

**Supplemental Table 2: Localization of identified proteins**

Identified proteins were analyzed for a chloroplast transit peptide using ChloroP (Emanuelsson et al., 1999; Protein Sci. 8, 978-84).

Proteins without a transit peptide were further grouped into plastid-encoded proteins, proteins that have a reported function in plastids or an Arabidopsis orthologue with a clear transit peptide, proteins that do not fall into any of the above categories but were detected in other plastid proteome studies (see also Supplemental Table 3), those with an unknown localization and putative true contaminants.

**CHLOROP predicts a Plastid Transit Peptide**

gi 99742	A41370	O	2-dehydro-3-deoxy-phosphoheptonate aldolase
gi 7573355	CAB87661	O	diaminopimelate decarboxylase-like protein
gi 7489279	T07790	O	transaldolase
gi 7489244	T07050	O/U	hypothetical protein R1
gi 7489185	T03843	C	prohibitin
gi 7488146	T05416	O/U	probable phosphoglycerate dehydrogenase
gi 7485588	T01258	U	hypothetical protein
gi 7484671	T09153	O	glucose-6-phosphate isomerase
gi 7450791	T09555	U/C	fibrillarin
gi 7441880	T08899	C	dnaK-type molecular chaperone HSC70-9
gi 7438127	T02431	O/U/C	acetyl-CoA carboxylase
gi 7437011	T07937	C	tryptophan synthase beta chain
gi 7433617	T09541	O	transketolase
gi 7431231	T06401	O/U/C	malate dehydrogenase
gi 7387849	O04974	O/U	2-isopropylmalate synthase B
gi 7331143	AAF60293	O/U	chaperonin 21
gi 729409	P41342	U/C	elongation factor TU
gi 7229675	AAF42936	U	glucose 6 phosphate/phosphate translocator
gi 7109469	AAF36733	O	putative enolase
gi 6939228	AAF31730	O	putative phosphoribosylformylglycinamide synthase
gi 6730768	AAF27157	U	putative alanine aminotransferase
gi 6723394	CAB66403	U	putative protein
gi 6714392	AAF26081	U	putative mitochondrial LON ATP-dependent protease
gi 6714365	AAF26055	U	unknown protein
gi 6690395	AAF24124	O	phosphoglucose isomerase
gi 6685804	O24578	U	adenylosuccinate synthetase
gi 6578124	AAF17705	O	ornithine carbamoyltransferase
gi 6456169	AAF09157	U	putative aminopeptidase
gi 6358779	AAF07360	U	unknown protein
gi 6319165	AAF07191	O	branched-chain amino acid aminotransferase

gi 6226239	O24381	U/C	plastidic ATP/ADP-transporter
gi 6014908	Q42948	O	dihydropicolinate synthase
gi 585421	P38418	U	lipoxygenase
gi 5701896	CAA47373	O	glutamate-ammonia ligase
gi 5532608	AAD44809	O/U	6,7-dimethyl-8-ribityllumazine synthase
gi 5123836	CAB45387	O	NAD-malate dehydrogenase
gi 5042434	AAD38273	U	hypothetical protein
gi 4996602	BAA78552	O	thylakoid-bound ascorbate peroxidase
gi 4874278	AAD31343	O/U	member of the phosphoribosyl pyrophosphate synthetase family
gi 4584503	CAB40743	O	starch branching enzyme II
gi 4583546	CAB40381	U	GrpE protein
gi 4210330	CAA11552	U	2-oxoglutarate dehydrogenase
gi 419757	S30145	O	ketol-acid reductoisomerase
gi 4105131	AAD02267	U	ClpC protease
gi 399333	P31300	O	cysteine synthase
gi 399213	P31542	O	ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B
gi 399212	P31541	U/C	ATP-dependent Clp protease ATP-binding subunit CLPA homolog CD4A
gi 3941322	AAC82334	O	gamma-glutamylcysteine synthetase
gi 3721540	BAA33531	U/C	sulfite reductase
gi 3334149	O22436	U	MG-protoporphyrin IX chelatase
gi 3121825	O24364	O	peroxiredoxin BAS1
gi 3023817	Q43793	U	glucose-6-phosphate 1-dehydrogenase
gi 2833389	Q43846	O	soluble glycogen [starch] synthase (SS III)
gi 2811029	O04866	O	acetylornithine aminotransferase
gi 267196	Q00775	O	granule-bound glycogen [starch] synthase
gi 2668492	BAA23769	U/C	metal-transporting P-type ATPase
gi 2565305	AAB82711	U	glycine decarboxylase P subunit
gi 2499535	Q41364	U/C	2-oxoglutarate/malate translocator
gi 2499497	Q42961	O	phosphoglycerate kinase
gi 2497542	Q40546	U	pyruvate kinase isozyme G
gi 2497541	Q40545	O	pyruvate kinase isozyme A
gi 2493809	Q42840	U	coproporphyrinogen III oxidase
gi 2492952	Q42884	O	chorismate synthase 1
gi 2454184	AAB86804	U	pyruvate dehydrogenase E1 beta subunit
gi 2252472	CAB10698	O	argininosuccinate lyase
gi 21579	CAA36612	O	starch phosphorylase
gi 2117355	S51590	C	mitochondrial processing peptidase

gi 1842188	CAA69726	U	mitochondrial phosphate translocator
gi 1711381	P52877	O	phosphoserine aminotransferase
gi 1710807	P08926	O	rubisco subunit binding-protein alpha subunit
gi 1708993	P53780	U	cystathionine beta-lyase
gi 1583601	2121278A	U	zeta carotene desaturase
gi 1477480	AAB67843	O	carbamoyl phosphate synthetase large chain
gi 1351271	P48496	O	triosephosphate isomerase
gi 134103	P21240	U/C	rubisco subunit binding-protein beta subunit
gi 133248	P19683	O	31 kDa ribonucleoprotein
gi 130173	P04045	O	alpha-glucan phosphorylase, L isozyme 1
gi 124429	P23525	U/C	37 KD inner envelope membrane protein
gi 1172754	Q05728	O/U	phosphoribosylformylglycinamide cyclo-ligase
gi 1170242	P42045	U/C	ferrochelatase
gi 1168260	P46248	O	aspartate aminotransferase
gi 114421	P17614	U/C	ATP synthase beta chain
gi 114165	P23981	O	EPSP synthase 1
gi 1097877	2114378A	U	aminolevulinic dehydratase
gi 1076758	S49340	U/C	heat-shock protein 82K
gi 1066499	AAB41904	U/C	NADH-dependent glutamate synthase
gi 100437	A35016	O	cystathionine gamma-lyase

#### Plastid encoded

gi 7525018	NP_051044	U/C	ATPase alpha subunit
gi 3915961	P09976	U	YCF2 hypothetical 267 kDa protein
gi 231660	P12222	U	YCF1 hypothetical 226 kDa protein
gi 133424	P06271	U	DNA-directed RNA polymerase beta chain
gi 4887543	CAB43488	U	ATP-dependent Clp protease subunit ClpP

#### No transit peptide bu true chloroplast proteins (by annotation, Arabidopsis orthologue localization, or reported chloroplast function

gi 7447845	T04985	U	hypothetical protein T16L1.170	Chloroplast, putative transaminase
gi 7438086	S76557	O	hypothetical protein	Chloroplast, noTP since Synechocystis protein
gi 7433550	T05362	O	glycine hydroxymethyltransferase	ATH orthologue has a clear transit peptide, RC1
gi 7431783	T06228	O	Fe-dependent glutamate synthase	Chloroplast, no TP since fragment
gi 7431781	S67499	U/C	glutamate synthase	Chloroplast, no TP since fragment
gi 7431768	T16982	U/C	glutamate dehydrogenase	described chloroplast function

gi 7431333	T03406	U/C	probable isocitrate dehydrogenase	described chloroplast function
gi 7267551	CAB78032	C	outer envelope membrane protein OEP75 precursor homologue	CP-envelope
gi 6856558	AAF29977	U	isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	ATH orthologue has a CP transit peptide
gi 6831644	Q42362	O	30S ribosomal protein S8	CP annotated
gi 5931761	CAB56614	U	acetolactate synthase small subunit	ATH orthologue has a CP transit peptide
gi 585449	P37222	O	NADP-dependent malic enzyme	annotated as CP protein
gi 585010	P37294	U	phytoene synthase	CP, no transit peptide because of cyanobacterial origin
gi 5822270	1QGNA	O	cystathionine gamma-synthase	CP
gi 482934	CAA54043	U	glutathione reductase	CP
gi 4567203	AAD23619	U	putative beta-hydroxyacyl-ACP dehydratase	Chloroplast protein
gi 3157931	AAC17614	O	similar to pyrophosphate-dependent phosphofructokinase beta	ATH orthologue has a CP TP
gi 3121731	O04916	U	aconitate hydratase	ATH orthologue has a CP TP
gi 2982255	AAC32115	C	probable NADH-glutamate synthase	reported CP function
gi 2833379	Q42581	U	ribose-phosphate pyrophosphokinase 1	ATH orthologue has a CP TP
gi 2829901	AAC00609	U	putative 10kd chaperonin	ATH orthologue has a CP TP
gi 266463	P29696	O	3-isopropylmalate dehydrogenase	CP annotated
gi 2498077	P93554	O	nucleoside diphosphate kinase I	ATH orthologue with a CP TP
gi 2493734	P74361	U	CLPB protein	Chloroplast, no CP TP since Synechocystis protein
gi 2077957	CAA73318	U	putative FTSH protease	chloroplast annotated
gi 120714	P09317	O	glyceraldehyde 3-phosphate dehydrogenase	Chloroplast
gi 116527	P12210	O	ATP-dependent Clp protease proteolytic subunit	chloroplast
gi 1076722	S49173	O	hypothetical protein	peroxiredoxin-like
gi 100284	A39267	O	superoxide dismutase (Fe)	ATH orthologue has a CP TP
gi 7486826	T04912	C	hypothetical protein T10I14.140	highly homologous to CP targeted protein
gi 7450428	T03270	O	probable histidinol-phosphate transaminase	Chloroplast

#### Unknown localization but orthologue was detected in other plastid proteome analyses

gi 6018208	AAF01789	U/C	82-90 kD heat shock protein	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 6016683	AAF01510	U	putative clathrin heavy chain	in Kleffmann et al., 2004
gi 4874272	AAD31337	U	Strong similarity to gb Y09533 involved in starch metabolism	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 477819	B48529	U/C	ubiquinol-cytochrome-c reductase	in Kleffmann et al., 2004
gi 464848	P33628	U/C	tubulin alpha chain	in Kleffmann et al., 2004
gi 462013	P35016	U/C	endoplasmic reticulum protein	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 461944	Q04960	U	DNAJ protein homolog	in Kleffmann et al., 2004
gi 4204861	AAD11550	U	heat shock protein 90	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 4101473	AAD01191	U	K <sup>+</sup> -efflux antiporter-1	in Kleffmann et al., 2004, Ferro et al., 2003, Froehlich et al., 2003

gi 1729864	P54411	U	T-complex protein epsilon subunit	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 1708313	P51818	C	heat shock protein 81-3	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 1515105	CAA68885	U	heat shock protein 90A	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 1351202	P28551	U/C	tubulin beta chain	in Kleffmann et al., 2004
gi 134672	P11796	U	superoxide dismutase (Mn)	in Kleffmann et al., 2004, Ferro et al., 2003, Peltier et al., 2002
gi 113217	P23343	U/C	actin 1	in Kleffmann et al., 2004
gi 7450157	S74252	O	putative heat shock protein	in Kleffmann et al., 2004 and Froehlich et al., 2003
gi 7362740	CAB83110	U	putative protein	in Kleffmann et al., 2004
gi 7486039	T02491	U	hypothetical protein/putative ABC transporter	in Kleffmann et al., 2004 and in Froehlich et al., 2003

#### Unknown localization

gi 2811028	O04658	U/C	hypothetical 47.9 kDa protein
gi 1552717	AAB08578	U/C	squalene synthase
gi 1170938	P43281	U/C	S-adenosylmethionine synthetase 2
gi 2340166	AAB67319	U	glutathione S-conjugate transporting ATPase

#### Putative contaminants

gi 7649159	AAF65769	U/C	histone H2A
gi 7529745	CAB86930	U	putative protein
gi 7489246	T07405	U/C	oxoglutarate/malate translocator
gi 7488227	T04622	U	prohibitin-like protein
gi 7451352	T06379	U/C	SAR DNA-binding protein 2
gi 6056371	AAF02835	U	nucleolar protein
gi 3928138	CAA10267	U	mitochondrial elongation factor TU
gi 3334123	Q96250	U/C	ATP synthase gamma chain
gi 2689078	AAB88906	C	cytochrome c oxidase subunit II
gi 266989	Q01474	C	GTP-binding protein SAR1B
gi 232202	P30109	U/C	glutathione S-transferase
gi 1549222	BAA13463	U/C	NtSar1 protein
gi 127041	P23686	U/C	S-adenosylmethionine synthetase 1
gi 122101	P04915	O/U/C	histone H4
gi 1172555	P42055	U/C	34 kDa outer mitochondrial membrane protein porine
gi 114208	P25317	U/C	probable glutathione S-transferase
gi 1093432	2104177A	U	catalase
gi 1076621	S46306	C	cytochrome b5

gi 1061420	AAA81348	U/C	p-type H <sup>+</sup> -ATPase
gi 1049255	AAA80347	U/C	H <sup>+</sup> -pyrophosphatase
gi 100961	S17947	C	protein URF13
gi 100424	S17917	U/C	ADP,ATP carrier protein
gi 4883746	AAD31625	C	histone H3