PROTEOMICS

Supporting Information for Proteomics

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Membrane proteins from the cyanobacterium *Synechocystis* sp. PCC 6803 interacting with thioredoxin

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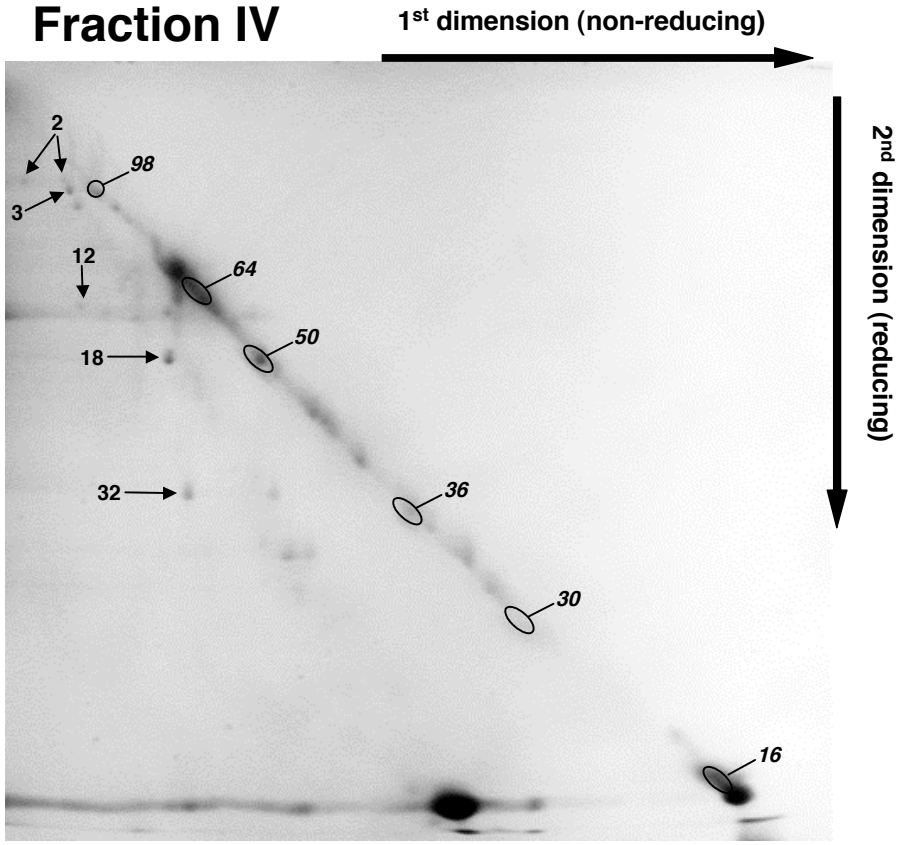
Fraction IV
1st dimension (non-reducing)
2nd dimension (reducing)
2
98
3
12
64
18
50
32
36
30
16

Supplemental Table 1. Identification by PMF of *Synechocystis* sp. PCC 6803 membrane proteins interacting with thioredoxin

No. [a]	Protein	ORF [b]	Fraction	Mowse score	Peptides matched	% seq. coverage
1	Preprotein translocase SecA	*sll0616*	III	183	30	33
2	Phycobilisome core-membrane linker polypeptide (L_{CM})	*slr0335*	I	173	32	37
			II	160	22	37
			III	163	26	36
3	ClpC	*sll0020*	I	129	15	21
			II	93	12	23
			III	161	23	37
4	ClpB1	*slr1641*	III	78	11	14
5	Polyribonucleotide nucleotidyl transferase, α-subunit	*sll1043*	I	219	22	35
6	FtsH	*slr1604*	III	99	12	18
7	Aspartyl-tRNA synthetase	*slr1720*	I	81	7	15
8	Ferredoxin-sulfite reductase	*slr0963*	I	109	18	30
			II	161	18	38
9	60-kDa chaperonin 1 (GroEL 1)	*slr2076*	I	183	26	44
			II	127	17	37
			III	175	18	38
10	Transcription termination factor NusA	*slr0743*	III	105	14	26
11	Pyruvate dehydrogenase component E2	*sll1841*	II	148	18	53
12	ATP synthase, α-subunit	*sll1326*	I	140	8	22
			II	77	10	28
			III	109	15	37

13	Rubisco large subunit (RbcL)	*slr0009*	II	96	18	37
14	ATPase of the AAA-family	*slr0374*	I	140	11	22
			II	188	26	46
			III	170	19	40
15	ATP synthase, β-subunit	*sll1329*	I	235	17	51
			II	159	23	63
			III	161	27	75
16	Carboxysomal protein CcmM	*sll1031*	II	192	24	38
17	Type 2 NADH dehydrogenase, NdbC	*sll1484*	III	91	13	37
18	Elongation factor EF-Tu	*sll1099*	I	244	31	72
			II	191	27	66
			III	165	28	62
19	Oxyanion-translocating ATPase, ArsA	*sll0086*	III	124	15	59
20	Putative GTP-binding protein	*sll0245*	I	144	8	31
			III	152	15	42
21	Urea transporter, ATP-binding subunit (UrtD)	*sll0764*	I	103	9	29
			II	112	14	44
			III	94	9	30
22	RecA	*sll0569*	I	119	10	36
			III	88	8	28
23	RNA polymerase, α-subunit	*sll1818*	I	131	6	26
			II	137	13	40
24	Phosphoribulokinase	*sll1525*	I	89	13	31
25	Twitching motility protein PilT	*slr0161*	I	91	6	18
			III	75	11	34
26	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH2)	*sll1342*	I	132	11	36

27	Hypothetical protein	*slr0658*	III	114	14	55
28	Pyruvate dehydrogenase component E1, α-subunit	*slr1934*	I	231	32	64
			II	132	14	34
29	Nitrate/nitrite transporter, ATP-binding subunit (NrtD)	*sll1453*	III	139	12	48
30	Pyruvate dehydrogenase component E1, β-subunit	*sll1721*	I	89	12	33
31	30S ribosomal protein S2	*sll1260*	I	132	11	39
			II	95	15	46
32	Universal stress protein Usp1	*slr0244*	I	110	9	44
			II	71	6	28
			III	113	7	34
33	Universal stress protein Usp2	*slr0670*	I	75	4	19
			III	103	13	66
34	β-type carbonic anhydrase	*slr1347*	II	98	15	52
35	Glutathione-S-transferase	*sll1545*	I	82	6	28
			III	148	13	57
36	Serine-O-acetyl transferase	*slr1348*	III	93	7	30
37	30S ribosomal protein S3	*sll1804*	I	165	17	58
			II	108	10	41
			III	119	16	68
38	50S ribosomal protein L3	*sll1799*	II	86	10	60
39	Hypothetical protein	*slr1702*	III	131	11	53
40	Heme oxygenase 1	*sll1184*	III	79	11	45
41	Phycobilisome rod-core linker polypeptide (L_{RC})	*sll1471*	III	108	12	50
42	Response regulator Rre1	*slr1783*	I	129	7	35
43	1-Cys peroxiredoxin	*slr1198*	I	117	10	43
			III	75	8	31

44	Transcription antitermination protein NusG	*sll1742*	I	110	10	51
45	Hypothetical protein ycf50	*slr2073*	I	86	5	41
			II	78	6	42
46	Precorrin isomerase	*slr1467*	I	84	5	31
47	Acetolactate synthase, small subunit	*sll0065*	III	121	9	61
48	Phycocyanin β-subunit	*sll1577*	I	88	6	47
			III	103	9	76
49	Hypothetical protein	*sll1106*	III	80	8	46
50	Photosystem I protein PsaD	*slr0737*	III	87	5	39

a) No., spot numbers in Figures 4 and 5, b) ORF, open reading frames according to the Cyanobase (http://bacteria.kazusa.or.jp/cyano/cyano.html).

Supplemental Table 2. Proteins indicated in Figure 3A identified by PMF

Fraction	Band [a)]	Protein	ORF [b)]	Mass [c)] exp./theor. (kDa)	Mowse score	Peptides matched	% seq. coverage
II	A	Rubisco large subunit (RbcL)	*slr0009*	55/52.5	138	11	27
II	B	Carboxysomal protein CcmM	*sll1031*	52/56.9	138	12	24
III	C	ATP synthase, β-subunit	*sll1329*	58/51.7	151	14	44
III	D	NrtA	*sll1450*	49/49.2	100	8	22

a) Band, protein band in Figure 3A, b) ORF, open reading frames according to the Cyanobase, c) Mass exp./theor., experimental and theoretical mass values

Supplemental Table 3. *Synechocystis* sp. PCC 6803 Fraction IV membrane proteins interacting with thioredoxin

No. [a]	Protein	Cys [b]	ORF [c]	Mass [d] exp./theor. (kDa)	Mowse score	Peptides matched	% seq. coverage
2	Phycobilisome core-membrane linker polypeptide (L_{CM})	3	*slr0335*	101/100.2	144	14	14
3	ClpC	1	*sll0020*	95/91.1	139	14	22
12	ATP synthase, α-subunit	2	*sll1326*	57/53.9	141	8	22
18	Elongation factor EF-Tu	1	*sll1099*	51/43.8	89	8	24
32	Universal stress protein Usp1	4	*slr0244*	38/31.2	88	7	33

a) No., spot numbers in Supplemental Figure 7, b) Cys, number of cysteines in the amino acid sequence, c) ORF, open reading frames according to the Cyanobase, d) Mass exp./theor., experimental and theoretical mass values

Supplemental Table 4. Localisation of *Synechocystis* sp. PCC 6803 membrane proteins

No. [a)]	Protein	ORF [b)]	Location [c)]	Reference [d)]
1	Preprotein translocase SecA*	*sll0616*	TM	Srivastava *et al*., 2005
2	Phycobilisome core-membrane linker polypeptide (L_{CM})	*slr0335*	PM	Pisareva *et al*., 2007
3	ClpC*	*sll0020*	TM, PM	Srivastava *et al*., 2005 Huang *et al.*, 2006
6	FtsH*	*slr1604*	PM	Pisareva *et al*., 2007
8	Ferredoxin-sulfite reductase	*slr0963*	PM	Pisareva *et al*., 2007
9	60-kDa chaperonin 1 (GroEL 1)	*slr2076*	TM	Srivastava *et al*., 2005
12	ATP synthase, α-subunit*	*sll1326*	TM, PM	Srivastava *et al*., 2005 Huang *et al*. 2002, 2006
13	Rubisco large subunit (RbcL)	*slr0009*	PM	Pisareva *et al*., 2007
15	ATP synthase, β-subunit*	*sll1329*	TM, PM	Srivastava *et al*., 2005 Huang *et al.*, 2006
16	Carboxysomal protein CcmM	*sll1031*	PM	Pisareva *et al*., 2007
17	Type 2 NADH dehydrogenase, NdbC*	*sll1484*	PM	Pisareva *et al*., 2007
18	Elongation factor EF-Tu	*sll1099*	TM	Srivastava *et al*., 2005
24	Phosphoribulokinase	*sll1525*	TM	Srivastava *et al*., 2005
26	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH2)	*sll1342*	TM	Srivastava *et al*., 2005
28	Pyruvate dehydrogenase component E1, α-subunit*	*slr1934*	TM	Srivastava *et al*., 2005
41	Phycobilisome rod-core linker polypeptide (L_{RC})*	*sll1471*	TM	Srivastava *et al*., 2005
48	Phycocyanin β-subunit	*sll1577*	TM, PM	Srivastava *et al*., 2005 Huang *et al.*, 2006
50	Photosystem I protein PsaD*	*slr0737*	TM, PM	Srivastava *et al*., 2005 Huang *et al.*, 2002

a) No., spot numbers in Figures 4 and 5, b) ORF, open reading frames according to the Cyanobase, c) Location. PM, plasma membrane; TM, thylakoid membrane,

d) References:

Huang, F. *et al.* (2002) Proteomics of *Synechocystis* sp. strain PCC 6803. Identification of plasma membrane proteins. *Mol. Cell. Proteomics* **1**, 956-966

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Srivastava, R. *et al.* (2005) Proteomic studies of the thylakoid membrane of *Synechocystis* sp. PCC 6803. *Proteomics* **5**, 4905-4916