD*
		MEGDLKQKLLRRRKEEEEEEEELSLAKRVWNEKVMWIVAAPAIFTRFSTFGIS VISQAFVGHIGSKELAAYALVFTVLIRFANGVLLGMASALSTLCGQAYGAKEYG
Glyma.		MMGVYLQRSWIVLFLTAVCLLPVFIFTSPILLLLGQDESIAQVAGNIALWSIPVM
03G005		FAFIVSFTCQTFLQSQSKNIIIAFLAASFIVIHVFLSWLLTMKFKFGIPGAMISAGL
800.1.		AYWIPNIGQLIFVTCGWCSDTWKGFTFLAFKDLWPVVKMSLSAGAMLCLELW
Wm82.		YNTILVLLTGNMKNAEVEIDALSICLNINGWEMMISLGFMAAASVRVANELGR
a2.v1		GSAKAAKFSIIVSVLTSLAIGFLLFIFFLFFRERLAYIFTSNKEVAFAVGDLSPLLSVS ILLNSVQPVLSGVAIGAGWQSIVAYVNMGCYYAIGIPVGIVLGNVLDLQVKGIW IGMLFGTLIQTIVLIVITYKTNWDEQVTIAQKRISRWSKVDSPDHENEVERKNVS*

Glyma. 03G036 200.1. Wm82. a2.v1	MCTGAESRGDINGDPVISKVGGGDYEDRMRTIELEGGGEERACNCGTFVQGGLL QGIHHHLTALNLP TLSASELKEELQSLAKVACPIIMTSLMMYSRSASVSMFLGR QGKVELAGGSLALGFANITANSVLKGLTMGMDPICCQAYGAKRWSVLNQFTL RTLCLLLLVAIPISVLWLNMEPILQMLGQDPEVTKVAQVYMFVSIPELLAQAH NPLRSFLRTQGLTTPVTIAASCAALLHLPINYLATYLN LGVKGIALATGLNSIN MTLGLLLYILFSKKPLKPWQGATLLSAFHGWKPLL SLALPSCISVCLEWWWYEI MLFLCGLLSNPQATVATMGILIQTLGFLYVFPFSLSIALTTRIGHSLGAGQASKA QSTAMIGFFTAFTLGITAFILLFFVRKSWGKLF TNETQIIELVT TILPILGLCEVSNW PQTVSCGILSGTARPYLGARINLC AFYLVLGPVSVFATFIYKYELVGLWSGMVAA QASCLCMMVYTLIQTDWGQQCKRALELAQKATEQENKNDEESGLLGSDQ*
Glyma. 04G089 000.1. Wm82. a2.v1	MCNPKPSSSSPFLCPTKNHIITPDPKLNHPPVDDQLKDELHRWPTPNEVIAEM KAIGKISGPTALTGLILYSRAMISMVFLGYLGEMELAGGSLSIGFANITGYSVISGL AMGMEPICGQAYGAKQLKTGLTLQRTVLLLLSTSLPISLTWLN MKNILLWCG QDQQISSTAQTFIIFSIPDLFLLSLLHPLRIYLR TQSITLPLTYCSAISVLLHVPLNFL LVVHFKMGVSGVAIAMVWTNLNLFIFLSSFVYFSRVYKDSWVPPSTDCLRGWSS LLALAVPNCVSVCLEWWWYELMIILCGLLLNPKSTIASMGILIQTTALVYVFPSS LSLAVSTRVGNELGANRPAKARISMIVSLACAV ALGVAAMLFTTLMRHRLGRF FTSDREILHLTSIALPIVGLCELGNCPQTTGCGVLRGSARPTVGANINLGSFYLVG MPVAVLLGFVVGKMGFPGLWLGLLAAQASCASLMIFVLCTTDWNAQVRRANE LTNANSAPFKQTEYCNNVRLREIVATEDHDHEITNRPSHYTHYK*
Glyma. 04G097 700.1. Wm82. a2.v1	MDTSCQQKGFFTFLPQNITKAPHYCCPVIDNLRSEAKHMGNILNEGEHEHPLIK SKLPPQPHGSNNHSLFQRSCSESKKLWHIAAPSIFTRLAMFSITVVTQSLAGHLG DLDLAAISIACTVLISITFGFLLGMA SALETLCGQAYGAGQQRILGVYLQRSWV LFLSSILLPVFIFATPVLKLIGQPVAVAEQAGLVAVWLIPLHLSFPFQFTLQRFLQ CQLKTGIIAWVSGVALAVHVLVSWVFVYRMRIGIVGTALSIGFSWWLSVLGML GYTLFGGCPRSWTGFSVEAFVGLWEFFKLSLASGVMLALENFYRLLIVSGYM HNTEIAIDALSVCVTIYGWESMIPLAFLGATGVRVANELGAGNAKGARFATVV SVVTTLFVGFI FVLVIVSFNKNLALIFTSSSSVIQMVNELAMLLAFTVLLNCIQPV LSGVAVGSGRQAVVAYINIGSYYLIGIPLGVLLGWLLPSGIGMWTGMMSGTVV QTLILAIITMRYDWEKEVQKAQILVEEEATFNDQ*
Glyma. 04G097 900.1. Wm82. a2.v1	MGSLKGD SGHANGENLTEALLPTRDAQQQHQTDDEEQRF GDKLWLETRKLW LIVGPSIFSRLASFTMNVVTQAFAGHLGDVELAAISIANNVLVGFNFGLLL GMA SALETLCGQAFGAKRYHLLGIYMQRSWIVLFMCCFLLLPFYVFATPLLKFLGQP DDVAEWSGVVAVWLIPLHFSFAFQFPMQRFLQCQLKTAVIAWVSLGLVNV VTSWLFIYVWDFGLYGAAISLDISWWVLVFGMYAYIAYGGCPLTWNGFSLEAFS GLWEFTLSSASGVMLCLENWYKILLMTGQLENATI AVDALSVCMTINGWE MMIPLAFFAGTGVRVANELGAGNGKAAKFATQVSVAQSTIIGLIFCVLIMIFHE HIAIYFTTSTSVLQAVDNMSLLLAITILLNSVQPVLSGVAVGSGWQAYVAYINIG CYYLIGFPLGIIMGWVFKSGVIGIWGGMIFGGTAIQTLILIIVTIRCDWEKEEEKAC FRVSKWSKSNNGNLEASN*
Glyma. 04G102 100.1. Wm82.	MLITSCVTLCVRIPLCWVLVFKTRQNNVGGALAMSISIWSNVFFHGLYMRYSP CAKTGAPIFMELFQRLWEFFRFAIPSAVMICLEWWPFELIILLSGLLLN PQLETSV LSVCTRISNELGVGNPRGARVSVRAAMPFAVVETTIVSGTLFACRHVFGYIFSNE KEVVD SVTLMAPLVCIWVILDNIQGVLAGVARGC*

a2.v1		MESSRELAAPLLVLRKSGEQENNGVESTFCQEFKRVSSMAAPMVAVTVSQYL LQVVSLMMVGHLLGILVSFSGVAIATSFAEVTGFSVLLGMSGALETLCCQTYGAE
Glyma. 05G001 700.1. Wm82. a2.v1		EYRKFGNYIWCAIVTLTLVCLPISLVWIFTDKILMLFSQDPEISHAAREYCIYLIPA LFGHAVLQALTRYFQTQSMIFPMVFSSITALCLHVPICWGLVFKLGLRHIGAAL AIGVSYWLNWVWLAIYMIFSPACQKTKIVFSSNALLSIPEFLKLAIPSGLMFCFEW WSFEVLTLLAGILPNPQLETAVLSVCLNTTTLHYFIPYAVGASASTRVSNELGAG NPKTAKGAVRVVVLGVAEAVIVSSVFISCRHVLGYAYSNDKEVIDYVAEMAPL LCVSVTADSLIGALSGIARGGGFQEIGAYVNLGAYYLVGIPMGLLLGFHLQLRA KGLWMGTLGSLTQVILAIVTALTDWHKEATKARERVVENSIVHYEA* MRQLSPTSNPKVQDEPNMLATLIPKSPTCQQQQQMQRNHHNNNNNTTHLSLS LNEAKCIANISFSMVL TGLLLYSRSMISMLFLGHLGELALAGGSLAIGFANITGYS VLSGLAMGMEPICGQAFGARRFKLLGLTMQRTVLLLLVTSLISLFFWLNMRKI LLLCGQEEDIANEAELYILSLPDLVLQSLHPLRIYLRQSITLPLTCCA AVSILL HVPINYL FVSILKLGIKVALSAVVTNLNLVWLLIVYVVVSGTHKKTWPGISREC FQGWNSWKTLMNLAIPSCVSVCLEWWWYEIMILLCGLLVNPHASVASMGLI QTTALIYIFPSSLSFGVSTRVGNELGAGNPRRAKLAAMVGLCFSEVFGLSALAF VSVRNWASMF TLDGQIIALTS AVLPIIGLCELGNCPQT TVCGVLRGTARPKLG ANINLGCFYLVGMPVAVWLGFAGFDFKGLWLGMLAAQGSCMMTMMFVLA RTNWEGQALRAKELTDSDSGEEKNLMEEEEQEEEGFLGSCATKEGSV* MSATSKEGENLSTNDRANRHPSTPSSHTKKCPLNANFVKMVVEELRVQRGIAL PLVAMNLAWFAKLAITTAFLGHLGELNLAGGALGFSFANVSGFAVLNGLSGA MEPICGQAHGAKNVRLHKTLLMTTLLLLLVTPLSFLWLNVDKILILFGQQQE ISIVAKTYVSYLPDLFIKALLCPLKAYLSSQCMTLPTMFSSAVALAFHIPVNILLS KTMGLRGVSI AVVWTDLIVMVMLAIYVVVLERRNGSMLWKEGGWWDQNM DWSRLIKLSGSCCLNTCLEWWCYEILLFLTGHLANAKQAVGVLAIVLNFDYLL YAVMLSLATSVSTRVSNELGANRAGQAYKSARVSLAVSVISGCIGGSIMVAARG VWGNLFSHQKGVVKGVEKAMLLMALVEVFNFVPTVCGGIVRGTGRPWLSMY ASLGGFYFLTPLGVVFAFKLRFGLGLLIGLLIGIAACLVLLT FIVRINWVEEA TKAQTFVCNAQVHEQVSRNEVNELTENPEGDQVCKETSITPYSCI* MNLARFAKTAITTAFLGHLGELNLAGGALGFSFANVTGFSVLNGLRGAMETK NVRLHKTLLMTTLLLLLVTPLSFLWLKVDKILIRFGQQQEISIVAKTYVSYLTP DLLVTSLLCPLKAYLSSQCMTLPTMFSSAVTLAFHIPVNILLSKTMRLRGVSI WINDLMVMVMLAIYVVILERRNGSMLWKEGGWWDQNMMDWIRLIKLSGSC CLNTCLEWWCYEILVLLTGHLANAKQAVGVLAIVLNFDYLLYSVMLSLATCVS TRSAVSVISVCIGGVVKGLKKTMLVIALVEVFNFVPTVCGGMVRGTARP* MEGAAEKERLQCWSIRREVKAVVELAFPIGITALIFYARSMVSMFLGHLGELEL AAGSLGMAFANITGYSVLSGLALGMEPMCSQAFGAKRVKVLSTLHRCVMFLL VCSIPISLLWLNMSILLLLHQDPNITLMAHTYLIFSLPDLT HSFHPIRIYLRQ GVTHPVTLASLAGTLLHLPFNLYLLVTRLRLGLAGVAAASAASNLSILLFLGA AVCFTGLHCAAPSRDCFSGWKPLLRLAAPSCVSVCLEWWWYEIMILLCGILVDPTA TVASMGILIQTTS LIYVFPSSLGFAVSTRVGNELGANRPSRAKLSAVVSVFLAAIM GFSAMFFAVGMRRRWGRMFTADEDIIRITSMALPILGICELGNCPQTVGCGIVR GMARPNTAANVNLGAFYLVGMPVAVGLGFWFDVGFCGLWLGLLSAQVCCA

	GLMLYVIGTTDWEFEAHRAQWLTLVEDGVMDGQKQPLTSVVTEAPST*
	MRIVREEVVEEVKRLWLA VPLFSVGILLHILQAISIMFVGHLGTLPLSGASMASF
Glyma.	ASVTGFNLLPFYLFASSKL VIGVSYCTGHILWSIKWSRTVPYAWHTHAEIHACCF
05G243	NDMIPSLFAYGILRCILKFLQTQKIVFPMVLTSGIAAVLHVLFCWLLVFKSGLAN
100.1.	RGAALANSISYWVNAILISLYVRFSSACKHSWTGFSKMALHNLLDFLKLEWTFK
Wm82.	LMVLMSGLLPNPKLETSVFSICLNTFGLGWMIPFGFSAAIETEYAIYSTHVCASF
a2.v1	VRCQVVSYIRFIVTIESTKSLMSTATINIKTPKEKEKKIIQPIKIQFTYLSSPKVYFFSS AIYSNCSRKCPHTMFSMNSSILVSENVKNKNVQGGAE*
	MCNPKPSSSSPFLCPTKNHIISTPDPKLINHPPPVDDQLQDELHRWPTPNEIVAE
	MKAIGKISGPTALTGLIISRAMISMVFLGYLGEMELAGGSLSIGFANITGYSVISG
Glyma.	LAMGMEPICGQAYGAKQLKTLGLTLQRTVLLLLSSSLPISLTWLNMKNILLWCG
06G091	QDHEISSTAQTFILFSIPDLFLLSLLHPLRIYLRQSITEPLTYCSAVSVLLHVPLNFL
100.1.	LVVHLKMGVSGVAIAMVWTNLNLFLLSSFIYFSGVYKDSWVPPSTDCLRGWSS
Wm82.	LLALSVPTCVSVCLEWWYELMIILCGLLLNPKATIASMGILIQTTSLVYVFPSSL
a2.v1	SLAVSTRVGNELGANRPAKARISMIVSLACAVALGVTAMLFTTLMRHRWGRFF TSDQQILHLTSIALPIVGLCELGNCPQTTGCGVLRGSARPTVGANINLGSFYLVG MPVAVLLGFVGKMGFPGLWLGLLAAQGS CAALMIFVLCTTDWNAQVQRANE LTNANSAPSKLPTTECNNVRLPEILVMDTEDHHDEIITKTPSLETDPLIHTSK*
Glyma.	
06G099	MASALETLCGQAYCAGHHRMLGVYLQRSWVVPVFHSDVAGVHFCHARVEV
600.1.	NRETHCGGGTGGFSGALVDPFHLSFPFQFTLQRFLQCQLKTGIIAWVSGWLL*
Wm82.	
a2.v1	MEENLLVLAKSGGEEQKVAWEGLGEEMKRMIDIAGPMVVVTASQRLLQVVSV MMVGHLNDDFLSSAALAISLTAVTGF5FLMGMASGLETICGQAYGAQQHKKI
Glyma.	GVQTYTAIFALT FVCLPFTFLWINMEKILVFIGQDPLIAKEAGKFIIWLIPALFAYA
06G103	ILQPLVRYFQMQSLLLPMLMTSCVTLCVHIPLCWVLVFKTRLNNVGGALAMSIS
400.1.	TWSNVIFLGLYMRYSRCAKTRAPISMELFQGLREFFRFAIPSAVMICLEWWSFE
Wm82.	LIILLSGLLLNPQLETSVLSICLNTTSILYAIPFGIGAASTRISNELGAGNPHGAC
a2.v1	VSVLAAISFAIIE TT VSGTLFACRHVFGYVFSNEKEVV DYVTVMAPLVCISVILD NIQGVLAGVARGCGWQHIGVYVNIGAFYLCGIPMAILSFFAKMRGKGLWIGV QVGSFAQCVLLSTITSCINWEQQTIKARKRLFGSEFSADDRLI*
	MDSTSVHKDIDEPLLSEEPSSPQPPSFTQSFSSRHGSDGELERILSNTSVPFAKRI
	GPATWVELKFLFH LAAPAVIVYLYNYVMSMSTQIFSGHLGNLELAAASLGNTGI
Glyma.	QVFAYGLMLGMGSAVETLCGQAYGAKKFNMLGIYLRSTVLLTLAGILLTIYIF
06G305	SEPILIFLGESPRIASAAALFVYGLIPQIFAYAINFPIQKFLQAQSIVAPSAYISAATL
200.1.	LVHLVLSYVVVYKVGLGLLGASLVLSVSWWIIVIAQFVYIVKSERCKHTWRGFSF
Wm82.	QAFSGLAEFFKLSAASAVMLCLETWYFQILVLLAGLLPHELALDSLSICTTFSG
a2.v1	WVFMISVGFNAAA SVRVSNELGARNPKSASF SVMVVTLSIFIISVIVALVVLAI RD IISYAFTDGEEVAAA VSDLCPLLALSIVLNGIQPVLSGVAVGCGWQTFVAYVNV GCYYGIGIPLG SVLGFYFKLSAKGIWLGMLGGTVLQTHILVWVTFRTDWNNEVE EAAKRLNKWENKTEPLVN*
Glyma.	MEEGSETGKWGW MKRRRAMREELKKVGTIAAPMVVASVLQYLLQVVSLVMV
06G318	GHLNQLSLSTVAIATSLTNVSGFSVLSGMAGGLETGGQAFGAGQYEKFGQYT

700.1.	YTAVISLSLICFPITILWTFMDKILTLLGQDPTISLEARKYAIWLIPALFGSAILKPLT
Wm82.	RFFQTQSLISPMILTSAIALCFHGATCWTLVFKLELGHVGA AISFSLCVWFNVML
a2.v1	LLSFVRYSSACEKTRIPFSKNALVGVGDFFRFAVPAAVMVCLKWWACEILVLLA GLFPNPKLETSVLSICLTISTLHFTIPYGFGA ASTRVSNELGAGNPQAVRVAVSA TMFLAVTEGLIVSATLFGCRHILGYAYSDDRMVVHYVAVMTPLLCLSIFTDSLQ GVLSGVARGSGWQH LGAYVNLGAFYLVGIPVGIVLGFVAHLRAKGLWIGIVTG SIVQSILLSLVTALTNWKKQAMMARERIFDVKPPDENESNHMTSA* MGIWRNEISEEAKKQLWLSGPMVVFVSFQYSLQMISLMFVGHLDELLLAGVSL ATSFVNVTGFSVLLGMSSALDTFCGQSYGAQQYH MVGIHMQR AIVII MLATIP
Glyma.	MSFIWAYLRPILVVLHQDKTIAAQAQLYATYLIPSLSANALLRCITKFLQTQNIV
07G099	LPMMLASGFTTLAHALLCWLLVLKFG LGIKGAAIAFCISNWLNTVLLALYIRFSS
900.1.	SCKSTWTGFSRESLQNIPQFLSLAFPSALMVCLEQWTFQIMVLLSGALPNPKLQT
Wm82.	SVLSICFNTTGLFWMIPFGVSVA ASTRISNELGAGCPKAAYLAVKVTLMSFVVG
a2.v1	ALGFILLMVTRNIWGHIFTNIPEVIRYVASMTPILASSVFVDSIQTALSGIVRGCG WQKLGA FVN LGSYYLVGLPFAIVLAFVLHIKGEGLLLGIVIALTMQVVGFVLITL RTNWEKEANKAAKRIRSNGVPTDANALPSDQN* MALWKEEAKKQLWLAGPMVVFVSFQYSLQVISLVFVGHLDELLLASTSLATSF VNATGFNVLMGMSSALDTFCGQAYGAKQFHMLGVHTQGAMLVLT LVTIPLSI
Glyma.	IWVFLGPILVALHQDKEIAAHAQLYARYLIPSLSANGLLRCITKFLQTQNIVFPM
07G100	VLATGLTSFLHFFLCWVLVQKVGLGIKGS AIAICISNWFNTIILALYIKLSPSCKTT
000.1.	WTGFSKESLHNIPKFLKLAFFSTLMVCLESWTFEIMVLLSGALPDAKLQTSMLSI
Wm82.	CLNTSGIFWMIPFGISAAGSTRISNELGAGSPKAAYLAVKVTMFLASAVGILEFA
a2.v1	SLMILWRVWGRVFTNVHEVVKYVTSMMPLVASSTFIDS IQTAFQGVARGCGW QKLGA YVN LGSYYFLGVPFSVVS AFV FHMKGQGLFLGILIALTVQVVCFLVTL RANWEKEAKKA AKRVGGDGVQLGDLPCDQNANTA* MGIWDKEIADEVTKQLWVAGPMICVCVCQYSLQMMSLMFVGHLDELLLAGA SLATS FVNVTGFNVLMGMSSALDTFCGQGRAMLV LILVTIPVSIH VVFLGPILVA
Glyma.	LHQDKEIAAQAQQYARLLIPSLSANGLLRLLHILLCWTFVLKLGLGFKGSVIAIC
07G100	ISNWFNTILLTYIRFSPSCKTTWTELDL FSLGGILNNPVDFCLEAWTFEIMVLLS
100.1.	GALPNAKLQTSVLSICLNTTGIFWMVPFEVSAAGSTRISNELGAGRAKAAYLAV
Wm82.	KVTMFLASAVGILEFAALLVRRVWGRAFTNVHEVVTYVTSMPIVASSPFIDSI
a2.v1	QTAFQGVARGCGWQKLGAFFNLGSYYFLGVPFAIVTAFVLHMKGQGLLLGIVL ALIVQVVCFLVVT LR TNWEKEANKAATRVGGSIVQVEHIKLS* MCESEKSEQRHDDKEKQTEELGGVLT RRSTIMWDVIGEAKSLWELAFPTALTGLI FYARSMVSMFLGLH LGDTELAAGSLAIAFANITGYSVLSGLSLGMEPLCSQAFG AKRPKLLSLTLQRCVIFLLFSSIPISLLWLNMSKV FILLHQH THITQMAQTYLVFL
Glyma.	LPDLVTNSFLHPIRVYLRAQNITHPVTLASLAGTLLHVPFNLLL VQRGLPGVAA
07G124	ASAASSFSILSLLVLYVWISGVHLATWTAPSRECFGGWEPLRLAAPS CVSVCLE
600.1.	WWWYEIMILLCGVLVDPTASVAAMGIFNPDDVVDLCLPLVSGICGFHARGEPA
Wm82.	WREQGPRARMSAVVAVFFAAVMGFS AVVFATAMRRRWGRMFTGDEGILRLT
a2.v1	AAALPILGLCELGNCPQT VGC GVVRGTARP NVAANVNLGAFYLVGMPVAVG LAFWLEVGF CGLWLGLLSAQVCCAGLMLYMIGTTDWEYQACRAQLLTALDQ GSDGHKQPLLA AVDNNNS*
Glyma.	MASSLSTTSFLCTHSLKSPTLKPLTKPHCFARFRARVRVPPKASSQNNNNANNS

07G156	VETPSLQPSSPKPPYNSSSSLLRHFSNGWFKFDELGMEIVLIALPAALALAADPIA
100.1.	SLIDTAFVGHIGAVELA AAVGVSA SVFNLVSKAFNVPLLNVTTSFVAEEQALIRKE
Wm82.	EESILSDENGKDQSKLLPSVSTSLALAAATLGIAETVVLTLGSGILMNIMGIPADS
a2.v1	PMRGPAEQFLTLRAFGAPAIVLALAAQGTFRGFLDTKTPLYAVGVGNFLNAIL DPILIFLFGLGIGGA AVATVISEYLIAFILLWKLSDKVLLIPSEFDGRKFFSYLKSGG LVSARTLAVFITVTLSTSVAAQQGPIPMAGHQICMQVWLSVSLNDALALAGQ ALLARNYSLGNYEQARLVYIRVIQIGLGAGITLSIILFFGFGAFSSLFSTDSEVLDV AWSGIWVAVAGSQPVNALAFVIDGIYYGVSDFGYAAYSMLVGLVSTFLLVAAP VGLPGVWTGLFIFMALRVLAGVWRLSSKSGPWDTIWYRDGAED* MLAEQKSQNTYPTVTEVLEEAKRMTDIGFPIAAMSLVGYLKNMTLVVCMGRL GSLELAGGSLAIGFTNITGYSVLSGLAMGMEPLCTQAFGSRNFSLLSLTLQRTIL MLLLFSLPISLLWLNLESLMLCLRQNPDITRVATLYCCFAIPDLIANCFLHPLRIY LRSKGTTWPLLWCTLISILLHLP TLTLFTLNLGVPGIAISSFVANFSNLFLLLY MFYTRVRKESLHVPLLMPRHMSHNVTTCSSSTIAKEWGVLMKFISQSCLAVCL EWWWYELMTISAGYLHNPRVSLATAGIVIQTTSMLMYTLPTALSASVSTRVGNEL GAGQGERARLSTVVAIGLALVSSIFGLLWTTMGRERWGRVFTSDSEVLQLTMA VLPIIIGLCELANCPQTTSCGILRGSARPGVGAVINFCSFYLVGAPVAIVLAFYWK LGMVGLCYGLLAAQIACVVSIFVVVYKTDWERESLKATCLVGKSSCGTFAYED QTAVKCEGVVFLHNSEK* MGSKTEEVVDYTLMEGAVEKEGQHCWSIRREVKA VGELAFPIALTALIFYARS MVSMLFLGHLGELELAAGSLGMAFANITGYSVLSGLALGMEPLCSQAFGAKRV NVLSLTLHRCVMFLLLC SIPISLLWLNMSNILVDLLHQDPNITLMAHTYLLFSLP DLLTHSFLHPIRIYLRAQGVTHPVTLASLAGTLLHLPFNILLVTRLRLGLAGVAA ASAASNLSILLFLGA AVFFSGLHCSAPSRECLSGWKPLLRLAAPSCVSVCLEWW WYEIMIILCGLLVDPTATVASMGIQITSLIYVFPSSLGFAVSTRVGNALGANRPS RAKLSAVVSVFLAAIMGFSAMFFAVGMRRRWGTMFTADEDILRITSMALPILGI CELGNCPTVGC GVVRGTARPNTAANVN LGAFYLVGMPVAVGLGFWFDVGF CGLWLGLLSAQVCCAGLMLYVIGTTDWEFEAHRAQLLTLVEDGVMDGQKQP LTGVVTETPSS* MDREDQKASLLSQLIHITVEDRLKVDNIQRNKDKQQAIERAELYEEVRKQLWL AGPLISVSM LNYSQQIISVMFVGHLGQLPLSGASMATSFASVTGFSLLVGMASAL DTLCGQSYGAKQHMLGIHMQRAMLVLMIVSINLAFIWANTRSILVALGQDP EISAEAGQYAQLMIPSLFAYGILQC LNRFLQTQNI VFPMVFSSGVTTLLHILICWT MVFKSGLGNKGAAIAN AISYWINVLILILYVKFSPSCSKTWTGFSKEALHGIPSFL KLAIPSALMVCLEMWSFEMMVLLSGLLPNPKLETSVLSICLNTSTSVWMIPFGLS GAVSTRVSNELGAGHPRAARLAVYFVFIMAIIEGTFVGAVMIIRNIWGYAYSNE AEVVQYVAIMLPILATSIFLDALQCVLSGTARGCGWQKKGAFINLGSYYLVGIPS AILFAFVLHIGGKGLWLGII CALVVQVSCLLIITRTDWEQEAKKV KDRVYDSMR AEVIVS*
Glyma.	MRIGREEVVEEVKRLWLAVPLFSVGILQYILQAISVMFIGHLGTLPLSGASM ASS
08G050	FASATGFNLLLGLATALDTFCGQSNGAGQYHMLGIHMQRSMLVVLMM SVFLS
700.1.	IIWYNTEPILKAMHQDKAISKEAGSYTQYMIPSLFAYGLLQCILKFLQTQKIVFP
Wm82.	MVLTSGIAAVLHVLLCWLLVFKSGLGIKGAALANSISYWINVILISLYVRFSAC
a2.v1	KHSWTGFSKMALHNLLDFLKLAAPSAVMHCLKVWTFELMVLM SGLLPNPKLE

	TSVLSICLNTFGLAWMIPFGFSAAVSVRVSNELGSGNPQAASLAVRVVLSMALIE GVILVSAMILLRNVWGHVYSNDKEVIRYVSFMMPVLALSSFLDGIQGTLSGILA GCGWQKIGAYVNLGSFYLVGVPCAVVLAFIVHMKAKGLWMGIIFAFIVQVSLY IITFRTNWEEQARKAQRRVELITIPPTTRDSVLPHQKQELVP*
Glyma. 08G244 400.1. Wm82. a2.v1	MAYGGGGFAISYPLAKALHIISWIVLFLTAICLLPLFIFTSPILTLLGQDESITEVAR TICICSIPILFSYIVSNNCQTFQLQSQSNVVISFLAALSIIHVLSLWLFTMQFKYGIPR AMISTILAYWIPNIGQLIFITCDWCPETWKGFSLAFKDLWPASKLSISFGAMLS* MEDHDDQTHPLLTRRHHTPDSSAVVFTATSDDIAPIGGAGDFAREFFAESKKL WYLAGPAIFTSVCQYSLGGVTQVFSVHVNTLALAAVSVENSVIAGFSLGITFGM 08G282 600.1. Wm82. a2.v1
Glyma. 09G042 700.1. Wm82. a2.v1	GSALETLCGQAYGAGQVHMLGVYMQRSWVILNATAILLSLLYIFAGHMLRAIG QTEAISAAAGEFALWMIPQLFAYAVNYPQKFLQAQSRIMVMAWIAAAAALVL HTLFSWLLILEFGWGLVGAADVNLASWWFIDIAQLVYIVSGACGEAWSGFTFK AFHNLWGFVRLSLASAVMLCLEVWYFMALVLFAGYLKNAEVSVDALSICMNI LGWTIMVSFGMNAAVSVRVSHELGAHPRTAKFS MVAEGKSQKPYPTAAEVVEELKRMGDIGVPIAAMSLAGYIKNMVLVVCMGRL GSLELAGGALAIGFTNITGFSVLSGLAMGMEPLCTQAFGSRNFSLVSLTLQRTIL MLLAASLPISLLWLKLEPLMLWLHQNPETIKVASVYCCFFSIPDLIANSFLHPIRIYL RSKGTTPWPLLWCTLLSILIHIPVAFFTFKLHLGVPGIAMSFAFVANFNTLFFLLSY MLYMRVSKGSLSMPLLLSSTCQLPSPSPQQQQQHHHQDQTSKTTTLGKEWG MLIRFSIQSCLGVCLEWWYEFMTILAGYLYNPRVALATAGIVIQTTSMLYTLPT ALSASVSTRVGNELGAGQPERAKLSTIVAIGLSLASSILGLLWTTIGRERWGRVFT SDSEVLELTMSVLPPIGVCELANCPQTTSCGILRGSARPGVGAGINFYSFYLVGAP VAIVIAFVWKLGLVGLCYGLLAAQIACVVSILVVVYNTDWERESMKAKSLVGIF KSSCDHDDHHYGDQTVKCEEGLLSFSMRKNSDQKK* MVINIKQAYFFILMDIMDENGSSSNAPKNKRNLPSVSVFFKDARHVFKMDSIAKE ILGIAFPSALAVAADPIASLIDTAFIGHLGPVELAAAGVSIALFNQASRITIFPLVSI TTSFVAEENTIEKINTEKKLSDKAKSKEQVMLDDHSLQDIEKVASKENNETENV EMNDCNTSICKSTSDTSSSSSNKSVPKDGRKKRHVASASTALLFGTILGLLQATT 09G102 800.1. Wm82. a2.v1
Glyma. 09G134 000.1. Wm82. a2.v1	LIFAAKPLLAAMGLKPDSPMLNPAIKYLRLRSLGAPAVLLSLAMQGIFRGFKDT TTPLYVILSGYALNVILDPVLIFYCKLGIKGAASHVLSQYLMALALMVILTRKVD LVPPSIKDLQIFRFLKNGGLLLARVIAVTFQCQTLAASLAARFGPIPMAAFQTCLQ VWLTSSLLADGLAVAVQAILACSF AEKDYEKVLVAATR TLQMSFVLGVGLSFA VGFGLYFGAGIFSKSVLVVHLIRIGLPFVAATQPINSLAFVFDGVNYGASDFAYS AYSLVTVSLASVASLFLLSKSKGFVGIWIALTIYMSLRMFAGVWRMGTGTGPWR FLRGRSMS* MTILSTSLTSIYAGHIGDIELSSIALYQGVMSAIYFYLLFGMSSALATLCGQAFGA GQIQSTCIYVQRSWIILTATCTILLPIFVYATPILKLLGQDEGIAELAGRYSIQVHR QKNPTFAYFGFGLCGLPDLRSCCCGTSSTSSCWCCWSCYVGDGGSVHVLGLVT SCISLTSVLHCQLAPSSKMTSLEMINCFESVIPYMFSAIAFPVQRFLLAQSKVKVI MCIAFVDLLIQNGLPYIFINVFGWGVTS LAITANIVGWLYAVALVYITIDWCRE KWISLQSSVMNCLEQWYITCIMLHAGLLDNPNVIGVGSYSICFNIQGWDDMLLL GINTVICIGSIPSKCSCLQYAWQVAAIYSFCMKMFLSLLL GILFMTVIFFSKDEFAK

		IFTDSEDMILADSDLAHLLGVTIVLNSASQVMMSGVAIGSRWQVMVGYNLACY IVGLPIGIFLGFKLHLGVKGLWGGTMCSSILQILVLFTHLTKTKWSKEMEQT MRLWSNNITTSKMLYEREQCGVI*
		METPLVVQNFTSEADYFPVKSLKDVKFVLWAETVKIWRIALPVALTHLFQVLT NSSTSIYAGHLGDIELSSISVSQGVMSYIFQLFGMSSALATLCGQAFGAGQIQS
Glyma.		TCIYVQRSWIILTATCIILLPIYIYATPILKLLGQDEGIANLAGRYSIQVIPHMFSAI
09G134		VFPTLRFLQAQSKVKVIMCIAFVLLIQNGLLYIFINIFGWGITGLAMVSNIGWL
100.1.		YAGALVYITISWCKEEWSGFSWMAFRDLLAFKLSLQSSVMGCLEQWYMTCI
Wm82.		MLLAGLLDNPIAVGSYSICFSVQGWHFMLLLGISTAISVRISNALGMSQPRAA
a2.v1		KYTFCVTMFQSLLLGVLFMNVIFLTKEDFAIIFTNSEDMIQAVADLAYLLGVTM VLNSASQVMMSGVAIGSGWQVMVAFINLACYIYIVGLPIGYFLGFKQHLGVKGLW GGTMCGLVQILILLIRKTNWTKEVEQTAHRMRIWNVNNFRSDLAENVT* METPLVTEKFTSESDYLPVKSLKDVKFVLWTETVKIWRIAFPMAISALFQFLT TSIYAGHIGDIELSSISVYQGVISALYFYLLFGMSSALVTLGQAYGAGQIQSTCIY
Glyma.		VQRSWIILTATCIILLPIYVYATPILNFIGQDQEIADLAGRYSIQVIPYMFSCAIAFP
09G134		FQTFQSQIKVKVITICIALAVLIQNVLLYIFINVFGWGTTGLAMVTNIIGWVYA
200.1.		AALVYITIGWCKEWTGFSWMAFRDLWSFAKLSLASSVMSCLDQWYSTCIILL
Wm82.		AGLLDNPIDVGSYSICFNVQGWHSMLLLGISAAISIRVSYILGKSHPRAAIYSFC
a2.v1		VTMFQSLLLGIVFMTVIFLSKDEFKIFTNKDMIRAVADLAYLLGVSMVINSAS HVMGSAVGSGWQVMVGYNLACYIYIVGLPIGIFLGFNQHLGVKGLWGGTM CGRILQMLVLLVIIWKTNWSKEVEQTAHRMRIWSINNLHSDAMGNVT* MCHPTLDVTSNCKCCSTSPDCPISIKDPLISKNNQNNNTSSLPPPPPPQHNNNTT TTTTTKTKPPPPPPSTTTTKTKATTSKPHNFPESIKEVFSISKIAIPMILTGLLLYC RSMISMLFLGHLGELALAGGSLAVGFANITGYSILSGLAVGMEPICGQAFGAKR
Glyma.		FTLLGLCLQRTILLLLFTSLPITLLWLYMKQILLLCGQDEAIATQAQQYLVSIPD
09G146		LIAQSFLHPLRIYLRQTSLPLTLCASFSILLHIPINYFLVAHLKLGKVALGGV
800.1.		WTNENLVASLILYIVFSSTHKKTWGGFSFECFTQWKSLLNLAIPSCVSVCLEWW
Wm82.		WYEIMILLCGLLVNPVKATVASMGIQTTSLLYIFPSSLFSVSTRVGNKLGAQKP
a2.v1		SKARLSAIVGLSCSFMMSGVLALFFALMVRNTWASMFTKDKIITLTSMVLPILGLC ELGNCPQTTGCGVLRGTARPKVGANINLGC FYLVGMPVSIWLAFFTG YDFQGL WLGLLAAQGS CAVTMLVVL CRTDWEFEAQRAKLTGMGV DHNHHEVDDPE KPLKHESKEDSLLLADSDENEQ*
Glyma.		MKRPLPPSVSSDNVEDRKMKKKVKALDTTMMWSAWRASMFDDNLLFEVLKHI
09G178		DTSDVGMHKQAVTQGS HVIESEGMMDFLVGLLVFWRRVSLEASTFEIIVLLTGA
700.1.		LPNSKLQTSVLSICLNTTG VFWMV PFGVSVAGSIRISNELGDGSAKAAYLAVKV
Wm82.		TMFLGSAVGILEFAVLMLVRKVWGRAFTNIHEVATYVTAIPIVASSAFIDSIQTA
a2.v1		FQGVARGCDRQKLGALINLGSYLLGV PFAIVTACVLHTKGQVKSSH FVIIKKD LTINNILKKGIVLALIVQVVCFLVVTLR TKWEKEVSCPIFNSVAMLSFINYGY*
Glyma.		KMALWKEEAKKQLWLAGPMV FVS VFQYSLQVISLMFVGHLD ELLASASLATS
09G178		FVNATGFNVLMGMSSALDTFCGQAYGAKQFHMLGVHTQGAMLVLT LVTIPLS
800.1.		IIWVFLGPILVALRQDKEIAAHAQLYARYLIPSLSANALLRCITKFLQTQNI VFTM
Wm82.		VLASGLTSLHFFLCWALVQKIELGIKGS AIAICISNWFNTIILALYIKLSPSCKTT
a2.v1		WTGFSKESLHNIPRFLRLAFPSTLMVCLESWTFEIMVLLSGALPNAKLQTSVLSIC LNTSGIFWMIPFGISAAGSTRISNELGAGSPKAAYLAVKVTMFLASAVGILEFASL

	MLLWRVWGHVFTNVHEVVKYVTSMMPLVASSTFIDSIQTAFQGVARGCGWQ KLGAYVNLGSYYFLGVPFSVVSFAVFHMKGQGLFLGILIALIVQVVCFLLVTLRA NWEKEIEI*
	MKRVSQRQEVVEEMKKQAWLAGPLFTVGVQLQYSLQVISVMFVGHLLGELPLSGAS LATSFASVTGFNLLMGMASALDTLCCQSFGAGQHHMLGIQMQRATFVLSFVS
Glyma. 09G178 900.1. Wm82. a2.v1	VFLAIMLVFTKHILVAMHQQVAIAEEAGVYAIYMIPSLFAYGIFQCCLKFLQTQ NIVFPMVLSSAVVALLHIPLCWVLVIKSGIGSKGAAIANSVSYWLVNLLIGFYVK FSSCAKTWTGFSVKALQNIPEFLKISIPSACMLCLKAWTFELMVLLSGLLPNPQ LETSVLSICLNTFVIAWMIPFGLSCAVSTRVSNELGAGHPQAASLAVRVALFLVL ADGIMMVLVMILLRKIWGNLYSSDTHVIKYVAAVMPILATCSFLDGIQSVLSGI ARGSGWQKIGAIVNLGSFYFVGVPSSVVLAFVLHMKGKGLWLGVSAFIVQVIL FGVITIRTSDWKEANKAAMRVKDTKIPQELPQRDPFTITEMN*
	MERGDQONQSASLQSPLIKHSHSSSSSGRGIERREVIEEVKKQLWLAGPLISVTLLNF CLSIISVMFVGHLLGELSLSGASMATSFASVTGFSLLVGMASSLDTFCGQSYGAKQ
Glyma. 09G179 000.1. Wm82. a2.v1	YHMLGIHLQRAMFTLMIVSIPLAIIWANTRSILTFLGQDPEIAAEAGSYARFMLP SLFAYGLLQCLNRFLQTQNIWFPMCMSSAITLLHVLICWILVFKSGLGNRGAA VANSISYWLVNTILSLYVMFSPSCAKSWTGFSKEALHNIPSFVRLAIPSAVMVCL EMWSFELMVLLSGLLPNPKLETSVLSICLNTTAAAWMIPFGLSGAGSIRVSNELG AGRPWNARLAVRVVLVLAIEGIIIVGTVMILVRNIWGYAYSNEVEVVEYVATMF PILAAASNFLDGLQCVLSGTARGCGWQKIGAFVNLGSYYIVGIPSSIVFAFVLHIG GKGLWLGIICALIVQMCSLMIITRTDWDQEAKKATDRVNSVTLESLS*
	METPLMFNSDLNSTGTTELQYAPEGLVDTNNGDYTEMSSGLADFKNVFSVESVK LWTIAAPIAFSILCNYAVNSFTTIFVGHLLGDLELSSVLSLSVSNFSFGFLGMA SALLETLCGQAFGAGQVEMLGVMQRSWLILLGACICLTPIIYIAEPILLLLQGEPE IAELAGVFTIQSIPQMFSLAINFPTQKFLQAQTKVGFLAWVGFGAFIFHIILLWILL KVLALGTTGAAYSTTAWVIALAQTAYVIGWCKDGRGFSWLAFKDLWAF VKLSVASAVMLCLEVWYFMILIVLTGHLDNAVIAVGSLSICMTINGFEGMLFIGI NAAISVRVSNELGSGRPRAAKYSVIVTIESLVIGLICAAIILITKDHFIIFTESKEM IKAVSKLAGLLGLTMILNSVQPVISGVAVGGGWQALVAYINLFCYYIMGLPLGF LLGYKLGVRVEGIWVGMICGTILQTLILLYIVYKTNWNKEVELASSRMRKWTGQ EIEINLANSQQPVTH*
	MCTGAESRGIVDGNNPVTNSKVGGVYHEINGMRSTEGGDGEGKRNSGCSGRFI QGLHQHLHQLLKALFPTLSLSEVKEELKSLANACPMMMTNVLLYSRAISMLY LGRQGKVELAGGSLAIGFANITANSFLKGLTMGMDPICCQAYGAKRWSVLSQT FCKTLCLLLLVAIPISLLWLNMAPLLHWLGQDPEVTKVAQVYVMVFSIPELLAQV
Glyma. 09G276 100.1. Wm82. a2.v1	HLNPLRSFLRTQGLTTPLTIAASFAAILHLPINYLATYLELGVKGIALATGLNSI NMILGLVLYLVSEKPLKPWEGVTILSSFHDWRPLLTLALPSCISVCLEWWCYEI MLFLCGLLSNPQTTIATMGVLIQTTGFLYVFPFSLAALTTQIGHSLGAGQPSRA QNTAKIGLFIAFALGVSAFVFLFVRNVWGKLFTNETQIVDMVTAILPILGLCEI GNWPQTAACGILSGTARPYVGARINLCAYLIGLPVAIFAFAFMHRYQLRGLWF GMLAAQISCFCMMVYTLVQTDWGHQSRRAEQLAQTTDEENVNNDKSGLLD SDL*
Glyma. 10G099	MLPLLMLFSSIRNAFSSDELGLEILNISLPTTLALAADPIASLIDTAFIGHIGPVELA AVGVSAIFNQISKITIIPLSVTTSLVAEEDAVDEQNQQSEREMLMKVSNEVDK

900.1.	LDVHDHAEKAGNSSSANVGRVAKLDHDKSYIPSASSGIVIGLLGVLQALFLIF
Wm82.	TAKPMLSYMGVDSNSPMFKPAQQYLTLRSFGAPAVIISMAIQGVFRGIKDTKTP
a2.v1	LYATVMGDVTNIILDPLLMFVLRLLGVNGAAISHIISQYLIAMLLWSLMKQVVLL PPSIQDFRFGKILKNGFLLLIKVASATFCVTLSTSLAARKGSTTMAAFQICLQIWM ATSLADGLAVAAQAIISAFARDDYKKVIASASRVLQLGLILGLVLSVLLLSLL PFASRLFTNDINVLQLISIGIPYVAATQPINALAFVFDGVNYGASDFTYSAYSMIM VALVSILSLYMLSSSLGFTGIWIALLIYMTLRIFAGFWRIGTGSGPWSFLKENSVEL Q*
Glyma.	
10G231	MITVFLSKDNLAIFTSSKDMQLTVADQAYLLGLTMIINSAAQLMSGVAIGSGW
800.1.	KLTVAYINLTCYYMVGLPLGFYLVSH*
Wm82.	
a2.v1	MDAPLLLAKGEGAALVTENG DYVAVRELKEVKVFWIETKRVWQIAMP IVFNI WCQFGVNSVTSMFVGHLGDIQLSAISLINSVIGTFAFGFMLGMGSATETLCGQA FGAGQVNMLGVYMQRSWVILSVTSILLPIYIFAGPILKFLGQQEDIADLAGSFSI LVIPQFLSLPFNFPTQKFLQAQSKVNIIAWIGLVALILHIGMLWLLIYVLD FGLAG AALAFDITSWGITVAQLVYVVIWCKDGWTGLSWLAFKDIWAFVRLSLASAVM LCLEVWYMMSVIVLAGNLDNALVAVDSLICMNINGWEAMLFIVNAAVSVR VSNELGLGHPRAAKYSVYVTVFQSLFLGIFFMAIILATRDYIAIFTNSEVLHKAV AKLGYLLAVTMVLNSVQPVVSGVAIGGGWQALVAYINIGCYLFLGLPLGFLLG YEANLGVEGLWGGMICGIVIQTLLLLLLILYKTNWKKEVEQTTERMRIWGGQDI GVDKIVAST*
Glyma.	
10G232	MCHISSQLPCKCNSMKSQEAEEESDMKITNPLIQKDITVTPPHHHVLKELISISKIA LPMILTGLLLYCRSMISMLFLGRLGELALAGGSLAVGFANITGYSILSGLAVGME PFCGQAYGAKKFTLLGLCLQRTILLLLFTSIPISLLWLYMKHILLCCGQDEAIATQ AQSYLLYSIPDLLAQSFHLPLRIYLRQSITLPLTLCATFSILLHIPINYLLVSHLNW GIKGVALSGVWTNFNLIASLILYVFSGTHKKTWGGFSFECFTQWKSLLDLAIPS CISVCLEWWWYEIMILLCGLLVNPRATVASMGIQTTSLYILPSSISFSVSTRVG NKLGAQKPSKAKLSAIVGLSCSFMLGFLAFVFTILVRNIWASMFTQDKEIITLSTL VLPII GLCELGNCPQTGCGVLRGTARPKVGANINLGCFYLVGMPVAVWLGF AGLDFQGLWLGLLAAQGSCAVTMLVVMSTQDWDVEALRAKKLTSVVVAVD DSKEVGAEKPPKAEIKEDSLLSLADSEEDKQSWV*
Glyma.	
10G239	MEENLIITKQSEKQRTWDGLGEEMKRIIRVAGPMVFVYASQNLLQVVSIMMIG HLNDELFLSGAALAI SLATVTGFSLLTGMASGLETICGQAYGARQYQKTGVQTY TAIFSLTCVCLPLTIIWISLENILVFIGQDPLIAHEAGNFIIWLLPALFAYAILQPLV RYFQM QSLLPMLATSCVTLCLHIPLCWALVFKTELSNVGGALAMSISIWL NVI 300.1.
Wm82.	FLVLYMRYSPACEKTRAPVSMELFQGIWEFFRFAIPSAVMICLEWWSFELLILLSG LLPNPQLET SVLSICLNTISTLYAIAFGIAAASTRISNELGAGNPHSARVAVLAS a2.v1
	MSFAIMEATIISGILFVCRHVFYGTFSNKKEVVDYVTVMAPLVCISVILDNIQGV AGIARGCGWQHIGVYVNLGAFYLCGIPVAASLAFLAKMSGKGLWIGLQVGAF VQCALLSTVTSTCNWEQQAMKARKRLFDSEISAENILV*
Glyma.	
10G267	MEENLLAKQREKQKVTWDGLGEEMKRIICIAVPMVIVTATQYLLQVVSIMMVG HLNNNLYLSGAALAI SLATVTGFSVLGMA SGLETICGQAYGAQQYEKGVQ

400.1.	YTAIFSLTVVCLPLTFIWISMEKILVFIGQDPLIAQEAGKFLIWLVPALFAHAIMQ
Wm82.	PFVRYFQMQLSLLPMLISSCVTLCHIPLCWALVFQTMNNIGGALAMSISIWLN
a2.v1	VTFLGLYMRYSPACAKTRAPISMELFQGIWEFFRFAIPSAVMICLEWWSFELLILL SGLLPNPQLETSVLSICLNTISTLFSIPFGIAAASTRISNELGAGNPHAAHVAVL AAMSFAMETAIVSGTLFVCRHDFGYIFSNEKEVVVDYVTVMAPLICISVILDSIQG VLAVARGCGWQHIGVYVNLGAFYLCGIPVAATLAFLAKMRGKGLWIGVQV GAFVQCILFSTITSCINWEQQAIAKARKRLFDSEISADNRLV*
Glyma.	
10G267	MSFTITEATIVSGTLFACRHVFGYIFSNEKKVVVDYVTVMAPLICISVILDSIQGVLA
600.1.	GVARGCGWQHIGVYVNLVAYYLCGIPVAASLAFLEKMRGKGLWIGVQVGAFAV
Wm82.	QCVLLSIITSCINWEQQAIAKARKRLFDSEFPADNRLV*
a2.v1	
	MEESLVKKHEQERV TWGVYSEEMRRVCHIAGPMVAVVSSQYLLQVVSTMIVG HLGELYLSSAAL AISLSGVTGFSLLMGMASGLETICGQAYGGQQYQRIGIQTYYTA
Glyma.	IFSLILVSIPVSLLWINMETILVFIGQDPLISHEAGKFTIWLVPALFAYAILQPLVRY
10G267	FQIQSLLLPMFASSCVTLIIHVPLCWALVFKTSLSNVGGALAVSISIWSNVIFLVLY
700.1.	MRYSSACAKTRAPISMELFKGMWEFFRFAIPSAVMVCLEWWSYELLVLLSGLLP
Wm82.	NPQLETSVLSVCLNTIATLYTIPFGIGAASTRVSNELGAGNSHAARVAVLAAM
a2.v1	SLAVIETSIVSATL FACRNVFGYIFSNEKEVVVDYVTAMAPLVCISVILDSIQGVLTG IARGCGWQHIGVYVNLGAFYLCGIPMAALLAFLVRLGGKGLWIGIQSGAFVQ CILLSIITGCINWEKQAIAKARKRLFDEKISADNRLV*
	MKRVGYLVGPMITVTL SQYFLQIISMVMVGHGLKLALSSTAIAISLCAVSGFSLIF AMSCALETQCGQAYGAHQYRKFVQMYTAIVSLTLACLPLSPLWVYLGLKILIFL
Glyma.	GQDPLISQEAGKFALCMT PALFDYATLQALVRYFLMQSLTPNEKTCISHLFNSL
10G267	VISSITLCFHVAFCWLLVFKFGFNLGAFFIGTSYWLVNILLVLYMKFSIECKK
800.1.	TWVPISTELFHGIGEFFRCAIPSAGMICLEWWSFELLFLLSGLLPNPELETSVLSIC
Wm82.	LSVTTTIYTIPEAIGSAASTRVSNALGGGSPQLAQVSVSAAMTLAASAAAILVSSIIF
a2.v1	ACRQVVGYA FSNELDVVDYFTMVPLLSISVILDTLHDTLSGIARGCGWQHRG AYVNLDAYYVVGPIAAILGFCLQLRGKGLWIGILTGAFCQTMVSLITSCTNW EKQVCLHFQVHALHLAQS*
	MCQLSSSPSTLCDSNEGHPNMPTTKIHEEPAHMLPLLPKPPTTLFEQGQNNHQ TKTHFSLALNEVKCIANIALPMVLTGLLLYSRVISMLFLGRV GELALAGGSLAI GFANITGYSILSGLAMGMEPICGQAFGAKRFKLLGLAMQRTIVLLLLTSVLISFL
Glyma.	WLNMMKKLLILCGQQEDIAEAQSFILFSIPDLVAQSLLHPLRIYLRQSITLPLTYT
11G026	ASLSILLHVPINYFLVSVLKLGIKGIAGAVWTNFNLVVSLILYI WVSGVYKKTW
300.1.	PGVSLKGILSGWKSLLNLAIPSCISVCLEWWWEIMILLCGLLINPQATVASMGV
Wm82.	LIQTTALYIFSSLSFAVSTRVGNELGAENPKKAKVAALVGLCISYGLGFSALFF
a2.v1	AVSVRQAWASMFTRDAEIIALTSMVLPIIGLCELGNCPQTTVCGVLRGTARPKL GANINLGC FYLVGMPVAVRLSFFAGFDKGLWLGLLAAQASCMFTMLIVLART NWEQVQRAKELTSSSEEQDQNCFFSSCATKEYCSDSLLV*
Glyma.	MGFRSGFDEL RVQRGIALPMVAMNLA WFAKTAITTAFLGRLGELSLAGGALGF
11G028	TFANVTGFSVLNGLCGAMEPIYVDRMLTLLMTISLLLLVSLPITFLWLVNDKILIL
900.1.	FGQQQDISTVARTYVSLIPDLFVASLFCPLKAYLSSQTITLPTMFSSAVALAFHIP
Wm82.	INIVLSRTMGLRGISMAVWITDLIVVLLAIYVLILERKKESMWKEGGWWDQSIE

a2.v1	DWIRLLKLCGSCCLNTCLEWWCYEILVLLTGHLTNAKQAVGVLAIVLNFDYLL FSVMLSLATCVCTRVSNELGANQAGLAYRSACVSLALGFISGCIGSLVMVAARG IWGPLFSHDVGIKGVKKTMLLMGLVEVFNFPLAVCGGIVRGTARPWLGMYA NLGGFYFLALPLGVVSAFKLRLGLVGLFIGLLTGIVTCLTLLLVIARLNNWVEEA AQAQTLTGQEQVKELSKYDAEELIDAHKKDVV* MAFKLKSPLLCSLHSPSRQNPNSTLSNHHFSRRFFAPSIPPTLCLSGAASASTFH RHRFFVTARSQDEDQITEALEQEEEEKDNEEISRQGEKKELAKQGIWDQIKEIVMF TGPATGLWICGPLMSLIDTAVIGQRSSIELAALGPATVVCDYMCYVFMFLSIATS
Glyma. 11G112 100.1. Wm82. a2.v1	NMVATALAKQDKEEVQHHSVLLFVGLSCGIAMLLFTRLFGAAIITAFTGPKNV HVVPAASNYVKIRGLASPALLVGWVAQSASLGMKDSLGPLKALAAATVINVA GCVLLCTYLGYGIVGAAWATMVSQVVASYMMIQNLNMKGYNALAFSIPSGKE LLTIFGLAAPVFITLMSKVAFYALLIYFATSMGHTMAAHQVMVQTYLMCTVW GEPLSQTSQSFMPELIYGVNRSLSKARMLLRSLVIGAILGLLGLIIGTSVPWLPNI FTPDRMVIQEMHKVLIPYFIALAVTPPTVSLEGTLLAGRDLKFISLSMSGCFCVGS LVLWALSSRYGLLGCWFSALFQWARFSMALQRLLSPKGILYSEDTEQYKLLKL RTA* MALKLSSLSLHSSLRHQHHPNSSHSNHRIPLRFFAPSLPPTSCLSGAASVSTFHRTL FAVTVRAFQSQDESKSSDVFEDEEKDEEISRQGEKKELAKQSIWSQIKEIVMFTGP ATGLWICGPLMSLIDTAVIGQRSSIELAALGPATVVCDYMSYVFMFLSIATSNMV
Glyma. 11G112 200.1. Wm82. a2.v1	ATALAKQDKEEVQHHSVLLFIGLSCGVGMLLFSRLFGASLITAFTGPKNNAHV PAASNYVKIRGLAWPALLVGWVAQSASLGMKDSLGPLKALAAATVINFAGCI LLCTYLGYGIVGAAWATMVAQVVAAYMMIQNLNMKGYNALAFSIPTGKEIL MILGLAAPVFLTLMSKVAFYALLIYFATSMGHTMAAHQVMVQTYGMCTVW GEPLSQTAQSFMPELIYGVNRSLSKARLLLSLVITIGAMLGLLGLIVGTSVPWLF PYVFTPDRMVIQEMHKVLIPYFIALAITPPTHSLGTLLAGRDLKFISLSMTGCFC VGTLLVLWALSSRFGLGCVFSLALFQWARFSIALRRLLSPKGILYSEDTDQYKLR KLRTA*
Glyma. 11G133 900.1. Wm82. a2.v1	MSLILGLALAFLLGTGLHFGAKLFTKDVNVLHLIRIEIPFVAATQSLNSLAFVFD GINFGASDFAYS AISLDAVAIVSIICLLILSSASGFIGTWIAMTIYMDLRAIVGFLRI GTRSGPWELLNY* MDSTSVHKDIDEPLLVSNEPSPEPPSCTQSFSSKHGSDGELERILSNTSVPFAKRL GPATWVELKLLFHLAAPA VIVYLINYVMSMSTQIFSGHLGNLELAAASLGNTGI
Glyma. 12G099 300.1. Wm82. a2.v1	QVFAYGLMLGMGSAVETLCGQAYGAKKFDMLGIYLQRSTVLLTLAGIILTIYIF SEPILIFLGESPRIASAAALFVYGLIPQIFAYAVNFPIQKFLQAQSIVAPSAYISTATL LVHLVLSYFVVYEVGLGLLGASLVLSVSWWIIVIAQFVYIVKSEKCKHTWRGFSF QAFSGLPEFFKLSAASAVMLCLETWYFQILVLLAGLLPHELALDSLSICTTVSG WVFMISVGFNAAASVRVSNELGARNPKSASFVSVVVTLSFIISVIVALVVLAIIRD VISYASQTVKRWLLLSQIFVLYLLFLLFSTAFNLSYLGWLLDVDGKLLLRM*
Glyma. 12G122 000.1. Wm82.	MEQVDLVPPSIKHLQLDRFLKNDKGMSASLVARQGPTSMAAFQAILAGAFAN KDFDKATATASRVLQRHTLCKCDALFVILHMGLVLGLALAFILGTGLHFGAKIF TQDANVHHLIQIGIPFVAVTQPLNSLAFVFYGINFGASDFAYS AFSMVVVAILSII CLLILSSVGGFIGIWVALTIYMGLRAFAGFWRIGTGSGPWFEFLRSS*

a2.v1	MGSAEKEPLLTAEGTRSNSKHESSSHGQLERILSDDTLPFLNRVGPATWIELKLL FFLAAPAVIVYLINYLMSMSTQIFSGHLGNLELAAASLGNTGIQMFAYGLMLG MGSAVETLCGQAFGAQKYGMLGVYMQRSTILLSLAGVVLTVIYVFSEPMFLFLG Glyma. 12G194 000.1. Wm82. a2.v1	ESPRIASAAALFVYGLIPQIFAYAANFPIQKFLQAQSIVAPSAYISAATLVVHLGM SWVAVYEIGLGLLGASLVLSLWWIMVIGQYVYIVKSERCRTWQGFTWEAFSG LYGFFKLSAASAVMLCLETWYFQILVLLAGLLPNPELALDSLSICTTISGWVFMIS VGFNAAASVRVSNELGARSPKSASFVSVVTVISFIISVIAALVVLALRDVISYAFT GGEEVAAA VSDLCPLLALSLVLNGIQPVLSGVAVGCGWQAFVAYVNVGCYYG VGIPLGAVLGFYFQFGAKGIWLGMLGGTVMQTIILLWVTFRTDWTKEVEEAAK RLTKWEDKKEPLLN*
Glyma. 12G225 600.1. Wm82. a2.v1	MLGIYLQGSCIISLIFSIIISIIWFYTEPILVLLHQSPDIARTAALYMKFLIPGVFAYSF LQNISRFLQTQSVVMPLVALSALPLLIHIGIAYGLVQWPGLSFAGAPLAASISQW ISMLLLALYVMYAKKFKQAWQGFSMHSHFYVFTNMKLALPSAAMVCIRLLVL VFLAGLLPDSQITTSLIAICLNTQFIAHMPVPVGLGAAERLVEEFASVTPLLAISIVL DAVEGVIQGVARGCGWQHSTGLWIGLICGQLCQVGTFLFLRRRAKWTKNLS GVKDKEHPLVV*	MDENGCSNEPNNKWKMPFLVFFRDARLIFKLDALSREILGIAFPAALAVVADPI ASLIDTTFIGHLGPVELAAAGVSIALFNQASRITIFPLVSITTSFVAEEDTIQRLINK ETETDNIENTITKENVEAPKKFKGETDESNNVVAKSTFTSGDVEKLATGNMGI NNENVTSTKSKPKVGKKRIASASTALLFGTILGLLQTAILTFAAKPLLYAMGLK HDSPMLIPAEKYLRLRSIGSPAVLLSLAMQGIFRGFKDTTTPPLYVIVSGYAFNVLL DPILIFYLKLGLKGAAMAHVISQYMMAITLLLLLMKRVHLVPPSIKDLQIFRFLK NGGLLLTRVSVTFCMTLAASLAARLGSIPMAAFQPGQLIWLASSLLADGLAV AVQTMLACSF AEKDYNKATAAATRTLQMSFVLGVGLSFAVALGLYFGPGIFSK NANVVHLIKISMPFVAATQPINSLAFVFDGVNYGASDFAYSAYSLVLVSLVSIPIE ILLFRSKQFVGIWIALTIYMILRMLVGIWRMGTGTGPWYYLRKGPWCYMRGHS LP*
Glyma. 12G237 400.1. Wm82. a2.v1	MDENRSSNEPNNKWKMPFLVFFKDARNVFKLDALSREILGIALPSALAVSADPIA SLIDTAFIGRLGPVELAAAGVSISSLNQASRITIFPLVNITTSFVAEEDTIQKLNTK AAENGNSKAKFGETIVPEDHMLQDMEKGT PKVMNTDAPTEFREDKDESQEYN ATGNNDTNIGDGANTICKFSSVTSSKSKDKVGKKKRLIASASTALLFGTILGLI QAAVLIFATKPLLGVMGVKRDS PMLKPAESYLRLRSFGAPAVLLSLAMQGIFRG FKDTTTPPLYVIVSGYALNVILDPIFIFTLKLGKGAIAHVLSQYMMAF TLLLILM KKVHLLPPRIKDLQIFRFLKNGGLLMLKVIAVTFCVTLATSLAARLGSIPMAAFQ TCLQVWMTSSLLADGLAVAVQAILACSFTEKDYKKQQQQQQGHCK*	MENVEIQIEEIEKMOVASSSEGTGVPLL RASDNNGRDQNTRSPQAEGWWNKV LDMEEAKHQLLFS LPMILTNLFYHLIILVSVMLVGHLGELQLAGATLANSWFSV TGVAVMVGLSGALETLCGQGFGAKEYQMLGIYLQASCIISLIFSIIISIIWFYTEPIL VLLHQSPDIARTAALYMKFLIPGVFAYSFLQNILRFLQTQSVVIPLVVL SALPMLV HIGVAYGLVQWSGLSFTGAPVAASISLWISLLLLALYVMYAKKFKQTWKGFSTH SFRYVFTNMRLALPSAAMVCLEYWAFEVLVFLAGLMPDSQITTSLIAICINTEFIA YMITYGLSAAASTRVSNELGAGNPERAKHAMSVTLKLSLLGLCFVLALGFGH NIWIQFFSDSSTIKKEFASVTPLLAISILLDAIQGVLSGVSRGCGWQH LAAYINLA

Glyma. 13G275 500.1. Wm82. a2.v1	TFYLIGLPISCFLGFKTNLQYKGLWIGLICGLLCQSGTLFLFIRRAKWTKLDLSRD NDKERPLVV*
	MKEEIEKMVASNSSDDSIGTPLVIRGSDNNGRDQNTRLHQVEGWWNKVLDME EAKCQLLFSPLMILTNTFYYLITSISVMLVGHLGELQLAGSTLANSWFNVTGSAV MVGLSGALETLCGQGFGAKEYQMLGIYLQASCIISLIFSIIISIIWFYTEPILVLLHQ SHDIARTTALYMKFLIPGLFAYSFLQNILRFLQTQSVVMPLVALSAPLLIHIGIA YGLVQWPGLSFTGAPVATSISQWISMLLLALYVMYAKKFKQTWQGFMSHSFHY VFTNMKLALPSAAMVCLEYWAFEVLVLLAGLLPDSQITTSLIAICLNTQFIAYM VPVGLGAAGSTRVSNELGAGNPEQAKHAMNVTVKLSFLFSFCFALALGFGHNI WIQLFSGSAKIKEEFASMIPLLAISIVLDAVQGVMMQGVARGCGWQHSTVYINLA TFYLVGLPISCLLGFKTNLHYKGLWIGLICGLLCQVVTLFLFLRLAKWTKLDLSG DKDKDHPLVV*
	MLKSRLDGTVTHFTPLLDVSHHKENTRQYRWWNSKILDLEEAKHQLLFSLPM FLTNLFYLLIVLVSVIFAGHLGDLQLAGATLANSWFVTGLAVMIGASYFNNEK QDKILDLEEAKHQLLFSLPMFLTNLFYLLIVLVSVIFAGHLGDLQLAGATLANS WFSVTGLAVMVGLSGALETLCGQGFGAAEYQMLGIYLQASCIISLIFSIIISIIWFY TEPILVLLHQSQDIARTTSLYTKFLIPGLFALSFLQNILRFLQTQSVVNFIGAPVAV SISLWISIPLLVMYIMYAERFRQWTGFSFESFNIFYTDLKLALLSAAMVCFEYWA FEIMVFLAGLLPDPTISTSLIAICTNTELIAYLITYGLSAAASTRVSNELGSGHLDR AKHAMGVSLKLSLLLGLCFVLALAFGHNIWIQMFSDSSKIKEELASLTPFLSISIL LDSVQGVLSGVIRGCGWQHLLAAYVNLATFYLIGLPISGLLGFKFNLQVKGLWIG LICGLACQTGTL SFLAWRAKWTCLNVSLDRDEIQPPSA*
Glyma. 13G339 800.1. Wm82. a2.v1	MQDIGAPSVSLQLCITSLNKLPLFVWFLKQHNSEFGVSDMAEKESIHSFGDWRR IPICTFFQDARLVFKADSLGREILSIALPAAMALTADPIASLVDTAFIGQIGPVELA AVGVSIALFNQVSRIAIFPLVSVTTSFVAEEDTLSGANPQTEEGRCLEAGQPTDTE TKELLPQKVTTGGNVHNSDFVGESFNIAKEERKRRHIPSASSAIFIGGILGLIQAIFL ISAAKPLLNFMGVTSDSPMLHPAKQYLKLRLSLGAPAVLLSLAMQGVFRGFKDT KTPLYATVAGDVTNIALDPLFMFVFRLLGVSGAAIAHVISQYLISVILLWRLLQV DLIPPSINHLQLDRFLKNGFLLLMRVIAVTFCVTLAASLAARQGPTSMAAFQVC LQVWLAVSLLADGLAVAGQAILAGAFANKDFNRATATASRVLQMGLVLGLA LAFILGTGLHFGAKIFTQDANVLHLIQIGIPFIAVTQPLNSLAFVFDGVNFGASDF AYSAFSMVVVAILSIIISLLILSSAGGFIGIWVALTIYMGLRAFAGFLRIGTGSGPWE FLRSS*
	MGVVEIYKRKTLQSSANNFNCRGRRYILWAAALMLMEAIHFTTSQYQLQYHG GFTRIPFLRKRNHISFGYGHHPHHHFLRHSPSLSSPFIALGSKPSSYTSQDHHSD SASVDVKRELISLTLPALASQAIDPLAQLMETAYIGRLGTVELASAGVSISIFNIIS KLFNIPLLSVATSFVAEDIAKSSSAADAKTQQLSSVSTALLLALALGFFEALALY LGAGAFHLHIGVPTQNPTYVPAHFSLRAVGAPAVVLSLALQGIFRGFKDTKT PVICLGIGNFSAVFLFPLLMYYFRLGVTGAAISTVISQYIGTMLMIWCLNKRAELL PPKMGDQLQFGSYIKSGGFLGRTLAVLSTMTLGTSAARHGPPVAMAAHQICMQ VWLAVSLLTDALAASGQALIASSVSRHEYKVVKVTSFVLRIGLVMGICLTAILG ASFGSLATIFTQDSEVLQVVKTLALFVSASQPFNALAYIFDGLHYGVSDFRYA AFSMMFVGAVSSAFLVFAPPLFGLQGVWLGLVLFMALRAAAGAVRLLSKNGPW WFLHRDLQIAEVVS*

Glyma. 14G032 400.1. Wm82. a2.v1	MSSLEHQPLLPRLDSDSHIQNLSSDAIEEFLEHRPIALRWWSKLIVWESRLLWLL SGASIVVSIFNYMLSFVTLMFTGHLGSLELAGASVASVGIQGLAYGIMLGMASA VQTVCGQAYGAKKHGAMSILQRAILHIGAAVILSFLYWFSGDFLKAIGQSDSI AERGQVFARGIILQLYAF AISCPMQRFLQAQNIVNPLAYMSVGVFLVHILLSWL VIYVLGYGLQGAALTSFSWWLLVLFNGLYIIFSPRCKETWAGFSVKAFKGIWPY FKLTVASAVMLCLEVWYNQGLVLLSGLLSNPTISLDSISICMNYLNWDMQFML GLSTAASVRVSNELGASHPRVAKFSVFVNGTSILISVVFCTIILIFRVLSKLFTSD SDVIDAVSNLTPLLAISVFFNGIQPILSGVAIGSGWQALVAYVNLASYVVGLTV GCVLGFKTSLGVAGIWWGMILGVLIQTVTLILTARTNWQAEVEKAVVRINKSA ENDTLDQLVADT*
Glyma. 14G078 000.1. Wm82. a2.v1	MDSPLLENIDNSTTYVEEKKTLNSVVKKFGFESKKLWKIAGPAILTSICQYSLGA LTQTFAGLVGDLELAAVSVENS SVAGLAFGVMLGMGSALETLCGQAYGAGQS TMLGVYMQRSWVILFVTALILLPLYIWSPPILRLFGQTAEISDAAGKFALWMIPQ LFAYAINFPMVKFLQAQRKVLVMLWISVVVLVLHTFFSWFLIFKLGWGLIGAAI TLNTSWWWVIVIAQLLYIFITKSDGAWNGFTWLA FSDLFGFVKLSLASAVMLCLE FWYLMILVVITGRLKNPLVPVDAISICMNINGWDAMIAIGFNAAISVRVSNELG AGDFKAAKFSVWVVSITSVFIVVAMIGVLSTKDYFPYLF TTSVPVANETTRLAA LLGVTVLLNSLQPVLSGVAVGAGWQSLVACINIVCYVIGLPAGIILGFPLGLGA EGIWSGMIAGIVLQTTILIVTSIRNWKKEAEEAESRVKKWGGAIAIDQ*
Glyma. 14G158 100.1. Wm82. a2.v1	MLGVYMQRSWVIVNATAILLSLLYIFAGPMLRAIRQTEAISAAGGEFAVWMIPQ LFAYAVNYP AQKFLQAQSRIMVMAWIAAAAALVLHTLFSWLLILEFWWGLVSA VVVLNASWWFIDIGQLHTFSSIL*
Glyma. 15G034 600.1. Wm82. a2.v1	MPNIGAPSVSLQLCITSLNKLPLLWFLKQHSEFGFSNMAEKESMYSLGDWRRI PICTFFKDARLVFKADSLGREILSIALPAAMALTADPIASLVDTAFIGQIGPVELA AVGV SIALFNQVSRIAIFPLVSVTTSFVAEEDTLSENPHIEEGRCLETGPPKDAE TKELLPHKVTGGNNHNSDFVGEFCFNIKEEHKRRHIPSASSAIFIGGILGLIQAIF LISAAKPLLNFMGVTS DSPMLHPAKQYLKLRTLGA PAVLLSLAMQGVFRGFKD TKTPLYATVAGDVTNIALDPLFMFVFR LGVSGAAIAHVISQYLISAILLWRLMEQ VDLVPPSIKHLQLDRFLKNGFLLL MRVIAVTFCVTLAASLAARQGPTSMAAFQV CLQVWLAVSLLADGLAVAGQAILAGAFANKDFDRATATASRVLQMGLVLGL ALAFILGIGLHFGAKIFTQDANVLHLIQIGIPFVAVTQPLNSIAFVFDGVNFGASD FAYSAFSMVVVAILSIICLLILSSAGGFIGIWVALTIYMGLRAFAGFLRIGTGS GPW EFLRSS*
Glyma. 15G107 100.1. Wm82. a2.v1	MMESQNQNLLRQPLINSTHHHHHSADSRLEEVLSDPTLPWSKRILSATWIELNL LFPLAAPAILVYVFNNLMSNVTRAFAGHLGNLELAAANLGN SGIQLFAYGLML GMGSAVETLCGQAYGANKYEMLG IYMQRAIIVLTITGIPLTVVYIFCKPILLLLGE PPEVASVAAMFVYGLIPQIFAYAVNFPIQKFLQAQSVVAPSTYISAATLV LHVAL SWVVVYKLGFGIMGSSLMLSLSWWIIVGAQFLYVVSASKFKDTWSGFSVEAFSG LWDFVKLSAASAVMLCLETWYFQVLVLITGLLDNPQLSLDSISVCMAITGLTMH IGIGFNAAASVRVSNELGA EHPKSAAFSVIVNMISFIIAVIEAVVVLALRRVVS Y AFTDGETVANAVSDLCPYLAVTLILNGIQPVLSGVAVGCGWQAIVAYVNVGCY YGIGIPLGCVLGFTFGLGVQGIWSGMIGGTMLQTLILLWITLRTDWNKEVNTAK

	KRLNKGWYKKEPKIQS*
Glyma. 15G150 300.1. Wm82. a2.v1	MVAEEKSQKTYPPTAEVVDELKRMGDIGVPIAAMSLVGYIKNMVLVVCMGRL GSLELAGGALAIGFTNITGFSVLSGLAMGMEPLCTQAFGSRNFSVSLTLQRTII MLLVASLPISLLWLKLEPLMLWLHQNPEITKVASVYCFFSIPDLIANSLLHPIRIYL RSKGTTWPLLWCTLLSILIHPIVAFLTFLHLGVPGIAMSAFVANFNNTLFFLLSY MLYMRVSKGSLSMPLLISSRPLSSSPRQHQQDQTSKTTTTLTKGKMWGLIRFSI QSCLGVCLEWWWYEFMTILAGYLHNPRVALATAGIVIQTTSMLMYTLPTALSAS VSTRVGNELGAGQPERARLSTIVAIGMSLASSILGLLWTTIGRNRWGRVFTSDSE VLELTMSVLPIIGVCELANCPTTSCGILRGSARPGVGAGINFYSFYLVGAPVAIV MAFVWKLGLVGLCYGLLAAQIACAVSILVVVYNTDWERESLKAKSLVGIYKSS CDDQHHGDQTVKCEEGVVFLEKE*
Glyma. 15G274 600.1. Wm82. a2.v1	MDENGSSSNAPKNKRNLPSVFFKCDARHVFKMDSIAKEILGIAFPSALAVAADP IASLIDTAFIGHLGPVELAAAGVSIALFNQASRITIFPLVSITTSFVAEESTIEKINTE KKLTDKTKSKEVMHDDHSLQDIEKGASKEKNETPTESSAVRGNTTCVPENVEM DDCNTSICKSTTETSSSSNKS SVSKAGRKKRHIASASTALLFGTILGLLQATTLIFAA KPLLAAMGLKPDSPMLNPAIKYLRRLSLGAPAVLLSLAMQGIFRGFKDTTTPLY VILSGYALNVILDPVLIFYCKLGIGAAISHVLSQYLMALALMVILTRKVDLVPPS IKDLQIFRFLKNGGLLLARVIAVTFCQTLAASLAARFGPIPMMAAFQTCLQVWLTS SLLADGLAVAVQAILACSF AEKDYEVLVAAATRTLQMSFVLGVGLSFAVGVGL YFGAGIFSKSVLVVHLIRIGLPFVAATQPINSLAFVFDGVNYGASDFAYSAYSLVT VSLASVASLFLSKSKGFVGIWIALTIYMSLRMFAGVWRMGTGTGPWRFLRGRS MS*
Glyma. 16G149 100.1. Wm82. a2.v1	MEETLLLPKENKRVSSNSMSSSSCSGFVQEFKKFLLQVVSLMMAGRSSWRTLPC RYCIGHFLCRLHDNNSFLLSLMGMAGALETQCGQSFGTEQFHKLGNVVFCAIL FLILSSAPISILWIFMDKLLVLLGQDHAISLVAGNYCIWLIPTLFGYSRFGSLFSDSE LDLSNACNLSCCFSAFYTYLLAALSIGISYWLSVMLLIVYTQCFKKHQRFVLLSH PICTYDLLSGGRSLELLVIFAGLLPNPKLETSLVLSIWCVSP*
Glyma. 16G157 300.1. Wm82. a2.v1	MGDNKDHDFFSHKFPTTSQVMEEMKELWGMALPITAMNMLVFVRVAVSVLFL LGRLGSLELAGGALSIGFTNITGYSVLVGLAAGLEPVCSQAFGSKNWDLLSLSLQ RMVLILLMAIVPISLLWLNLERIMLFMGQDSAITGMASLYCFYSLPDLTNTLLQ PLRVFLRSQKVTKPMMYCSLVAVLFHVPLNYLLVVVMGLGVPGVAMASVMT NLNMVVLMAGYVCVCRKREVVLKWRCGGGGVVCGLGQLMGFAVPSCLMIC LEWWWYIEIVTVLAGYLPRPTLAVAATGILIQTTSMMYTVPMALAGCVSARVG NELGAGKPYKAKLAATVALGCAFVIGFINVTWTVILGQRWAGLFTNDEPVKA LVASVMPIMGLCELGNCPQTTGCCILRG TARPGIGAHINLGSFYFVGTPVAVGL AFWFKVGFSGLWFGLLSAQVACAVSILYVVLVRTDWEAEALKA EKLTRIEMGS CNGLRNKENERDEESKGLLVNGNGNKNKDDTC*
Glyma. 16G180 000.1. Wm82. a2.v1	METPLVIQKHTSEPDYLPVESLKDVMFVLR TETVKIWRVALPMALLALFQLLMD SSTSIYAGHIGDIELSSIGVYQGVIGAIYFYLLFGMSSALATLCGQAFGAGKIQSTC IYVQRSWIILTATCIILLPIYVYATPILKLLGQDEGIAEVAGRYSIQVIPYMF SFAVA FPIQRFLQAQSKVKVIMCIAFVDLLIQNGLLYIFINVFGWGITGLAIVTNIVGWLY AVALVVYTIGWCKEEWSGFCWMAFRDLWAFAKLSLASSVMNCLEQWYITCIM LLAGLLDNPVIAVGSYSICFNVQGWDDMLRLGINTAISVRVSN TLGMSHPRAAI YSFCVTMFQSLLL GILFMTVIFFSKDEF AKIFTDSEDMILAAADLAYLLGVTIVLN

	SASQVMSGVAIGSGWQVMVGYINLACYIVGLPIGIFLGFKLHLGVKGLWGGT MCGSILQTLVLFTIIWKTNWSKEVEQTAHRMRLYVEQ*
Glyma. 16G180 100.1. Wm82. a2.v1	MYGWICVAKAEVCQPRCPGASTPYSLVLMDSSTSIYAGHIGDIELSSIAVYQAFR IQRFLQAQSKVKVIMCIAFVDLLIQNGLLYIFINVFGWGITGLAMVTNIIGSLCAL ALVVYTIGWCREEWGRFSQLQKRNLWAFKLSLASSVMNCLEQCFNVQGW YMLLLGINTAISLKDVKFVLWTETVKIRRTLPAVALSQLFQFLTNSSTSIYVGRVG DIELSSISVYQGVSSI* METPLVIQKFTSESDYLPVKSLKDLKFVLWTETVKIWRIAAPMALSALLQFLT TSIYAGHLGDIELSSISVYQGVISAIYFDLLFGMSSALVTLCGQAFGAGQIQSTCIY
Glyma. 16G180 200.1. Wm82. a2.v1	VQRSWIILTATCIILLPIYVCATPILKFIGQDHEIADLAGRYSIQVIPYMFSCAITFPF QTFLQAQIKVKVITCIALAVLVIQNVLLYIFINVFGWGTTGLAMVTNITGWVYA MALVVYTIGWCKEWTGFSWMAFRDLWSFAKLSLASSVMSCLEQWYGTCIILL AGLLDNPVIDVGSYSICFNVQGWHTMLLLGISVAISIRVSNLTGMSPRAAIYSF CVTMFQSLLLGIVFMIAIFLSKDEFKIFTDSEDMIRAVADLAYLLGVSMVINSAS QVMSGVAVGSGWQVMVGYINLACYVVGLPIGIFLGFNQHLGVKGLWGGTM CGRILQMLVLLIIWKTNWSKEVEQTAHRMRIWSINNLHSNDMGNVT* MCHPTLDVTCNCQCCSTSPDCPISITNPLISKPQNTTTPPPPHQHNNTTTKTK TPPPSTTATKTTTAPKPHHVPEAIKEVFSISKIVIPMILTGLLLYCRSMISMLFLGH LGELALAGGSLAIGFANITGYSILSGLAVGMEPICGQAFGAKRFTLLGLCLQRTIL
Glyma. 16G198 700.1. Wm82. a2.v1	LLLFTSLPISLLWLYMKQILLLCGQDVAIATQAQSYLVYSIPDLIAQSFLHPLRIYL RTQSITLPLTLCASFILLSHIPINYFLVAHLKLGKGVALGGVLTNFNLVASLILYIV FSGTHKKTWGGFSFECFTQWKSLLNLAIPSCVSVCLEWWWYEIMILLCGLLVNP KATVASMGIQTTSLLYIFPSSLSFSVSTRVGNKLGAQKPSKARLSAIVGLSCSFM SGVLALVFALMVRNTWASMFTKDKDIITLTSMVLPPIGLCELGNCPQTTGCGVL RGTARPKVGANINLGC FYLVGMPVSIWLAFFTG YDFQGLWLGLLAAQGSCAV TMLVVLCRTDWEFEAQRACKLTGMGGAASGVDQSREVDPEKPLKHESNEDSL LLADSDENEQ* MLAEQKFQKTYPTVTEVLEEVRMTDIGFPIAAMSLVGYLKNMTLVVCMGRLG SLELAGGSLAIGLTNITGYSVLSGLAMGMEPLCTQAFGSRNLSLLSLTLQRTILM LLLFSLPISLLWLNLESLMLCLRQNPDIRVATLYCRFAIPDLIANSFLHPLRIFLR
Glyma. 17G027 900.1. Wm82. a2.v1	SKGTTWPLLWCTLILLSILLHPLTLTFLTFKLN LGVPGIAISSFVANFSNLFFLLLYMF YTRVPKESLHVSLLMSHNNLIITCSSSTSTIAKEWGMLMKFSIQSCLAVCLEWW WYELMTISAGYLDNPRVALATAGIVIQTTS LMYTLPTALSASVSTRVGNELGAG QGERANLSTVVAIGLALVSSIFGLLWTTMGRERWGRVFTSDSEVLQLTVAVLPII GLCELANCPQTTSCGILRGSARPGIGAVINFC SFYLVGAPVAIVLAFYWKLG MV GLCYGLLAAQIACVVSIFGVYKTDWERESLKARCLVGKASCGTFAYDEDQTD ALKCEEVVFLNSQK* MLTTLIPKSPTCQLHQMQNPHNNINTTHLSLSLVEAKCIANISFSMILTGLLLYS
Glyma. 17G131 700.1. Wm82. a2.v1	RSVISMLFLGHLGELALAGGSLAIGFANITGYSVLSGLAMGMEPICGQAFGAKR FKLLGLTMQRTVLLLLITSCLISLFFWLNMKKILLCAQE QDIANEAE LYFYSLP DLVLQSL LHPLRIYLR SQSITLPLTCCA AVSILLHVPVNYLFVSILNLGIKGV ALSA VITNLNLVVLLIYIVFSGTHKKTWPGISRECFNGWKLLNLAIPSCVSVCLEWW WYEIMILLCGLLVNPHASVASMGVLIQTTAL IYIFPSSLSFGVSTRVGNELGAGN PRRAKLAAIVGLCF SFVFGLSALAF AVSVRN VWASMFTLDGEI IALTTAVLP IIGL

	CELGNCPQTTVCGVLRGTARPKLGANINLGCFYLVGMPVAVWLGFAGFDFK GLWLGMLAAQGSCIVTMMFVLARTNWEGQALRAKELTSSDPREEKKLVEEEH EEKGFLGSCATKEASDLVV*
Glyma. 17G136 400.1. Wm82. a2.v1	MSATSKGESITANDWSNRQPSFSSHTQKCPSNANNFVKMVVEELRVQRGIAL PLVPMNLAWFAKLAITTAFLGHLGELNLAGGALGFSFANVTGFSVLNGLSGA MEPICGQAHGAKNARLLHKLTLLMTLLLLLVTPLSFLWLNLGKILILFGQQQE ISTVAKTYVSNLIPDLFIKALLCPLKAYLSSHCVTLPTMFSSAVALAFHIPVNIVLS KTMGLRGVAIAVWITDLMVMVMLAIYVVVLERRSEGLLWKEGGWWDQNNM DWIRLIKLSGSCCLNTCLEWWCYEILLFLTGHLANAKQANFDYLHYAVMISLA TSVSTRVSNELGANRAGQACESARVSLALS SVSGCIGGSTMVAARGVWGD LFS HDKGVVKG VKKAMLLMALVEVFNFPVTVC GGIVRGTGRPRLGMYASLG GFYF LTLPLGVVFAFKLRLGLAGFTIGLLIGIVACLILLTFIVRINWVQEATKAQTFVCI AQVQEQVPRYEVNELVENHENDQV*
Glyma. 17G136 500.1. Wm82. a2.v1	MSATSKQVENLSTNDKANHRPSSPSHTKKCPFNANFIKMOVLEELRVQRGIALP LVAMNLAWFAKTAITTAFLGHLGELNLAGGALGFSFANITGFSVLNGLSGAME PICGQAHGAKNVRLHKTLLMTTLLLLLASLPISFMWLNVDKILICFGQQQEIST VAKTYVSYLIPDLLVTSLLCPLKTYLSSQCMTLPTMFSSAVALAFHIPVNIVLSKT MGLRGVSI VAVWITDLMVMVMLAVYVVVLERRNEGMLWKEGGWWDQNVMD WIRLMKLSGSCCLNTCLEWWCYEILVLLTGHLANAKQALGVLAIVLNFYDYL SVMLSLATCVSTRVSNELGANSAGQAYKSARVSLAVGVISGCIGGSMMVASRG VWGNLFSHDKGVVKG VKKTMFLMALVEVFNFPVTVC GGIVRGTARPWL GMY ANIGGFYFLALPLGVVFAFKLRLGLAGLIIGFLIGVVACLILLTFIVRINWVQEA TKAQMLVCIPAQVQEQVPRNQVNELVR*
Glyma. 17G175 100.1. Wm82. a2.v1	MGLITYGKSAISTYFLGKLSKEALVGGSLAIGVANITGYSIISSLATSMDGISSQAC GAQQWTLIGQTLQCSIMILTLTCITISILWLNIEPVLLFCGQNPTISSIATTYLGFSL PDLIFTSLIISFKIFLRTQDVTLPFMFSATLAPFLHAIINNVVIHTFGLGIQGV ALVG SFTNIKFLIILLLYLWFSRNCNSNSWQGWYELLVLFSGVLPNATKTIATYGIIIQA TSLIYNFPYALSLAVSPKVGNELGANRSDKAKASSFYALLCAFITTIVATILTVNG SARPTLGAKINLVSFYVVG L PVAL LMSFVFDLGLLGLLLGLLLAQIVRASVMTIV LARTNWGASTEGKGV*
Glyma. 17G247 400.1. Wm82. a2.v1	MDSPLLENIDNSCSNVEEEKTPNTVVKRFGFESKKLWKIAGPAIVTSICQYSLGA LTQTFAGLVGDLDLA AVSVENSVIAGLAFGVMLGMGSALETLCGQAYGAGQI RMLGVYMQRSWVILFITALILLPLYIWSPILRLAGQTAEISDAAGKFAVWMIPQ LFAYAINFPIVKFLQAQRKVLVMLWISVVVLVLHTFFSWLVIFKLGWGLIGAAV TLNTSWWWVIVIAQLLYIFITKSDGAWSGFTWLAFSDLFGFVKLSLASAVMLCLEF WYLMILVVITGRLENPLIPVDAISICMNINGWDAMIAIGFNAAISVRVSNELGAG DFKAAKFSVWVVSITSV SIGVVVMIGVLLTKDYFPYLFTTSVPVANETTRLSALL AVTVLLNSLQPVLSGVAVGAGWQSLVAYINIVCYLVGLPAGIILGFKLGLGAE GIWSGMIAGIVLQTTILIIVTSIRNWKKEAEEAESRVRKWGG AISYDQ*
Glyma. 18G097 600.1. Wm82. a2.v1	MIVIFLSKDEFKIFTNSED MIRAVADLAYLLGVSIMSGVAVGSGWQVMVGNIN LACVYVVGLPIGIFLGFNQHLGVKGL*

Glyma.	
18G110	MDKLLVLLGQDHAISLVAGNYCIWLIPALFGYVVLQALVRYFQTQSLIFPMLVT
800.1.	SVVVLVLHIPICWVLVFELGLGQNEAALSIGISYWLSVMMLIVYTVLSVMSENLG
Wm82.	SFR*
a2.v1	MEDHEDHHTHPLLTPRHHTPDPAVVFTAKSDDIAPAGAGDFAREFFAESKKLW YLAGPAIFTSVCQYSLGAVTQVFSGHVSTLALAAISIENSVIAGFCLGITFGMGSA LETLCGQAYGAGQVHMLGVYMQRSWVILNATAILLTLLYIFAAPLLRAIGQTE AISAAAGDFAVWMIPQLFAYAVNYPQKFLQAQSRIMVMAWIAAAALVLHT VFSWLLMLKLRWGLVGAAVVLNASWWFIDLAQLVYIMGGACGEAWSGFTFK AFHNLWGFVRLSLASAVMLCLEVWYFMALILFAGYLNKNAEVSVDALSICMNIL GWTIMVSFGMNAAVSVRVSNELGACHPRTAKFSLLVAVITSTLIGVMLSMVLIIF RNQYPFLFSNDSEVRKIVVELTPMLALCIVINNVQPVLSGVAVGAGWQAVVAY VNIACYFFGIPLGLILGYKLDKGMGIWSGMLLGTILQTCVLFMVYRTDWNK EASLAEDRIKQWGGHEDSKTHAIAKNDQET* MVSSLSTFFLCTHSLKSPTLKLPTKFYCFARLFRVPPKASSRNKNANTDSVETPS LQPSSLKPPYDSSSSLLRCFSGVLKFVYWVLASDGWLTDFDESIVVLIALPAALALA ADPIASLIDTAFVGHIGAVELAAVGVVSASGFNLVSKAFNVPLLNVITASFVAEEQ ALIRKEEESIPSDKNDPFQMYIQIKLLPSVSTSLALAAATLGMAETVVLTGSGIL MNIMGIPADSPMRGPAEQFLTLRAFGTPAIVLALAAQGTFRGFLDTKTPLYAVG KVHNLKFEITNKYLLTEMFLGVGNFLKAILDPILIFLGLGGATVATLISEYLIAFI LLWKLSDKVLLIPSEFYGRKFFSYLKSETLLFDSNWILLCLEPAIPAEVFKDIPNIP PPPIPKMFLTLAVFITVMLSTSVAAQQGPIPPMAGHQICMQVWLSALLACNYSL GNYEQASLVIFRVMQIGLGAGITLSMILFFGFGAFSSLFSTDSEVLVDVARSGIWV AGSQPVNALAFVIDGIYYGVSDFGYAAYSMVISYHVGLVSSTFLLVAPVGLPG VWTGLFIFMALRVLAGLWMLSSKSGPWDTFWYKDGAED* MRSTKGGDGEGKRNCGCCGRFIEGLHQHLHQFLKALFPTLSLSEVKEELKSLA NIACPMMMTNVLLYSRSAISMLFLGRQGKVELAGGSLAIGFANITANSFLKGLT MGMDPICCQAYGAKRWSVLSQTFCKTLCLLLLVAIPISLLWLNMAPLLHWLGQ DPEVTKVAQVYMFVSIPELLAQVHLNPLRSFLRTQGLTTPLTIAASF AAILHLPIN YFLATYLELGVKGIALATGLNSINMILGLVLYLLVSKKPLKPWEGATILSSFHDW RPLLTLALPSCISVCLEWWCYEIMFLCGLLSNPQTTVATMGVLIQTTGFLYVFP FSLSAALTTQIGHSLGAGQPSRAQITATIGLFIAFALGFSAFVLLIVRNVWGKLF TNETQIVDMVTTILPILGLCEIGNWPQTAACGILSGTARPYVGARINLCAFYLIG LPVAVFAAFMHRYQLRGLWFGMLAAQISCFMCMVYTLVQTDWGHQSRRAEQ LAQATDEEISGFLDSDM* MFNNGFNSMETTELHHAPEGLVDTNNGGDYTEMMSGFADFKNVFSVESIKLWTIA APIAFSILCNYAVNSFTTIFVGHGLDLELSSVLSLSVVSNSFSFGFLGMASALETL CGQAFGAGQVEMIGVYMQRSWLILLGACICLTPIYIYAEPILLLLQGEPEIAELA GAFTIQSIPQMFSLAINFPTQKFLQAQTKVGFLAWLGFGAFIFHVILLWILLKVFS LGTGAAVAYCTTAWIIALAQTAAYVIGWCKDGWRGFSWLAFKDLWAFVKLSV ASAVMLCLEIWYFMILIVLTGHLDNAVIAVGSLSICMTINGFEGMLFIGINAAISV RVSNELGSGRPRAAKYSVIVTHIESLIIGLISAAIILATKDHFAIIFTESKEMIKAVSK LAGLLGITMILNSVQPVISGVAVGGGWQALVAYINLFCYYIMGLPLGFLGKYKL

	GYRVEGIWVGMICGTMLQTLILLYIVYKTNWNKEVEQASERM RKWTGQEIEIN LANSQQTFTR*
	MEEGSETGKWGW MKRRRAMREELKKVGTIAAPMVVASVLQYLLQVVSLVMV GHLNQLSLSSVAIAISLTNVS GFSVLSGMAGGLETLCGQAFGAGQYEKFGQYTY
Glyma. 18G293 100.1. Wm82. a2.v1	TAVISLSLICFPITILWTFMDKILTLLGQDPTISLEARKYAIWLIPALFGSAILKPLTR FFQTQSLISPMIL TSAIALCFHGATCWTLVFKLELGHVGA AISFSLCVWFNVMLL LSFVRYSSACEKTRIPFSKNALVGVGVFFRF AVPAAVMVCLKWWACEILVLLAG LFPNPKLET SVLSICLTISTLHFTIPYGF GAASTRVSNELGAGNPQAVRVAVSAT MFLAVTEGLIVSATLFGCRHLLGYAYSDDRMVVHYVAVMTPLLCLSIFTDSLQG VLSGVARGSGWQH LGAYVNLGAFYLVGIPVGIVLGFVAHLRAKGLWIGIVT GSI VQSILLSLVTALT NWKKQAMMARERIFDAKPPDENESNHMTSA*
Glyma. 18G293 200.1. Wm82. a2.v1	MAAPMLAANMCQYLLQVVSLMMVGH LGLLVSFSGVAIAISFAEVTGFCVLMG MAGALETLCGQTYGAE EFTEIGNYTFCAIVTLLLVCLPISLLWIFMDKILL LFGQ DPEISHVAHKYCIC SIPALYGFAVLQCQIRYFQTQSMIFPMVFSSIAVLCLHVPIC WGLVFKLGLGHVGAAYAIGISYWLNVIGLGIYMNYS PACEKTKIVFSFNALLSIP EFCQFAIPSGLMFCFEMWSFELLTLFAGLLPNPQLQTSVLSVCLNTTTLHYIIPYA VGASASTRISNELGAGNP KAAQDIVPILCGSFTADSLIGALSGIARGGGFQQIGA YVNLGAYYLVGVPLAFL LGFVLHFNAKGLWMGSLTGSVLQV IILT TVVTVLTDW QKEATKARERIVEKSIKVHND SVI*
Glyma. 18G293 300.1. Wm82. a2.v1	MEETLLLPKENKRVSSNSKSSSSSGSFVQEFKKVSLMAAPMVVSVSQFLLQVV SLMMAGIALATSFADVTGFNILMG MAGALETQCAQSFQTEQFHKLGN YVFCAI LFLILSSAPKSILWIFMDKLLVLLGQDH AISLVAGNYCIWLIPALFGYAVLQALV RYFQTQSLIFPMLVTSVVVLVLHIPICWVLVFELGLGQNEAALSIGISYWLSVMLL IVYTLSGGRSLELLVILAGLLPNPKLET SVLSICLKICNLHYFIPYGTGA AVSSRV NELGAGRPQAAREAVFAVIVLTFTDAIVFSSV LFCFRHVLGF AFSNEMEVVHSV AKIVPVLCLSFSVDGFLGVLCG SRLQKMG AISNLVAYYAVGIPVSLVFGFGLNFY GKGL*
Glyma. 19G001 600.1. Wm82. a2.v1	MESSREM NKELAAPLLVPRKSGDGQENNNNNGVEVVASSSESTFCQELKRVSS MAAPMVAVTVSQYLLQVVSLMMVGHFGILVSFSGVAIATSFAEVTGFSVLLGM SGALETLCGQTYGAE EYRKFGNYTWCAIVTTLVCLPISLVWIFTDKILL LFSQDP EISHAAREYCIYLIPALFGH AVLQALTRYFQTQSMIFPMVFSSIT ALCLHVPICWG LVFKLGLGHVGAALAIGVSYWLN VVWLAIYMIYSPACQKTKIVFSSNALLSIPEF LKLAIPSGLMFCFEWWSFEVLTLLAGILPNPQLETAVLSICLNTTTLHYFIPYAVG ASASTRVSNELGAGNPKTAKGAVRVV VILGVAEAAIVSTVFISCRHVLGYAYSN DKEVIDYVAEMAPLLCVSVTADSLIGALSGIARGGGFQEIGAYVNLGAYYLVGI PMGLLLGFHLQLRAKGLWMGTLSGSLTQV IILAIVTALIDWQKEATKARERVVE NSIKAHI*
Glyma. 19G120 200.1. Wm82. a2.v1	MEMEEELKETLMHHPNNTSLESVEKEESLRKRAW EESKMMWV VAGPAIFTRFS TFGIMVVSQSFIGHIGSTELAAYAIVMTVLVRFANGVLIGMASALDTLCGQAYG AKKYDMLGVYLQRSWIVLFMTSILL LPIYIFTTPLL EALGQDKTIAQVAGSISLWS IGIIFAFSVSFTSQMFLQSQSKNKIIAYLAAVSISIHVLLSWVLTVQFKFGLNGAMT STLLAYWIPNIGQLVFIMTKCPDTWKGF SFLAFKDLLPVIKLSLSSGAMLCLEIW YNTVLILLTG NMKNAEVSIDALAICLNISGWEMMIALGFFAAASVRVANELGR GNSKATKFSILITVLTFSIGFVFLVFLFLRGKLA YIFTPDPEVAKAVGDLSPLLSF

	SFLNSVQPVLSGVSVGAGWQSVVAYVNIGCYYLIGIPVGVLLDNLFHLEVKGI WIGMLFGTFVQTVMLTITFTKTDWDKQVEIARNRVNKWAVTTENEESSNRSSIS S*
Glyma. 19G120 300.1. Wm82. a2.v1	MEGHLKQKLLRNKERRTSSEQEEEEELSLVKRVWNESQVMWIVAAPAIFTRFSTF GISVISQAFVGHIGSKELAAAYALVFTVLVRFANGVLLGMASALSTLCGQAYGAK EYGMMGVYLQRSWIVLFLTAVCLLPVFIFTSPILMLLGQDESIAQVAGNIALWSI PVMFASIVSFTCQTFQLSQSKNVIIAFLAAFSIVIHVFLSWLLTMKFQFGIPGAMIS AGLAYWIPNIGQLIFVTCGWCSDTWEGFSFLAFKDLWPVVKMSLSAGAMLCLE LWYNTILVLLTGNMKNAEVEIDALSICLNINGWEMMISLGFMAAASVRVANEL GRGSAKAAKFSIIVSVLTSLAIGFLLFLFFLFFRERLAYIFTSNKDVAFAVGDLSP LSVSILLNSVQPVLSGVAIGAGWQSIVAYVNMGCYYAIGIPVGIVLGNVLDLQV KGIWIGMLFGTLIQTIVLIVITYKTNWDEQVTIAQKRISRWSKVDNADQENEAQ RKYVS*
Glyma. 19G120 700.1. Wm82. a2.v1	MSSALSTLCGQAYGAKEYAMMGVYLQRSWIVMSLTTLFLLPVFIFTRPILMLLG QDEIIAEVAGTISLWSIPIIFAFIASFTCQNFLQSQRNTIIALLAAFSIVIHVFLSWL LTIQFKLEIPGAMTSTSLAFWIPNIGQLIFITCGWCSDTWKGFSFLAFKDLWPVV KLSLSSGVMLCLELWYNTILVLLTGNMENAQIDALSICLNINGWEMMISLGF MAAASVRVANELGKGSSKAAKFSIVVTVLTSLAIGFVLFLFFLFLREKLAYIFTTN KDVAQAVGDLSPLLAISILLNSVQPVLSGVAIGAGWQSIVAYVNIGCYYYIGVPV GVLLGNVLNLQVKGIWIGMLFGTFILTVVLIVITYKTDWDKQVIIARNRINKWS KVESDHEIITSDN*
Glyma. 19G120 900.1. Wm82. a2.v1	MEGNLEKKLLSREKKSEEEEEEEKLSLVKRVWEESKVMWIVAAPAIFTRFTHFGI SVISQAFIGHIGSRELAAYALVFTVIIRFANGILLGMASALSTLCGQAYGAKEYD MMGVYLQRSWIVLFLTAICLLPLLIFTSPILTILGQDESIGQVAGTISLWSIPIIFAYI VSNNCQTFQLSQSKNVIIISFLAALSIIHVLSWLFTMQFKYGIPGAMISTILAYWI PNIGQLIFITCGWCPETWKGFSVLAFKDLWPVAKLSISSGAMLCLEFWYSTILILL TGNMKNAEVQIDALSICININGWEMMIAFGFMAAASVRVANELGRGSSKAAK FSIVVTVLTFSVIGFILFLFLREKVAYLFTSNEDVATAVGDLSPLLAVSLLLSI QPVLSGVAVGAGWQSTVAYVNIGCYYLIGIPVGIVLGNIIHLQVKGIWIGMLFG TLIQTIVLTIITYKTNWDEQVIIARSINKWSKVESDHETTTSDN*
Glyma. 19G244 000.1. Wm82. a2.v1	MEQVDLVPPSIKHLQLDRFLKNASLATRQGPTSRAAFQFIASKITCWFHAILAG AFANKDFDRATTTASRVLQICLILGLALAFILGIGLHFGAKIFTQDANVLQICLIL GLALAFILGIGLHFGAKIFTQDANVLQICLILGLTLTFILGIGLHFGAKIFTQDAN VLHLIQIGITFVVVTQPLNSLAFVFYGVNFGASDFAYSASFMSVRLLYGNSQVV VAILSIIICLLILSSAGGFIGIWVALTITYMGLRAFASFLRIGMGSGPWFLRSS* MWIPHYFSSFLRKEEQPNGGRKMNLTFVSSPFFPSFLAGTKEREA EYVMRWSV FGEEMKRVGYLAGPMINVTLSQYFLQIISMMMVGHLGKLVLSSTAIAISLCAVS
Glyma. 20G123 300.1. Wm82. a2.v1	GFSLIFGMSCALETQCGQAYGAQQYRKFGVQIYTAIVSLTLACLPLTLLWVYLG KILIFLGQDPLISQEAGKFALCMIPALFAYATLQALVRYFLMQSLTSPLFISSSITLC FHVAFCWLLVFKCGFNLGAAFSIGTSYWLNVVLLGLYMKFSTECEKTRVPISM ELFHGIGEFFRCAIPSAAGMICLEWWSFELLTLLSGLLPNPELETSVLSICLSVTTTIY TIPEAIGSAASTRVSNALGAGSPQSAQLSVSAAMTLAASAAILVSSIIFACRQVVG YVFSELVDVVDYFTDMVPLLCLSVILDTLHGTLSGIARGCGWQHGLGAYVNLGA YYVVGPIAAMLGFVWQLRGKGLWIGILTGAFCQTVMLSLITSCTNWEKQAIKA

	RERTFQRSFAVEDGLVLANGENSLNLSACLVGIGKSSNFGGTKDQNLELEEGKV LITRQV*
Glyma. 20G123 400.1. Wm82. a2.v1	MENSLLDKDEPENPSASAITWTVFSQEMKRVGYLAAPMITVTLSQYFLQIISM MMVGHGLKLALSSTAIAISLCAVSGFSLIFGMSCALETQCGQAYGAQQYRKFG VQIYTAIVSLTLACLPLTLFWVYLEKILIFLGQDPSISQEAGKFALCMIPALFAYAT LQALIRFFLMQSLISPLVISSITLCFHVAFSWLMVFKSGFGNLGAAFSIGTSYWL NVILLGLYMKFSTECERTRVPISMELFHGIGEFFTYAIPSAAGMVCLEWWSFELLTL LSGLLPNPELETSVLSICLSIITTIYTIPEAIGSAASTRVSNALGAGSPQSARVSVSA AMTLAVSEAILVSSIIFASRQVLGYVFSNEQDVVDYVTDMPVLLSISVIVDTLHGT LSGIARGCGWQHIGAYVNL*
Glyma. 20G123 500.1. Wm82. a2.v1	MEESLVKKHEEDRVVRWGVYSEEMRRICEIAGPMVAVVSSQYLLQVVSTMIVG HLGELYLSSAALAIISLGVTFGSLHMGMASGLETICGQAYGAQQYQRIGMQTY TAIFSLILVSIPVSILWINMESILVFIGQDPLISHEAGKFTIWLVPALFAYAILQPLV RYFQVQSLLLPMFASSCVTLIIHVPLCWALVFKTRLSNVGGALAVSISIWSNVIFL GLYMRYSACAKTRAPISMELFKGMWEFFRFAIPSAVMVCLEWWSYELLVLLSG LLPNPQLETSVLSVCLNTISTLYMIPFGIGAAASTRVSNELGAGNSHAARVAVLA AMSLAVIETSIVSATLFACRNVYGYIFSNEKEVIDYVTVMAPLVCISIILDSIQGVL TGIARGCGWQHLGVFVNLGAFYLCGIPMAALLAFLVRLGGQGLWIGIQSGAFV QTLLSIITGCINWEKQAIKARKRLFDDQFSADNILV*
Glyma. 20G155 500.1. Wm82. a2.v1	MCHITSHLPCKCNSNPEYVVSMPPEADMMITNPLIQKDITVTLTTLHEEKNDP RTMQTHHHVLKELISICKIAFPMTGLLLYCRSMISMLFLGRLGELALAGGSLA VGFANISGYSILSGLAVGMESICGQAYGAKKFSLLGLCLQRTILLLLFTCIPISLLW LYMKHILLCGQDEAIATQAQSYLLYSIPDLLAQSFHLPLRIYLRQSITLPLTLCA TFSILLHIPINYLLVSHLNWGIKGVALSQVWNTNLNLVASLILYVFSGTHKKTWG GFSFECFTQWKSLLNLAIPSCISVCLEWWYEMILLCGLLVNPRATVASMGI LQTTSLLYIFPSSISFSVSTRVGNKLGAQKPSKAKFSSIVGLSCSFMLGVFALVFTILV RNIWANMFTQDKEIITLTSFVLPVIGLCELGNCPQTTGCGVLRGTAARPKVGANI NLGCFYLVGMPVAVWLGFAGFDQGLWLGLLAAQGSCAVTMLVVLSTRTDW DAEALRAKKLTSVVVDDSKEVGAEKPPKAEIKEDSLLSLADSDEDKQSWVSTF W*
Glyma. 20G162 000.1. Wm82. a2.v1	MDAPLLLNVNGEALVAENGDYVAVRELKEVKVFWIETKRVWEIAMPVFN WCQFGVNSVTSMFVGHLDIQLSAISLINSVIGTFAGFMLGMGSATETLCGQA FGAGQVNMLGVYMQRSWVILSVTSILLPIYIFAAPILKLLGQQEDIADLAGSFSI LVIPQFLSLPFNFPTQKFLQAQSKVKVIAWIGLVALILHIGMLWFLIYVLDGFLA GAALAFDITSWGITVAQLVYVVIWCKDGWNGLSWLAFKDIWAFVRLSLASAV MLCLEVWYMMSVIVLAGHLDNAVIAVDSLICMNINGWEAMLFIVNAAVSV RVSNELGLGHPRAAKYSVYVIVFQSLFLGIFFMAILATRDYYAIIFTNSEVLHKA VAKLGYLLSVTMVLNSVQPVVSGVAIGGGWQALVAYINIGCYLFLGLPLGFVL GYTANLGVGLWGGMICGIVLQTLILLILYKTNWKKEVEQTAERMRIWSGQD IGVDKIVASA*
OsMA TE1	MGSSDSQAPLLLPRGSHRKEEEEEYAAAGKVRGCCGGDGEggWWREATAEA GRLASLAAPMIAVALLQLMMQLISTVMVGHLEVALAGAAIANSLTNVSGFSV LMGLACGLETICGQAYGAEQYHKLALYMRSIIVLLVVSVPAAIHWVFIPEVLPLI GQQPEIASEVGKYALWLIPGLFAFTVAQCLSKFLQTQSLIFPMVLSSSITLALFIPL

	<p>CWFMVYKVGGMGNAGAALSVSICDWVEVTVLGLYIVLSPSCEKTRAPLTWEAFS GIGSFLRLAVPSALMICLEWWSYELLVLLSGILPNPALETSVLSICISTVVLVYNLP HGIGTAASVRVSNELGAGNPEGARLVVGVALSVILCSAVLVSVTLLALRHFIGIA FSNEEEVINYVTRMVPVLSISVITDSLQGVLSGVSRCGWQHLGAYVNLGAFYL VGVPVALFFGFAMHLGGMGFWMGMVAGGATQVTLLSIITAMTNWRKMAEK ARDRVFEERIPTQSV VRVSQVAGEAQAGRVSVPMMAVTGLVMYSRALISMLFLGRLGELALAGGSLAL GFANITGYSVLSGLALGMEPICGQAFGARRGKLLALALHRTVLLLLAVALPISLL WVTSTGYILKQLGQDEGVADAAQTFAAYASADLAVLAVLHPLRVYLRSQLNT LPITACSLFSVLLHGPINYL LVRLRMGVAGVALAVALTDLNLLLALLCFLAISC AHRDSWVGPTSDCLRGWPALLRLAVPTATAVCLEWWWYELMIVLSGLLANP RATVASMGI LIQATSLVYVFPSSLGQGASTRVSHQLGAGRPAGARRAAGAALSI GLVVGAAAATFMVSVRSHWGRMFTSDGEILRLTAVALPIAGLCELGNCPQTAG CGVLRGSARPASGARINLASFYLVGMPVGVALAFGARLGFAGLWLGLLAAQA ACAVWMARAVAATDWDVEVARAKELTKASTTSGGTNHQHECNNSNTNTA NAKANTKTTTSPAANNINAGGGGSSDNRGYVPISESGHNDGSDDLEKLEEG MVATSGGCCCGDALGVDTKAGDKQQCSNGGAGTAEGNAGQRRGSASSER APLISVGDDEEAGEENDGDGGGGGHV MAGGDQRGDSPPSSHELSGRLEGILADGEAPWARRACKAAALEVRLAPIAAPA IVVYVPNNVLSISTQIFCGHLGNLELAASSLGNNGIQIFAYGLMLGMGSAVETL CGQAYGVHKYDMLGVYMQRSTVLLMATGVPLAVIYAFSRPILVLLGESPEIASA AAVFVYGLVPQIFAYAANFPIQKFLQAQSIVAPSAYTSAATLVHLVVGWL VVY QLGMGLLGASLVLSL SWWVIVAAQFVYIAASKRCRRTWTGFSWMAFSGLPEFL KLSTASAVMLCLETWYFQILILLAGLLDDPQLALDSLTVCM TLAGWMMISIGF NAAASVRVGNELGAGHPRAAAFSVVVVTAVSFVITVVMMAVFLMFRDYISYIFT EGETVARAVSDLCPLAATLILNGIQPVLSGVAVGCGWQKIVAYINVGCYYFVG IPLGFLLGK FHLGAKGIWTGMLGGTCMQTLILFWITFRTDWNKEVEEAKKRL NQWEDKKQPLLAGTVDY MGTESDQYPAHLSSSATVAGHGDDGESPEIAGAARLYVVGLIPQIFAYAANFPI QKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSL SWWVIV LAQFAYIVVSDRCRLTWAGFSSKA FSGLPEFLQLSAASAVMLCLETWYFQVTVL IAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAA FSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLN GIQPVL SGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGM IVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDI AKPLLANED MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGDGGGGHGVSGELESILGDET VPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLEL AAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVL LMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKF MQAQSIMAPSAYISAATLAFHLVLSYL VVYQFGLGLLGASLMLSISWWVIVVAQ FIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLL KDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVV VTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTILNGIQPVLS GVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGG TLM</p>
OsMA TE10	<p>RATVASMGI LIQATSLVYVFPSSLGQGASTRVSHQLGAGRPAGARRAAGAALSI GLVVGAAAATFMVSVRSHWGRMFTSDGEILRLTAVALPIAGLCELGNCPQTAG CGVLRGSARPASGARINLASFYLVGMPVGVALAFGARLGFAGLWLGLLAAQA ACAVWMARAVAATDWDVEVARAKELTKASTTSGGTNHQHECNNSNTNTA NAKANTKTTTSPAANNINAGGGGSSDNRGYVPISESGHNDGSDDLEKLEEG MVATSGGCCCGDALGVDTKAGDKQQCSNGGAGTAEGNAGQRRGSASSER APLISVGDDEEAGEENDGDGGGGGHV MAGGDQRGDSPPSSHELSGRLEGILADGEAPWARRACKAAALEVRLAPIAAPA IVVYVPNNVLSISTQIFCGHLGNLELAASSLGNNGIQIFAYGLMLGMGSAVETL CGQAYGVHKYDMLGVYMQRSTVLLMATGVPLAVIYAFSRPILVLLGESPEIASA AAVFVYGLVPQIFAYAANFPIQKFLQAQSIVAPSAYTSAATLVHLVVGWL VVY QLGMGLLGASLVLSL SWWVIVAAQFVYIAASKRCRRTWTGFSWMAFSGLPEFL KLSTASAVMLCLETWYFQILILLAGLLDDPQLALDSLTVCM TLAGWMMISIGF NAAASVRVGNELGAGHPRAAAFSVVVVTAVSFVITVVMMAVFLMFRDYISYIFT EGETVARAVSDLCPLAATLILNGIQPVLSGVAVGCGWQKIVAYINVGCYYFVG IPLGFLLGK FHLGAKGIWTGMLGGTCMQTLILFWITFRTDWNKEVEEAKKRL NQWEDKKQPLLAGTVDY MGTESDQYPAHLSSSATVAGHGDDGESPEIAGAARLYVVGLIPQIFAYAANFPI QKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSL SWWVIV LAQFAYIVVSDRCRLTWAGFSSKA FSGLPEFLQLSAASAVMLCLETWYFQVTVL IAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAA FSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLN GIQPVL SGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGM IVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDI AKPLLANED MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGDGGGGHGVSGELESILGDET VPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLEL AAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVL LMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKF MQAQSIMAPSAYISAATLAFHLVLSYL VVYQFGLGLLGASLMLSISWWVIVVAQ FIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLL KDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVV VTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTILNGIQPVLS GVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGG TLM</p>
OsMA TE11	<p>QKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSL SWWVIV LAQFAYIVVSDRCRLTWAGFSSKA FSGLPEFLQLSAASAVMLCLETWYFQVTVL IAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAA FSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLN GIQPVL SGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGM IVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDI AKPLLANED MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGDGGGGHGVSGELESILGDET VPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLEL AAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVL LMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKF MQAQSIMAPSAYISAATLAFHLVLSYL VVYQFGLGLLGASLMLSISWWVIVVAQ FIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLL KDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVV VTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTILNGIQPVLS GVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGG TLM</p>
OsMA TE12	<p>QKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSL SWWVIV LAQFAYIVVSDRCRLTWAGFSSKA FSGLPEFLQLSAASAVMLCLETWYFQVTVL IAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAA FSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLN GIQPVL SGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGM IVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDI AKPLLANED MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGDGGGGHGVSGELESILGDET VPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLEL AAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVL LMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKF MQAQSIMAPSAYISAATLAFHLVLSYL VVYQFGLGLLGASLMLSISWWVIVVAQ FIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLL KDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVV VTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTILNGIQPVLS GVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGG TLM</p>
OsMA TE13	<p>QKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSL SWWVIV LAQFAYIVVSDRCRLTWAGFSSKA FSGLPEFLQLSAASAVMLCLETWYFQVTVL IAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAA FSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLN GIQPVL SGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGM IVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDI AKPLLANED MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGDGGGGHGVSGELESILGDET VPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLEL AAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVL LMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKF MQAQSIMAPSAYISAATLAFHLVLSYL VVYQFGLGLLGASLMLSISWWVIVVAQ FIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLL KDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVV VTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTILNGIQPVLS GVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGG TLM</p>

	QTLILMWVTFRTNWNREVEEAMKRLNKWEDKTPLLSE
	MAGGVSDGGAHGAHGRLESILSDSSMPLARRAWAATTIELGLLTRIAAPAVV
	MYMINYLMSMSTQIFSGHLGNLELAAASLGNNGIQMFAYGLMLGMGSAVETL
	CGQAFGAHKYDMLGVYLQRSVLLTITGVPLAVIYGFSEPILVFMGQSPEIARA
	AAIFVYGLIPQIFAYAINFPIQKYMQAQSIVLPSAYISAATLALHVLSSWVVVYKV
OsMA	GLGLLGASLVLSISWWVIVAAQFAYIVTSPTCRHTWTGFTWQAFAGLWDFLKL
TE14	SAASAVMLCLESWYFQVLVLIAGLLPNPELALDALSVCMTISGWVFMISVGFNA
	AASVRVSNELGAGNPKAAYFSVWVVTISCAIISAILAVVILCLRNYISYLFTEGEV
	VSNAVADLCPLLAITLILNGIQPVLSGVAVGCGWQQFVAYVNIGCYIYGVPLG
	VLLGFVFKLGVKGIWGGMLGGTCMQTAILVWVTLRTDWNNEVEEAQKRLNK
	WEDKKKEPLLTGIRDNN
	MGKLVSKSWQESKLLWHIAFPAILTAVFQFSIGFVTVGVFVGHIGQVELAAVTVV
	ENVIEGFAYGVLLGMGSALETLCGQAVGAGQVSM LGVYIQRSWIICGATAVILT
	PTYVFTAGILIGLRQPTDIAAVAGTYTRWVIPQLFAYAANFPLQKFFQSQSKVW
OsMA	AMTAISGIALALHVVLNYIFLTRLGHLVAAALIGNVTWWLILAQFIYLVSGCF
TE15	PEAWKGFSMLAFKNLAAFVKLSLASAIMLCLELWYYTAVLILVGLLKDAKLQV
	DVMSVCINYQLWTLMV ALGFNAAVSVRVSNELGANRPKAAKFAVAMAVSTS
	AIVGAVFMAVFFIWRTQLPRFFSDDADVRESAKLGYLLAATIFLNSIQPVLSGV
	AIGAGWQSLVAFINIGCYLVGIPLGVLFGFKLKDAMGIWVGMSLGTLLQTAI
	LAFISFRTKWERQAMMAEERIREWGGRRND DALPSTTTPTADHDNVDR
	MAIPLQGKAQQQQGEGGKGDGAVDDDGDDQPSVASELRELWGMAAPITAL
	NCVVYLRAMVSVLCLGRLGPLDLAGGALAIGLTNITGHSVLFLGLASGLEPLCA
	QAFGSKNYDLLTSLQRAVLLLTLAALPIALLWLHVGPILVALGQDPTISASAA
	AYAAYALPDLAASAVLQPLRVYLSQGITKPMACSAIAVALHVPLNVLLVFG
OsMA	LGFGVRGVAAAQALTNTNMVLFLLAYIRWSRACDATWKGWARPAAVASGLA
TE16	GLVRLAVPSCVGVCLEWWWYEVVTVLAGYLPDPAAAVGAAGVLIQTSLMYT
	VPMALAACVSTRVGNELGGGKPRRRARMAAMVALGCAVVIGVVHVAWTAAF
	SREWVELFTREAAVRLAAAAMPILGLCELGNCPQTTGCGVLRGTARPAVGA
	RINLLSFYLVGTPVAVTLAFGARVGFGLWYGLLSAQAAACVALVLLAVVWRT
	DWHLEALRAKKL TGLEMIAAAEGDDDECKRLIAPLPPPDGHDVAVDVV
	MTPPPSPPPHERKTWAEVASEFRAQRGIAFPLIAMNLTWFAKLAVTTAFLGRL
	GDLQLAAGTLGFSFANVTGFAVLTGLCAAMPICGQAHGASNGKLLRKTLM
	ATILLGASIPAFWLHVDVALLRFGQQADMSSNARSYVVCLLPD LAVTSFVN
	PLKSYLSAQGVTLPTLFASALALALHVPLTMWMARTRGIQGVATAVWVSDLA
OsMA	VAVMLAGYVLVSERRRKAGGGGGWVEQTRGEWVRLRLAVPSC LNTCLEWW
TE17	CYEILVLLTGRLPDARRTVAVMAVTLNFDYLLFAGMLSLSVSASVRVSNELGAG
	EAWAARRAGMVSIVGGAVGGVGGGVAMVAARRAWGSIYSSDAGVREGVGR
	AMEVM AVLEVNFPLNVCGGIVRGTA RPAVGMYAVVAGFYVLALPLGVALA
	FKARLGIQGLLLGFLVGAAASLAVLLTFIARMDWPAEAQKARTRTTATVAQFH
	QHDEVVQP
	MAAPPSMEEPLLGGNGEEKKGGSSRLAVVAEVRKQLYLAGPLIAGWLLQNV
OsMA	VQMISVMFVGH LGELELSSASIATSFAGVTGFSLLAGMASSLDTL CGQAFGAKQ
TE18	HRLVG VYKQRAMVVLGLASVCVAAVWAYTGELLLLFGQDPEIAAAAAGSYIRW
	MIPALLAYGPLQCHVRFLQTQNAVMPVMLSSGAAAACHLPVCWLLVYGAGL

OsMA TE19	<p>GSKGAALANAVAYLANAAALAAAYVRLSPACRSTWTGFSSEAFHDLVGFMRLA VPSALMVCLEWWSFELLVLLSGLLPNPKLEASVLSICLNSGSLAFMIPFGLGSAIS TRVSNELGAGRPEAARLASRVVMALGLVVGVAIGLAMILVRHLWGYAYSNEE EVVQYVAKMMPILAVSFLFDDLQCVLSGVARGCGWQKIGAIVNLGAYYLVGIP AALCFAFVYHLGGMGLWLGIMCALIVQMLLLLAITVCTNWEKEALKAKERVF SSSLPADMT</p> <p>MTTCADDQTGCAFFAPLLSSKGAENVILVAGDEAEEQQPAPVLTSPKPPGRLAK AVNEAWSVSLGVAFPVTPSMFTCSARGEARSILGLAFPMILTGLLLYLRSISMML FLGHLGGLALAGGSLAIGFANITGYSVLSGLAMGMEPICGQAFGAGNYALLGV TMQRTVLLLIAAAPIGGLWVQMRPLLLFCGQDAAIAAVAETYIFASLPDLVLQ AFLHPVRIYLRQTSINLPLTVCAGLAIAIHLPIYVLLVVLGLGVKAVALASVLA NLNLVLFLLAYIFLKGVHKRTGGFLLSAESFRGWGELISLALPSCVSVCLEWWW YEIMILLCGLLLNPQATVASMGIQTTSLIYIFPSSLSFGVSTRVSNELGAGQPEE ASRAATVGLVLGFGFGAFASAFALVRNVWASMFTADPAIVALTASVLPILGLC ELGNCPQTTGCGVLRGSARPKDAASINLRSFYLVGTPVALVMAFWFHLDLFRGL WFGLLAAQATCTVRMLLVIGRTDWAAEAKRSKQLTGAGAAANMESDDRVAA DEKSRLPVDTDVERSSDHTDRC</p>
OsMA TE2	<p>MAAAAREEQPLLLRREEGEEEGEEVGVRRRWGSEAGKLAYLALPMVAVSLTN YAVQVFSNMMVGHLPGLVPLSSAAIATSLASVTGFSLLIGMASALETLCCGQAYG AKQYHTLGVHTYRAILTLVVCIPSLWVFMGKILVLIGQDPLISHGAGRYIVW LIPGLFANALIQPITKFLQSQSLIMPMLVASVATLVFHIPLCWLMVFKTGLGYTG</p> <p>AALISISYWLNVAMLVAYILLSSSCKETRTPPTIEAFKGLDGFLRLALPSALMICL EWWSFELLILMSGLLPNPELQTSVLSICLTSITLLFTIPYGLGAGGSTRVANELGA GNPEGARSAVYVLSVAVTEALIVCGTLLASRRLGRAYSSSEEVISFVAMMVPL VCITVVTDLQGVMSGIARGCGWQHLGAYVNLGSFYLLGIPMAILLGFVLHM GAKGLWMGIVCGSISQITLLSAITFFTQWQKMAENARERVFSEKPTPSRYHLV E</p>
OsMA TE20	<p>MEERIPLLSKRFPADGTAGVGGGREEEGGDRWWSGLAREAGKVGSMALPMA AMSVAQNAVQVASNMMVGHLPGLVPLSASAIATSLASVSGFSLLVGMASGLE TLCCGQAYGAKQYDKLGVQTYRAIVTLTVVTIPISLLWVFIGKLLTLIGQDPVISHE AGRYIVWLIPGLFAYAVCQPLTKFLQSQSLIFPMLWSSIATLLHIPLSWLLVFKT</p> <p>SMGFTGAALASISYWLNTFMLAAAYIRFSCSKVTRSPPTIEAFRGVGLFLRIALPS ALMLCFEWWSFELVLLSGLLPNPELESSVLSICLTTTSLMYTIPYGLGGAASRV ANELGAGNPEGARSAVHLVMSIAGTEAVLVTGMLFAAQRLGYAYSSDEEVVT YFTSMVPFVCISVAADSLQGVLSGIARGCGWQHLGAYVNLGSFYLVGIPVALLL GFGFKMEGKGLWLGACGSVLQFLLAVIAFFSNWQKMAEKARERIFGETPSEK QHLVLDATNSV</p>
OsMA TE21	<p>MAAKGSPEEEALLAGVGGDHQLVESDELAPAAAVVREEVKKQLWLAVPLVA GALLQNVIQMISVMFVGHGELPLAGASMASFASVTGLSLLLGMASALDTLC GQAFGSRQYHLLGVYKQRAMLLLTAVSVPLVVVWFYTGDLVAFGQDADIAA EAGAYARWMIPALFAYGPLQCHVRFLQTQNVVLPVMASAGAAALCHLVVCW ALVYAAGMGSKGAALSNAVSYWINVAILAVYVRVSSSCKKTWTGFSMEAFHD PLSFFRLAIPSALMVCLEMWSFELIVLLSGILPNPKLETSVLSISLNTAAFVWMIPF GLGSAISTRVSNELGAGRPRARLAVRVVVFMAVSEGLVIGLVLVGVRYIWGH</p>

	<p>AYSDEEEVVITYVAKMMLVIAVSNFFDGIQCVLSGVARGCGWQKIGACVNLGA YYIVGIPSAYLIAFVLHVGGMGLWLGIIICGLLVQVLLMAITLCTNWDKEAANA KDRVFSSSLPSDLAT</p> <p>MEKASCLEEALLLPESCKEEEITASDEVKRQLRLAGPLIAGSLLQNLIQMISVMF VGHLGELPLAGASMASSFAAVTGFSLLLGLASALDTLCGQAFGARQYHLLGVY KQRAMLLLTAVSVPLAVAWYYTGDILLFGQDADIAAEAGAYARWMIPALFA YGPLQCHVRFLQTQNMVVPVMAAAGAAALCHLGVCWALVHAAGMGSRGAL</p>
OsMA TE22	<p>ALGNAVSYWINVGVLA VYVRVSRSCKKTWTGFSMEAFRDPLSFFRLAIP SALM VCLEWWSFELLVLLSGLLPNPKLETSVLSITLNTANCLFMIPFGLGAAISTRVSNE LGAGRPRARLAVRVVTLATLEGLGMALVLACVRYVWGHAYSNEEEVVAY VAKMMLVLAVSNFLDGIQCVLSGVARGCGWQKIGACINLGAFYVVGVPAAYL AAFVLRAGGLGLWMGIICGVAVQTLLFLAITSRTDWQKEAKMAKDRVFSSSLP TDLAT</p> <p>MCTTTSAPSVPEVATPADGGGHHVYVSLPQCTDGGDVEGGHCRPVVHQVKC RGGDDDDGGGGGRGGGVMPAAGETVREAAALCRLACPIALTALMLYSRSALS MLFLGSLGDLPLAAGSLAVAFANITGYSVLSGLSLGMDPLCSQAFGARQPRLLG LTLYRSVLFLLCCSLPLSALWLNMAKILLFLGQDRDITAMAQDYLLFSLPDLFSFS LIHPLRVYLR SQGITQPLAVAAAAAVVFHVPANYVLVGRRLRGAPGVAAAASA SNFVLLAVLLAYVARRDEALREAGGPTAEWLAWGGLARLAAPSCVSVCLEW WWYEVMI LLCGLLPEPRPAVASMGVLMQTTALVYVFPSSLGFGVSTRVGNELG ANRPGRARAAAHVAVAGAAAMGLAAMAFATGMRHAWGRLFTADADILRL TAAALPVVGLCELGNCPQTVGCGVLRGTARPARAAHVNLGAFYLVGMPVAV VLAFLGLGVGFVGLWVGLLAAQVCCAGLMLCVVGSTDWEAQARRAQALTSSA AVSGKADAAEGGGRWPEKGEHQEWKRRHVALISSEADPETA EVL MSGGGGEVEAAAEAAPLLVPHDPQPAVGAEVRRQVGLAAPLVACSL LQYSLQ VVSVMFAGHLGELSLSGASVASSFANVTGFSVLLGMGSALDTFCGQSYGAKQY DMLGTHAQRAIFVLMMLMGVPLAFVLAFA GQILIALGQNPEISSEAGLYAVWLIP GLFAYGLLQCLTKFLQTQNI VHPLVVCSGATLVIHILLCWVMVHCFDLGNRGA ALSISLSYWFNVILLAIYVKVSEVGRRSWPGWSREALKLKDVNMYLRLAIPSTFM TCLEYWAFEMVVLLAGFLPNPKLETSISLISLNTMWMVYTIPSGLSAISIRVSNE LGARNPQAARLSVFVSGIMCLTEGILVAIITVLVRDIWGYLYSNEEEVVKYVAA MMPILALSDFMDGIQCTLSGAARGCGWQKVC SVINLCAYYTIGIPSAVTF AFVL KIDGKGLWLGIIICAMTVQILALVVM LRTSWNEEA EKARARVQGS DGRITLA MGGDERAVAAPLLQQQQDGGGGDGERRRRRWWWGWDGEEAAGQLAFA APMVATSMAYYAIPLVSVMYAGRLGELELAGATLGNSWGTVTGIALMTGLSGS LETLCGQGYGAKMYHMMGVYLQASIITSAFFSVLV SLLWFYSEPVLI FLRQDPEV TRTATLFLRYSIPAQFAYGFIQCTLRFLQTQS VVTPLVV FALLPLVLHFGITHAFV</p>
OsMA TE23	<p>HYLGFGYAGAGMSTSVSLWLSFLMLAAYVCLSERFKHTWEGFSTEAFRHVLP G LKLAIPSAVMVC FEYWAFEVLVLVAGLMPNSHMSTSIAMCENTE AISYMITYG FAAAISTRVSNELGAGNVAKAKKALAVTLVLSLLLGVAFLLLLGLGHDLWAGL FSKSDA VISEFASMTPLLIGSVVLDSTQGVLSGVSRGCGWQH LAAWTNLVAFYI VGLPLSILFGFKLGLQTKGLWLGQICGLLLQNAVLLFITLRTKWERLELT MNGK EDGFVC</p>
OsMA TE24	<p>MASTDPLLGGKEEEE GGGEVRRARRWWVGRVVDTEEAWAQTRFAVPMVL TN</p>

TE26	<p>MSYYAIPLVSVMFSGHLGDVHLAGATLGNSWATVTGYAFVTGMSGALETLCG QAYGARMYRMLGLYLQSSLLMSAAVSVLVSALWCFTEPLLLLLRQDPAVSAAA SAFVRAQVPGLFAFSFLQCLRLYLQTSVVAPLVACSLAPFLHVALAHLLVNA LGLGLAGAGAAVSITFWASCLMLLAYVLRSERFAETWNGFSAEAFRFVPTIKL ATPSAVMVCLEYWAFELLVLIAGLLPNPTVSTSLIAMCSSTEAIAYMITYGFSAA VSTRVSNEIGAGNVEGAKNAVAVTLKLSVFLAAAFVLLLGFHGLWAGLFSGS AIIAAEFAAVAPLMMASILLDSAQGVLSGVARGCGWQHLLAAVTNLVAFYVIG MPLSIFFAFKLKWYTKGLWMGLICGLTCQTCTLMVITARTKWSKIVDAMQEKK ASYVA</p> <p>MGHAVDGRLEALLSGGGGGGEEAAPWARRMAAAAALRLRLAPLAAPAVV VYMLIIVMSSATQIFCGQLGNVQLAASSLGNNGIQVFAYGLMLGMGSAVETLC GQAYGAGRHEMLGVYLQRSVLLTAAGVPLAALYACSERVLLLLGQSPEISRA AAGFARGLIPQIFAYAANFPIQKFLQAQSIVAPSAAVLAASFALHPLSWAAVR</p>
OsMA	VLGLGLPGAALALSATWWVLVAGQFAYIVRSPRCAATWTGFTWAAFHDLAA
TE27	<p>FARLSAASAVMLALEVWYFQVLILLAGMLPDPQIALDALTVCTSIQSWVFMISV GFNAAAASVRVGNELGAGNPRSAAFSTWMVTALSIIIAAIAGVVILLRDKLSYI FTQGEAVSRAVSDLCPLLVGTVLTCGIQPVLSGVAVGCGWQALVAYINIGCYLI GLPLGVLLGFKFDYGIKGLWGGMIGGTLIQTLILIWITFRTDWNKEVEDARRRL DKWDDTKQPLLVRNQ</p> <p>MEDEATSVAAPLLRPRGGVDAEAVKQQLWPAGARVAGEWWVESKKLWRVV GPAIFQRIALYGINVVSQAFIGHMGDLELAAFSIASTVVAGFNFGFLGMASALE TLCGQAFGAKKYHMLGVYLQRSWLVLMMFAVALTPTYVLMEDLLLLIGQPAD LASLAGKMSVWLLPQHFAAMMLPLTRFLQSQLKNWVTAVTAGVALALHLVI</p>
OsMA	TYLLVNTLHLGLLGAVAAANVAWWIVVLGQLVYVVGWCPLSWKGFSEAF
TE28	<p>ADFWEFIKLSSASGVMLCLENWYYRVLVLLTGYLNNAEIAVDALSICLTINGWE MMIPFGFLAATGVRVANELGAGSGKGARFAIVVSVTTSVAIGLVFWCLIIAYND KIALLFSSSKVVLDAVSDLSVLLAFTVLLNSVQPVLSGVAIGSGWQALVAYVNV GSYYLVGVPIGAILGWPLHFVGGIWSGLIGGTAVQTLILAYLTISCDWDEEAK KASTRMEVWASSK</p> <p>MCHCSSKVVAVAQCHQPLLPPPEACPALHDRPRSARGGGGAIAEVASIVRLA MPMVGAGLLMYMRSLVSMLFLGRLGRLPLAGGSLALGFANITGYSVLSGLAAG MDPVCGQAFGAGRTSVLAAALRRTVVLLLAASVPIAALWLAMHRVLVAAGQ DPDIAACAYEFILCSLPDLAVQSFLHPLRVYLRAQSITLPLTYAAAAALALHVPV NVLLVHGLGLGIRGVALAAVWTLNLFLLFLVAYAYFSGLIRGDDDDDDGGNGK AGEEGATTTTTTMEWGWLVKLSVHSCMSVCLEWWWYEIMVLLCGVLADPKA AVAAMGILIQTTSLLYIFPHSLSCAVSTRVGHELGAGRPERARLAARVGLACGA ALGVVACAFAASLRGVWARMFTADATILRLASSALPILGAAELGNCPQTVGCG VLRGSARPGRAARINVSIFYGVGMPAALALAFWPARDFRGMWAGMLAAQL VCAALMLLAVRRTDWDEQAARAREITGAVAGVVVGDDVVKGDHADA VKADSGLLVVTVLS</p> <p>MLIDPPCNRIHSARTQLQRCRTTTTGGLSALRYTVRGLSLLYMCTASSCAHTHT</p>
OsMA	HNRTEGGARTGLRSEMAPPAGTEAAGAGHRKNWRGESGNLWRIAGPVILTEI
TE3	<p>FQFLIGFVTAAFVGHIGKVELAAVSVVNGVVEGLAFGLLLGMGSALETLCGQA VGAGQPRMLGVYLQRSWVICLATSLALLPLYLLASPALRLLRQSAAISSVAGRY</p>

	<p>ARWCAPQLFAYAVNFPMQKFYQAQSRVWAVTAISAAALAAHALLNWLVVA RLGHGVVGAALVGDVSWWLLNAAQFAYLVGGSFPEAWSGFSRKAFTSLGGFV KLSLSSAVMLCLEMWYYTAVLILVGCLKNPEIQVGAISICMNYQLWTLMAVG FNAAVSVRVANELGANHPKAAKFSVIVAVVTSAAVGLVFTLVALVARKQLPRL FTDDDLVRETAKLGYLLAATIFLNSIQPVLSGVAIGAGWQSSVAFVNIGCYYL VGLPIAAVFGFRLSLNATGIWVGMLIGTILQTVILLVILYRTKWQKEAMLAERI KVGWGGVELP</p> <p>MSSTSGSAWDHSNNGGGGSPELREALLLGDGGSSPESREIKGIAVKKQDDLEEI RSVGELMRLAAEENRRLWYLAGPAIFTSLAQYSLGAVTQVFAGHLTTLELDAV STENMVIAGLAFGIMYGMGSALETLCGQAFGAKQHHMLGIYLQRSWVILTAM SVILLPIYLFATPILRFFHQDDEIAVLASRFSLYMIPQLFAYALNFPIQKFLQAQSK</p>
OsMA TE30	<p>VMAMAAVSAAVLLFHVALTWLLLVPLRMGLVGLAVALNVSWWLVVLGQLA YIVMGYCPGAWNGFDWLAFTDLLSFARLSLGS AIMICLEFWFYMFLIVVGNLP NAQVAVAAVSICTNLFGWQIMVFFGFNAAISVRVSNELGAGRPRARLAIAVV LVSSVAIGVAFFAAVLLLRDVYGAPFTGSPEVVRAVASLGVVFAFSLLLNSVQPV LSGVAVGAGWQWLVA YINLGCYCYVGIPVGYAIAFPLRRGVQGMWGGMLTG VGLQTAILVAITARTNWNKEASEAHARIQHWGGTAKLAVDDPI</p> <p>MGSVSPPAPEEDAAAVESAGAAARMFWHETKRLWAIGTPIAIGTITNYAISSVT TMFIGHLGNLPLAAASVGLSVFATFALGFLLGMGSALETLCGQAFGAGQVSML GVYLQRSWIILLGATVLMVPVYVLAEP LLLL VGQDPEVARAAGRFTLYILPGAF</p>
OsMA TE31	<p>AFAVNFPSGKFLQAQSKVGLAWIGVAGLAFHVGITYLAVSVLWGWLPGAAA AYDVSQWASSLAQVAYIMGWCREGWRGWSMAAFHDLAAFLRLSIESAVMLC LEIWYLG LITVLTGDLDDAQMAVDLSL GICMNINGYEGMIFIGLNAAISVRVSNE LGSGRPRAAMHAVVVVVAESLLIGLLCMALVLA FSDKLALVYTS DAHLLRAVS RIAGLLGVTMVLNSVQPVLSGVAVG GGWQGLVA YINLACYYLFGLPVGYLLG YYFNLGVGVPIPIPIPTYLPSLFFFPLI</p> <p>MASVPLLAEWPAGKEKEEGRVRRRLPALAREAWEEKKLWEIVGPAVFLRLVL YSFNIISQAFAGHIGDLELA AFSIANNVITGLNFGFLLGMASALETLCGQAYGAK QCSMLGIYLQRSWIILFVFAVLLVPTYVFTAPLLEALGQPAALARKAGMVSVM LP SHFQYAVLLPLNKFLQSQRKNWVTVVTAAA AFPVHIAVSWLLVSRLRFGVL</p>
OsMA TE32	<p>GAAMSLGVSGWLVTLLQLAYVVG GCPVTWSGFSPLAFVDLWGFVKLSVSSG VMVCLETWYYKILILLTGHLKNS ELAVNALSICMSFQSWEMMIPVGFLAGTGV RVANELGAGNGKGAKFATIVSTTTSFLIGLFFSALALAFHDKIALVFSSSNAVID AVDNISFLLAVTILLNGVQPVLSGVAIGSGWQAAVAYVNIGCY YFIGVP IGVLL GWSFNLGVFGIWAGMIAGTAIQTIILAHMTIQCDWNKEVLQASERVQRWGNP K</p> <p>MASRHSDEATQCHQQLLVM PAATASYPKLHDRPRLAGAAAGVLGEVASILCL AGPMVGAGILLYLRLSVSMVFLGRLGQLPLAGGSLALGFANITGYSVLSGLAGG MDPVCGQAFGAGRTDLLRAALRRTVVLLLAASVPISALWVAMHRVLVATGQ</p>
OsMA TE33	<p>DPDIAATAYAYILCSLPDLAVQCFLHPIRIYLRAQSVTLPLTYAAAAALLHVPI NVVLVDRLGLGIRGVALGAVCTNLNCLLFLAAYVCLSGMYGGRAKACASAAA PAAGEEDDDGGVREWWSLVRLSVHSCMSVCLEWWWYEIMVLLCGVLADPKA AVAAMGVLIQTTS LIYIFPHSLGCAVSTRVGHELGAGRPERARLVARVGVLGA ALGIVAFGF AVSVRAAWARMFTAEDAILRLAAAALPLLGAELGNCPQTAGC</p>

OsMA TE34	<p>GVLRG SARPERA ARINVA AFYGVGMPVALALAFWPAGLDFRGMWGGMLAA QLVCAWLMLRAVLGTDWAEQAERARELTGGGDGYAAVA AVIVDDDKAKQH AEMDKPQQVDNTLLMAIDCV MELAGGGTG VVRQRAEPLGAGLLLRGGGRSVGGGGIGCARRATLRGLALSPL ARRAVSAAGGHFLPRRAVRAAAAAGDGGFYGEEDAASDQPF PARASPSDDA NDSTAVRSLGGDHPGEIKKELLNLALPAIVGQAIDPVAQLLETAYIGRLGPVEL ASAAVGVSVFNIISKLFNIPLLSITTSFVAEDVARHDSQFTSEGNMSESSESGRKR LPSISSAILLAAAIGVIEASALILGSEILLSIMGVSHASTMHSPAKLFLSLRALGAPA VVVSLAIQGFIRGLKDTKTPLLYSGLGNISAVLLLPFLVYSLNLGLNGAALATIAS QYLGMFLLLWLSKRAVLLPPKIEDLDFVGYIKSGGMLLGRTLSVLITMTLGT MAARQGTIAMA AHQICLQVWLAVSLLSDALAVSAQALIASSFAKLDYEKVK VTTYVLKIGLLVGAALALLFASFGRIAELFSKDPMVLQIVGSGVLFVSASQPIN ALAFIFDGLHFGVSDFSYSASSMITVGAISSFLLYAPKVFGLPGVWAGLALFMG LRMTAGFLRLGSRAGPWWFLHQKEPTYKLHSSTC QKLIRLFSSISLQEACGNQCELLRRCSDLHCHHEGGDGGA AHRRQQWRRGG EERRRGGGVGGDRDQEA AVPRRAARRRHVAAERRPDDFRHVRP RRARPLQ RLHGHLLRRRHRLQLAGWHGEQPGHAVRPGVRREAAPHARRVQAAGDAGA</p>
OsMA TE35	<p>RAGERPDRGGLGLHRRDPPRRPGPGDRGGRRELHPVDDPDAVRLRAAAVPR PVPADAERRRAGDALRRRDGGEPRARLLAARAQARAGRQRRARQRLLPH QPLRAGHLRLATRVVMLLAFLVGTSEGLVMVIVRN LWGYAYSNEEEVADYIAK MMPILAVSILFDAIQCVLSGVVRGCGRQQIGAFINLGAYLAGIPVAFFFAFVCH LGGMGLWFGILCGLVVQMLLLLTITLCTNWDKEALKAKDRVCSSSLPKDLAT MEGQGLVSRSWQESKLLWRVAFPAVLVELLQFSIGFVTASFVGH LGVVELAAV TAVESILEGFAYGVLFGMGCALDTLCGQAVGAGRLDVLGLYVQQSWIVCGAT AVALTPTYAFAEPILRSLLRQPADVA AVAGPYALWSLPRLFAHAANFPLQKFF QTQSRVWALAAISAAVLAVHAALTYAAVVRLRYGLRGA AVAGNLSYWLIDA</p>
OsMA TE36	<p>AQFVYLVSGRFPDAWKGFTMTAFSNLAAFVKLSLVS AIMICLEFWYYAALLILV GLLKNARLQLDIMSICINYQFWTMMVAMGFSE AISVRVSNELGARRPKEAKFS VAVASLTSAMIGAIFMSIFFIWR TSLPSLFSDDKEVVDGAARLG YLLAVTVFFGNI GPVLSGVAVGAGWQILVAFVNIGCYLVGIPFGVLF GFKLKL GALGIWMGMLT GTLLQMAILFFIIMRTKWEAQAILAEKRIS ELGETTAND MNGESLLDRSSSADAAMND AVPGHRHHHPLSVFLRDARLAFRWDELGREIM GIAVPGALALMADPVASLVDTAFIGHIGPVELAAVGVSIAVFNQVSRIAIFPLVS VTTSFVAEEDATSSDREKYEINGENEFNVSDSEMEELVSHEEASAAPSKSSFETDS SDVKIEHKRKNIPSVSTALLGGVLG LLQALLVICAKPLLGYMGVKQGSAML</p>
OsMA TE37	<p>MPALKYL VVRSLGAPAVLLSLAMQGVFRGLKDTKTPLYATVAGDATNIVLDPI FMFVFQYGVSGAAIAHVISQYFIASILLWRLRLHVDLLPPSFKHMQFSRFLKNGF LLLARVIAATCCVTLASMAARLGSPMAAFQICLQIWLASSLLADGLAFAGQ AILASAFARQDHSKAAATASRILQLGLVLG LLSIFLGIGLRLGSRLFTDDQDVL HHIYLGIPFVSLTQPINALAFVFDGINYGASDFGYAAYS MILVAIVSIIFIVTLASY NGFVGIWIALTVYMSLRMLAGFLRIGTARGPWTFYAAQRMHSHEVVGLC</p>
OsMA TE38	<p>MNTLT YMLIPISWTTIQRIHHFQPNKRLTVGDSIDMDESTVEEPLLAVRRGGDG EDGAMASTAAEVKRLRLAGPLMAGFVLRNSVQMV SVMFVGH LGELQLAGSS LAASLASVTGFSLLSGMSSALDTLCGQAYGAGQHRL LGVYAQRAMLVLA AAA</p>

OsMA TE39	<p>VPIALVWASAGEILLFGQDPAIAAEAGAYARWMIPSLAAYVPLACALRFLQA QGIVVPVMASSGVA AVAHVAVCWALVHKAGMGSKGAALSGAVTYWTNFAV LAFYARLSGACKTTWTGFSMNAFRELRRFTELAVPSAMMVCLEWSSFEILVLLS GILPNPQLETAVLSISLSTASLLIMVPRGIGSSLSTRVSNELGGGHPRAARMAVRV ATAMTVLVCLVLVIAMILLRNWGYAYSNEEEVVAYIASMLPILAVSFFVDGIN GALSGVLTGCGKQKIGAHVNLGAFYLVGIPTAVLLAFVLHLNGEGLWLGI VCG SISKVGMLLFITLHTDWGKEVQKASPCKHFGLYHVFSGTSV MEKPAASVEEPLLVGAGEKKGESAAAAELKRLRLAGPLVASGVLRNVVQMV SVMFVGH LGELPLAGASLATSLANVTGFSLLFGMASALDTL CGQAYGARQHH LLGVYKQRAMLVLA VAAVPIALVWASAGEILLFGQDPAIAAEAGAYARWLIP SLVPFVPLVCHIRFLQAQSAVLPVMASCGVTAASHVAVCWALVRKAGMGSRG AALANAVSYGVNLTIMSLYVRLSRSEKTTWTGFSMEAFREL RQYAELAIPAAM MVCLEWWSFEFLVMLSGLLPNPKLETSVLSICLNTGALLVMVPIGLSTAISTRVW NELGAGNPQA AKLATRVVICMAMTEGSVVAFTMILLRNSWGHMYSDEAEVV TYIARMIPVLAISFFIDGMHSALSGVLTGCGKQKIGARVNLGAFYLAGIPMAVFL AFVLHLNGMGLWLGI VCGSLSKLILLFWITMSINWEKESTRAKELVFSSSLPVA MARSSAPESMEADHQLTATVTAASGDMPVTEQQQKQMVAVAAPPATEN ADAAGGGGGDNGDHLPTATSL LGGARRTGLHLFVLNARSALRLDELGAEVL RIAVPASLALTADPLASLIDTAFIGRIGSVEIAAVGVAIAVFNQVMKVCYPLVSV TTSFVAEEDAILSKGAAGADDDNDGDHDAKGHGASAAAVADPEKQQVVG DSAETNGAEVSTA AVRITDDKAAAAGVGVGKRRRFVPSVTSALIVGAFLGL</p>
OsMA TE4	<p>LQAVFLVAAGKPLL RIMGVKPGSPMMIPALRYLVVRSLGAPAVLLSLAMQGVF RGFKDTKTPLYATVTGDLANIALDPILIFTCRFGVVGAAIAHVISQYLITLIMLCK LVRKVDVIPSSLKSLKFRFLGCGFLLARVAVTFCVTLAASLAARHGATAMA AFQICAQVWLASSLLADGLAVAGQALLASAFAKKDHYKVAVTTARVLQLAVV LGVGLTAFLAAGMWFGAGVFTSDAAVISTIHRGVPFVAGTQTINTLAFVFDGV NFGASDYAFAAYS MVGVA AVTIPCLVLLSSHGGFVGIWIALAIYMSVRAFAST WRMGAARGPWKFLRK</p>
OsMA TE40	<p>EPLLA AAPPTPGKAADGDGPEEGRRLASAEAKRLRLAGPIVASCILQCVVNM VSMFVGH LGELPLAGASLATSLANVTGYSLTGMATAMDTL CGQAYGARQY HLLGVYKQRAMVVLA AACVPIALVWASAGRILLLLGQDAGIAAEAGAYARW MLPSLAAYVPLQCHIRFLQTQTVLPVTASSAATALLHPLVCWLLVFRAGMGS KGAALANAISYAVNLAILAVYVRASNTCKGRWSGFSGEAFKELRQFAALAMPS AMMICLEWWSFEILVLLSGLLPNPQLETSVLSICLNTGALLYMVPLGLCSSISTRV SNEIGAGQPQA AKRATRVVMYMALSEGLVISFTMFLLRNVWGYMYSNEQEVV TYIARMLPILDISFFIDGLHSSLSGVLTGCGKQKIGAAVN LGAFYLVGIPVAVLLA FYLHLNGMGLWLGI VCGSIKLLVLIIVSCCIDWEKEAILAKDRVFSSSLPVA MERTTEDDERPTVPLLEPKPASNEEEVGSVRRRVVEENKKLWV VAGPSICAR FSSFGVTVISQAFIGHIGATELAAYALVSTVLMRFSNGILLGMSALETLCGQSY GAKQYHMLGVYLQRSWLVL FCCAVILLPVYIFTTPLLIALGQDPEISAVAGTISL</p>
OsMA TE41	<p>WYIPVMFSYI WAFMLQMYLQAQSKNMIVTYLAFLNLGIHLFLSWLLTVKFQLG LAGVMGSMVISFWIPVFGQLAFVFFGGCPLTWTGFSSSAFTDLGAIMKLSLSSGV MLCLELWYNTILVLLTGYMKNAEVALDALSICLNINGWEMMISIGFLSAIGVRV ANELGAGSARRAKFAIFNVVTTSLIGFVLFVLFVFFRGS LAYIFTESKAVADEVA</p>

OsMA TE42	DLAPLLAFSILLNSVQPVLSGVAIGSGWQSVVAYVNVTSYYLIGIPLGAILGYVLG FQAKGIWIGMLLGTLVQTLVLLFITLRTNWKQVEITRERLNRWYMDENGRSQ NSIGNA EVGSVRRRVVEENKKLWVAVGPSICARFSSFGVTVISQAFIGHIGATELAAYALV STVLMRFSNGILLGMA SALETLCGQSYGAKQYHMLGIYLQRSWLVLFC CAVILL PVYIFTTPLLIALGQDPEISAVAGTISLWYIPVMFSYIWAFTLQMYLQAQSKNMIV TYLAFLNLGIHLFLSWLLTVKFQLGLAGVMGSMVISFWIPVFGQLAFVFFGGCP LTWTGFSSSAFTDLGAIMKLSLSSGVMLCLELWYNTILVLLTGYMKNAEVALDA LSICLNINGWEMMISIGFLSAIGVRVANELGAGSARRAKFAIFNVVTT SFLIGFVL FVLFLFFRGLAYIFTESKAVADEVADLAPLLAFSILLNSVQPVLSGVAIGSGWQS VVAYVNVTSYYFIGIPLGAILGYVLGFQAKGIWIGMLLGTLVQTLVLLFITLRTD WKKQVEITRERLNRWYMDENGRSQNSIGNA MTATSPPMRSVAAAALVLTPTPTLNRLSFPFAHRHCPSTAAPRWRPARCRGKP AVEDVVHDDEEETWRREANPERKDGGEEMLRGRWFMVDEIGMEILTIALPAV LALAADPITALIDTAFVGHVGSTELAAVGVSISIFNLVSKLLNVPLLNVTTSFVAE QQAVDADYNSSVENSHIGEEISISQEKAGEQRKFLPAVSTSLALAAGIGLMETVA LILGSGTLLDIVGVPVDSMPMRIPAEQFLT LRAYGAPPVIVALAAQGA FRGFMDT KTPLFAVVAGNLVNALLDAIFIFPLGLGVSGAALATVTSEYLTAFILLWKLNSKI VLFSWNIVSGDIIRYLKSGALLIARTIAVVL TFTVSTSLAAREGSVPMAGYEICLQ VWLTISLLNDALALAGQALLASEYAKGNYKKARIVLYRVLQIGGVTGAALSTTL LLGFGYLSMLFTDDAAVL DVAQTGVWFVTVSQPINAVAFVMDGLYYGVSDFA FVAYSTLFAGAISSAVLLVAAPKFGLGGVWAGLTLFMSLR AIAGFWRLGSKGGP WKIIWSETE MERPGDEHDDCRTAPLLEPKHAHGEGSNNDKQEEDEEEV GSLGPRVLVESKK LWVVAGPSICARFSTFGVTVISQAFIGHIGATELAGYALVSTVLMRFSGGILLGM ASALETLCGQSYGAKQYHMLGIYLQRSWIVLLCCAVLLLPIYLF TTPLLIFLGQD PKIAAMAGTISLWYIPVMISNVGNFTLQMYLQAQSKNMIVTYLAMLNLGLHLF LSWLLTVQFHLGLAGVMGSMVIAIWIPVFGQLAFVFFGGCPLTW TGFSSAAFT ELGAIVKLSLSSGVMLCVELWYNTILVLLTGYMKNAEIALDAL SICLNINGWEM MISIGFLSATGVRVANELGAGSARRAKFAIFNVVTT SFSIGFMLFVLFLIFRGRLA YIFTESKVVADAVAELSPLLA FSILLNSIQPVLSGVAVGSGWQSVVAYVNVTSYY LFGIPIGVILGYVLGFQVKGIWIGMLLGTLVQTIVLLFITLRTDWEKQVEIARQRL NRWSMDENGRQQNPGENP MEELKLMRRLCLPISALNLLHYVKSMVTVLCLGRLGRAELAGGALAVGLTNVT GYSVLSGLALGLEPLAGQAFGSGTGRTRSRPRRALRRAVLLLLAASFPVAALWA CAGPAARAARQDAAVARAAGSYCRYAIPDLAAA SVLLPARVYLRSKGETRRL ASCAALAVALVHAPATAYLGARLRVPGVAMAA CMTSFATLAFLWISLTWAPA QNEPDEPADLEEWAGVGQWAEWADLLRLSLPSCLSVCLEWWYELMTIAAG YLRDPHTALATAAIVIQTTSLLYTIPVTLS SAVSTRVANELGAGRPRSAQVSFVV AMGIAMMGSCVGLTWTTFGRGLWVQVFTTDPTIQSLTTSVLPVIGLCELANCP QTTGCGVLRGSARPAVGAAINLYSFYLVGAPVALVLA FGLDMGFLGLCLGLLS AQVVCLISVGFATFQTDWEAEALKAFHLVGGGDEKCGDDLPC LAHKENV MAETSSARSPLLDVDESSGASEELLRREPVP RSVLSRLAAWEAGNLWRISWASIL ITLLSFTLSLVTQM FVGHLELELAGASITNIGIQGLAYGIMIGMASAVQTVCGQ
OsMA TE43	
OsMA TE44	
OsMA TE45	
OsMA TE46	

OsMA TE5	<p> AYGARKFRAMGIVCQRALVLQFATAIVIAFLYWYAGPFLRLIGQAADVAAAG QLYARGLVPQLLAFALFCPMQRFLQAQNIVNPVAYITMAVLIFHILISWLTVFVL GFGLLGAALTLSFSWWVLVALTWGLMVWTPACKETWTGLSVLAFRGLWG YA KLAFASAVMLALEIWYVQGFVLLTGFLPDPEIALDSLSICINYWNWDFQIMLGL SYAASIRVGNELGAGHPNVARFSVFVITASVAFSILATILVLVRLYPLSTLYTSST TVIEAVIKLTPLLSISIFLNGIQPILSGVAVGSGWQVVVAYVNVGAYYLIGLPICG VLGKYSLSGAAGIWWGLIIGVSVQTVALIITARTNWDNEVMKAIQRLRQTAVD DGTVPVDDIE MSAHLRLLSAAPLPALLPTRRLPAVPTPALAARAARLVLSRPLTEPQPPRLPRG AAARCRGVAVAGADGDEPAAAAAGTAGLWEQVRDIVVFAGPALGLWICGPL MSLIDTMVIGQTSSLQLAALGPGTVFCDYLCYIFMFLSIATSNMVATSLAKKDEE LAQHQVSMMLLFVALTCGLGMFLFTKLFGTQVLTFTGSGNYDIISAANTY AQIR GFAWPAVLVGLVAQSASLGMKDSWGPKALAAASVINGVGDLLCSVCGYGI AGAAWATMVSQIVAAFMMMQLNLKRGFRAFSTIPSSSELLQIFEIAAPVFITM TSKVAFYALLTYSATSMGAILAAHQVMVNVLCMCTVWGEPLSQT AQSFMP LIYGAKCNLMKARMLLKSVMIGAITGTTVGAVGTLVPWLPFSLFTNDFMVVQ QMHKVLIPYFCALLVTPSVHSLEGTLLAGRDLRFLSQSMGACFGIGTFLLMV MSSPRRDGRGAVDDLTA SL LHKGDGGEAVFVVVVVPPVAEEEEPPPVLTCKPP GRFARAVKEAWSVPFPMMPMSMSAGAAAGAEARSILGLALPMLTGLLLYL RSMIS MLFLGRGLGGLALAGGSLAIGFANITGYSVLSGLAMGMEPICGQAFGAGHYDLL GVTMQRVTLLLVAASVPIAGLWVHMRPLLLLCGQDAAIAAVAETYILASLPDL LLQAFLHPVRIYLRTQSINLPLTVCAALAIALHLPINYVAVSVLGLGIKGV ALAS VLANLNLVLF LFGYIWFKGVHKRTGGFALSADCLRGWGELVSLALPSCISVCLE WWWYEIMILLCGLLANPQATVASMGILIQTTSLIYFPSSLGFGVSTRVSNELGA NRPERACRAATVGLMLGFAFGGVASAFACHVRGAWATMFTADPAIVALTAS VLPILGACELGNCPQTTGCGVL RGSARPKDAASINLRSFYLVGTPVALILAFWY HYDFRGLWLGLLAAQATCVVRMLLVIGETDWTAEAKRAQQLTGAADIKDCG GKGDHVAVIEQPDEQC MAYTEPLLLSARHTTQTSPRHLLRSRHAAAAAADGRMVVAVQDDET GALV AAVGKGDEDDDDDDDAVAGEEDEDEDDAPVVRTARGAWEVFAAESRRLWAI GAPIAFNVICLYGTNSTTQIFVGHIGNRELSAVAIGLSVVS NFSFGLLGMGSALE T LCGQAFGAGQVAM LGIYMQRSWIILAASAALLSPLYVFAGPILRLLGQEE SIA AAAGEFTVRIIPQMFALAINFPTQKFLQAQSKVTVLAWIGFAALLAHVGLLALF VSALGWGIAGAAAAYDVSSWLTALAQVAYVVGWCRDGWTGLSRKAFNELW AFVKLSLASAVMLCLEIWYMMVLVVL TGHLD DAEIAVDSSISICMNINGWEGML FIGLNAAISVRVSNELGSGRPRATMHAVVVVLVQSLAFGLLAMVLILATR NHF AVIFTGDRHLQKAVANIAYMLAVTMVLNSIQPVW RSAADGREWWRTLIWRVT TASASLSASYLATSSDGV MGDGRGDEEECRVALLNGGGAKEGWQVVSGDGKLR RRVWEESRKLWVIV APAIFSRVVTYSMNVITQAFAGHLGDLELAAISIAN TVVVG FNFGLMLGMASAL ETLCGQAFGAKKYHMMGVYMQRSWIVLLACAVLLLPMYIYAEDVLLLTGQPP ELSAMAGRVSVWFIPLHLSFAFLFPLQRFLQCQMKNFASAAASGVALCVHVAIS WLLVSRFRFGLVGIALTLNFSWWATAAMLFA YVACGGCPETWNGLSLEAFAG CHAMLLTEFVCLICSLENWYYRILILLTGNLKNAAIAVDALSICMTINAWELMIP </p>
OsMA TE6	
OsMA TE7	
OsMA TE8	

OsMA TE9	LAFFAGTGVRVANELGAGNGKGARFATIVSSVTSLVIGLFFWVLIVGLHDKFAL IFTSSDVVLDAVDNLSVLLAFTILLNSIQPVLSGVAVGSGWQSMVAYVNIGTYYL IGIPMGILLGWLFLKGLVLIWAGMIGGTAVQTLILAIITIRCDWDKEAMIASTRM DKWSQVR MAGLKKMEEVTAAAAAVAASSTAEEKRAAAVVVPDAALTMNGAAGAEKTA AAAAAPEDLPAPAALSGWPRRVGLYLFVMNIRSVFKLDELGSEVLRIAVPASLA LAADPLASLVDTAFIGRLGSVEIAAVGVSAIFNQVSKVCIYPLVSVTTSFVAEED AIISKCIEENSSQDLEKASPVDSETNNLPVSGPDKVECVNSCIPTECTNPSDQGCK RKYIPSVTSAVIVGSFLGLLQAVFLVFSAKFVLNIMGVKNDSPLMRPAVRYLTIRS LGAPAVLLSLAMQGVFRGFKDTKTPLYATVVGDAANIILDPILMFVCHMGVTG AAVAHVISQYLITMILLCRLIRQVDVIPPSTLSLKFGRFLGCGFLLLARVAVTFC VTASSLAARHGPTIMAAFQICQQLWLATSLADGLAVAGQAVLASAFKND KGKVVVATSRVLQLSIVLGMGLTVVLGVGMKFGAGIFTKDIDVIDVIHKGIPFV AGTQTINSLAFVFDGINFGASDYTYSAYSMVGVAAISIPCLVYLSAHNGFIGIWI ALTIYMSLRRTIASTWRMGAARGPWVFLRK

Table S4. The primers used in this study

Name	Primer sequence
Primers for Gene cloning and Construction of expression vector	
GmMATE13-F	5'-ATGATGCCCTTTTGATGTTAT-3'
GmMATE13-R	5'-CTAAAGCCCAACATTGTTTACC-3'
GmMATE75-F	5'-ATGGACGAGAATAGAAGTTCCAAC-3'
GmMATE75-R	5'-TCACTAAGGCAGTGAGCGACCTC-3'
Primers for qRT-PCR in tamba black soybean	
q18S rRNA-F	5'-ATGATAACTCGACGGATCGC-3'
q18S rRNA-R	5'-CTTGGATGTGGTAGCCGTTT-3'
qGmMATE13-F	5'-CTCCCTACTACTCTGGCTTTGGC-3'
qGmMATE13-F	5'-TTGTTTCATCAGCAGCATCTTCC-3'
qGmMATE75-F	CCAACGAACCCAACAAGTGG
qGmMATE75-R	CCGGTCCTAAACGGCCTATG
Primers for subcellular localization	
GmMATE13-F-XbaI	5'-GCTCTAGAATGATGCCCTTTTGATGTTAT-3'
GmMATE13-R-SmaI	5'-TCCCCCGGGAAGCCCAACATTGTTTACC-3'
GmMATE75-F-XbaI	5'-GCTCTAGAATGGACGAGAATAGAAGTTCCAAC-3'
GmMATE75-R-SmaI	5'-TCCCCCGGGCTAAGGCAGTGAGCGACCTC-3'