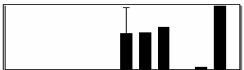
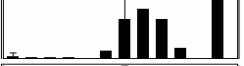
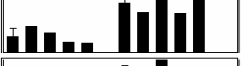
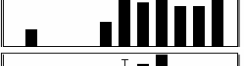
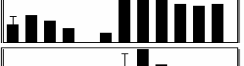
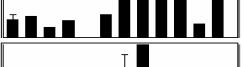
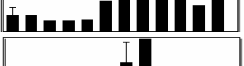
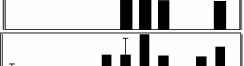
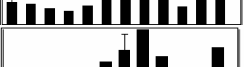

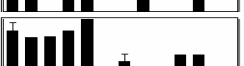

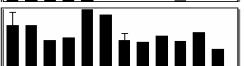
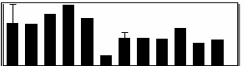
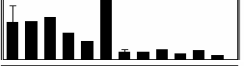
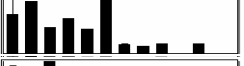


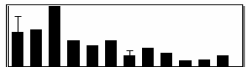
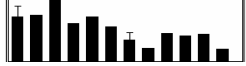
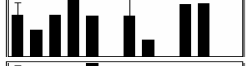
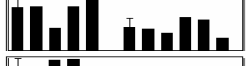
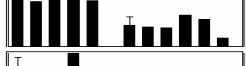
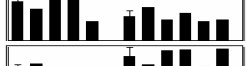
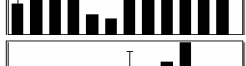

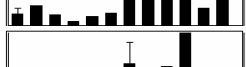
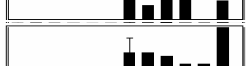




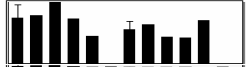
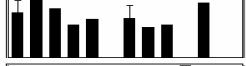




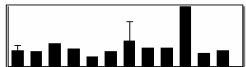
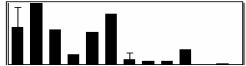
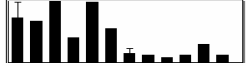
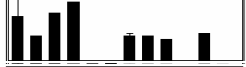

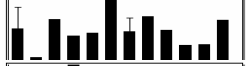
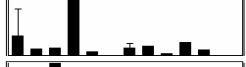
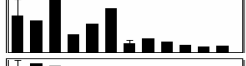
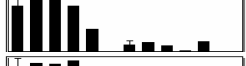
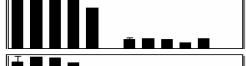
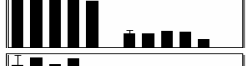
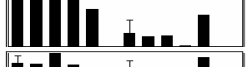
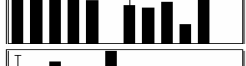





**Supplemental table 2.** Summary of identifications and quantifications obtained from the analysis of 2DE-IPG-PAGE for each protein spot that passed the criteria for reproducibility and that was used for quantification. Apparent molecular mass and pI for each spot are listed. Proteins were identified by peptide mass finger printing by MALDI-TOF MS and by nano-LC-ESI/MS and spectral data were searched against the maize assembled EST (unigene) collection (ZmGI, TIGR), maize genome (AZM, TIGR) and rice genome (OsGI2, TIGR). Mascot scores are indicated, number of matching peptides, the highest peptide score (if MS/MS) and experimental ambiguity are indicated and provide indications of the 'strength' of protein identification. Assigned protein names are based on TIGR annotations or based on information from BLAST searches against the predicted proteomes of rice and *A. thaliana*. Closest *A. thaliana* homologues can be found in Supplemental Table 1 or PPDB). Differential accumulation of proteins in BS and M chloroplast stroma is indicated by an averaged value as well as by a graphic representation. The graphs represents, from left to the right: M average spot volume (the standard deviation is indicated), normalized M spots volumes from 5 individual gels, BS averaged spot volume (the standard deviation is indicated), normalized BS spot volumes from 5 individual gels.

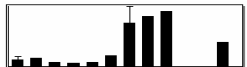
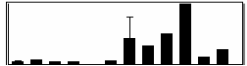
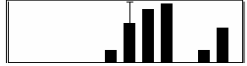
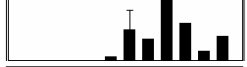
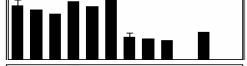
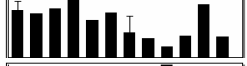
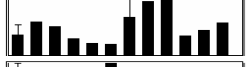
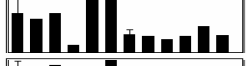
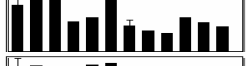
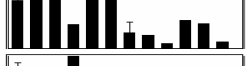
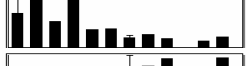
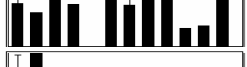



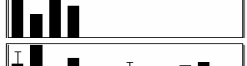


2-DE gel Spot	Exp. MW	Exp. pI	Accession Number (ZmGI)	Protein Name	Ratio (BS/M)	Spot volumes	Predicted MapMan BIN	Mascot	highest peptide (MS/MS)	Exp. ambiguity	AZM acc. #	Mascot	Exp. ambiguity	OsGI acces. #	OsGI name	Mascot
215	37	5.9	TC219223, TC219224	ferredoxin reductase (FNR1)	0.18		1.1 PS.lightreaction	84, 70	83		AZM4_11351, AZM4_11520	83		9630.m00037	Oxidoreductase NAD-binding domain, putative	128
206	38	5.9	TC219223 TC219224	ferredoxin reductase (FNR1)	0.48		1.1 PS.lightreaction	151,151,67,67	66,66	TC221973,TC219226,TC221973,TC219226	AZM4_11351, AZM4_91927	113, 92		9630.m00037, 9634.m00084	Oxidoreductase NAD-binding domain, putative, ferredoxin--nadh reductase, leaf isozyme, chloroplast precursor(ec	137, 89
290	26	6.5	TC235206, TC235205	oxygen evolving enhancer 2 (OEE2)	0.41		1.1.1 PS.lightreaction - Photosystem II	320, 166	72, 62		AZM4_102521	325		9635.m00415, 9635.m00416	PsbP	57
283	27	6.5	TC235206	oxygen evolving enhancer 2 (OEE2)	0.47		1.1.1 PS.lightreaction - Photosystem II	195	45		AZM4_102520	142		no ID		
294	26	6.2	TC235205	oxygen evolving enhancer 2 (OEE2)	0.50		1.1.1 PS.lightreaction - Photosystem II	228,68	69		AZM4_102521	234		no ID		
286	26	6.2	TC235206	oxygen evolving enhancer 2 (OEE2)	0.65		1.1.1 PS.lightreaction - Photosystem II	172	55		no ID			no ID		
355	15	5.8	TC238911	photosystem II protein W-like protein	0.72		1.1.1 PS.lightreaction - Photosystem II	97	65		AZM4_49819	133		9629.m07037	Photosystem II reaction centre W protein, PsbW, putative	65
292	26	6.3	TC226969	Thylakoid luminal 29.8 kDa protein (OEE2-like TL30)	0.53		1.1.1 PS.lightreaction - Photosystem II	132	57		AZM4_80708	114		no ID		
89	56	6.0	TC224055	ATP synthase beta chain (β-CF1)	0.59		1.1.4 PS.lightreaction - ATP synthase	82	41		AZM4_12435	80		9633.m03285, 9634.m03804, 9638.m01773, 9640.m00996	ATP synthase F1, beta subunit	57, 82, 82, 63
90	56	5.9	TC224055	ATP synthase beta chain (β-CF1)	0.65		1.1.4 PS.lightreaction - ATP synthase	68			no ID			no ID		
169	42	6.1	TC219359	Fructose-bisphosphate aldolase	1.44		1.3 PS.calvin cyle	345	75		AZM4_123619	317		9639.m00637	Fructose-bisphosphate aldolase class-I	147
209	37	6.1	TC219359	Fructose-bisphosphate aldolase	2.16		1.3 PS.calvin cyle	187	43		AZM4_123619	157		no ID		
194	39	6.1	TC219359	Fructose-bisphosphate aldolase	2.47		1.3 PS calvin cyle	355	70		AZM4_123619	325		9639.m00637	Fructose-bisphosphate aldolase class-I	155
433	37	6.2	TC219359	Fructose-bisphosphate aldolase	3.31		1.3 PS.calvin cyle	102			no ID			9639.m00637, 9639.m00638	Fructose-bisphosphate aldolase class-I	52, 42
757	39	6.2	TC219359	Fructose-bisphosphate aldolase	3.42		1.3 PS.calvin cyle	103			no ID			no ID		

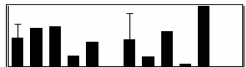
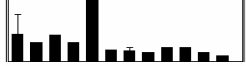
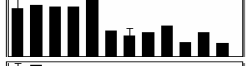
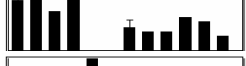
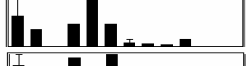

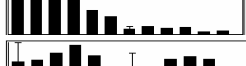


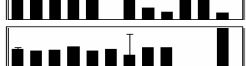
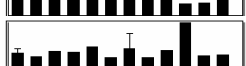
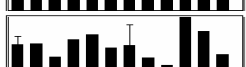
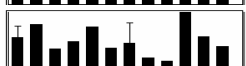
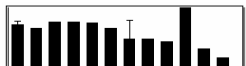
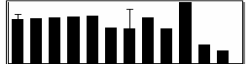
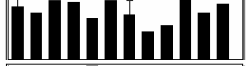
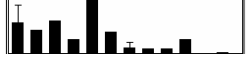

187	40	5.9	TC219361	Fructose-bisphosphate aldolase	10.00		1.3 PS. calvin cyle	216	59	AZM4_103212	182	9639.m00637, 9639.m00638	Fructose-bisphosphate aldolase class-I, Fructose-bisphosphate aldolase class-I	47, 47
220	36	6.6	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	1.88		1.3 PS. calvin cyle	103		no ID		9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	77
228	34	6.6	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	2.04		1.3 PS. calvin cyle	133	37	AZM4_114830	133	9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	76
385	38	6.6	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	3.69		1.3 PS. calvin cyle	183	58	AZM4_114830	183	9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	159
384	40	6.6	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	5.79		1.3 PS. calvin cyle	55		no ID		9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	51
381	40	6.5	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	10.00		1.3 PS. calvin cyle	76	39	AZM4_114830	73	9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	76
629	39	6.6	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	10.00		1.3 PS. calvin cyle	272	63	AZM4_114830	272	9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	223
630	39	6.5	TC219897	Glyceraldehyde 3-phosphate dehydrogenase A	10.00		1.3 PS. calvin cyle	94	34	AZM4_114830	89	9632.m03644	glyceraldehyde-3-phosphate dehydrogenase, type I	61
173	41	5.6	M (TC234510), BS (TC239473)	M (glyceraldehyde-3-phosphate dehydrogenase (B)), BS (sedoheptulose-1,7-bisphosphatase)	2.52		1.3 PS. calvin cyle	M(543)/BS(265)	M(71)/BS(57)	M (AZM4_124239), BS (AZM4_113569)	M (483), BS (226)	9631.m00283	M (glyceraldehyde-3-phosphate dehydrogenase, type I)	M (350)
195			TC234510	glyceraldehyde-3-phosphate dehydrogenase (B) (comigration with FBA)	0.45		1.3 PS. calvin cyle	327	84	AZM4_124239	293	9631.m00283	glyceraldehyde-3-phosphate dehydrogenase, type I, putative	232
763	43	5.8	TC219624, TC219203	Phosphoglycerate kinase	0.51		1.3 PS. calvin cyle	83, 205		no ID		no ID		
163	42	5.6	TC221089, TC225896	Phosphoribulokinase	2.54		1.3 PS. calvin cyle	370, 149	76, 51	AZM4_39942, AZM4_61423, AZM4_82239	201, 85, 195	no ID		
770	28	6.3	TC234954	Ribulose-5-phosphate-3-epimerase	10.00		1.3 PS. calvin cyle	89	48	no ID		no ID		
113	49	5.9	TC237072	RuBisCO Activase	1.59		1.3 PS. calvin cyle	339	67	AZM4_80494	286	9639.m04488	RuBisCO activase small isoform precursor	126
132	45	5.9	TC237072	RuBisCO Activase	2.13		1.3 PS. calvin cyle	293	77	AZM4_80494	242	9639.m04488	RuBisCO activase small isoform precursor	122
780	52	6.4	TC233714	RuBisCO large subunit (train)	19.64		1.3 PS. calvin cyle			no ID		no ID		
776	53	6.5	TC233714	RuBisCO large subunit	30.01		1.3 PS. calvin cyle	134		NP004621	no ID	no ID		
777	52	6.5	TC233714	RuBisCO large subunit	37.38		1.3 PS. calvin cyle	182		NP004621	no ID	no ID		

572	124	6.6	TC233714	RuBisCO large subunit	10.00		1.3 PS.calvin cyle	193	51	AZM4_51730	100	9638.m01774	Ribulose bisphosphate carboxylase large chain, catalytic domain, putative	172
779	53	6.7	TC233714	RuBisCO large subunit (train)	17.89		1.3 PS.calvin cyle			no ID		no ID		
784	15	6.3	TC234040	RuBisCO small subunit	3.03		1.3 PS.calvin cyle	62,72		no ID		no ID		
773	26	6.3	TC234040	RuBisCO small subunit	10.00		1.3 PS.calvin cyle	77	40	no ID		no ID		
772	27	6.4	TC234040	RuBisCO small subunit	2.51		1.3 PS.calvin cyle	94	47	no ID		no ID		
226	35	5.6	TC239473	sedoheptulose-1,7-bisphosphatase	2.27		1.3 PS.calvin cyle	258,73	58	AZM4_113569	245	no ID		
51	72	6.1	TC235000	Transketolase	2.39		1.3 PS.calvin cyle	87		no ID		no ID		
564	140	6.1	TC235000	Transketolase	10.00		1.3 PS.calvin cyle	77	46	no ID		9634.m00340	transketolase	64
50	73	6.1	TC235001	Transketolase (train)	1.94		1.3 PS.calvin cyle			no ID		no ID		
49	73	6.2	TC235000	Transketolase	3.29		1.3 PS.calvin cyle	167		no ID		no ID		
307	23	5.9	TC240700	β-hydroxyacyl-ACP dehydratase	0.10		11.1 lipid metabolism.FA synthesis and FA elongation	65	36	no ID		9636.m01261	Hypothetical protein	36
202	38	5.4	TC223360	S-malonyltransferase	0.38		11.1 lipid metabolism.FA synthesis and FA elongation	56	34	AZM4_1951, PUHIX67TD	56, 56	no ID		
359	14	5.2	AI966827	lipid transfer protein 7a2b	0.10		11.6 lipid metabolism.lipid transfer proteins etc	45	45	no ID		no ID		
57	62	6.3	TC222347	Ferredoxin-nitrite reductase	0.67		12.1 N-metabolism.nitrate metabolism	110	46	no ID		no ID		
137	44	6.1	TC220868	Glutamine synthetase (GS2)	0.66		12.2 N-metabolism.ammonia metabolism	174	41	AZM4_12662	64	9632.m05496	Glutamine synthetase, catalytic domain, putative	41
140	44	6.3	TC219944	Aspartate transaminase (ASP5 A.th)	0.20		13.1.2.1 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	433	75	AZM4_140403, AZM4_69012	109, 186	9630.m05507	retrotransposon protein, putative, unclassified	256
135	44	6.3	TC219944	Aspartate transaminase (ASP5 A.th)	0.22		13.1.2.1 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	231	64	AZM4_140403	98	9630.m05507	retrotransposon protein, putative, unclassified	167
156	43	6.3	TC219944	Aspartate transaminase (ASP5 A.th)	0.30		13.1.2.1 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	395	73	AZM4_140403, AZM4_69012	102, 132	9630.m05507	retrotransposon protein, putative, unclassified	230

143	44	6.4	TC219944	Aspartate transaminase (ASP5 A.th)	0.32		13.1.2.1 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	194	56		AZM4_140403, AZM4_69012	65, 56	9630.m05507	retrotransposon protein, putative, unclassified	156
138	44	6.3	TC219944	Aspartate transaminase (ASP5 A.th)	0.48		13.1.2.1 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	425	57		AZM4_140403, AZM4_69012	115, 190	9630.m05507	retrotransposon protein, putative, unclassified	250
297	25	6.1	TC234316	Lactoylglutathione lyase	0.98		13.3.2.2 amino acid metabolism.aspartate family.threonine.degradation	62			no ID		no ID		
368	46	5.6	TC220616	3-isopropylmalate dehydrogenase	0.54		13.4.2.1 amino acid metabolism.alanine-valine-leucine group.leucine.synthesis	267	63		AZM4_51952	114	9631.m06408	putative 3-isopropylmalate dehydrogenase	85
124	47	5.6	TC220615, TC234316	3-isopropylmalate dehydrogenase	0.40		13.4.2.1 amino acid metabolism.alanine-valine-leucine group.leucine.synthesis	71	36	TC220616	AZM4_69259	69	9631.m06408	putative 3-isopropylmalate dehydrogenase	36
211	37	6.1	TC235388, TC235390	Cysteine synthase 1	0.62		13.5.3.1 amino acid metabolism.serine-glycine-cysteine group.cysteine.synthesis	44, 361	83	TC235390, TC235389	AZM4_138367, AZM4_27612	50, 83	9629.m07405, 9629.m07406, 9629.m07407	cysteine synthase A, putative	234
118	49	6.3	TC235924	ATP sulfurylase 2	1.69		14 S-assimilation	283, 63	65, 45		AZM4_119032	151	9632.m00109	ATP-sulfurylase	67,214,67
72	61	6.3	TC235924	ATP sulfurylase 2	2.16		14 S-assimilation	69	39		no ID		no ID		
190	39	5.8	TC227295	TC227295 unknown	2.86		17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	230	55		AZM4_90949	404	9636.m02890	oxidoreductase, zinc-binding dehydrogenase family, putative	99
627	39	5.9	TC227295	TC227295 unknown	10.00		17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	244	62		AZM4_90949	269	9636.m02890	oxidoreductase, zinc-binding dehydrogenase family, putative	99
98	53	6.4	TC222533, TC242174	glucose-1-phosphate adenylyltransferase large chain	4.49		2.1.2 major CHO metabolism.synthesis.starch	353, 103	73, 61		no ID		no ID		
99	53	6.3	TC222533, TC242174	glucose-1-phosphate adenylyltransferase large chain	4.60		2.1.2 major CHO metabolism.synthesis.starch	153, 43	41, 43		no ID		no ID		
331	18	6.2	AZM4_47023	Ferredoxin-thioredoxin reductase subunit A (FTR-A)	0.10		21.1 redox.thioredoxin				AZM4_47023	61	no ID		
441	18	5.3	TC220465, TC221334, TC228810	Thioredoxin-M2, -M4	0.31		21.1 redox.thioredoxin	43, 64	43, 38	TC228810	AZM4_129228, AZM4_90887, PUJBE47TD	64	AZM4_90887P, UJBE47TD	no ID	
348	15	5.4	TC221334, TC220464	Thioredoxin-M4, -F	0.10		21.1 redox.thioredoxin	86, 136	57, 39		AZM4_129228, AZM4_81115, PUJBE47TD	133, 82, 136	9640.m00810	retrotransposon protein, putative, unclassified	66
340	17	5.4	TC221334	Thioredoxin-M4, -M2	0.74		21.1 redox.thioredoxin	372	98		AZM4_129228, PUJBE47TD	287, 290	PUJBE47TD	no ID	
347	15	5.3	TC221334	Thioredoxin-M4, -M2	0.86		21.1 redox.thioredoxin	65	34		AZM4_129228, PUJBE47TD, AZM4_90887	53	no ID		
78	58	6.3	TC227052	glutathione-disulfide reductase	0.86		21.2 redox.ascorbate and glutathione	283	44		no ID		no ID		

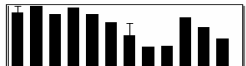
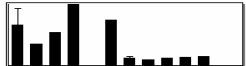
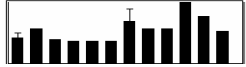
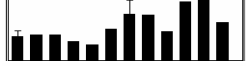
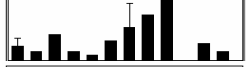
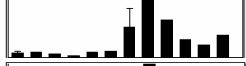
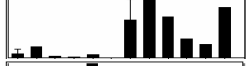
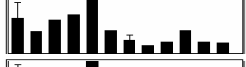
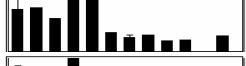

79	58	6.3	TC227052	glutathione-disulfide reductase	1.57		21.2 redox, ascorbate and glutathione	114	35	no ID	no ID			
288	26	5.0	TC234346, TC234345	2-cys peroxiredoxin-like (2CysB)	0.14		21.5 redox, periredoxins	326, 346	92, 92	AZM4_102908	49	9630.m03177	Similar to 2-cys peroxiredoxin bas1, chloroplast precursor (thiol-specific antioxidant protein) (fragment). [barley] 60	
291	26	5.2	TC234346, TC234345	2-cys peroxiredoxin-like (2CysB)	0.21		21.5 redox, periredoxins	340, 379	74, 74	TC234346	74	9630.m03177	Similar to 2-cys peroxiredoxin bas1, chloroplast precursor (thiol-specific antioxidant protein) (fragment). [barley] 58, 237, 58	
341	17	5.8	TC234346	2-cys peroxiredoxin-like (2CysB)	0.56		21.5 redox, periredoxins	57	29	no ID	no ID			
309	22	5.4	TC234346	2-cys peroxiredoxin-like (2CysB)	0.10		21.5 redox, periredoxins	101	44	no ID	9630.m03177	Similar to 2-cys peroxiredoxin bas1, chloroplast precursor (thiol-specific antioxidant protein) (fragment). [barley] 101		
362	53	5.3	TC234346	2-cys peroxiredoxin-like (2CysB)	1.09		21.5 redox, periredoxins	101	42	9630.m03177	58	no ID		
459	47	5.3	TC234345, TC234346	2-cys peroxiredoxin-like (2CysB) (DIMER Train)	0.38		21.5 redox, periredoxins	188, 185	52, 52	no ID	9630.m03177	Similar to 2-cys peroxiredoxin bas1, chloroplast precursor (thiol-specific antioxidant protein) (fragment). [barley] 99		
125	47	5.2	TC234345, TC234346	2-cys peroxiredoxin-like (2CysB) (DIMER Train)	0.24		21.5 redox, periredoxins	184, 255	60, 60	no ID	9630.m03177	Similar to 2-cys peroxiredoxin bas1, chloroplast precursor (thiol-specific antioxidant protein) (fragment). [barley] 144		
324	19	5.4	TC223042	Peroxiredoxine-like (II-E)	0.14		21.5 redox, periredoxins	279, 74	63	AZM4_14798	279	9634.m04053	AhpC/TSA family, putative 47	
311	21	5.2	TC223042	Peroxiredoxine-like (II-E)	0.17		21.5 redox, periredoxins	344, 62	89	AZM4_23244	74	9634.m04053	AhpC/TSA family, putative 75	
315	21	5.5	TC223042	Peroxiredoxine-like (II-E)	0.25		21.5 redox, periredoxins	97	53	AZM4_14798	97	no ID		
313	21	5.4	TC223042	Peroxiredoxine-like (II-E)	0.26		21.5 redox, periredoxins	292	79	AZM4_14798	292	9634.m04053	AhpC/TSA family, putative 77	
342	17	5.6	TC237182	Superoxide dismutase [Cu-Zn]	0.75		21.6 redox, dismutases and catalases	277	110	no ID	9636.m04566	Copper/zinc superoxide dismutase, putative 123		
264	29	5.5	TC236534	Adenylate kinase	0.26		23.4 nucleotide metabolism, phosphotransfer and pyrophosphatases	50		no ID	no ID			
271	28	5.6	TC236532, TC236534	Adenylate kinase	0.36		23.4 nucleotide metabolism, phosphotransfer and pyrophosphatases	103, 105		TC236534	no ID	no ID		
108	51	5.5	TC236532, TC236534	Adenylate kinase	0.20		23.4 nucleotide metabolism, phosphotransfer and pyrophosphatases	347, 59	78, 0	AZM4_13718	233	9636.m00076	adenylate kinase, chloroplast (ec 2.7.4.3) (atp-amtrnosphorylase) 59	
241	33	5.7	TC218860	inorganic pyrophosphatase-like	0.69		23.4 nucleotide metabolism, phosphotransfer and pyrophosphatases	461, 137	88	TC218859, TC218859	AZM4_3565	279	9630.m05227	inorganic pyrophosphatase, putative 301
448	17	6.6	TC238875	nucleoside diphosphate kinase II	0.18		23.4 nucleotide metabolism, phosphotransfer and pyrophosphatases	38	38	no ID	9640.m03506	Nucleoside diphosphate kinase 38		

77	58	6.4	TC220472	$\beta$ -D-glucosidase	6.76		26.3 misc gluco-, galacto- and mannosidases	220	79	no ID		no ID			
458	55	6.4	TC220472	$\beta$ -D-glucosidase	8.31		26.3 misc gluco-, galacto- and mannosidases	84	38	AZM4_118020	60	no ID			
679	57	6.5	TC220472	$\beta$ -D-glucosidase	10.00		26.3 misc gluco-, galacto- and mannosidases	245	63	AZM4_118020, AZM4_2007	76, 63	no ID			
680	54	6.5	TC220472	$\beta$ -D-glucosidase	10.00		26.3 misc gluco-, galacto- and mannosidases	104	58	AZM4_118020, AZM4_12435	92, 63	no ID			
278	28	5.7	TC222544	glutathione S-transferase (GST10)	0.42		26.9 misc glutathione S transferases	66	26	no ID		no ID			
276	28	6.0	TC222544	glutathione S-transferase (GST10)	0.53		26.9 misc glutathione S transferases	271	103	AZM4_127368	245	no ID			
785	42	6.4	CF646019, AZM4_135414	mRNA binding protein (Csp41a-like)	1.88		28 (Regulation) transcription and translation - unspecified	39, 64	39, 64	AZM4_135414	85	no ID			
232	34	4.5	TC235457, TC235458	nucleic acid-binding protein Cp31	0.46		28 (Regulation) transcription and translation - unspecified	104, 42	41, 42	TC235457		no ID	9636.m04513	RNA-binding protein 3	42
231	34	4.7	TC235457, TC235458	nucleic acid-binding protein Cp31	0.55		28 (Regulation) transcription and translation - unspecified	106, 43	41, 43	TC235457		no ID	9636.m04513	RNA-binding protein 3	43
222	35	4.1	TC236626	nucleic acid-binding protein Cp33	0.33		28 (Regulation) transcription and translation - unspecified	54,442	,98	AZM4_112176, AZM4_112180, AZM4_112207	81, 148, 58	9637.m03347	Similar to cp31AHv protein	166	
282	27	5.8	TC238798	plastid-specific ribosomal protein 2 (RP-2)	0.28		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	380	59	AZM4_128226	213	9637.m00836	plastid-specific ribosomal protein 2 precursor	136	
200	38	6.5	TC219835	ribosomal protein L1	0.96		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	133	57	no ID		no ID			
319	20	5.1	TC222916	ribosomal protein L12.1	0.10		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	332	87	AZM4_108777	330	no ID			
117	49	4.9	TC221841	ribosomal protein S1	0.10		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	211	67	no ID		no ID			
122	48	4.9	TC221841	ribosomal protein S1	0.10		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	211	67	no ID		9631.m01992	Similar to 30s ribosomal protein s1, chloroplast precursor (cs1). [spinach]	97	
146	44	4.9	TC221841	ribosomal protein S1	0.10		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	190	61	no ID		no ID			
205	38	6.2	TC239133, TC235751	ribosomal protein S5 (RP-S5), enoyl acyl carrier MIX	0.87		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	89, 72	59, 47	no ID		9631.m03343	putative ribosomal protein	89	
306	23	6.3	TC224551, BM079225	ribosomal protein L10	0.10		29.2.2 protein.synthesis.misc ribosomal protein	49, 188	0,79	no ID		no ID			

304	24	5.9	TC237934	Elongation factor P (EF-P)	0.94		29.2.3 protein.synthesis.initiation	96	51	no ID		9639.m00151, 9640.m00143	Elongation factor P (EF-P), putative	43	
123	47	6.0	TC222181, TC226641	elongation factor Tu	0.39		29.2.3 protein.synthesis.initiation	500, 525	82, 132	TC222181	no ID	no ID			
133	45	6.0	TC222181, TC226641	elongation factor Tu	0.44		29.2.3 protein.synthesis.initiation	552, 376	99, 99	AZM4_91499, AZM4_91500	528, 533	9630.m03668	translation elongation factor Tu	257	
121	48	6.0	TC222181, TC226641	elongation factor Tu	0.45		29.2.3 protein.synthesis.initiation	126, 79	49, 79	no ID		no ID			
26	88	5.8	TC222353	elongation factor G (EF-G)	0.13		29.2.4 protein.synthesis.elongation	75	49	no ID		no ID			
36	85	5.8	TC222353	elongation factor G (EF-G) TRAIN	0.18		29.2.4 protein.synthesis.elongation			no ID		no ID			
6	125	5.4	TC226754	EF-Ts (PSRP-7 - homologue of <i>C. reinhardtii</i> PETS)	0.14		29.2.99 protein.synthesis.misc	66	66	no ID		no ID			
771	28	6.4	TC237618, TC237619	Ribosome recycling factor	0.82		29.2.99 protein.synthesis.misc	273, 231	59, 61	no ID		no ID			
245	32	6.4	TC220737	Membrane-associated 30 kDa protein (Vipp1)	0.10		29.3 protein.targeting	51	51	no ID		no ID			
261	29	6.1	TC245457, TC225197	ClpP protease (ClpP1?)	0.58		29.5 protein.degradation	43	43	TC245457	no ID	no ID			
47	73	5.8	TC219522	Chaperonin 60 (β-Cpn60)	0.85		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	247	55	AZM4_103597, OGVDF90TH	55, 62	AZM4_140740, GYABS2TV	9634.m00139, 9634.m00140	TCP-1/cpn60 chaperonin family	247
67	61	5.8	TC219523, TC219522	Chaperonin 60 (β-Cpn60)	1.16		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	167,167		TC219525,TC219523	no ID	9634.m00139, 9634.m00140	TCP-1/cpn60 chaperonin family	174	
273	28	5.8	TC233810, TC236117	Chaperonin 20 (Cpn21)	0.99		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	346, 179	67, 75	AZM4_73208	126	9630.m05353, 9630.m05354, 9637.m02334	chaperonin, 10 kDa, putative	193, 104	
274	28	5.8	TC236117	Chaperonin 20 (Cpn21) train	0.86		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	100		no ID		no ID			
66	62	5.5	TC220350, TC236031	Chaperonin 60 (α-Cpn60)	0.67		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	87		TC236031	no ID	no ID			
68	61	5.6	TC220350, TC235184, TC236031	Chaperonin 60 (α-Cpn60) TRAIN	0.78		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	156,156		TC235184,TC236031	no ID	9631.m06368, 9640.m01758	putative rubisco subunit binding-protein alpha subunit precursor (60 kDa chaperonin alpha subunit), rubisco subunit binding-	64, 114	
43	76	5.4	TC220215, TC235785	Chaperonin 70 (DnaK)	0.86		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	211/102		TC235785	no ID	no ID			
454	40	4.0	TC222867	GrpE	0.19		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	86	45	no ID		no ID			

316	21	6.4	TC228225	peptidyl-prolyl cis-trans isomerase (TLP21)	0.49		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	301	74	AZM4_42293	195	9633.m00033	similar to Arabidopsis thaliana Peptidyl-prolyl cis-trans isomerase	115
314	21	6.2	TC228225	peptidyl-prolyl cis-trans isomerase (TLP21)	0.10		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	78	38	AZM4_42293	70	no ID		
154	43	5.3	TC239826	peptidyl-prolyl cis-trans isomerase (Tlp40)	0.36		29.6 protein.(un)folding (includes isomerases and chaperones - if not heat induced)	484	80	AZM4_104750, AZM4_67669	327, 160	9636.m02914	peptidyl-prolyl cis-trans isomerase, chloroplast precursor (ec 5.2.1.8) (40 kda thylakoid lumen ppiase) (40 kda thylakoid	231
786	34	5.9	TC237704	Aldose-1-epimerase	10.00		3.5 minor carbohydrates, starch, OPP, glycolysis	100	63	AZM4_111522	63	9637.m01315	apospory-associated protein C-like protein	63
450	20	6.7	TC237508	Vacuolar ATP synthase subunit C (VATC_ARATH)	0.10		34.1 transport.p- and v-ATPases	248	112	AZM4_102857	158	no ID		
244	32	5.4	TC223951	ABC transporter putative	0.10		34.16 transport.ABC transporters and multidrug resistance systems	109	54	AZM4_11952	54	no ID		
221	36	5.4	TC238048	SHOOT1 protein	0.31		35.2 not assigned. unknown	92	69	AZM4_93135	55	no ID		
223	35	5.4	TC238048	SHOOT1 protein	0.39		35.2 not assigned. unknown	199	80	AZM4_139502	98	no ID		
224	35	5.5	TC238048	SHOOT1 protein	0.55		35.2 not assigned. unknown	122	67	no ID		no ID		
248	31	5.3	TC222257	Fruit protein PKIW1502	0.32		35.2 not assigned.unknown	80,283	,90	AZM4_53484	76	no ID		
634	34	5.6	TC238795	inositol monophosphate family protein	10.00		35.2 not assigned.unknown	166	72	AZM4_12532	72	no ID		
303	24	5.6	TC230439	unknown TC230439	0.39		35.2 not assigned.unknown	59	59	AZM4_68343	268	9636.m03984	expressed protein	67
256	30	6.6	CF032674	unknown CF032674	1.88		35.2 not assigned.unknown	39	39	no ID		no ID		
251	31	4.8	CF032674	unknown CF032674	0.10		35.2 not assigned.unknown	39	39	no ID		no ID		
323	19	5.5	TC237508	Vacuolar ATP synthase subunit C (VATC_ARATH)	0.57		35.2 not assigned.unknown	110	73	AZM4_102857	100	no ID		
253	31	6.6	TC235613	Y230_ARATH	0.37		35.2 not assigned.unknown	111,81	,33	TC235612,TC235612 AZM4_26007	62	no ID		
252	31	6.2	TC235613	Y230_ARATH	0.37		35.2 not assigned.unknown	37	37	no ID		no ID		
254	31	6.4	TC235613	Y230_ARATH	0.37		35.2 not assigned.unknown	64,388	,64	TC235612,TC235612 AZM4_26007, AZM4_81439	171, 76	9633.m00110	3-beta hydroxysteroid dehydrogenase/isomerase protein, putative	110



260	29	6.1	TC220990	AT4g15940-like unknown	0.58		35.2 not assigned.unknown; probably tyrosine metabolism	104	36	no ID	no ID				
275	28	5.7	TC233905, TC233906, TC233912	Triosephosphate isomerase	0.19		4 glycolysis	73,73	73,73	TC233912,TC233906	no ID	no ID			
255	30	5.2	TC221577	Ribose-5-phosphate isomerase	1.67		7.2 OPP.non-reductive PP	440	92		no ID	no ID			
257	30	5.3	TC221577	Ribose-5-phosphate isomerase	1.97		7.2 OPP.non-reductive PP	306	71	AZM4_51443	126	no ID			
55	65	5.3	TC221577	Ribose-5P-isomerase dimer	2.38		7.2 OPP.non-reductive PP	375	82			no ID			
60	62	6.1	TC234846	NADP-dependent malic enzyme	6.89		C4BS_8.2.10 TCA / org. transformation.other organic acid transformaitons.malic	82				no ID			
33	86	6.2	TC234846	NADP-dependent malic enzyme	9.39		C4BS_8.2.11 TCA / org. transformation.other organic acid transformaitons.malic	371	69			no ID			
15	96	5.9	TC233444	pyruvate orthophosphate dikinase (PPDK)	0.36		C4MS_6 gluconeogenese/ glyoxylate cycle	634	68			no ID			
144	44	6.0	TC220999	Malate dehydrogenase [NADP]	0.33		C4MS_8.2 TCA / org. transformation.other organic acid transformaitons	213	74			no ID	9636.m04570	malate dehydrogenase, NADP-dependent	74
141	44	5.9	TC220999	Malate dehydrogenase [NADP]	0.45		C4MS_8.2 TCA / org. transformation.other organic acid transformaitons	328	90			no ID			