

**Supplemental table** Catalog of proteins identified from Triton-insoluble pea chloroplast fraction. SDS-PAGE band numbers, correspond to polypeptides in figure 2, and apparent masses are noted in parentheses. Uninterpreted tandem mass spectrometry data were searched against the NCBI non-redundant database (June, 2004; Viridiplantae) using Mascot (Matrix Sciences) and XTandem (www.thegpm.org) which allows for single amino acid substitutions for cross-species searching. Genbank identification number, predicted mass, Mascot or XTandem (log(e)) score and number of identified tryptic peptides are shown. Subcellular target predictions were performed using ChloroP and TargetP prediction algorithms. If predictions from these two algorithms did not agree then a third algorithm (Predotar) was employed. Plastid targeting for the ChloroP algorithm were either Yes (Y) or No (N) based upon a probability score (in parentheses). Abbreviations for TargetP and Predotar subcellular localization algorithms are: C, chloroplast; O, other; M, mitochondria; N, neither plastid or mitochondria. TargetP prediction class (1 through 5) for each protein is noted in parentheses. Plastid-encoded (PE) and outer membrane (OM) proteins are noted. Abbreviations for plant sources are as follows: A, Arabidopsis thaliana; Cd, Ceratophyllum demersum; Ca, Cicer arietinum; C, Citrullus lanatus; Dc, Daucus carota; D, Drimys winteri; Ea, Encephalartos altensteinii; G, Glycine max; H, Helianthus anuus; Hordeum vulgare; Ls, Lactuca sativa; Lc, Lens culinaris; Ll, Liliun longiflorum; Lj, Lotus japonicus; La, Lupinus albus; Le, Lycopersicon esculentum; Md, Malus domestica; Ms, Medicago sativa; M, Mesembryanthemum crystallinum; Np, Nicotiana paniculata; Ns, Nicotiana sylvestris; Nt, Nicotiana tobacum; Oa, Opilia amentacea; Os, Oryza sativa; Pp, Physcomitrella patens; P, Pisum sativum; Pr, Prunus subhirtella; St, Solanum tuberosum; S, Spinacia oleracea; Sa, Sterculia apetala; Sl, Stylonychia lemnae; V, Vigna unguiculata; Z, Zea mays

<i>gi number</i>	<i>predicted mass</i>	<i>Mascot/</i>		<i>ChloroP (score)</i>	<i>TargetP (class)</i>	<i>Predotar</i>	<i>plant</i>	<i>protein</i>
		<i>XTandem score</i>	<i>matched peptides</i>					
<b>Band 1 (144 kDa)</b>								
15220209	157,055	396	23	N (0.494)	C (5)	N	A	starch excel protein
7431783	111,051	339	10	Y (0.579)	C (2)		G	glutamate synthase (ferredoxin)
12044358	156,582	-31.6	9	N (0.488)	C (5)	N	A	SEX1 protein
<b>2 (144 – 126 kDa)</b>								
6573745	172,811	132	4	N (0.494)	C (5)	N	A	unknown protein– similar to chloroplast R1 protein
7450925	154,514	73	3	Y (0.507)	C (4)	C (0.97)	Nt	protoporphyrin IX magnesium chelatase
37051123	63,822	-30.0	6	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor
13518436	121,501	-20.6	4		C (PE)		Lj	RNA polymerase beta subunit
1498315	109,982	-5.1	2	Y (0.574)	C (2)		P	Import intermediate associated protein 100
28416677	35,042	-1.9	1	Y (0.551)	C (1)		A	unknown protein
<b>3 (126 kDa)</b>								
7160671	63,979	110	3	N (0.445)	O (2)	N	A	endoribonuclease E
15240319	130,913	56	4	Y (0.562)	C (1)		A	glycoside hydrolase starch-binding domain protein
<b>4 (122 – 113 kDa)</b>								
7488820	98,786	828	21	Y (0.580)	C (1)		P	polyribonucleotide nucleotidyltransferase
7488813	110,523	337	7	Y (0.574)	C (2)		P	import intermediate-associated 100K protein precursor
7488796	69,741	265	12	N (0.463)	O (3)	C (0.50)	P	DNA-binding protein PD2
13518436	121,501	127	4		C (PE)		Lj	RNA polymerase beta subunit
15240319	130,913	70	2	Y (0.562)	C (1)		A	glycoside hydrolase starch-binding domain protein
4582783	98,742	-18.0	5	N (0.429)	O (4)	N	V	starch synthase, isoform V
<b>5 (113 kDa)</b>								
7488813	110,523	1746	59	Y (0.574)	C (2)		P	import intermediate-associated 100K protein precursor
11465946	121,156	522	18		C (PE)		Nt	putative RNA polymerase beta subunit
7488796	69,741	393	12	N (0.463)	O (3)	C (0.50)	P	DNA-binding protein PD2
4582783	99,137	183	7	N (0.429)	O (4)	N	V	starch synthase, isoform V
20453114	112,121	-5.9	3	Y (0.569)	C (1)		A	putative chloroplast inner envelope protein
15231854	15,225	-1.8	1	N (0.431)	O (1)	M (0.96)	A	histone, H2B putative
<b>6 (109 – 103 kDa)</b>								
7488796	69,741	918	37	N (0.463)	O (3)	C (0.50)	P	DNA-binding protein PD2
7488813	110,523	244	7	Y (0.574)	C (2)		P	import intermediate-associated 100K protein precursor
7619891	91,369	197	5	Y (0.569)	C (1)		P	acetyl-CoA carboxylase alpha subunit
32129333	102,334	-24.1	6	Y (0.562)	M (3)	M (0.83)	Oj	putative DNA gyrase subunit
4582783	98,742	-20.2	5	N (0.429)	O (4)	N	V	starch synthase, isoform V
1703061	67,702	-5.3	2		C (PE)		P	acetyl-CoA carboxylase carboxyltransferase subunit beta
<b>7 (103 kDa)</b>								

7619891	91,369	1377	41	Y (0.569)	C (1)		P	acetyl-CoA carboxylase alpha subunit	
15228353	102,261	237	11	Y (0.589)	C (1)		A	putative DNA gyrase subunit A	
1703061	67,702	115	3		C (PE)		P	acetyl-CoA carboxylase carboxyltransferase subunit beta	
15242755	58,180	-12.5	3	Y (0.577)	C (2)		A	hydrolase family	
7488796	69,741	-11.2	5	N (0.463)	O (3)	C (0.50)	P	DNA-binding protein PD2	
1345570	105,227	-5.5	1	Y (0.564)	C (3)	C (0.50)	P	starch branching enzyme 1	
473605	16,617	-2.3	1	N (0.428)	O (2)	N	Z	histone H2B	
<b>8 (99.8 kDa)</b>									
7619891	91,369	2141	80	Y (0.569)	C (1)		P	acetyl-CoA carboxylase alpha subunit	
3913218	83,099	397	12	Y (0.572)	C (3)		P	magnesium-chelatase subunit chld precursor	
100080	67,377	263	8		C (PE)		P	acetyl-CoA carboxylase beta-carboxyltransferase	
15242755	58,428	224	10	Y (0.577)	C (2)		A	putative protein	
15228353	102,261	71	4	Y (0.589)	C (1)		A	putative DNA gyrase subunit A	
28393617	100,554	-77.8	15	Y (0.577)	C (2)		A	unknown protein	
25278006	85,023	-27.4	8	Y (0.574)	C (3)	C (0.99)	A	unnamed protein product	
169128	102,711	-4.2	3	Y (0.561)	C (4)	C (0.99)	P	nuclear encoded precursor to chloroplast protein	
<b>9 (97.7 kDa)</b>									
461753	102,818	1295	38	Y (0.561)	C (4)	C (0.99)	P	ATP-dependent Clp protease ATP-binding subunit	
3913218	83,099	1149	39	Y (0.572)	C (3)		P	magnesium-chelatase subunit chld precursor	
1076524	96,660	690	15		C (OM)		P	chloroplast outer envelope protein OEP86 precursor	
1703061	67,702	541	17		C (PE)		P	acetyl-CoA carboxylase carboxyl transferase subunit beta	
15242755	58,428	133	5	Y (0.577)	C (2)		A	putative protein	
30681440	104,538	114	2	Y (0.589)	C (1)		A	DNA gyrase subunit A -related	
7619891	91,369	86	4	Y (0.569)	C (1)		P	acetyl-CoA carboxylase alpha subunit	
3721540	78,370	-21.4	5	Y (0.561)	C (1)		Nt	sulfite reductase	
15242755	58,180	-14.8	4	Y (0.577)	C (2)		A	hydrolase family	
7488796	69,498	-4.8	2	N (0.463)	O (3)	C (0.51)	P	DNA-binding protein PD2	
25084218	93,726	-4.7	3	Y (0.575)	C (1)		A	putative helicase	
30698050	96,855	-3.9	1	Y (0.597)	C (1)		A	AAA-type ATPase family protein	
<b>10 (94.0 kDa)</b>									
1703061	67,702	636	27		C (PE)		P	acetyl-CoA carboxylase carboxyl transferase subunit beta	
710465	96,526	220	6		C (OM)		P	OEP86=outer envelope protein	
15226791	62,547	111	6	N (0.478)	C (4)	C (0.99)	A	unknown protein	
7488180	52,637	108	4	Y (0.561)	C (1)		A	probable RNA helicase	
37051123	63,822	-8.2	3	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor	
7488796	69,498	-7.4	3	N (0.463)	O (3)	C (0.51)	P	DNA-binding protein PD2	
22137204	78,998	-4.7	1	N (0.451)	O (4)	C (0.60)	A	putative ABC transporter	
15232029	40,551	-3.2	2	N (0.432)	O (2)	C (0.82)	A	zinc finger (C2H2 type) family protein	
26450692	60,895	-1.9	3	N (0.478)	C (4)	C (0.99)	A	unknown protein	
<b>11 (90.2 kDa)</b>									
7488180	52,637	258	10	Y (0.561)	C (1)		A	probable RNA helicase	
13548330	82,669	255	6	Y (0.536)	C (3)		A	putative protein	
15237634	84,615	249	7	Y (0.558)	M (4)	M (0.99)	A	DNA gyrase subunit B - like protein	
15221411	97,120	213	10	Y (0.542)	C (2)		A	unknown – similar to pentatricopeptide repeat protein	
399942	75,583	205	6	Y (0.589)	C (1)		P	chloroplast stroma 70 kD heat shock-related protein	
3721540	78,370	98	4	Y (0.561)	C (1)		Nt	sulfite reductase	
100080	67,377	77	3		C (PE)		P	acetyl-CoA carboxylase beta-carboxyltransferase	
28416497	81,000	-36.5	8	Y (0.561)	C (1)		A	unknown protein	
25406387	96,326	-19.9	5	Y (0.542)	C (2)		A	hypothetical protein	
7488796	69,741	-2.0	1	N (0.463)	O (3)	C (0.50)	P	DNA-binding protein PD2	
15081216	53,096	-1.3	1	Y (0.544)	C (5)	C (0.44)	A	glycine-rich protein GRP17	
<b>12 (84.9 kDa)</b>									
399942	75,583	995	33	Y (0.589)	C (1)		P	chloroplast stroma 70 kd heat shock-related protein	
2833384	84,192	540	21	Y (0.518)	O (4)	C (0.94)	P	glycogen [starch] synthase precursor	
15228245	72,847	492	23	N (0.428)	O (2)	N	A	putative DNA gyrase subunit B	
9621818	76,828	104	3	Y (0.549)	C (1)		G	acetyl-CoA carboxylase carboxyl transferase alpha subunit	
7433621	80,744	86	2	Y (0.592)	C (1)		S	transketolase precursor, chloroplast	

1363492	88,728	78	1		C (OM)		P	outer envelope membrane protein OEP75 precursor
3721540	78,370	69	2	Y (0.561)	C (1)		Nt	sulfite reductase
7436975	79,023	-5.8	2	N (0.447)	O (3)	N	Bn	tetrafunctional protein precursor, glyoxysomal
15081216	53,096	-1.1	1	Y (0.544)	C (5)	C (0.44)	A	glycine-rich protein GRP17
<b>13 (83.2 - 79.8 kDa)</b>								
1363492	88,728	653	18		C (OM)		P	outer envelope membrane protein OEP75 precursor
2833384	84,192	457	13	Y (0.518)	O (4)	C (0.94)	P	glycogen [starch] synthase precursor
12658639	64,124	321	14	Y (0.587)	C (1)		G	ferredoxin:sulfite reductase precursor
15237634	84,615	235	4	Y (0.558)	M (4)	M (0.99)	A	DNA gyrase subunit B - like protein
13518437	79,832	204	6		C (PE)		Lj	RNA polymerase beta subunit-1
27363456	69,242	-8.0	1	Y (0.500)	C (3)	N	A	ATP-dependent RNA helicase-like protein
445605	75,453	-4.0	1	Y (0.589)	C (1)		P	heat shock protein hsp70
15450593	78,413	-3.7	2	N (0.454)	O (2)	C (0.24)	A	putative acyl-CoA synthetase
<b>14 (73.6 kDa)</b>								
12658639	64,124	232	12	Y (0.587)	C (1)		G	ferredoxin:sulfite reductase precursor
1076416	72,391	210	9	Y (0.551)	C (2)		A	sulfite reductase (ferredoxin) precursor
9558534	48,760	-2.0	1	N (0.441)	O (3)	N	Os	unknown protein
<b>15 (70.8 kDa)</b>								
3721540	78,370	119	4	Y (0.561)	C (1)		Nt	sulfite reductase
7453538	64,498	-6.9	2		C (OM)		P	Toc64 chloroplast protein translocon
15228245	72,847	-4.4	1	N (0.428)	O (2)	N	A	putative DNA gyrase subunit B
<b>16 (67.3 kDa)</b>								
15239867	84,440	186	6	N (0.469)	S (1)	N	A	xylosidase
11358808	81,475	64	2	Y (0.561)	C (1)		A	RNA helicase RH3 [imported]
3721540	78,370	-9.1	4	Y (0.561)	C (1)		Nt	sulfite reductase
1185390	61,979	-7.7	2	Y (0.559)	C (2)		P	alpha Cpn60 precursor
7488180	52,637	-6.9	2	Y (0.561)	C (1)		A	probable RNA helicase
<b>17 (65.3 - 61.4 kDa)</b>								
2506277	63,287	649	20	Y (0.562)	C (1)		P	rubisco binding-protein beta subunit (60 kd chaperonin)
1710807	61,998	603	19	Y (0.559)	C (2)		P	rubisco binding-protein alpha subunit (60 kd chaperonin)
15626365	68,096	301	6	Y (0.540)	C (2)		P	granule-bound starch synthase
532217	52,830	-21.7	4		C (PE)		Oa	ribulose 1,5-bisphosphate carboxylase
21616072	56,901	-11.2	4	Y (0.540)	C (3)	C (0.26)	P	Tic62 chloroplast import protein
21536525	48,326	-8.3	3	Y (0.539)	C (5)	C (0.83)	A	dihydrolipoamide S-acetyltransferase, putative
870726	58,387	-2.9	1	Y (0.579)	C (3)	C (0.60)	Nt	biotin carboxylase subunit
<b>18 (59.0 - 57.8 kDa)</b>								
114522	54,649	300	6		C (PE)		P	ATP synthase alpha chain
532217	52,830	143	4		C (PE)		Oa	ribulose 1,5-bisphosphate carboxylase
114560	53,147	95	3		C (PE)		P	ATP synthase beta chain
37051123	63,822	-22.6	7	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor
15626365	67,626	-14.4	3	Y (0.540)	C (2)		P	granule-bound starch synthase
21536525	48,326	-5.2	2	Y (0.539)	C (5)	C (0.83)	A	dihydrolipoamide S-acetyltransferase, putative
<b>19 (56.4 kDa)</b>								
462187	57,371	1121	43	N (0.498)	M (3)	M (0.99)	P	serine hydroxymethyltransferase (serine methylase)
114560	53,147	699	25		C (PE)		P	ATP synthase beta chain
3893097	54,206	697	29		C (PE)		P	ribulose 1,5-bisphosphate carboxylase, large subunit
21464567	60,757	-58.1	8	Y (0.589)	C (1)		A	putative dihydrolipoamide dehydrogenase
15292887	60,145	-51.5	7	Y (0.577)	C (1)		A	unknown protein
114522	54,649	-48.6	9		C (PE)		P	ATP synthase alpha chain
21536525	48,326	-27.7	5	Y (0.539)	C (5)	C (0.83)	A	dihydrolipoamide S-acetyltransferase, putative
3219361	58,808	-14.5	4	Y (0.558)	C (2)		G	biotin carboxylase precursor
<b>20 (54.2 kDa)</b>								
3893097	54,206	956	60		C (PE)		P	ribulose 1,5-bisphosphate carboxylase, large subunit
3219361	58,808	-96.3	14	Y (0.558)	C (2)		G	biotin carboxylase precursor

169158	57,293	-86.3	12	N (0.498)	M (3)	M (0.99)	P	serine hydroxymethyltransferase
21536525	48,326	-18.0	2	Y (0.539)	C (5)	C (0.83)	A	dihydrolipoamide S-acetyltransferase, putative
11357296	53,781	-5.0	1	Y (0.507)	C (3)	C (0.94)	A	fructokinase-like protein
<i>21 (51.8 kDa)</i>								
3869088	49,629	543	28	N (0.432)	O (2)	N	Np	elongation factor-1 alpha
3746903	57,521	532	23	Y (0.571)	C (1)		P	signal recognition particle 54 kDa subunit precursor
6572433	52,941	200	9		C (PE)		O a	1,5-bisphosphate carboxylase/oxygenase large subunit
15230922	50,106	184	9	Y (0.592)	C (1)		A	dihydrolipoamide S-acetyltransferase
30680397	56,873	-4.7	2	Y (0.561)	M (2)	M (0.99)	A	DNA topoisomerase, ATP-hydrolyzing, putative
<i>22 (49.2 – 47.2 kDa)</i>								
5917745	49,770	362	13	N (0.432)	O (2)	N	LI	elongation factor-1 alpha 2
532217	52,830	201	7		C (PE)		Oa	ribulose 1,5-bisphosphate carboxylase, large subunit
7387729	15,957	-7.4	1	N (0.431)	O (2)	N	Nt	histone H2B
15237634	84,615	-4.3	1	Y (0.558)	M (4)	M (0.99)	A	DNA gyrase subunit B - like protein
28973141	55,611	-4.0	1	Y (0.562)	C (1)		A	unknown protein
<i>23 (45.4 kDa)</i>								
6015084	53,131	707	28	Y (0.595)	C (1)		P	elongation factor tu (EF-TU)
120663	48,580	229	5	Y (0.536)	C (2)		P	glyceraldehyde 3-phosphate dehydrogenase b
4733939	51,633	137	3	Y (0.544)	C (3)		G	geranylgeranyl hydrogenase
421845	48,028	108	2	Y (0.573)	C (2)		A	recombination protein recA homolog
3738234	77,963	-32.3	5	Y (0.561)	C (1)		Nt	sulfite reductase
20857316	51,838	-32.1	3	Y (0.580)	C (2)		A	geranylgeranyl reductase
3659909	54,559	-3.6	1	Y (0.522)	M (4)	N	A	histidyl-tRNA synthetase
4558676	111,490	-2.6	1	Y (0.505)	C (1)		A	hypothetical protein
<i>24 (44.0 – 41.9 kDa)</i>								
120663	48,580	930	29	Y (0.536)	C (2)		P	glyceraldehyde 3-phosphate dehydrogenase b
3915699	44,656	551	14	N (0.447)	M (3)	N	P	aminomethyltransferase (glycine cleavage t protein)
3914605	48,217	361	11	Y (0.590)	C (1)		Md	ribulose bisphosphate carboxylase/oxygenase activase
7488841	35,878	244	8	Y (0.502)	C (5)	M (0.58)	P	ribonuclease S5 homolog
2500098	48,159	241	6	Y (0.574)	C (2)		A	DNA repair protein RecA
7434544	50,594	225	10	Y (0.583)	C (1)		St	phosphoglycerate kinase precursor
133405	39,194	196	7		C (PE)		P	DNA-directed RNA polymerase alpha chain
121344	47,346	-16.7	4	Y (0.557)	C (3)	C (0.99)	P	glutamine synthetase leaf isozyme, chloroplast precursor
3738234	77,963	-16.6	4	Y (0.561)	C (1)		Nt	sulfite reductase
3122053	49,294	-14.6	3	N (0.431)	O (3)	N	P	elongation factor 1-alpha
15224351	41,915	-14.0	1	Y (0.579)	C (1)		A	cysteine synthase (cpACS1)
15231854	15,225	-7.0	1	N (0.431)	O (1)	M (0.96)	A	histone, H2B putative
4678934	42,275	-5.8	1	Y (0.508)	M (5)	C (0.47)	A	putative protein
<i>25 (41.0 kDa)</i>								
15230174	47,885	728	18	Y (0.586)	C (1)		A	putative fatty acid desaturase SBZIP, diiron protein
133405	39,194	694	26		C (PE)		P	DNA-directed RNA polymerase alpha chain
7488841	35,878	438	14	Y (0.502)	C (5)	M (0.58)	P	ribonuclease S5 homolog
7431421	31,335	284	12	N (0.463)	M (5)	N	Le	(S)-2-hydroxy-acid oxidase
120658	43,597	262	7	Y (0.564)	C (2)		P	glyceraldehyde 3-phosphate dehydrogenase a
7488822	48,266	180	5	Y (0.570)	C (2)		P	ppf-1 protein, chloroplast membrane protein
15450707	47,174	-35.4	5	Y (0.573)	C (1)		A	pyruvate dehydrogenase E1 alpha subunit
3914605	48,217	-30.7	6	Y (0.590)	C (1)		Md	ribulose bisphosphate carboxylase/oxygenase activase
3850621	42,158	-23.7	4	N (0.489)	O (4)	C (0.97)	A	putative RNA binding protein
15224351	41,915	-20	2	Y (0.579)	C (1)		A	cysteine synthase (cpACS1)
4678934	42,275	-9.2	2	Y (0.508)	M (5)	C (0.47)	A	putative protein
1885326	39,026	-5.2	2	Y (0.552)	C (2)		P	phosphoribulokinase
289208	47,733	-5.0	1	Y (0.574)	C (2)		A	DNA repair protein (RecA homolog)
3738234	77,963	-4.4	3	Y (0.561)	C (1)		Nt	sulfite reductase
7267399	33,696	-1.7	2	Y (0.569)	C (3)	C (0.99)	A	putative tetrahydrofolate synthase
<i>26 (39.4 – 38.5 kDa)</i>								
120658	43,597	835	30	Y (0.564)	C (2)		P	glyceraldehyde 3-phosphate dehydrogenase a

15230174	47,885	715	28	Y (0.586)	C (1)		A	putative fatty acid desaturase SBZIP, diiron protein
7488841	35,878	441	13	Y (0.502)	C (5)	M (0.58)	P	ribonuclease S5 homolog
15223294	47,600	319	13	Y (0.573)	C (1)		A	pyruvate dehydrogenase E1 alpha subunit
15217485	42,764	273	11	N (0.495)	O (4)	C (0.31)	A	putative RNA-binding protein
228403	40,907	240	9	N (0.431)	O (2)	N	Lc	glycolate oxidase
3915035	45,221	138	7	Y (0.558)	M (5)	C (0.94)	H	acyl-ACP desaturase (stearoyl-ACP desaturase)
15224351	41,915	126	9	Y (0.579)	C (1)		A	cysteine synthase (cpACS1)
38344868	46,145	-52.7	8	Y (0.566)	C (2)		Os	unknown protein
3850621	42,158	-34.8	6	N (0.489)	O (4)	C (0.97)	A	putative RNA binding protein
7488822	48,266	-28.2	4	Y (0.570)	C (2)		P	ppf-1 protein, chloroplast membrane protein
37051123	63,822	-15.7	3	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor
7387729	15,957	-6.1	1	N (0.431)	O (2)	N	Nt	histone H2B
15220670	44,245	-6.0	1	Y (0.579)	C (1)		A	pyruvate dehydrogenase E1 beta subunit –related
32489062	42,348	-4.9	2	N (0.447)	O (3)	C (0.60)	Os	stearoyl-ACP desaturase
4678934	42,275	-4.3	2	Y (0.508)	M (5)	C (0.47)	A	putative protein
133405	39,194	-3.8	2		C (PE)		P	DNA-directed RNA polymerase alpha chain
<b>27 (37.4 kDa)</b>								
15217485	42,764	293	8	N (0.495)	O (4)	C (0.31)	A	putative RNA-binding protein
7488841	35,878	218	4	Y (0.502)	C (5)	M (0.58)	P	ribonuclease S5 homolog
461987	49,623	208	6	N (0.432)	O (2)	N	Dc	elongation factor 1-alpha (EF-1-alpha)
120661	42,122	168	6	Y (0.524)	C (2)		Nt	glyceraldehyde 3-phosphate dehydrogenase a
231970	34,279	165	9	N (0.428)	O (3)	N	S	cysteine synthase (o-acetylserine sulfhydrylase)
15220670	44,245	130	6	Y (0.579)	C (1)		A	pyruvate dehydrogenase E1 beta subunit –related
15219038	37,525	118	5	Y (0.566)	C (2)		A	unknown protein
3334130	27,754	76	4	Y (0.569)	C (4)	C (0.97)	G	biotin carboxyl carrier protein of ACCase
3850621	42,158	-25.8	5	N (0.489)	O (4)	C (0.97)	A	putative RNA binding protein
26453355	43,941	-14.4	5	Y (0.597)	C (1)		Le	mRNA binding protein precursor
4995796	51,910	-7.8	2		C (PE)		Sa	proton-transporting ATP synthase
21280837	37,377	-3.8	3	Y (0.566)	C (2)		A	unknown protein
8886873	29,613	-2.0	1	Y (0.588)	C (1)		A	biotin carboxyl carrier protein isoform 1
<b>28 (36.3 – 34.8 kDa)</b>								
266742	43,163	367	11	Y (0.532)	C (4)		P	protochlorophyllide reductase
399024	38,747	310	9	Y (0.528)	C (2)		P	fructose-bisphosphate aldolase 1,
114640	41,841	293	11	Y (0.578)	C (1)		P	ATP synthase gamma chain
118049	35,240	273	8		C (PE)		P	apocytochrome f plastoquinol--plastocyanin reductase
7488830	42,106	260	5	Y (0.589)	C (1)		P	probable malate dehydrogenase
13430510	49,847	159	6	N (0.432)	O (2)	N	A	putative elongation factor 1-alpha protein
7488841	35,878	144	2	Y (0.502)	C (5)	M (0.58)	P	ribonuclease S5 homolog
15236930	44,152	108	3	Y (0.584)	C (5)	M (0.91)	A	putative protein - low similarity to vestitone reductase
15418698	43,717	107	4	Y (0.569)	C (1)		Le	transaldolase
1350625	23,481	81	2	Y (0.568)	C (1)		P	50S ribosomal protein L1
3334130	27,754	81	3	Y (0.569)	C (4)	C (0.97)	G	biotin carboxyl carrier protein of ACCase
15212142	41,494	70	4	Y (0.571)	C (3)		Os	putative O-acetylserine (thiol) lyase
15450597	37,525	67	4	Y (0.566)	C (2)		A	unknown protein
26450902	44,831	-7.2	1	Y (0.581)	C (1)		A	unknown protein
21280837	37,378	-7.1	2	Y (0.566)	C (2)		A	unknown protein
3080425	43,723	-6.2	2	Y (0.584)	C (5)	M (0.91)	A	putative protein
8886873	29,613	-2.5	1	Y (0.588)	C (1)		A	biotin carboxyl carrier protein isoform 1
<b>29 (33.8 kDa)</b>								
81946	43,319	701	46	Y (0.537)	C (4)	C (0.95)	P	protochlorophyllide reductase precursor
65613	37,897	462	19		C (PE)		P	plastoquinol—plastocyanin reductase cytochrome f
510190	34,193	273	6		C (OM)		P	chloroplast outer envelope protein 34
1350625	23,481	195	4	Y (0.568)	C (1)		P	50S ribosomal protein L1
15229443	37,780	114	3	Y (0.568)	C (1)		A	chloroplast ribosomal L1 – like protein
3293201	34,157	-40.0	7		C (OM)		P	GTP-binding protein
11022877	41,360	-12.8	2		C (PE)		Cd	photosystem II CP43 protein
32487387	41,183	-10.8	4	Y (0.567)	C (2)		Os	unknown protein
18377706	107,797	-2.0	1	Y (0.530)	C (5)	N	A	DNA-binding family protein
15238764	20,313	-1.5	1	N (0.470)	M (4)	C (0.99)	A	Gar1 RNA-binding region family protein

## 30 (32.8 kDa)

81946	43,319	703	29	Y (0.537)	C (4)		P	protochlorophyllide reductase precursor
118049	35,240	498	22		C (PE)		P	apocytochrome f plastoquinol--plastocyanin reductase
1350625	23,481	486	24	Y (0.568)	C (1)		P	50S ribosomal protein L1
510190	34,193	370	12		C (OM)		P	chloroplast outer envelope protein 34
15229443	37,780	284	11	Y (0.568)	C (1)		A	chloroplast ribosomal L1 - like protein
1346848	52,126	187	5		C (PE)		P	photosystem II 44 kDa reaction center protein
119157	49,850	128	3	N (0.431)	O (2)	N	Sl	elongation factor 1-alpha (EF-1-alpha)
3293201	34,157	-59.0	8		C (OM)		P	GTP-binding protein
31432862	42,766	-8.4	3	Y (0.519)	C (4)	N	Os	putative pyruvate dehydrogenase
15005009	37,870	-6.4	1	Y (0.581)	C (1)		A	APG1

## 31 (31.6 kDa)

119905	40,454	332	10	Y (0.553)	C (1)		P	ferredoxin-NADP reductase
266742	43,163	307	11	Y (0.532)	C (4)	C (0.95)	P	protochlorophyllide reductase
1350625	23,481	220	6	Y (0.568)	C (1)		P	50s ribosomal protein L1
65613	37,897	194	7		C (PE)		P	plastoquinol--plastocyanin reductase cytochrome f
6635349	21,664	162	3	N (0.474)	C (5)	N	Ls	37 kDa chloroplast inner envelope membrane protein
15230982	23,834	139	2	Y (0.583)	C (2)		A	putative peroxidoredoxin
15450737	37,780	139	5	Y (0.568)	C (1)		A	50S ribosomal protein L1
13877771	35,120	129	4	Y (0.543)	C (4)	C (0.98)	A	unknown protein
15237163	32,980	125	5	Y (0.506)	M (5)	C (0.99)	A	fibrillarin-like
3914666	30,506	80	3	Y (0.576)	C (2)		A	50S ribosomal protein L4, (R-protein L4)
29893583	46,354	-15.1	4	Y (0.592)	C (1)		Os	unknown protein
7439756	15,671	-13.3	3	N (0.428)	O (1)	N	Le	histone H2B

## 32 (30.3 kDa)

119905	40,454	986	43	Y (0.553)	C (1)		P	ferredoxin-NADP reductase
131384	35,100	203	9	Y (0.518)	M (5)	C (0.36)	P	chloroplast oxygen-evolving enhancer protein 1 (33 kDa)
13877771	35,120	107	5	Y (0.543)	C (4)	C (0.98)	A	unknown protein
4583548	39,939	96	5	Y (0.550)	C (2)		A	chloroplast FtsYhomolog
81946	43,319	88	2	Y (0.537)	C (4)	C (0.95)	P	protochlorophyllide reductase precursor
7413642	30,567	-18.0	3	Y (0.545)	C (5)	C (0.99)	A	putative protein
15983608	38,846	-14.8	3		C (PE)		Pr	photosystem II D1 protein
1350550	31,537	-14.4	2	N (0.438)	O (2)	N	C	serine acetyltransferase
37051123	63,822	-12.6	4	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor
16974682	35,364	-10.5	2	Y (0.588)	C (2)		Ms	iron-superoxide dismutase precursor
7387729	15,957	-6.6	1	N (0.431)	O (2)	N	Nt	histone H2B

## 33 (28.5 kDa)

7446357	32,131	396	13	Y (0.587)	C (1)		P	RNA-binding protein
4930128	35,083	325	13	Y (0.553)	C (1)		P	ferredoxin--NADP reductase
1361979	31,859	216	10	N (0.438)	O (2)	N	C	serine O-acetyltransferase
400994	29,890	123	4	Y (0.531)	C (1)		P	chloroplast 50S ribosomal protein L2
6840824	27,451	93	5	N (0.439)	O (4)	N	V	iron-superoxide dismutase precursor
3986172	34,416	91	4	N (0.464)	S (1)	C (0.44)	P	endoxyloglucan transferase
15233005	34,239	83	2	Y (0.530)	C (2)		A	unknown protein
23296698	34,811	-9.5	1	Y (0.530)	C (2)		A	unknown protein
25991545	29,828	-8.1	2	N (0.456)	O (5)	N	Z	satase isoform III
21309	24,513	-5.3	2	Y (0.586)	C (1)		S	28 kD RNA binding protein
7487951	33,796	-4.6	1	Y (0.585)	C (2)		A	magnesium-protoporphyrin IX methyltransferase

## 34 (27.9 kDa)

7446357	32,131	338	10	Y (0.587)	C (1)		P	RNA-binding protein
400994	29,890	258	8	Y (0.531)	C (1)		P	chloroplast 50S ribosomal protein L2
729842	35,709	189	6	Y (0.575)	C (2)		P	membrane-associated 30 kDa protein
1172558	29,579	150	4		C (OM)		P	outer plastidial membrane protein porin
133247	25,330	97	4	Y (0.586)	C (1)		S	28 kDa ribonucleoprotein, chloroplast (28RNP)
1361979	31,859	80	2	N (0.438)	O (2)	N	C	serine O-acetyltransferase
1076251	32,001	76	2	Y (0.586)	C (1)		M	RNA-binding protein
15076863	32,941	74	3	Y (0.572)	C (3)		P	putative heme oxygenase 1

7439754	15,035	-7.9	3	N (0.432)	O (2)	N	Le	histone H2B-3 (fragment)
7487951	33,796	-6.5	1	Y (0.585)	C (2)		A	magnesium-protoporphyrin IX methyltransferase
<b>35 (27.4 – 26.8 kDa)</b>								
1172558	29,579	554	26		C (OM)		P	outer plastidial membrane protein porin
729842	35,709	243	8	Y (0.575)	C (2)		P	membrane-associated 30 kDa protein
7431035	28,633	74	2	Y (0.514)	C (4)	C (0.47)	A	3-oxoacyl-[acyl-carrier-protein] reductase
1076251	31,963	-9.9	3	Y (0.586)	C (1)		M	RNA-binding protein
10178029	37,206	-6.2	2	Y (0.576)	C (3)	C (0.96)	A	unnamed protein product
<b>36 (26.8 – 25.2 kDa)</b>								
400986	27,867	411	14	Y (0.554)	C (2)		P	50S ribosomal protein L15
1172558	29,579	335	10		C (OM)		P	outer plastidial membrane protein porin
2780194	42,305	249	10	N (0.487)	O (4)	N	La	adenine nucleotide translocator
15081739	31,249	209	7	Y (0.519)	C (3)		A	chlorophyll a/b-binding protein CP29
629728	29,403	159	8	N (0.452)	O (3)	N	St	porin I, 36K
629557	33,937	82	4	Y (0.587)	C (4)	C (0.99)	A	RNA-binding protein RNP-D precursor
11762118	33,755	73	2	Y (0.514)	C (4)	C (0.47)	A	3-oxoacyl-[acyl carrier protein] reductase
6634469	37,750	-24.6	4	Y (0.548)	C (2)		Le	putative ascorbate peroxidase
298036	31,139	-22.4	5	Y (0.538)	C (3)	C (0.96)	A	light harvesting complex b4
28950693	15,082	-14.3	3	N (0.431)	O (1)	M (0.99)	A	putative histone H2B
14597792	41,176	-13.2	5	Y (0.538)	M (5)	C (0.95)	Pp	unnamed protein product
37051123	63,822	-12.6	3	Y (0.579)	C (2)		P	ferredoxin:sulfite reductase precursor
18377498	31,823	-3.2	1	Y (0.516)	C (2)		A	putative protein
21592994	33,854	-2.7	2	Y (0.579)	C (1)		A	unknown protein
<b>37 (24.7 kDa)</b>								
400986	27,867	454	19	Y (0.554)	C (2)		P	50S ribosomal protein L15
115814	28,565	300	10	Y (0.562)	C (2)		Ms	chlorophyll a/b binding protein 8
7440606	28,352	290	12	Y (0.531)	C (1)		Nt	ribosomal protein L3 precursor, chloroplast
15081739	31,249	276	10	Y (0.519)	C (3)		A	chlorophyll a/b-binding protein CP29
133913	27,167	129	3		C (PE)		P	chloroplast 30S ribosomal protein S2
729930	28,513	108	6	N (0.467)	S (1)	N	P	nonseed lectin precursor
15229506	31,442	99	3	N (0.445)	O (3)	C (0.92)	A	xyloglucan endotransglycosylase, putative
11022885	35,634	91	3		C (PE)		D	photosystem II D2 protein
133248	35,255	88	3	Y (0.552)	C (3)		Ns	31 kDa ribonucleoprotein
6634469	37,750	-35.0	8	Y (0.548)	C (2)		Le	putative ascorbate peroxidase
37051123	63,822	-34.7	6	Y (0.579)	C (2)		G	ferredoxin:sulfite reductase precursor
445116	31,311	-23.1	7	Y (0.521)	C (2)		Hv	light-harvesting complex IIa protein
18377498	31,823	-10.2	6	Y (0.516)	C (2)		A	putative protein
3738333	35,142	-9.9	6	Y (0.583)	C (2)		A	putative chloroplast initiation factor 3
18176428	28,837	-8.4	3	Y (0.570)	C (1)		A	unknown protein
7413646	14,544	-6.1	2	N (0.433)	O (1)	N	A	histone H2B
737169	35,787	-3.5	1	Y (0.587)	C (1)		A	RNA-binding protein
21592994	33,854	-2.7	1	Y (0.579)	C (1)		A	unknown protein
<b>38 (24.0 kDa)</b>								
400986	27,867	331	11	Y (0.554)	C (2)		P	50S ribosomal protein L15
133913	27,167	302	13		C (PE)		P	chloroplast 30S ribosomal protein S2
3928140	28,357	294	18	Y (0.571)	C (2)		Ca	chlorophyll a/b binding protein 8
7440606	28,352	231	9	Y (0.531)	C (1)		Nt	ribosomal protein L3 precursor, chloroplast
7439754	15,035	167	7	N (0.432)	O (2)	N	Le	histone H2B-3 (fragment)
2129885	20,977	101	7	N (0.432)	O (1)	N	P	HMGI/Y protein
6634469	37,750	-6.1	2	Y (0.548)	C (2)		Le	putative ascorbate peroxidase
<b>39 (23.3 kDa)</b>								
15487307	28,995	254	8	Y (0.524)	C (3)		G	ferritin
3928140	28,357	237	8	Y (0.571)	C (2)		Ca	chlorophyll a/b binding protein
7488821	23,482	220	7	Y (0.511)	O (3)	N	P	pore protein 24K chain
2129885	20,977	220	11	N (0.432)	O (1)	N	P	HMGI/Y protein $\beta$
15241858	14,535	187	10	N (0.433)	O (1)	N	A	histone H2B, putative
8569250	24,209	183	6	Y (0.594)	C (1)		P	carbonic anhydrase

122083	15,213	150	5	Y (0.547)	C (3)	Ea	histone H3
19184	30,575	138	6	Y (0.563)	C (3)	Le	chlorophyll a/b-binding protein CP29
13518426	23,366	100	3		C (PE)	Lj	30S ribosomal protein S4
21536493	13,259	-16.7	6	Y (0.547)	C (2)	A	unknown protein