Supplementary Table 1. Soybean pulvinus proteins as identified by LC-MS/MS and Scaffold analysis program. The MS/MS spectra were examined against the UniProt database in order to retrieve GO terms for functional analysis. Fifty-five proteins had names; a further 116 proteins initially identified as "uncharacterized" were named using UniRef cluster homology and 24 proteins remained uncharacterized even at the 50% homology level.

Identified Proteins	Gel Spot(s)	UniProtKB	MW	Gene	GO Term(s)		
40S ribosomal protein S12	178	C6SVV7	15 kDa	Gma.54991	GO:0006412		
Alpha-form rubisco activase	40	D4N5G0	52 kDa	RCAalpha	GO:0010150	GO:0009753	
Aminomethyltransferase	49	I1KNF5	44 kDa	Gma.2009	GO:0006546		
Annexin	110	C6TFT8	36 kDa	Gma.6613			
ATP synthase subunit alpha, chloroplastic	22	Q2PMS8	56 kDa	atpA	GO:0015991	GO:0015986	
ATP synthase subunit alpha, mitochondrial	17	Q01915	55 kDa	ATPA	GO:0015991	GO:0015986	
ATP synthase subunit beta	26, 28, 29	I1NFS4	60 kDa	Gma.1312	GO:0015991	GO:0015986	
ATP synthase subunit beta	26	I1LEP2	59 kDa		GO:0015991	GO:0015986	
ATP synthase subunit beta, chloroplastic	29	Q2PMV0	54 kDa	atpB	GO:0015991	GO:0015986	
Beta-amylase	15, 16, 17, 28, 29, 30, 51, 62	P10538	56 kDa	BMY1	GO:0000272		
Betaine aldehyde dehydrogenase	10	B0M1A6	55 kDa	Gma.1571	GO:0009737	GO:0009651	GO:0009414
Cysteine synthase	96	C6TMX6	34 kDa	Gma.50149	GO:0006535		
Cytochrome b6-f complex iron-sulfur subunit	166	I1LUB3	24 kDa		GO:0022900	GO:0015979	
Elongation factor 1-alpha	16, 19, 20, 23, 25, 27, 39, 45	P25698	49 kDa	TEFS1	GO:0006184		
Ferritin	147	C6TI81	28 kDa	Gma.30035	GO:0006879	GO:0006826	
Fructose-bisphosphate aldolase	85, 97	I1JSJ3	43 kDa	Gma.55167	GO:0006096		
Glucose-1-phosphate adenylyltransferase	42, 44	I1M6B5	55 kDa		GO:0005978		
Glutamine synthetase	63	C6T8F0	39 kDa	Gma.32852	GO:0006542	GO:0006807	
Glutamine synthetase	67	I1MZF3	39 kDa	Gma.34078	GO:0006542	GO:0006807	
Glutamine synthetase	67, 68, 80	Q9FUK4	39 kDa	Gma.57937	GO:0006542	GO:0006807	
Glutamine synthetase	57, 72	I1M170	48 kDa		GO:0006542	GO:0006807	
Glutathione peroxidase	167	I1KP94	25 kDa	Gma.2160	GO:0006979		

Glycinin G1	75	P04776	56 kDa	GY1			
In2-1 protein	128, 137	Q9FQ95	27 kDa	Gma.13691			
Late-embryogenesis abundant protein 1	74, 75, 90, 91	C6TLT7	36 kDa	LEA-1	GO:0009269		
Late-embryogenesis abundant protein 2	90, 91	C6T750	34 kDa	LEA-2	GO:0009269		
Malate dehydrogenase	84, 85	I1JB84	33 kDa	Gma.2876	GO:0044262	GO:0006108	GO:0006099
Malate dehydrogenase	83, 84, 85, 87	H2D5S3	35 kDa	Gma.44441	GO:0044262	GO:0006108	GO:0006099
Malate dehydrogenase	83, 84, 85, 87	Q9SPB8	36 kDa	Mdh1	GO:0044262	GO:0006108	GO:0006099
Malic enzyme	13	I1JMI9	69 kDa	Gma.40835	GO:0006108		
Nucleoside diphosphate kinase	181	I1KJI7	17 kDa	Gma.1449	GO:0006241	GO:0006183	GO:0006228
Phosphoglycerate kinase	71, 82	I1MJC6	39 kDa	Gma.34268	GO:0006096		
Phosphoribulokinase	61	I1L540	45 kDa	Gma.55320	GO:0005975		
Phosphoribulokinase	61	I1J4L6	45 kDa		GO:0005975		
Profilin	183	A7XZJ7	14 kDa	Gma.32917	GO:0030036		
Proteasome subunit alpha type	138, 140	C6TH59	26 kDa	Gma.2259	GO:0006511		
Proteasome subunit alpha type	93	I1L3S2	31 kDa		GO:0006511		
Proteasome subunit beta type	144	I1JJI4	29 kDa	Gma.57932	GO:0051603		
Protein disulfide isomerase L-3b	7	C6KXH6	59 kDa	PDIL-3b	GO:0045454		
Ribulose bisphosphate carboxylase large chain	3, 16, 17, 18, 19, 23, 30, 32, 38, 39	P27066	53 kDa	rbcL	GO:0009853	GO:0019253	
Rubisco activase	40, 41, 51, 52, 64, 66	D4N5G3	49 kDa	RCA11	GO:0010150	GO:0009753	
S-adenosylmethionine synthase	46, 47, 58, 59, 60	I1MHR0	43 kDa	Gma.51643	GO:0006730	GO:0006556	
S-adenosylmethionine synthase	59, 60	I1KMK1	43 kDa	Gma.54660	GO:0006730	GO:0006556	
S-adenosylmethionine synthase	47	I1JQV8	43 kDa	Gma.55102	GO:0006730	GO:0006556	
Serine hydroxymethyltransferase	19	I1K3S6	45 kDa		GO:0006544	GO:0006563	GO:0006730
SGT1-2	53	B6EBD5	41 kDa	Gma.4629			

Stem 31 kDa glycoprotein	135, 142, 143	P10743	29 kDa	VSPB	
Sulfurtransferase	102, 104	I1KTY9	42 kDa		
Superoxide dismutase [Cu-Zn]	179	I1JRI7	15 kDa		GO:0006801
Superoxide dismutase [Cu-Zn]	173	I1LKZ3	21 kDa		GO:0006801
Superoxide dismutase	139	I1LCI3	28 kDa	Gma.16827	GO:0006801
Triosephosphate isomerase (Fragment)	141, 144	I1M4W9	27 kDa		
Triosephosphate isomerase	140	I1NAD0	33 kDa	Gma.56055	
Triosephosphate isomerase	140	C6TK33	33 kDa	Gma.56433	
Triosephosphate isomerase	138, 140	C6T7V6	33 kDa	Gma.6904	

Proteins identified by UniRef

Cluster Name	Gel spot(s)	UniProtKB	UniRef ID	MW	Gene	GO Terms	
(+)-pulegone reductase	88	C6TIQ5	UniRef50_Q6WAU0	38 kDa	Gma.8065		
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	146	I1LE06	UniRef50_Q9BV57	26 kDa	Gma.56164		
20 kDa chaperonin, chloroplastic	148, 149	C6TJG0	UniRef50_Q02073	27 kDa	Gma.10871	GO:0006457	
26S protease regulatory subunit 6A homolog A	36, 37	I1LBA2	UniRef90_Q9SEI2	47 kDa		GO:0030163	
26S protease regulatory subunit 6B homolog	43, 45, 47	I1MZN7	UniRef90_Q9SEI4	47 kDa	Gma.1686	GO:0030163	
2-Cys peroxiredoxin BAS1-like, chloroplastic	145	I1JQ73	UniRef50_Q9C5R8	24 kDa			
3-oxo-Delta(4,5)-steroid 5-beta-reductase	37	I1K843	UniRef50_Q9STX2	44 kDa	Gma.4849		
40S ribosomal protein S19-like protein	182	C6SVR8	UniRef50_G7IYM0	16 kDa	Gma.54683	GO:0006412	
60S acidic ribosomal protein P0	93, 95	C6TGA6	UniRef90_P50346	34 kDa	Gma.8646	GO:0042254	GO:0006414
60S ribosomal protein L23	182	C6T0H9	UniRef90_P49690	15 kDa	Gma.54799	GO:0006412	
Acid phosphatase-like protein	123	I1KJR7	UniRef50_Q9SW12	28 kDa	Gma.16109		
Actin	53, 55	I1MDT4	UniRef100_G7IL85	42 kDa	Gma.56363		
Actin depolymerizing factor 1	180	C6SYJ7	UniRef90_A9P876	16 kDa	Gma.54636		
Actin-11	53, 55, 57	I1JY56	UniRef90_P53496	42 kDa			
Actin-11	55	I1M4W2	UniRef90_P53496	42 kDa			

Alanine aminotransferase 2	45	I1J547	UniRef90_A8IKE5	54 kDa		GO:0009058	
Allantoinase	134, 135	I1M261	UniRef50_G7IP08	57 kDa		GO:0000256	
Alpha-form rubisco activase	41	I1M841	UniRef90_D4N5G0	52 kDa	Gma.10987		
Alpha-form rubisco activase	66	I1MZA9	UniRef90_D4N5G0	47 kDa			
Apyrase 2	33, 91	I1ML46	UniRef50_Q9SPM5	50 kDa	Gma.33771		
Argininosuccinate synthase, chloroplastic	45	I1K099	UniRef50_Q9SZX3	52 kDa	Gma.55729	GO:0006526	
Aspartic proteinase	33	I1LAZ3	UniRef50_O04057	57 kDa	Gma.42568	GO:0006629	GO:0006508
AT5g63860/MGI19_6	46	I1JXY7	UniRef50_Q9FN03	47 kDa			
ATP synthase subunit d, mitochondria	161, 162	C6SZJ2	UniRef50_Q9FT52	20 kDa	Gma.54629	GO:0015986	
ATP synthase subunit d, mitochondria	162	C6SYC1	UniRef50_Q9FT52	20 kDa		GO:0015986	
Caffeic acid 3-O-methyltransferase	68	C6TIJ7	UniRef50_O23760	40 kDa	Gma.54887	GO:0032259	
Caffeoyl-CoA O-methyltransferase	131	I1JE07	UniRef90_Q40313	37 kDa			
Chaperonin CPN60-1, mitochondrial	10	I1LCI1	UniRef90_Q05045	61 kDa		GO:0042026	
Chlorophyll a-b binding protein 21, chloroplastic	124	C6TNE6	UniRef90_P27493	28 kDa	Gma.25185	GO:0009765	
Chlorophyll a-b binding protein 6, chloroplastic	154, 155	I1JCY0	UniRef50_Q01667	27 kDa	Gma.32962		
Chloroplast HSP70	24	I1MJU7	UniRef90_A2TJV6	74 kDa	Gma.31188	GO:0006457	
Cystatin (Fragment)	105	I1M778	UniRef50_P25973	23 kDa	Gma.3314		
Cysteine proteinase RD19a	118	I1MC68	UniRef50_P43296	40 kDa	Gma.55946	GO:0006508	
Cysteine proteinase RD21a	122	I1M8Q5	UniRef50_P43297	51 kDa		GO:0006508	
Cytochrome c oxidase subunit 5b-2, mitochondrial	182	C6TAW8	UniRef50_Q9SSB8	18 kDa	Gma.30782		
Cytosolic ascorbate peroxidase 1	126, 129, 130	I1LKA6	UniRef90_Q76LA8	27 kDa	Gma.1246	GO:0006979	
D-3-phosphoglycerate dehydrogenase	6	I1NFX7	UniRef50_G3C901	63 kDa	Gma.35523	GO:0006564	
DEAD-box ATP-dependent RNA helicase 15	46	I1JUD5	UniRef90_Q56XG6	48 kDa	Gma.2609		
Dihydroflavonol reductase	106, 107	I1LLS1	UniRef90_B0LVF3	30 kDa	Gma.37094	GO:0044237	
Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial	29	I1KH71	UniRef50_Q5M729	59 kDa		GO:0006090	
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	60	I1JJB5	UniRef50_Q8H107	50 kDa		GO:0006099	
Disease resistance response protein 1	164	C6SX05	UniRef100_E0YNQ4	21 kDa			

Elicitor-inducible protein EIG-J7	169	I1LNL7	UniRef50_G7J3U5	20 kDa	Gma.5756		
Enolase 2	29	I1JPW5	UniRef90_Q9LEI9	48 kDa	Gma.31115	GO:0006096	
Eukaryotic initiation factor 4A-1	42, 44	I1KUR0	UniRef90_P41376	48 kDa	Gma.31208		
Eukaryotic initiation factor 4A-1	42, 44	I1L1K7	UniRef90_P41376	47 kDa	Gma.6107		
FAM10 family protein At4g22670	39	I1MUT2	UniRef50_Q93YR3	44 kDa			
Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic	108	I1JCG8	UniRef50_Q8W493	40 kDa			
Fructokinase-2	95	I1M561	UniRef50_A2YQL4	35 kDa	Gma.5886	GO:0006014	
Fumarylacetoacetase	72	I1KZY9	UniRef50_P16930	46 kDa	Gma.2794	GO:0009072	
Glutathione S-transferase DHAR3, chloroplastic	150	I1NJ59	UniRef50_Q8LE52	23 kDa	Gma.30056		
Glutathione S-transferase GST	141	I1KK66	UniRef50_G7L5M2	26 kDa	Gma.33740		
Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (Fragment)	74, 75, 76, 77, 83, 84	I1JXG9	UniRef90_P09094	37 kDa	Gma.41848	GO:0006006	
Glycosyl hydrolase family 18 protein	35	I1MKL0	UniRef50_Q9M159	48 kDa	Gma.2559		
Heat shock 70 kDa protein (Fragment)	1, 3	I1JPC5	UniRef50_P81672	68 kDa	Gma.58383		
Heat shock 70 kDa protein 3	1, 3	I1LQR4	UniRef90_O65719	71 kDa	Gma.51582		
Heat shock 70 kDa protein 3	3	I1N557	UniRef90_O65719	71 kDa			
Heat shock 70 kDa protein, mitochondrial	4, 12	I1M2K9	UniRef90_P37900	72 kDa	Gma.28256	GO:0006457	
Heat shock 70 kDa protein, mitochondrial	4	I1KL72	UniRef90_P37900	72 kDa		GO:0006457	
Heat shock 70 kDa protein, mitochondrial	4	I1ME25	UniRef90_P37900	72 kDa		GO:0006457	
Hydroxyacylglutathione hydrolase, mitochondrial	133	I1MB50	UniRef50_Q16775	29 kDa	Gma.6651		
Inositol-3-phosphate synthase 1	31	I1K4L3	UniRef50_Q9JHU9	56 kDa	Gma.31628	GO:0006021	GO:0008654
Isoflavone reductase homolog 2	98, 99	I1JSN3	UniRef90_Q9SDZ0	28 kDa	Gma.1950		
Lactoylglutathione lyase	116	I1KND9	UniRef50_P44638	27 kDa	Gma.37335		
L-ascorbate peroxidase T, chloroplastic	115, 117	I1JZ45	UniRef50_Q42593	45 kDa		GO:0006979	
Malate dehydrogenase [NADP], chloroplastic	70	I1LCM5	UniRef90_P21528	46 kDa	Gma.55222	GO:0005975	GO:0006108
Mediator of RNA polymerase II transcription subunit 37a	1	I1K668	UniRef90_Q9LKR3	73 kDa	Gma.34300		
Methyl binding domain protein	48	I1JWB8	UniRef50_G7JE44	32 kDa	Gma.1196		
MLP-like protein	171	C6SZA9	UniRef50_B7FKA0	17 kDa	Gma.31695	GO:0006952	GO:0009607
MLP-like protein	170, 171	C6SYW1	UniRef50_B7FKA0	17 kDa	Gma.57049	GO:0006952	GO:0009607

NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	136	C6TIE6	UniRef50_O22769	28 kDa			
Oxygen-evolving enhancer protein 1, chloroplastic	111, 112, 113	I1MNK0	UniRef90_P14226	35 kDa	Gma.55000	GO:0015979	GO:0042549
Oxygen-evolving enhancer protein 2-1, chloroplastic	153	I1JJ05	UniRef50_Q42029	28 kDa	Gma.55126	GO:0015979	
Oxygen-evolving enhancer protein 2-1, chloroplastic	152	I1N123	UniRef50_Q42029	28 kDa	Gma.55221	GO:0015979	
Peroxiredoxin	174, 176	C6SWE0	UniRef90_B3GV28	17 kDa	Gma.54780	GO:0055114	
Phosphoglycerate mutase	6, 14	I1L6W0	UniRef50_D8TI51	61 kDa	Gma.48063	GO:0006007	
Probable mitochondrial-processing peptidase subunit alpha-2	43	I1KGH6	UniRef50_O04308	54 kDa	Gma.10742	GO:0006508	
Probable mitochondrial-processing peptidase subunit alpha-2	23, 43	I1KPV1	UniRef50_O04308	55 kDa		GO:0006508	
Probable nucleoredoxin 1-2	2	I1KXE7	UniRef50_Q7Y0F2	64 kDa	Gma.11948	GO:0045454	
Protein disulfide isomerase-like 1-1	7, 8, 68	I1KAB7	UniRef50_Q53LQ0	56 kDa	Gma.10984	GO:0045454	GO:0006662
Protein disulfide isomerase-like 1-1	8	I1JZ42	UniRef50_Q53LQ0	48 kDa		GO:0045454	GO:0006662
Putative DNA repair protein RAD23-3	48	C6TIN6	UniRef50_Q84L31	41 kDa	Gma.55970	GO:0006289	GO:0043161
Putative DNA repair protein RAD23-3	34, 48	I1LEX5	UniRef50_Q84L31	43 kDa		GO:0006289	GO:0043161
Putative RNA-binding protein rbpA	172	I1LJC9	UniRef50_Q44560	16 kDa	Gma.41300		
Pyruvate dehydrogenase, putative	79	C6T827	UniRef90_B9RFW4	39 kDa	Gma.54725		
Pyruvate dehydrogenase, putative	79	I1JJD2	UniRef90_B9RFW4	39 kDa			
Quinone oxidoreductase-like protein At1g23740, chloroplastic	89	I1MLW9	UniRef50_Q9ZUC1	35 kDa	Gma.3654		
Quinone oxidoreductase-like protein At1g23740, chloroplastic	89	I1N5R5	UniRef50_Q9ZUC1	34 kDa			
RuBisCO large subunit-binding protein subunit alpha, chloroplastic (Fragment)	7	I1LL25	UniRef90_P85903	62 kDa	Gma.10732	GO:0042026	
RuBisCO large subunit-binding protein subunit alpha, chloroplastic (Fragment)	7, 8	I1LR60	UniRef90_P85903	62 kDa		GO:0042026	
RuBisCO large subunit-binding protein subunit beta, chloroplastic	9, 10, 11	I1MJ28	UniRef90_P08927	63 kDa		GO:0042026	
Sedoheptulose-1,7-bisphosphatase, chloroplastic	75, 76, 77	I1LMN5	UniRef50_P46284	42 kDa	Gma.2026	GO:0005975	
Sedoheptulose-1,7-bisphosphatase, chloroplastic	77	I1MZ53	UniRef50_P46284	42 kDa		GO:0005975	
Serpin-ZX	63	I1K7W5	UniRef50_Q9S7T8	43 kDa			
SGT1-2	53	I1MPF6	UniRef90_B6EBD5	40 kDa			
SHOOT1 protein	93	I1K480	UniRef90_Q9AT39	38 kDa			
Soluble inorganic pyrophosphatase	141	C6SYN5	UniRef90_G7KEZ5	24 kDa	Gma.51876	GO:0006796	
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	65	I1L8G3	UniRef50_O82662	45 kDa	Gma.54773		

Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	65	I1LYN0	UniRef50_O82662	45 kDa	Gma.57093		
Transaldolase (Fragments)	50	I1KZJ0	UniRef50_P86071	48 kDa	Gma.54889	GO:0006098	
Translationally-controlled tumor protein homolog	158	I1L0Z3	UniRef90_Q944T2	15 kDa	Gma.55531		
Trypsin inhibitor A	145	I1KYX1	UniRef50_P01070	23 kDa	Gma.1048	GO:0010951	
Tubulin A	24, 25, 27, 39, 43	I1K3X9	UniRef100_Q2TFP2	50 kDa	Gma.58392	GO:0007018	GO:0051258
Tubulin alpha-2 chain	24	I1JV03	UniRef90_B9DGT7	50 kDa	Gma.55053	GO:0007018	GO:0051258
Tubulin alpha-6 chain	24, 27	I1K2I1	UniRef90_P29511	50 kDa	Gma.58389	GO:0007018	GO:0051258
Tubulin beta-2 chain	18, 19, 20, 21, 38	I1JT28	UniRef90_Q56YW9	51 kDa	Gma.34151	GO:0007018	GO:0051258
Tubulin beta-2 chain	38, 39	I1KPA1	UniRef90_Q56YW9	50 kDa	Gma.35057	GO:0007018	GO:0051258
Tubulin beta-2 chain	21	I1J752	UniRef90_Q56YW9	51 kDa	Gma.57130	GO:0007018	GO:0051258
Tubulin beta-2 chain	19	I1LDR2	UniRef90_Q56YW9	50 kDa	Gma.6303	GO:0007018	GO:0051258
Tubulin beta-2 chain	19, 21, 38	I1K2Y0	UniRef90_Q56YW9	50 kDa		GO:0007018	GO:0051258
Uncharacterized protein At5g39570	15, 16, 17	I1N675	UniRef50_Q9FKA5	41 kDa	Gma.25034		
Uncharacterized protein At5g39570	17	I1LWM2	UniRef50_Q9FKA5	43 kDa	Gma.48834		
UTP--glucose-1-phosphate uridylyltransferase	23, 25, 27, 28	I1MBR7	UniRef90_Q9LKG7	51 kDa	Gma.56729		
V-type proton ATPase catalytic subunit A	5, 6	I1KVU0	UniRef90_O23654	69 kDa	Gma.1434	GO:0015991	
V-type proton ATPase subunit B2	20, 21	I1L655	UniRef90_Q9SZN1	54 kDa		GO:0015991	
V-type proton ATPase subunit E3	119, 120	I1KPH2	UniRef50_P0CAN7	27 kDa	Gma.49394	GO:0015991	

Unknown or uncharacterized proteins

UniProt Protein Name	**Gel spot(s)**	**UniProtKB**	**MW**	**Gene**	**GO Term(s)**
Uncharacterized protein (Fragment)	96	I1JPE6	45 kDa		GO:0009089
Uncharacterized protein	157	I1KJH7	21 kDa	Gma.11258	GO:0015986
Uncharacterized protein	17	C6TGU6	45 kDa	Gma.13206	GO:0006886
Uncharacterized protein	43	I1L281	59 kDa	Gma.13759	GO:0005975
Uncharacterized protein	95	I1JN31	55 kDa	Gma.14675	GO:0006508

Uncharacterized protein	69, 82	I1JEI0	44 kDa	Gma.2190	GO:0007047	GO:0030244
Uncharacterized protein	49, 51, 61, 63, 65, 67, 68, 86	I1JGY9	49 kDa	Gma.24854	GO:0006508	
Uncharacterized protein	30	I1N7G4	61 kDa	Gma.27992	GO:0006508	
Uncharacterized protein	132	C6THR8	36 kDa	Gma.31275		
Uncharacterized protein	163	C6SVX3	18 kDa	Gma.31311	GO:0006950	
Uncharacterized protein	51	C6T9R1	42 kDa	Gma.32429	GO:0006629	
Uncharacterized protein	138	I1LU40	26 kDa	Gma.3521		
Uncharacterized protein	106, 107	I1LLS2	28 kDa	Gma.37094	GO:0044237	
Uncharacterized protein	165	I1JHP9	23 kDa	Gma.3898	GO:0008152	
Uncharacterized protein	86	I1KAJ5	37 kDa	Gma.55012		
Uncharacterized protein	160	C6T2Y2	19 kDa	Gma.6437	GO:0022904	
Uncharacterized protein	78	I1LZ92	38 kDa	Gma.6545	GO:0006167	GO:0006166
Uncharacterized protein	76	I1L340	30 kDa	Gma.9083		
Uncharacterized protein	55	C6TKV3	46 kDa		GO:0006222	
Uncharacterized protein	68, 69, 81	I1JBH8	40 kDa		GO:0045454	GO:0006662
Uncharacterized protein	156	I1JML1	21 kDa		GO:0015986	
Uncharacterized protein	130	I1K4S0	28 kDa			
Uncharacterized protein	50	I1KYR2	40 kDa		GO:0006508	
Uncharacterized protein	95	I1JVA6	33 kDa			

Supplementary Table 2. The eight most significant biological GO processes as calculated by agriGO software. All eight process are the farthest along the GO map as was possible. The last four GO terms are intermediate terms which are not directly annotated with the proteins but are upstream of the annotated terms.

Child GO Term	Process	Identified Proteins	Gel Spot(s)	UniProtKB	E-value
GO:0015991	*ATP hydrolysis coupled proton transport*				2.74E-13
		V-type proton ATPase catalytic subunit A	5, 6	I1KVU0	
		V-type proton ATPase subunit B2	20, 21	I1L655	
		V-type proton ATPase subunit E3	119, 120	I1KPH2	
		ATP synthase subunit alpha, chloroplastic	22	Q2PMS8	
		ATP synthase subunit alpha, mitochondrial	17	Q01915	
		ATP synthase subunit beta	26, 28, 29	I1NFS4	
		ATP synthase subunit beta	26	I1LEP2	
		ATP synthase subunit beta, chloroplastic	29	Q2PMV0	
GO:0015986	*ATP synthesis coupled proton transport*				9.93E-08
		ATP synthase subunit alpha, chloroplastic	22	Q2PMS8	
		ATP synthase subunit alpha, mitochondrial	17	Q01915	
		ATP synthase subunit beta	26, 28, 29	I1NFS4	
		ATP synthase subunit beta	26	I1LEP2	
		ATP synthase subunit beta, chloroplastic	29	Q2PMV0	
		ATP synthase subunit d, mitochondria	161, 162	C6SZJ2	
		ATP synthase subunit d, mitochondria	162	C6SYC1	
		Uncharacterized protein	156	I1JML1	
		Uncharacterized protein	157	I1KJH7	
GO:0051258	*protein polymerization*				6.44E-06
		Tubulin A	24, 25, 27, 39, 43	I1K3X9	
		Tubulin alpha-2 chain	24	I1JV03	

		Tubulin alpha-6 chain	24, 27	I1K2I1	
		Tubulin beta-2 chain	18, 19, 20, 21, 38	I1JT28	
		Tubulin beta-2 chain	38, 39	I1KPA1	
		Tubulin beta-2 chain	21	I1J752	
		Tubulin beta-2 chain	19	I1LDR2	
		Tubulin beta-2 chain	19, 21, 38	I1K2Y0	
GO:0007018	*microtubule-based movement*				3.52E-05
		Tubulin A	24, 25, 27, 39, 43	I1K3X9	
		Tubulin alpha-2 chain	24	I1JV03	
		Tubulin alpha-6 chain	24, 27	I1K2I1	
		Tubulin beta-2 chain	18, 19, 20, 21, 38	I1JT28	
		Tubulin beta-2 chain	38, 39	I1KPA1	
		Tubulin beta-2 chain	21	I1J752	
		Tubulin beta-2 chain	19	I1LDR2	
		Tubulin beta-2 chain	19, 21, 38	I1K2Y0	
GO:0045454	*cell redox homeostasis*				1.29E-02
		Protein disulfide isomerase L-3b	7	C6KXH6	
		Probable nucleoredoxin 1-2	2	I1KXE7	
		Protein disulfide isomerase-like 1-1	7, 8, 68	I1KAB7	
		Protein disulfide isomerase-like 1-1	8	I1JZ42	
		Uncharacterized protein	68, 69, 81	I1JBH8	
GO:0006508	*proteolysis*				4.48E-02
		Aspartic proteinase	33	I1LAZ3	
		Cysteine proteinase RD19a	118	I1MC68	
		Cysteine proteinase RD21a	122	I1M8Q5	

		Probable mitochondrial-processing peptidase subunit alpha-2	43	I1KGH6	
		Probable mitochondrial-processing peptidase subunit alpha-2	23, 43	I1KPV1	
		Uncharacterized protein	95	I1JN31	
		Uncharacterized protein	30	I1N7G4	
		Uncharacterized protein	50	I1KYR2	
		Uncharacterized protein	49, 51, 61, 63, 65, 67, 68, 86	I1JGY9	
GO:0006457	*protein folding*				2.99E-03
		20 kDa chaperonin, chloroplastic	148, 149	C6TJG0	
		Chloroplast HSP70	24	I1MJU7	
		Heat shock 70 kDa protein, mitochondrial	4, 12	I1M2K9	
		Heat shock 70 kDa protein, mitochondrial	4	I1KL72	
		Heat shock 70 kDa protein, mitochondrial	4	I1ME25	
GO:0015979	*photosynthesis*				1.56E-02
		Cytochrome b6-f complex iron-sulfur subunit	166	I1LUB3	
		Oxygen-evolving enhancer protein 1, chloroplastic	111, 112, 113	I1MNK0	
		Oxygen-evolving enhancer protein 2-1, chloroplastic	153	I1JJ05	
		Oxygen-evolving enhancer protein 2-1, chloroplastic	152	I1N123	
GO:0006108	*malate metabolic process*				1.71E-05
		Malate dehydrogenase	84, 85	I1JB84	
		Malate dehydrogenase	83, 84, 85, 87	H2D5S3	
		Malate dehydrogenase	83, 84, 85, 87	Q9SPB8	
		Malic enzyme	13	I1JMI9	

	Malate dehydrogenase [NADP], chloroplastic	70	I1LCM5	
GO:0006007	*glucose catabolic process*			4.99E-02
	Phosphoglycerate mutase	6, 14	I1L6W0	
GO:0009119	*ribonucleoside metabolic process*			4.59E-04
GO:0009084	*glutamine family amino acid biosynthetic process*			1.91E-03
GO:0006119	*oxidative phosphorylation*			2.04E-06
GO:0045333	*cellular respiration*			8.18E-03