

**Supplemental Table.** All 241 proteins identified on the CN-PAGE of the chloroplast stroma proteome of *Arabidopsis thaliana* rosette leaves. Accession number, protein name, associated BIN, predicted location by TargetP and Predotar (C=chloroplast/plastid; M= mitochondria; s= Secreted) and identifications in other proteomics papers are indicated. Note that in absence of published information on *Arabidopsis* proteins, the medline reference concerning the native state is from many different plant species and even bacteria and only in a few cases from *A. thaliana*.

relative concentration range (1= highest, 5 = lowest)	Accession	(a) exp.ambiguity (b)	Lab Annotation (c)	cTP (d)	cTP (e)	MapManBin (f)	oligomeric state (Medline Ref) (g)	Calc. MW (h)	Calc. processed MW (i)	uncured exp. native MW (j)	relative amount (k)	rel norm. concentration (l)	ProteomicsPub. (m)
3	At5g36790.1	At5g36700.1	2-phosphoglycolate phosphatase-2 (PGP-2)	C	C	1.2 PS.photorepiration	homodimer (11581250)	40	33	91	0.2000	0.00548	
3	At5g36700.1	At5g36790.1	2-phosphoglycolate phosphatase-1 (PGP-1)	C	C	1.2 PS.photorepiration	homodimer (11581250)	40	33	91	0.2000	0.00548	
2	At2g21170.1		triosephosphate isomerase 1 (TPI-1) (plastid)	C	C	1.3 PS.calvin cyle	dimer (2392479 and 2732453)	33	27	93 128 144 94 107	1.2948	0.04389	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
3	At3g54050.1		fructose-bisphosphatase (FBPA)	C	C	1.3 PS.calvin cyle	homotetramer (7703243)	45	39	145 111 136	0.2126	0.00452	
5	At1g14030.1		Rubisco LS methyltransferase (LSMT)	C		1.3 PS.calvin cyle; 29.4 protein.posttranslational modification		55	48	111	0.0033	0.00006	
1	ATCG00490		Rubisco large subunit (RBCL)	c-enc	c-enc	1.3.01 PS.calvin cyle.rubisco large subunit	heteroheadecamer L8S8 (3133767)	53		224 103 990 236 627 282 624 604 598 983 556 757 360 616 105 191 803 333 350	46.0195	0.85221	12775770(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
1	At1g67090.1	At5g38430.1 At5g38410.1 At5g38420.1	Rubisco small subunit-4 (RBCS-4)	C	C	1.3.02 PS.calvin cyle.small subunit	heteroheadecamer L8S8 (3133767)	20	15	370 360 355 639 600 738 348 480 465 268 440 450	3.0400	0.20250	12938931(Total chloroplast envelope); 11719511(Thylakoid lumen proteome); 12775770(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
1	At5g38430.1	At1g67090.1 At5g38410.1 At5g38420.1	Rubisco small subunit 1b (RBCS-1b)	C	C	1.3.02 PS.calvin cyle.small subunit	heteroheadecamer L8S8 (3133767)	20	15	480 465 440 268 42 360 370 639 738 348	3.0400	0.20250	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope);
1	At5g38420.1	At1g67090.1 At5g38410.1 At5g38430.1 at5g38410.1	Rubisco small subunit 2b (RBCS-2b)	C	C	1.3.02 PS.calvin cyle.small subunit	heteroheadecamer L8S8 (3133767)	20	15	600 348 738 639 370 360 42 268 440 480 465	3.0400	0.20250	12938931(Total chloroplast envelope);
1	At5g38410.1	At5g38420.1 At1g67090.1 At5g38430.1 at5g38420.1	Rubisco small subunit 3b (RBCS 3b)	C	C	1.3.02 PS.calvin cyle.small subunit	heteroheadecamer L8S8 (3133767)	20	15	480 465 440 268 42 360 370 639 738 348 600	3.0400	0.20250	
2	At1g56190.1	At3g12780.1	phosphoglycerate kinase-1 (PGK-2)	C	C	1.3.03 PS.calvin cyle.phosphoglycerate kinase	monomer (7724671)	50	40	129 132 123 28 59	1.3892	0.02894	MitoDB(Mitochondrial proteome);
2	At3g12780.1	At1g56190.1	phosphoglycerate kinase-1 (PGK-1)	C	C	1.3.03 PS.calvin cyle.phosphoglycerate kinase; 4.10 glycolysis.phosphoglycerate kinase	monomer (7724671)	50	43	119 270 123 132 59 58 600 721	1.6871	0.03590	12775770(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 14617066(Nuclear proteome);
2	At1g12900.1	At3g26650.1 At1g42970.1	glyceraldehyde-3-phosphate dehydrogenase A-2 (GAPA-2)	C	C	1.3.04 PS.calvin cyle.GAP	heteroheadecamer (A8B8) and heteroteradecamer with CP12 and PRK (8-2-4) (12423361)	43	38	602 604 946 721 751 753 465 224 319 219 450 440	0.6170	0.01577	12775770(Total chloroplast envelope);
2	At1g42970.1	At1g12900.1 At3g26650.1	glyceraldehyde-3-phosphate dehydrogenase B (GAPB)	C	C	1.3.04 PS.calvin cyle.GAP	heteroheadecamer (A8B8) and heteroteradecamer with CP12 and PRK (8-2-4) (12423361)	48	43	946 949 604 751	0.5614	0.01337	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 15322131(Thylakoid-stripped);

2	At3g26650.1	<i>At1g12900.1,At1g42970.1</i>	glyceraldehyde 3-phosphate dehydrogenase A-1 (GAPA-1)	C	C	1.3.04 PS.calvin cyle.GAP	heterohecamer (A8B8) and heteroteradecamer with CP12 and PRK (8-2-4) (12423361)	42	38	721 946 949 604 602 465 753 751 219 319 450 440 224	0.6451	0.01654	15322131(Thylakoid-stripped);
2	At4g38970.1	<i>At2g21330.1</i>	fructose-bisphosphate aldolase-2 (SFBA-2)	C	C	1.3.06 PS.calvin cyle.aldolase; 4.07 glycolysis.aldolase	homotetramer (class I) and dimer (class II) (9675026 and 12232396)	43	38	181 185 186 179 219 224	0.5094	0.01358	12775770(Total chloroplast envelope);
2	At2g21330.1	<i>At4g38970.1</i>	fructose-bisphosphate aldolase-1 (SFBA-1)	C	C	1.3.06 PS.calvin cyle.aldolase; 4.07 glycolysis.aldolase	homotetramer (class I) and dimer (class II) (9675026 and 12232396)	43	42	185 181 179 219 224	1.6402	0.03952	12938931(Total chloroplast envelope); 11719511(Thylakoid lumen proteome);
2	At3g60750.1		transketolase-1 (TKL-1)	C	C	1.3.07 PS.calvin cyle.transketolase; 7.2 OPP.non-reductive PP	dimer (12913150 and 9523694)	80	73	149	3.3655	0.04199	12775770(Total chloroplast envelope);
2	At3g55800.1		sedoheptulose-bisphosphatase (SBPase)	C	C	1.3.08 PS.calvin cyle.seduheptulose bisphosphatase	homodimer (3032163)	42	36	100 94 107 152 118	0.5523	0.01416	12938931(Total chloroplast envelope);
2	At3g04790.1		ribose 5-phosphate isomerase (PRI)	C	C	1.3.09 PS.calvin cyle.Rib5P Isomerase; 7.2 OPP.non-reductive PP	homodimer ( 10620366)	29	25	69 184 106 124 8994	0.5848	0.02150	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
3	At5g61410.1		ribulose-5-phosphate-3-epimerase (RPE)	C	C	1.3.10 PS.calvin cyle.Rib isomerase; 7.2 OPP.non-reductive PP	heamer (chloroplasts) or dimer (cytosolic) (10625676)	30	25	643	0.1040	0.00417	12938931(Total chloroplast envelope);
3	At1g32060.1		phosphoribulokinase-2 (PRK-2)	C	C	1.3.11 PS.calvin cyle.PRK	heterotetradecamer with CP12 and GAPDH (12423361)	44	38	465 480 109 321 219 224 604 602 949	0.2272	0.00548	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
2	At2g39730.1		Rubisco activase	C	C	1.3.12 PS.calvin cyle.rubisco interacting		52	46	190 949 959 610 604 485 768 770 328 480 323	0.5154	0.01097	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 14617066(Nuclear proteome); 14729914(thylakoid stripped); 15322131(Thylakoid-stripped);
5	At5g35360.1		acetyl-CoA carboxylase (ACCase)	C	C	11.1.01 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	heterotetrameric (plastid) or homomeric (cytosol) except in graminae where the homomeric is also present in plastid. In Brassicaceae both form homo and hetero are present in plastids. (11299381, 15215578)	58	51	191	background level	background level	12938931(Total chloroplast envelope);
5	At5g46290.1		Ketoacyl-ACP Synthase I (Lipid Gene Database; Beisson)	C	C	11.1.03 lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	dimer (11286890)	50	45	129	background level	background level	12938931(Total chloroplast envelope);
4	At2g05990.1		Enoyl-ACP reductase, plastid	C	C	11.1.06 lipid metabolism.FA synthesis and FA elongation.enoyl ACP reductase	homotetramer (8126737, 8535786, 2194572 and 6756317)	41	33	616	0.0140	0.00041	12938931(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen);
4	At5g36880.1		acetyl-CoA synthetase (acetate-CoA ligase)	C	C	11.1.08 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	monomer (10859180)	77	73	95 104	0.0215	0.00026	
5	At2g43710.1		acyl-[acyl-carrier-protein] desaturase-1 (stearoyl-ACP desaturase)	C	C	11.1.15 lipid metabolism.FA synthesis and FA elongation.ACP desaturase; 11.2.01 lipid metabolism.FA desaturation.desaturase	dimer (7118934)	46	42	949	background level	background level	

5	At3g02630.1	acyl-[acyl-carrier-protein] desaturase-2 (stearoyl-ACP desaturase)	C	C	11.1.15 lipid metabolism.FA synthesis and FA elongation.ACP desaturase; 11.2.01 lipid metabolism.FA desaturation.desaturase	dimer (7118934)	45	42	949	background level	background level	
4	At2g15620.1	nitrite reductase (ferredoxin)	C	C	12.1.02 N-metabolism.nitrate metabolism.nitrite reductase	monomer (9232882)	66	63	74/157	0.0153	0.00022	MitoDB(Mitochondrial proteome);
3	At5g04140.1	ferredoxin-dependent glutamate synthase/glu1/Fd-GOGAT 1	C	C	12.2.01 N-metabolism.ammonia metabolism.glutamate synthase	monomeric (15501908 and 10357231 and 8453303)	177	170	774 319 224 253	0.2853	0.00168	12938931(Total chloroplast envelope);
1	At5g35630.1	glutamate-ammonia ligase (GS2), chloroplast	C	C	12.2.02 N-metabolism.ammonia metabolism.glutamine synthase	tetra and octamer (15197594)	47	42	328 345 234 485 200 229	7.0097	0.15232	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
3	At4g31990.1	aspartate aminotransferase, chloroplast (transaminase A/AAT1/Asp5)	C	C	13.1.1.2 amino acid metabolism.central amino acid metabolism.aspartate.synthesis	homo or heterodimer (Plant Physiol. 92 (1990), pp. 587-594)	50	45	163 174	0.1462	0.00311	12938931(Total chloroplast envelope);
4	At5g10920.1	argininosuccinate lyase (AtArgH)	C	C	13.1.2.3 amino acid metabolism.synthesis.glutamamate family.arginine		58	53	191	0.0193	0.00035	
4	At1g75330.1	ornithine carbamoyltransferase	C	C	13.1.2.3 amino acid metabolism.synthesis.glutamamate family.arginine	homotrimer (11538003)	41	36	224	0.0282	0.00073	
4	At1g80600.1	acetylornithine transaminase/AOTA/AC OAT)	C	M	13.1.2.3 amino acid metabolism.synthesis.glutamamate family.arginine		49	44	111	0.0116	0.00025	
3	At3g27740.1	carbamoyl phosphate synthetase small subunit	C		13.1.2.3 amino acid metabolism.synthesis.glutamamate family.arginine; 23.1.1 nucleotide metabolism.synthesis.pyrimidine	heterodimer (11574542, 209307, 2658488)	47	43	163	0.0592	0.00124	
4	At1g29900.1	carbamoylphosphate synthetase	C		13.1.2.3 amino acid metabolism.synthesis.glutamamate family.arginine; 23.1.1 nucleotide metabolism.synthesis.pyrimidine	heterodimer (11574542, 209307, 2658488)	130	123	173 174	0.0270	0.00019	
3	At3g58610.1	ketol-acid reductoisomerase	C	C	13.1.4.1 amino acid metabolism.synthesis.branch chain group.common	homodimer (9218783 and 10320328)	64	57	179 151	0.2770	0.00469	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
4	At1g31180.1	3-isopropylmalate dehydrogenase-3, chloroplast,	M		13.1.4.4 amino acid metabolism.synthesis.branch chain group.leucine specific	Tri or tetramer (7557336)	44		111	0.0116	0.00025	
4	At5g14200.1	At1g80560.1, At1g31180.1	-		13.1.4.4 amino acid metabolism.synthesis.branch chain group.leucine specific	Tri or tetramer (7557336)	44		111	0.0116	0.00025	
4	At1g80560.1	3-isopropylmalate dehydrogenase-1	C	C	13.1.4.4 amino acid metabolism.synthesis.branch chain group.leucine specific	Tri or tetramer (7557336)	43	40	111	0.0116	0.00025	12938931(Total chloroplast envelope);
3	At2g43750.1	cysteine synthase	C	C	13.1.5.3 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine	heteroheamer ( 1375015 and 9692924) NB: OAS-TL form free homodimer 68 kDa and SAT free homotetramer	42	35	118	0.0708	0.00182	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);

4	At4g33680.1	aminotransferase, classes I and II	C		13.1.6.2 amino acid metabolism.synthesis.aromatic aa.phenylalanine and tyrosine	50	47	129 136	0.0235	0.00047	
4	At5g48220.1	indole-3-glycerol phosphate synthase (IGPS)	C	C	13.1.6.5 amino acid metabolism.synthesis.aromatic aa.tryptophan	42	36	109	0.0090	0.00021	monomer (10329177 and 8747456)
4	At3g54640.1	tryptophan synthase, alpha subunit (TSA1)	C	C	13.1.6.5 amino acid metabolism.synthesis.aromatic aa.tryptophan	33	29	174	0.0150	0.00049	heterotetramer A2B2 (7476868)
5	At5g63890.2	histidinol dehydrogenase	C	C	13.1.7 amino acid metabolism.synthesis.histidine	50	47	148	0.0031	0.00006	dimer (1989490)
4	At1g67280.1	glyoalase I -1, putative (lactoylglutathione lyase)	C	M	13.2.3.2 amino acid metabolism.degradation.aspartate family.threonine; 24 Biodegradation of enobiotics	39	32	119 147 170 198	0.0196	0.00058	11719511(Thylakoid lumen proteome);
3	At3g23940.1	dihydroxyacid dehydratase	C		13.3.3.1 amino acid metabolism.aspartate family.isoleucine.synthesis	65	61	138	0.0745	0.00118	dimer (2831190)
5	At3g22890.1	ATP sulfurylase (ATPS1)	C	C	14.01 S-assimilation.APS	51	46	129 148	0.0046	0.00009	tetramer (8274013)
4	At5g14910.1	epressed protein - also in CN-PAGE -stroma	C	C	15.2 metal handling.binding, chelation and storage	19	15	150 155	0.0015	0.00014	14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped);
4	At2g02500.1	4-Diphosphocytidyl-2C-methyl-D-erythritol synthase (ISPD) - mevalonate-independent	M	C	16.1 secondary metabolism.isoprenoids	34		69	0.0163	0.00052	
4	At5g60600.1	GepE protein (CLB4)	C	C	16.1 secondary metabolism.isoprenoids	82	78	107	0.0620	0.00071	12938931(Total chloroplast envelope);
4	At2g38040.1	putative alpha-carboxyltransferase ;	C	C	16.99 secondary metabolism.unspecified	85	80	983	0.0175	0.00020	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope);
3	At1g23740.1	oidoreductase, zinc-binding dehydrogenase family	C		17.2.3 hormone metabolism.auin.induced-regulated-responsive-activated	41	41	151 126	0.0521	0.00130	12938931(Total chloroplast envelope);
3	At3g45140.1	lipoygenase AtLO2, plastid	C	C	17.7.1 hormone metabolism.jasmonate.synthesis s-degradation	102	96	172 174 212 120 133 119 103	0.7533	0.00753	12938931(Total chloroplast envelope); 14729914(thylakoid stripped); 15322131(Thylakoid-stripped);
4	At2g29630.1	thiamine biosynthesis (thiC family)	C	C	18 Co-factor and vitamine metabolism	72	68	157	0.0143	0.00021	
3	At5g54770.1	THI1 -involved in thiamine synthesis (vitamine B1)	C	C	18 Co-factor and vitamine metabolism	37	32	202 198 253 212 199	0.1073	0.00316	12938931(Total chloroplast envelope);
3	At2g44050.1	6,7-dimethyl-8-ribityllumazine (DMRL) synthase (COS1) (vit B2 synthesis)	C	M	18 Co-factor and vitamine metabolism	24	17	738	0.0520	0.00359	hecontamer (60) (icosaeader of 12 pentamers) (10595538, 14523158, 10419541)
4	At4g18480.1	Mg-protoporphyrin I chelatase- CHL1-1	C	C	19 tetrapyrrole synthesis	46	40	109	0.0090	0.00021	heterotrimer (11678270)
4	At1g48520.1	Glu-tRNA(Gln) amidotransferase subunit B (GATB or GLU-ADT subunit B)	M	C	19 tetrapyrrole synthesis	61		199	0.0195	0.00033	homodimer (1970821)
4	At3g25660.1	glutamyl-tRNA amidotransferase subunit A	C	M	19 tetrapyrrole synthesis	57	52	191	0.0308	0.00054	homodimer (1970821, 6617644)
4	At3g48730.1	At5g63570.1 glutamate-1-semialdehyde 2,1-aminomutase 2 (GSA 2)	C	C	19 tetrapyrrole synthesis	50	48	115 103	0.0325	0.00065	12938931(Total chloroplast envelope);

3	At5g63570.1	At3g48730.1	glutamate-1-semialdehyde 2,1-aminomutase 1 (GSA1)	C	C	19 tetrapyrrole synthesis		50	46	111 103 115	0.2083	0.00417	12938931(Total chloroplast envelope);
4	At5g08280.1		hydroxymethylbilane synthase	C		19 tetrapyrrole synthesis	monomer (8192681 and 1986793)	41	32	152	0.0047	0.00013	12938931(Total chloroplast envelope);
4	At2g40490.1		uroporphyrinogen decarboxylase (UPD)	C	C	19 tetrapyrrole synthesis	homodimer (11679753)	44	40	126	0.0123	0.00030	12938931(Total chloroplast envelope);
4	At1g69740.1		porphobilinogen synthase-1 (delta-aminolevulinic acid dehydratase-1) (ALAD-1)	C	C	19 tetrapyrrole synthesis	homo-octamer (10913315)	47	41	328 343	0.0072	0.00016	
3	At1g03475.1		coproporphyrinogen III oxidase	C	C	19 tetrapyrrole synthesis	homodimer (11489187)	41	35	82	0.1260	0.00280	
4	At4g37000.1		red chlorophyll catabolite reductase (RCCR) - also accelerated cell death 2 (ACD2)	C	C	19.1* tetrapyrrole degradation	monomer? (12223836)	36	32	61	0.0243	0.00068	12938931(Total chloroplast envelope);
3	At5g48300.1*		ADP-glucose pyrophosphorylase - small subunit 1 (APS1)	C	C	2.1.2.01 major CHO metabolism.synthesis.starch.A GPase	heterotetramer 2L2S (12111225)	57	49	234 306 990	0.0755	0.00145	
5	At5g19220.1		ADP-glucose pyrophosphorylase (ADG2) (APL1)	C	C	2.1.2.01 major CHO metabolism.synthesis.starch.A GPase	heterotetramer 2L2S (12111225)	58	52	103	0.0025	0.00004	12938931(Total chloroplast envelope);
4	At5g24300.1		starch synthase	C	C	2.1.2.02 major CHO metabolism.synthesis.starch.starch synthase	homo and heterodimer (9492303 and 11361132)	72	66	154 157	0.0408	0.00062	
4	At5g03650.1		starch branching enzyme class II (SBELII)	-		2.1.2.03 major CHO metabolism.synthesis.starch.starch branching		83		132	0.0698	0.00073	
4	At4g09020.1		glycoside hydrolase family 13 similar to isoamylase	C		2.1.2.04 major CHO metabolism.synthesis.starch.debranching	homotetra to homoheamer (10333591)	86	78	96	0.0340	0.00038	
4	At1g66430.1		pfkB family carbohydrate kinase	C	C	2.2.1.01 major CHO metabolism.degradation.sucrose.fructokinase		41	37	63	0.0255	0.00062	
4	At3g29320.1		starch phosphorylase-1	C		2.2.2.02 major CHO metabolism.degradation.starch.starch phosphorylase	homo and heterodimer (9492303 and 11361132)	109	101	234	0.0758	0.00068	
4	At1g10760.1		Sex1 - R1 protein - controls starch phosphorylation	C		2.2.2.03 major CHO metabolism.degradation.starch.glucan water dikinase		157	148	319	0.0233	0.00014	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
4	At5g26570.1		glycoside hydrolase starch-binding domain-containing protein, similar to SE1	C	C	2.2.2.03 major CHO metabolism.degradation.starch.glucan water dikinase		131	125	282	0.0300	0.00021	
3	At4g21860.1		methionine sulfoxide reductase domain-containing protein	C	C	20.2 stress.abiotic		22	15	48	0.0285	0.00148	
4	At2g04030.1		cpHSP90	C	C	20.2.1 stress.abiotic.heat		89	82	119	0.0840	0.00088	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
3	At2g42540.1		cold-regulated protein (cor15a)	M		20.2.2 stress.abiotic.cold		13		46 61	0.0268	0.00382	12938931(Total chloroplast envelope);
3	At2g42530.1		cold-regulated protein (cor15b)	C	C	20.2.2 stress.abiotic.cold		15	11	61 46	0.0268	0.00382	12938931(Total chloroplast envelope);
4	At3g02730.1		thioredoxin F1	C	C	21.1 redo.thioredoxin		19	13	154 155 212	0.0018	0.00015	
4	At1g50320.1		thioredoxin X	C	C	21.1 redo.thioredoxin		20	13	154	0.0035	0.00037	
5	At4g03520.1		thioredoxin m2	C	C	21.1 redo.thioredoxin		20	13	155	0.0003	0.00002	14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
4	At1g03680.1		thioredoxin M1	C	C	21.1 redo.thioredoxin		20	14	96 89	0.0135	0.00096	11826309(thylakoid peripheral&lumen);

3	At5g42980.1		thioredoxin H-type 3 (TR-H-3)	-		21.1 redo.thioredoxin		13	34	0.0363	0.00274	15276431(Mitochondrial proteome);	
5	At1g07890.1		glutathione peroxidase (likely chloro's) (AtGP1)	-		21.2 redo.ascorbate and glutathione	monomer and homodimer (7703247)	28	94	background level	background level		
3	At5g16710.1		dehydroascorbate reductase-2 (DHAR-2), plastid	C	C	21.2 redo.ascorbate and glutathione	monomeric (12077129)	29	24	64 116 101	0.0523	0.00200	12938931(Total chloroplast envelope);
4	At3g54660.1		glutathione reductase,	C	C	21.2 redo.ascorbate and glutathione		61	53	186	0.0133	0.00016	MitoDB(Mitochondrial proteome);
3	At1g63940.1		monodehydroascorbate reductase (MDHAR)	C	C	21.2 redo.ascorbate and glutathione	monomeric (12077129)	53	48	109 89 60	0.1325	0.00250	MitoDB(Mitochondrial proteome);
4	At1g19570.1		dehydroascorbate reductase-1 (DHAR1)	-		21.2 redo.ascorbate and glutathione	monomeric (12077129)	24	44		0.0075	0.00029	MitoDB(Mitochondrial proteome);
4	At4g23100.1		gamma-glutamylcysteine synthetase (GSH1)	C	C	21.2 redo.ascorbate and glutathione	dimer (Planta 1990 180(4) 603-612)	59	51	81	0.0525	0.00092	
3	At2g20270.1		glutaredoxin protein family	C	C	21.4 redo.glutaredoxins		19	13	34	0.0363	0.00274	
4	At3g52960.1		Peroiredoxin II E (PrE)	C	C	21.5 redo.periredoxins	monomer, dimer or decamer (11706208, 15333640 and 12702727 and 11969410)	25	17	84	0.0050	0.00024	11826309(thylakoid peripheral&lumen);
2	At3g11630.1	<i>At5g06290.1</i>	2-Cys Peroiredoxin A (PrA)	C	C	21.5 redo.periredoxins	monomer, dimer or decamer (11706208, 15333640 and 12702727 and 11969410)	29	21	360 58 59 480 91 219 270 215 119 111	0.6214	0.02959	12938931(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen);
2	At5g06290.1	<i>At3g11630.1</i>	2-Cys Peroiredoxin B (PrB)	C	C	21.5 redo.periredoxins	monomer, dimer or decamer (11706208, 15333640 and 12702727 and 11969410)	30	21	219 111 270 119 480 91 360 59 58	0.6119	0.02781	
3	At4g25100.1		FE-SOD -1 (FSD1)	-		21.6 redo.dismutases and catalases		24		148	0.0490	0.00209	12775770(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 15060130(Plasma Membrane proteome); 15276431(Mitochondrial proteome); 11826309(thylakoid peripheral&lumen);
4	At3g20330.1		chloroplast aspartate transcarbamylase / ATCase (PYRB)	C	C	23.1.1 nucleotide metabolism.synthesis.pyrimidine	trimer (8029359)	43	36	154	0.0348	0.00093	
4	At2g35040.1		phosphoribosylaminoimidazolecarboxamide formyltransferase	C		23.1.2 nucleotide metabolism.synthesis.purine		65	60	222	0.0560	0.00090	
3	At4g18440.1		adenylosuccinate lyase	C		23.1.2 nucleotide metabolism.synthesis.purine	tetramer (8366112 and 11841213)	60	53	282	0.0858	0.00156	
5	At3g57610.1		adenylosuccinate synthetase (ADSS)	C		23.1.2 nucleotide metabolism.synthesis.purine	homodimer (10669609)	53	49	148	0.0031	0.00006	
4	At1g74260.1		phosphoribosylformylglycinamide synthase	M	C	23.1.2 nucleotide metabolism.synthesis.purine		152		142	0.0680	0.00042	
5	At5g48960.1		similarity to 5'-nucleotidase	C	C	23.2 nucleotide metabolism.degradation		73	64	166	0.0045	0.00007	
3	At5g63980.1		3(2),5-bisphosphate nucleotidase			23.2 nucleotide metabolism.degradation		38		46 61	0.1035	0.00231	
3	At5g47840.1		adenylate kinase or ATP-AMP transphosphorylase	C	C	23.4 nucleotide metabolism.phosphotransfer and pyrophosphatases		31	25	69 68	0.0555	0.00201	
3	At5g63310.1		NDPK2-stromal	C	C	23.4 nucleotide metabolism.phosphotransfer and pyrophosphatases	heamer (8645740)	26	19	133	0.0190	0.00102	12938931(Total chloroplast envelope);

3	At5g09650.1		Inorganic phosphatase like	C	C	23.4 nucleotide metabolism.phosphotransfer and pyrophosphatases	33	26	61 52	0.0443	0.00123	12938931(Total chloroplast envelope);
4	At1g35420.1		dienelactone hydrolase family	C	C	26.1 misc.misc2 monomer (2380986)	34	30	28	0.0070	0.00022	
5	At4g15110.1		cytochrome P450-type monoxygenase CYP97B3; beta hydroylase	M	C	26.10 misc.cytochrome P450	65		163	background level	background level	
5	At1g09390.1		GDSL-motif lipase/hydrolase family protein	S		26.28 misc.GDSL-motif lipase	40		360	background level	background level	
3	At1g75690.1		DnaJ domain family	C	C	26.29* misc. DnaJ domain with unknown function	16	12	34	0.0363	0.00274	15322131(Thylakoid-stripped);
4	At4g04020.1		fibrillin	C	C	26.31* misc. fibrillins	35	29	112	0.0053	0.00017	11719511(Thylakoid lumen proteome); 14617066(Nuclear proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
3	At3g05625.1		epressed protein (TPR)	C		26.33* misc. tetratricopeptide repeat (TPR) unknown function	29	23	71	0.0253	0.00106	
4	At5g53490.1		peptapetide repeat TL17.4 (PPR)	C	C	26.54* misc. Pentapeptide repeat (PPR) unknown function	26	17	99	0.0025	0.00014	11719511(Thylakoid lumen proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
5	At1g78380.1		putative glutathione transferase	-		26.9 misc glutathione S transferases dimer (8551521)	26		106	background level	background level	
3	At3g55040.1		gluthatione Transferase Lamda -2 (GSTL2) - chloroplast spinach	C	C	26.9 misc glutathione S transferases dimer (8551521)	33	27	50	0.0430	0.00140	
3	At4g02520.1	At2g02930.1	glutathione transferase Phi (ATGSTF2)	-		26.9 misc glutathione S transferases dimer (8551521)	24		64	0.0285	0.00107	
4	At5g26742.1		DEAD bo RNA helicase (RH3) - mRNA etiolated seedling	C	C	27.1 RNA.processing	81	74	980	0.0205	0.00028	
4	At3g03710.1		3'-5' eoribonuclease	C		27.1 RNA.processing homotrimer? (11680851 and 8605883)	100	94	410	0.0615	0.00055	
5	At1g77060.1		isocitrate lyase and coA biosynth domain	C	M	27.3.99 RNA.regulation of transcription.unclassified	37	33	147 119	0.0033	0.00009	
3	At1g31190.1		Inositol monophophatase-1	C		27.3.99 RNA.regulation of transcription.unclassified	40	34	85	0.0560	0.00141	
3	At4g24770.1		RNA binding protein CP31	C	C	27.4 RNA.RNA binding	36	26	28	0.2647	0.00696	12938931(Total chloroplast envelope); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
4	At2g37220.1		RNA binding protein CP29 B'	C	C	27.4 RNA.RNA binding	31	26	68	0.0045	0.00016	12938931(Total chloroplast envelope); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
3	At3g63140.1		mRNA binding protein, Rap41 or CSP41	C	C	27.4 RNA.RNA binding maybe change to endo nuclease hetero-59-mer (12605670 + 10874046)	44	36	946 224 126 107	0.2330	0.00583	12938931(Total chloroplast envelope);
3	At3g48420.1		haloacid dehalogenase-like hydrolase-2	C	C	28.1 DNA.synthesis/chromatin structure	34	27	94 73 69	0.0813	0.00251	12938931(Total chloroplast envelope);
4	At5g52520.1		tRNA synthetase class II	C	M	29.1 protein.aa activation	61	54	199	0.0195	0.00033	
4	At3g48110.1		aminoacyl-t-RNA synthetase	C		29.1 protein.aa activation dimer (6706990)	119	112	350	0.0205	0.00016	

4	ATCG00820	30S rps19 ribosomal protein S19	c-enc	c-enc	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	11		908	0.0058	0.00070	
4	ATCG01120	30S rps15 ribosomal protein S15	c-enc	c-enc	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	11		908	0.0058	0.00070	
4	At5g40950.1	50S ribosomal protein L27	C		29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	22	20	919	0.0153	0.00088	11826309(thylakoid peripheral&lumen);
4	At1g79850.1	30S ribosomal protein S17 chloroplast	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	16	11	915	0.0015	0.00012	12938931(Total chloroplast envelope);
4	At4g01310.1	50S ribosomal protein L5p family	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	28	24	224	0.0038	0.00014	12938931(Total chloroplast envelope);
4	At1g05190.1	50S ribosomal protein L6p family	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	25	18	925	0.0130	0.00062	12938931(Total chloroplast envelope);
4	At1g32990.1	50S ribosomal protein L11p	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	23	17	919	0.0153	0.00088	12938931(Total chloroplast envelope);
4	At1g35680.1	50S ribosomal protein L21	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	24	15	929	0.0149	0.00063	12938931(Total chloroplast envelope); 14617066(Nuclear proteome);
4	At3g52150.1	PSRP-2 associates with 30S	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	28	21	929	0.0149	0.00063	12938931(Total chloroplast envelope); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
3	At1g07320.1	50S ribosomal protein L4	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	31	27	929	0.0915	0.00333	14617066(Nuclear proteome); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
4	At2g33800.1	30S Ribosomal p S5 Isolog L13	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	33	27	929	0.0248	0.00072	14617066(Nuclear proteome); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
4	At3g63490.1	50S ribosomal protein L1p family	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	38	30	929	0.0248	0.00072	14617066(Nuclear proteome); 15322131(Thylakoid-stripped);
4	ATCG00650	30S rps18 ribosomal protein S18	c-enc	c-enc	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	12		915	0.0015	0.00012	12775770(Total chloroplast envelope);
5	At1g75350.1	50S ribosomal protein L31 chloroplast	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	16	13	212	0.0010	0.00009	12938931(Total chloroplast envelope);
4	At3g15190.1	30S ribosomal protein S20	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	22	14	925	0.0095	0.00050	
4	ATCG00380	30S rps4 ribosomal protein S4	c-enc	c-enc	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	23		929	0.0149	0.00063	
4	At3g44890.1	50S ribosomal protein L9	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	22	18	919	0.0153	0.00088	



3	At2g43030.1	50S ribosomal protein L3	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	29	24	929	0.0505	0.00200	
3	At3g25920.1	50S ribosomal protein L15	C	C	29.2.1 protein.synthesis.chloroplast - plastid ribosomal protein	hetero-59-mer (12605670 + 10874046)	30	23	929	0.0753	0.00290	
3	At5g13510.1	ribosomal protein L10	C	C	29.2.2 protein.synthesis.misc ribosomal protein	hetero-59-mer (12605670 + 10874046)	25	20	922	0.0250	0.00127	
4	At1g74970.1	30S ribosomal protein S9	C	C	29.2.2 protein.synthesis.misc ribosomal protein	hetero-59-mer (12605670 + 10874046)	23	17	919	0.0153	0.00088	12938931(Total chloroplast envelope);
3	At1g78630.1	30S ribosomal protein S5	C	C	29.2.2 protein.synthesis.misc ribosomal protein	hetero-59-mer (12605670 + 10874046)	27	21	922 929	0.0260	0.00114	11826309(thylakoid peripheral&lumen);
4	At1g13930.1	60S ribosome protein?	-	-	29.2.2 protein.synthesis.misc ribosomal protein		16		128	0.0105	0.00044	12938931(Total chloroplast envelope); 15060130(Plasma Membrane proteome);
5	At3g08740.1	elongation factor P (EF-P)	C	C	29.2.4 protein.synthesis.elongation		26	21	360	background level	background level	
4	At5g13650.1	elongation factor protein, typA/bipA like	C	C	29.2.4 protein.synthesis.elongation		74	68	980	0.0225	0.00032	
3	At1g62750.1	elongation factor Tu-G (EF-G)	C	C	29.2.4 protein.synthesis.elongation		86	78	132 128	0.2153	0.00234	12938931(Total chloroplast envelope);
2	At4g20360.1	elongation factor Tu (EF-Tu-1), plastid	C	C	29.2.4 protein.synthesis.elongation		52	45	111 151 148 129 163 480 132 949 959 604	0.4967	0.01035	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 14617066(Nuclear proteome); 15322131(Thylakoid-stripped);
5	At4g25370.1	ClpS1	C	-	29.3 protein.targeting	heteroheadecamer (14593120)	26	19	355 348	0.0017	0.00009	12938931(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen); 14593120(Plastid Stroma);
5	At2g20890.1	TF1 - thylakoid formation1	C	C	29.3 protein.targeting		34	27	270	background level	background level	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
4	At5g55220.1	Trigger Factor	C	C	29.3 protein.targeting		62	59	146 163	0.0443	0.00072	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope);
4	At1g65260.1	Vipp1 - mutant HCF155 - PspA like	C	C	29.3 protein.targeting	homo60mer?(15210715)	36	30	932	0.0210	0.00068	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 15322131(Thylakoid-stripped);
3	At4g12060.1	ClpS2	C	-	29.3 protein.targeting	heteroheadecamer (14593120)	27	20	348 355	0.0497	0.00237	12938931(Total chloroplast envelope); 14593120(Plastid Stroma);
4	At3g05350.1	aminopeptidase-2	-	-	29.5 protein.degradation		63		263	0.0075	0.00010	
4	At1g63770.1	aminopeptidase-1	C	M	29.5 protein.degradation		103	100	133	0.0555	0.00048	12938931(Total chloroplast envelope); 15215502(Vacuolar proteome);
3	At1g11750.1	ClpP6 (nClpP6)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	29	24	348 355	0.0481	0.00241	12938931(Total chloroplast envelope); 14593120(Plastid Stroma);
3	At5g45390.1	ClpP4 (nClpP4)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	31	25	360 370	0.1265	0.00475	12938931(Total chloroplast envelope); 14593120(Plastid Stroma);
4	At1g12410.1	ClpR2 (nClpP2)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	31	25	360	0.0109	0.00043	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope);
3	At1g02560.1	ClpP5 (nClpP1)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	32	26	360 355	0.0618	0.00281	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 14593120(Plastid Stroma);
4	At1g66670.1	ClpP3 (nClpP3)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	34	26	370	0.0230	0.00081	12938931(Total chloroplast envelope); 14593120(Plastid Stroma);
3	At4g17040.1	ClpR4 (nClpP9)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	33	26	360	0.0519	0.00200	12938931(Total chloroplast envelope); 14593120(Plastid Stroma);
4	At1g09130.1	ClpR3 (nClpP8)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	36	32	370	0.0230	0.00081	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 14593120(Plastid Stroma);

4	At1g49970.1		ClpR1 (nClpP5)	C	C	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	43	38	370	0.0230	0.00081	14593120(Plastid Stroma);
3	ATCG00670		ClpP1 (pClpP)	c-enc	c-enc	29.5.05 protein.degradation.serine protease	heteroheadecamer (14593120)	22		348 355	0.0481	0.00240	14593120(Plastid Stroma);
4	At5g65620.1		Zn oligopeptidase A (M3 family)	C	M	29.5.07 protein.degradation.metalloprotease		89	80	107	0.0620	0.00071	
4	At3g19170.1		Zn-MP - Zn-metalloprotease	C	M	29.5.07 protein.degradation.metalloprotease		121	112	120	0.0858	0.00063	12938931(Total chloroplast envelope);
3	At5g17710.1		GrpE-1	C	C	29.6 protein.folding	dimer/tetramer and in comple with HSP70 (11752390)	35	29	202 152 154	0.0473	0.00127	
3	At2g44650.1		Cpn10-1	C	C	29.6 protein.folding	heptamer and multiple forms (7738007 and 14499591)	15	11	170	0.0130	0.00150	
3	At1g36390.1		GrpE-2	C	C	29.6 protein.folding	dimer/tetramer and in comple with HSP70 (11752390)	31	24	197	0.0575	0.00195	
3	At3g01480.1		Tlp-40	C	C	29.6 protein.folding		48	44	46	0.2085	0.00464	11719511(Thylakoid lumen proteome); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
4	At5g49910.1	At4g24280.1	cpHSP70-2 (Dnak homologue)	C	C	29.6 protein.folding	heterotrimer (11752390)	77	67	215	0.0245	0.00032	12938931(Total chloroplast envelope);
2	At3g62030.1		peptidylprolyl isomerase ROC4	C	C	29.6 protein.folding		28	20	47 107 71	1.6748	0.07278	12938931(Total chloroplast envelope); 11719511(Thylakoid lumen proteome); 15322131(Thylakoid-stripped);
3	At1g55490.1	At3g13470.1 At5g56500.1	Cpn60-beta-2	C	C	29.6 protein.folding	heterotetradecamer (8754688)	64	58	807	0.1373	0.00224	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope);
2	At5g20720.1		Cpn21 (also Cpn20)	C	C	29.6 protein.folding	multiple form and compleed with CPN60 (7738007 and 14499591)	27	21	148 171	0.6505	0.02730	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
3	At5g50920.1	At3g48870.1	ClpC1	C	C	29.6 protein.folding	dimer ((14593120)	103	99	199 253	0.2498	0.00250	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 14593120(Plastid Stroma); 15322131(Thylakoid-stripped);
3	At4g24280.1	At5g49910.1	cpHSP70-1 (DnaK homologue)	C	C	29.6 protein.folding	heterotrimer (11752390)	77	67	123	0.5685	0.00726	12938931(Total chloroplast envelope); 14617066(Nuclear proteome); 11826309(thylakoid peripheral&lumen);
3	At2g28000.1		Cpn60-alpha-1	C	C	29.6 protein.folding	heterotetradecamer (8754688) and HMW comple with CPN21 when ADP or ATP added)	62	57	803 234 800	0.1698	0.00288	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 11826309(thylakoid peripheral&lumen);
3	At3g48870.1	At5g50920.1	ClpC2	C		29.6 protein.folding	dimer ((14593120)	106	101	199	0.1623	0.00162	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 14593120(Plastid Stroma);
3	At5g56500.1	At3g13470.1 At1g55490.1	Cpn60-beta-3	C	C	29.6 protein.folding	heterotetradecamer (8754688)	63	60	807	0.1373	0.00224	MitoDB(Mitochondrial proteome);
3	At3g13470.1	At5g56500.1 At1g55490.1	Cpn60-beta-1	C	C	29.6 protein.folding	heterotetradecamer (8754688) and HMW comple with CPN21 when ADP or ATP added)	63	58	807	0.1373	0.00224	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 14617066(Nuclear proteome);
4	At5g15450.1		ClpB3 -HSP100 family	C	C	29.6 protein.folding	dimer ((14593120)	109	102	986 627	0.0373	0.00034	14593120(Plastid Stroma);
5	At5g23120.1		HCF136 Tat Ttp	C		29.9* protein assembly and cofactor ligation		44	36	224	background level	background level	11719511(Thylakoid lumen proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);

5	At1g17160.1	ptkB type carbohydrate kinase protein	C		3.5 minor CHO metabolism.others		40	32	147	0.0013	0.00004	
4	At5g66530.1	aldose 1-epimerase	C	C	3.5 minor CHO metabolism.others	dimer (7317442)	34	30	61	0.0113	0.00031	
4	At1g04420.1	aldo/keto reductase family	C	C	3.5 minor CHO metabolism.others		46	41	111	0.0116	0.00025	12938931(Total chloroplast envelope);
5	At1g56050.1	GTP-binding protein	C	C	30.5 signalling.G-proteins		46	38	105	0.0015	0.00009	
4	At1g35720.1	Annein - AnnAt1	-		31.1 cell.organisation		36		61	0.0145	0.00034	11826309(thylakoid peripheral&lumen);
4	At1g11430.1	DAG protein -related	C	C	33.99 development.unspecified		26	20	929	0.0149	0.00063	12938931(Total chloroplast envelope);
5	At4g33520.1	PAA1 - copper transport envelope	C		34.12 transport.metal		24	23	16	background level	background level	
5	At1g21440.1	carboxyvinyl-carboxyphosphonate phosphorymutase	C	C	35.1 not assigned.no ontology		36	32	119	background level	background level	
4	At1g56500.1	haloacid dehalogenase-like hydrolase-1	C	C	35.1 not assigned.no ontology		114	108	27	0.0190	0.00070	
5	At4g02530.1	thylakoid lumen protein TL16.5	C	C	35.1 not assigned.no ontology		24	16	76	0.0005	0.00003	11719511(Thylakoid lumen proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
3	At1g16880.1	uridylyltransferase-related	C	C	35.1 not assigned.no ontology		31	26	721 32 287	0.0760	0.00238	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
5	At1g15140.1	oidoreductase NAD-binding domain-containing protein	C	C	35.1 not assigned.no ontology		32	27	94	background level	background level	12938931(Total chloroplast envelope);
3	At4g39970.1	haloacid dehalogenase-like hydrolase-3	C	C	35.1 not assigned.no ontology		35	30	50	0.0430	0.00140	12938931(Total chloroplast envelope);
4	At2g31670.1	NADH-ubiquinone oidoreductase B16.6	M	M	35.1 not assigned.no ontology		29		41	0.0250	0.00094	
5	At3g01510.1	phosphatase; starch binding?	C	C	35.2 not assigned.unknown		66	59	311	0.0060	0.00009	
4	At2g30200.1	malonyl-CoA:Acyl carrier protein transacylase	C	M	35.2 not assigned.unknown		42	34	202	0.0078	0.00021	
4	At4g16060.1	epressed protein (carrier?)	-		35.2 not assigned.unknown		27		69	0.0163	0.00052	
4	At1g51100.1	epressed protein	C	C	35.2 not assigned.unknown		24	20	929	0.0149	0.00063	
4	At1g62780.1	epressed protein	C	C	35.2 not assigned.unknown		27	26	101 116	0.0238	0.00092	
3	At2g45990.1	epressed protein	-		35.2 not assigned.unknown		30		46	0.0775	0.00244	
3	At1g50900.1	Epressed protein - ankyrin domain	C	C	35.2 not assigned.unknown		19	12	16	0.0293	0.00246	
3	At2g33180.1	NifU_C domain protein	C		35.2 not assigned.unknown		18	11	16	0.0293	0.00246	
3	At4g21445.1	receptor-interacting protein (PRIP)	C		35.2 not assigned.unknown		18	11	16	0.0293	0.00246	
3	At5g66090.1	UspA domain domain (stress)	C	C	35.2 not assigned.unknown		23	16	38	0.1060	0.00564	
3	At4g34090.1	epressed protein	C	C	35.2 not assigned.unknown		37	33	28	0.2647	0.00715	
3	At1g09340.1	unknown protein	-		35.2 not assigned.unknown	hetero-59-mer (12605670 + 10874046)	43		946 604 602 151 126 107 450 319 224	0.2695	0.00691	12938931(Total chloroplast envelope);
5	At2g24020.1	epressed protein YbaB family	C	C	35.2 not assigned.unknown		20	14	61	background level	background level	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
4	At3g55760.1	importin doman protein	C	C	35.2 not assigned.unknown		66	59	113	0.0085	0.00013	
4	At2g47390.1	G-protein domain	C	M	35.2 not assigned.unknown		106	99	185	0.1090	0.00098	

3	At2g37660.1		3-beta-hydroxy-delta5-steroid dehydrogenase	C	C	35.2 not assigned.unknown		35	28	112 51 73	0.1498	0.00461	
3	At5g51820.1		plastid phosphoglucomutase (PGM1) (starch free mutant 1)	C	C	4.02 glycolysis.PGM		68	62	100 79	0.0860	0.00132	12938931(Total chloroplast envelope);
4	At4g24620.1		glucose-6-phosphate isomerase	C	C	4.03 glycolysis.G6PIsomerase	dimer (11758906)	67	62	163 160 166	0.0553	0.00089	12938931(Total chloroplast envelope);
5	At3g55440.1		triosephosphate isomerase 2 (TPI-2)	-		4.08 glycolysis.TPI	dimer (2392479 and 2732453)	27		128	0.0015	0.00005	MitoDB(Mitochondrial proteome);
4	At5g52920.1		pyruvate kinase-2 (typically homotetramer)	C	C	4.13 glycolysis.PK	heteroheamer (plastid) and homotetra (cytoplasm) (10880971 and 11913971)	64	57	304	0.0210	0.00035	
4	At3g22960.1		pyruvate kinase-1 (typically homotetramer)	C	C	4.13 glycolysis.PK	heteroheamer (plastid) and homotetra (cytoplasm) (10880971 and 11913971)	65	60	306	0.0150	0.00024	
4	At4g15530.1		pyruvate phosphate dikinase family protein	-		6.05 gluconeogenesis/ glycolate cycle.pyruvate dikinase	heteroheamer (plastid) and homotetra (cytoplasm) (10880971 and 11913971)	98		306	0.0683	0.00065	
4	At5g13420.1		transaldolase-1	C	C	7.2 OPP.non-reductive PP		48	41	91	0.0360	0.00078	MitoDB(Mitochondrial proteome);
4	At2g43090.1		aconitase	C	C	8.1.03 TCA / org. transformation.TCA.aconitase	monomer (1648348 and 7713917)	27	20	44	0.0075	0.00029	
3	At3g47520.1		malate dehydrogenase [NAD], plastidic	C	C	8.2.09 TCA / org. transformation.other organic acid transformaitons.cyt MDH	dimer (10574915)	42	34	154 323	0.0478	0.00131	12775770(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
3	At5g58330.1		malate dehydrogenase [NADP]	C	C	8.2.09 TCA / org. transformation.other organic acid transformaitons.cyt MDH	dimer (10574915)	48	43	96 109	0.1550	0.00352	12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome);
3	At1g04410.1		malate dehydrogenase, cytosolic,	-		8.2.09 TCA / org. transformation.other organic acid transformaitons.cyt MDH	dimer (10574915)	36		151	0.0398	0.00100	14617066(Nuclear proteome);
2	At3g01500.2	<i>At5g14740.1</i>	carbonic anhydrase-1 (CA1)	C	C	8.3 TCA / org. transformation.carbonic anhydrases	homoheam, octa or decamer (9413559, 413832, 10431928)	30		112 224 270 219 140 124 106 116 101 205 360	1.0516	0.04076	12938931(Total chloroplast envelope); 12775770(Total chloroplast envelope); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
5	At5g14740.1	At3g01500.1	carbonic anhydrase 2 (CA2)	-	C	8.3 TCA / org. transformation.carbonic anhydrases	homoheam, octa or decamer (9413559, 413832, 10431928)	37		112	background level	background level	12938931(Total chloroplast envelope); 15322131(Thylakoid-stripped);
5	At4g15510.1		OEC23-like-3 Tat ITP	C	C	1.1.02 PS.lightreaction - Photosystem II		32	21	929	background level	background level	11719511(Thylakoid lumen proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen);
4	At4g21280.1		psbQ OEC16 Tat Itp	C	C	1.1.02 PS.lightreaction - Photosystem II		24	16	919	0.0153	0.00088	11719511(Thylakoid lumen proteome); 14729914(thylakoid-pheripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);

3	At3g50820.1	At5g66570.1	psbO OEC33-like	C	C	1.1.02 PS.lightreaction - Photosystem II		35	27	125 153	0.0785	0.00261	11719511(Thylakoid lumen proteome); 14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
3	At5g66570.1	At3g50820.1	psbO OEC33	C	C	1.1.02 PS.lightreaction - Photosystem II		35	32	153 125	0.0785	0.00261	11719511(Thylakoid lumen proteome); 14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
2	At1g06680.1		psbP OEC23 Tat ITP	C	C	1.1.02 PS.lightreaction - Photosystem II		28	20	922 246	0.4300	0.01911	12938931(Total chloroplast envelope); 11719511(Thylakoid lumen proteome); 14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
5	At4g28660.1		psbW -like sequencing project	C	C	1.1.02 PS.lightreaction - Photosystem II		20	15	89 96	background level	background level	14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 15322131(Thylakoid-stripped);
4	At5g66190.1		FNR-1	C	C	1.1.07 PS.lightreaction.ferredoin reductase		40	34	126 107	0.0176	0.00043	12938931(Total chloroplast envelope); 11719511(Thylakoid lumen proteome); 12775770(Total chloroplast envelope); 14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);
3	At1g20020.1		FNR-2	C	C	1.1.07 PS.lightreaction.ferredoin reductase		41	35	107 126 151 132	0.1006	0.00258	14729914(thylakoid stripped); 15322131(Thylakoid-stripped);
4	ATCG00480		CF1b - atpB	c-enc	c-enc	1.1.08 PS.lightreaction - ATP synthase	tetracosamer (155058, 2142688, 10364459)	54		224	0.0460	0.00082	11719511(Thylakoid lumen proteome); 14729914(thylakoid-peripheral&lumen); 14729914(thylakoid stripped); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped);

(a) Accession number from Tair. Note that only gene model (typically .1) is indicated. However, in most cases the mass spectrometry data also matched the other gene models - such details can be found in PPDB

(b) In some cases the mass spectrometry matched to more than 1 protein, making the identification (somewhat) ambiguous. Accessions in italics indicate that the mass spectrometry based identification was only ambiguous in some of the protein spots the protein was identified.

(c) Internal annotation in PPDB

(d) plastid localization prediction according to TargetP

(e) plastid localization prediction according to Predotar

(f) Functional assignment according to the MapMan Bin classification (Thimm et al, 2004) and reported in PPDB

(g) Oligomeric state as reported in the literature for orthologues of this protein in other species than *A. thaliana* or in very selected cases of exactly this protein.

(h) Calculated molecular mass of the precursor proteins, as reported in PPDB

(i) Calculated molecular mass of the processed proteins, as reported in PPDB

(j) Experimental native mass as determined from the CN-PAGE gels. If proteins were identified more than in one spot (e.g due to aggregation, smearing or truly different oligomeric states), these additional native masses are also listed.

(k) Relative protein amount, normalized to total amount on the CN-PAGE gel.

(l) Relative concentration (multiplied by 100) in the stroma as determined by normalize spot volume divided by experimental mass. If more than protein was identified in a spot, the spot volume was divided by the number of its protein components.

(m) This protein was also identified in the listed medium/large scale proteome paper

\*over estimated, aggregated at HMW, interestingly with other starch enzymes!!; Not identified at correct denatured mass.