

Table S2. Proteins That Showed Multiple Localizations, Related to Figure 2

Phytozome v5.5 (Augustus u111.6) ID	Name	Localization	Predalga predicted localization	Putative function	Predicted Mw
Cre09.g416800	-	Cytosol and chloroplast	O	-	22.78
Cre12.g552450	-	Cytosol and chloroplast	O	-	11.85
Cre16.g685000	-	Cytosol and chloroplast	C	-	25.67
Cre07.g334800	FDX4	Cytosol and chloroplast	C	Ferredoxin	14.05
Cre09.g396400	UBQ2	Flagella and cytosol	O	Bi-ubiquitin	17.2
Cre03.g204577	DNJ31	Flagella and cytosol	C	DnaJ-like protein	61.75
Cre07.g321800	-	Flagella and cytosol	O	-	24.88
Cre11.g467617	LCI19	Flagella and cytosol	O	Gamma hydroxybutyrate dehydrogenase	30.24
Cre16.g685050	LCI15	Flagella and cytosol	C	PRLI-interacting factor L	34.34
Cre03.g158000	GSA1	Flagella, chloroplast and cytosol	C	Glutamate-1-semialdehyde aminotransferase	49.23
Cre17.g725500	-	Flagella, chloroplast and cytosol	C	-	13.82
Cre07.g337100	-	Flagella and mitochondria	C	-	10.75

Table S3. Proteins Used as Baits for the AP-MS Study, Related to Figure 5

Phytozome JGI v5.5 (Augustus u111.6) ID	Name	Protein description	Localization	Replica type (Biological, BR; Affinity Purification AR; Mass Spectrometry, MR)	Replica 1 MS ID	Replica 2 MS ID	Number of Preys with WD-score >1	Number of HCIPs (WD-score >47.52)
Cre01.g051500	ULP1	Uncharacterized thylakoid luminal polypeptide	Chloroplast not homogeneous with pyrenoid signal	MR	MAP30	T3B08	179	1
Cre01.g054850	-	-	Chloroplast not homogeneous with pyrenoid signal	AR	MAP17	T1D03	211	6
Cre02.g097800	HLA3	ABC transporter	Plasma membrane and late-secretory pathway	AR	MAP12	T2F06	372	36
Cre02.g120100	RBCS1	Rubisco small subunit 1	Pyrenoid matrix	BR	MAP23	T1D08	81	19
Cre02.g120150	RBCS2	Rubisco small subunit 2	Pyrenoid matrix	AR	MAP14	T2H06	104	20
Cre03.g151650	SMM7	-	Pyrenoid matrix	AR	MAP2	T1A12	303	5
Cre03.g162800	LCI1	Low-CO2-inducible membrane protein	Plasma membrane and late-secretory pathway	AR	MAP11	T1E12	266	7
Cre03.g179800	LCI24	Low-CO2-inducible membrane protein	Chloroplast homogeneous with pyrenoid signal	AR	MAP28	T2D06	249	3
Cre03.g191250	LCI34	Low-CO2-inducible protein	Chloroplast not homogeneous with pyrenoid signal	AR	MAP6	T2F03	239	5
Cre04.g223050	CAH2	Carbonic anhydrase, alpha type, periplasmic	ER	MR	MAP1	T1A07	323	34
Cre04.g223300	CCP1	Low-CO2-inducible chloroplast envelope protein	Mitochondria	AR	MAP22	T1C07	328	48
Cre04.g229300	RCA1	Rubisco activase	Pyrenoid matrix	AR	T3E8	T3E08	463	26
Cre05.g248450	CAH5	Mitochondrial carbonic anhydrase	Mitochondria	BR	MAP18	T1F02	290	19
Cre06.g283750	HST1	Homogentisate solanesyltransferase	Chloroplast not homogeneous with pyrenoid signal	AR	MAP32	T2F11	309	22
Cre06.g295450	HPR1	Hydroxypyruvate reductase	Mitochondria	MR	MAP21	T5D02	162	12
Cre06.g307500	LCIC	Low-CO2 inducible protein	Pyrenoid periphery punctate	MR	MAP4	T1C02	113	6
Cre06.g309000	LCIA	Anion transporter	Chloroplast envelope plus chloroplast homogeneous	AR	MAP9	T1C05	393	43
Cre07.g330250	PSAH	Subunit H of photosystem I	Pyrenoid tubules	AR	T2D2	T2D02	351	2
Cre08.g362900	PSBP4	Luminal PsbP-like protein	Pyrenoid periphery punctate	AR	MAP35	T3F12	234	24
Cre08.g372450	PSBQ	Oxygen-evolving enhancer protein 3	Chloroplast not homogeneous with pyrenoid signal	AR	MAP20	T3B04	134	3
Cre09.g394473	LCI9	Low-CO2-inducible protein	Pyrenoid periphery mesh	MR	T1E6	T1E06	200	4
Cre09.g415700	CAH3	Carbonic anhydrase 3	Chloroplast homogeneous with pyrenoid signal	AR	T1E9	T1E09	500	11
Cre10.g436550	EPYC1/LCI5	Low-CO2-inducible protein	Pyrenoid matrix	BR	LCI5MAP	T1C11	146	9
Cre10.g444700	SBE3	Starch branching enzyme	Pyrenoid periphery spherical	AR	MAP7	T2F05	212	4
Cre10.g452800	LCIB	Low-CO2-inducible protein	Pyrenoid periphery punctate	AR	T1E11	T1E11	136	3
Cre12.g485050	CAH6	Carbonic anhydrase 6	Flagella	MR	MAP5	T1D07	190	4
Cre12.g507300	LCI30	Low-CO2-inducible protein	Nucleus	MR	MAP27	T2C11	320	34
Cre12.g509050	PSBP3	OEE2-like protein of thylakoid lumen	Chloroplast not homogeneous with pyrenoid signal	AR	MAP25	T3G08	245	10
Cre12.g519300	TEF9	Predicted protein	Chloroplast homogeneous with pyrenoid signal	MR	MAP31	T1D04	180	1
Cre12.g560950	PSAG	Photosystem I reaction center subunit V	Chloroplast not homogeneous with pyrenoid signal	AR	MAP33	T3B03	145	2
Cre13.g577100	ACP2	Acyl-carrier protein	Chloroplast not homogeneous with pyrenoid signal	MR	MAP19	T3B02	189	26
Cre14.g626700	Fd/FDX1	Ferredoxin	Chloroplast not homogeneous with pyrenoid signal	AR	MAP29	T2D10	199	20
Cre16.g651050	CYC6	Cytochrome c ₆	Chloroplast not homogeneous with pyrenoid signal	AR	MAP10	T1D12	288	7
Cre16.g652800	-	-	Chloroplast homogeneous with pyrenoid signal	AR	MAP15	T1C01	281	2
Cre16.g662600	-	-	Chloroplast homogeneous pyrenoid disenriched	AR	MAP16	T1C04	371	23
Cre16.g663450	LCI11	Low-CO2-inducible membrane protein	Chloroplast homogeneous with pyrenoid signal	AR	MAP3	T1B12	284	6
Cre17.g721500	STA2	Granule-bound starch synthase I	Pyrenoid periphery spherical	AR	MAP13	T2F09	142	1
Cre17.g724300	PSAK	Photosystem I reaction center subunit psaK	Chloroplast not homogeneous with pyrenoid signal	AR	MAP34	T3B09	319	5
Totals							9451	513

Table S4. Cre16.g655050 BLAST Results, Related to Figure 6

Query cover is the percentage of the query sequence that matches the hit sequence. E-value is the expected value, the lower the E-value the more significant the hit.

Accession	Species	Query cover	E-value	Identity
XP_002950714.1	<i>Volvox carteri</i>	77%	4.0E-137	56%
KXZ52617.1	<i>Gonium pectorale</i>	71%	9.0E-127	56%
XP_005849673.1	<i>Chlorella variabilis</i>	31%	2.0E-53	56%
XP_005645512.1	<i>Coccomyxa subellipsoidea</i>	28%	2.0E-50	55%
XP_005847655.1	<i>Chlorella variabilis</i>	27%	5.0E-48	53%
XP_001698126.1	<i>Chlamydomonas reinhardtii</i>	10%	1.0E-29	100%
XP_013896920.1	<i>Monoraphidium neglectum</i>	16%	2.0E-29	60%
XP_002501227.1	<i>Micromonas commoda</i>	24%	1.0E-18	41%
XP_003062310.1	<i>Micromonas pusilla</i>	24%	2.0E-17	39%