

Supplementary Table S3: Genes that were differentially expressed during the study and their annotation. Genes expressed with a log₂ fold change of <-1.4 or >1.4 and $p < 0.05$ were considered differentially expressed. We used Cyanobase (<http://genome.kazusa.or.jp/cyanobase>) as a guideline to distinguish between genes of different functional categories. We have also designated several genes that are listed as unknown or hypothetical in CyanoBase, but are annotated in the Kyoto Encyclopedia of Genes and Genomes (KEGG) (<https://www.kegg.jp/>) or in recent literature. In the latter case, references are added. References not included in the main text are listed as footnotes.

ORF ID	Gene name	Time after light switch										Functional category and gene function (Cyanobase, KEGG, recent literature)	Reference (if not annotated in Cyanobase or KEGG)
		blue light					orange light		red light		red dilute		
		1h	4h	24h	48h	192h	4h	192h	4h	192h	192h		
Photosynthesis and respiration													
<i>sll1326</i>	<i>atpA</i>	-0.76	-1.54	-1.64	-0.64	-0.42	-0.11	-0.25	-0.14	-0.19	-0.20	ATP synthase alpha chain	
<i>sll1327</i>	<i>atpC</i>	-0.74	-1.45	-1.39	-0.72	-0.27	-0.03	-0.15	-0.07	-0.10	-0.04	ATP synthase gamma chain	
<i>sll1325</i>	<i>atpD</i>	-0.78	-1.64	-1.68	-0.69	-0.48	-0.09	-0.34	-0.05	-0.13	-0.12	ATP synthase delta chain of CF(1)	
<i>slr1330</i>	<i>atpE</i>	-1.03	-1.53	-1.50	-0.64	-0.35	0.00	-0.39	0.32	0.23	0.54	ATP synthase epsilon chain of CF(1)	
<i>sll1324</i>	<i>atpF</i>	-0.92	-1.81	-1.80	-0.74	-0.53	-0.04	-0.38	0.01	-0.14	-0.15	ATP synthase B chain (subunit I) of CF(0)	
<i>sll1323</i>	<i>atpG</i>	-1.00	-1.74	-1.89	-0.76	-0.61	-0.09	-0.38	-0.01	-0.12	-0.13	ATP synthase subunit b' of CF(0)	
<i>ssl2615</i>	<i>atpH</i>	-0.75	-1.34	-1.70	-0.77	-0.58	-0.06	-0.28	-0.01	-0.15	-0.26	ATP synthase C chain of CF(0)	
<i>sll1031</i>	<i>ccmM</i>	-1.15	-1.48	-1.75	-1.16	-0.59	0.15	-0.07	-0.02	0.02	0.16	Carbon dioxide concentrating mechanism protein CcmM, putative carboxysome structural protein	
<i>sll1032</i>	<i>ccmN</i>	-0.94	-1.41	-1.37	-1.02	-0.35	0.19	-0.17	0.08	-0.10	0.40	Carbon dioxide concentrating mechanism protein CcmN, putative carboxysome assembly protein	
<i>sll1471</i>	<i>cpcG2</i>	3.61	3.38	3.63	2.85	2.69	3.81	2.80	3.33	2.47	2.74	Phycobilisome rod-core linker polypeptide CpcG2	
<i>ssl0452</i>	<i>nblA1</i>	2.52	2.34	2.47	1.31	1.23	0.27	0.80	0.04	0.41	0.45	Phycobilisome degradation protein NblA	
<i>ssl0453</i>	<i>nblA2</i>	1.98	1.84	1.82	0.59	0.68	0.32	0.88	0.02	0.17	0.15	Phycobilisome degradation protein NblA	
<i>slr1687</i>	<i>nblB2</i>	1.80	1.66	1.41	1.74	1.60	-0.28	-0.08	0.01	0.01	-0.20	Phycobilisome degradation protein NblB	Li and Sherman 2002
<i>slr1311</i>	<i>psbA2</i>	1.43	2.36	2.12	2.40	2.47	-0.18	0.15	0.13	0.17	-0.21	Photosystem II D1 protein	
<i>sll1867</i>	<i>psbA3</i>	1.39	2.30	2.10	2.40	2.45	-0.22	0.12	0.16	0.17	-0.25	Photosystem II D1 protein	

<i>slr0906</i>	<i>psbB</i>	0.91	1.61	1.13	1.03	0.83	-0.11	0.30	-0.03	0.06	-0.26	Photosystem II core light harvesting protein	
<i>sll0849</i>	<i>psbD</i>	1.01	1.82	0.94	1.22	0.96	-0.37	0.06	-0.12	-0.06	-0.40	Photosystem II reaction center D2 protein	
<i>slr0927</i>	<i>psbD2</i>	1.14	2.07	1.45	1.75	1.44	-0.27	0.10	-0.03	-0.03	-0.32	Photosystem II reaction center D2 protein	
Other known categories and functions													
<i>sll1473</i>	<i>CcaS;</i> <i>hik32</i>	1.31	1.25	1.69	1.19	1.08	1.85	1.19	1.71	0.89	1.29	Hypothetical; two-component sensor histidine kinase Hik32	Hirose et al. 2008
<i>sll1475</i>	<i>CcaS;</i> <i>hik32</i>	0.77	0.81	0.95	0.92	0.87	1.91	0.98	1.51	0.96	1.22	Regulatory functions; two-component sensor histidine kinase Hik32	
<i>slr0473</i>	<i>cph1,</i> <i>hik35</i>	1.14	2.16	2.15	1.10	0.83	-0.20	0.78	-0.48	0.06	0.22	Regulatory functions; cyanobacterial phytochrome 1, two-component sensor histidine kinase Hik35	
<i>slr1251</i>	<i>cyp</i>	-1.12	-1.69	-1.31	-1.57	-0.63	-0.10	-0.59	0.08	-0.03	0.21	Translation; protein modification and translation factors; peptidyl-prolyl cis-trans isomerase	
<i>slr0676</i>	<i>cysC</i>	-1.28	-1.82	-1.55	-1.31	-0.82	0.07	-0.42	0.40	0.01	-0.12	Amino acid biosynthesis; serine family/sulfur assimilation; adenylylsulfate kinase	
<i>sll1441</i>	<i>desB</i>	-1.24	-1.27	-0.85	-1.57	-0.61	-0.32	-0.95	0.46	-0.24	-0.25	Fatty acid, phospholipid and sterol metabolism; acyl-lipid desaturase (omega-3)	
<i>sll0662</i>	<i>Fed7</i>	0.68	1.23	1.49	1.62	1.03	-0.08	0.12	-0.10	-0.10	-0.50	Hypothetical protein; 4Fe-4S type iron-sulfur protein ferredoxin 7	Marteyn et al. 2009 ¹
<i>sll1009</i>	<i>FrpC</i>	1.28	2.20	2.72	2.07	1.32	0.12	1.16	-0.28	0.66	0.00	Unknown protein; iron-regulated protein	
<i>sll0145</i>	<i>frr, rrf</i>	-1.16	-1.30	-1.41	-0.91	-0.75	-0.08	-0.22	-0.29	-0.17	-0.51	Translation; protein modification and translation factors; ribosome releasing factor	
<i>slr1604</i>	<i>ftsH</i>	1.66	1.55	1.24	1.16	1.12	-0.26	-0.27	-0.15	0.13	-0.25	Cellular processes; cell division protein FtsH	
<i>slr0228</i>	<i>ftsH</i>	1.53	1.55	1.08	1.40	1.20	-0.11	-0.21	0.08	0.15	-0.05	Cellular processes; cell division protein FtsH	
<i>ssl1911</i>	<i>gifA</i>	1.56	2.23	3.06	2.21	2.54	-0.46	-0.15	-1.27	-0.58	0.17	Hypothetical protein; glutamine synthetase inactivating factor IF7	García-Domínguez et al. 1999 ²
<i>sll1515</i>	<i>gifB</i>	1.23	1.95	2.52	2.44	2.42	-0.26	-0.59	-1.15	-0.75	-0.11	Unknown protein; glutamine synthetase inactivating factor IF17	García-Domínguez et al. 1999 ²
<i>slr1124</i>	<i>gpmB</i>	-1.35	-1.62	-1.31	-0.60	-0.60	-0.05	-0.39	0.41	0.27	0.03	Energy metabolism; glycolysis; phosphoglycerate mutase	
<i>slr1992</i>	<i>gpx2</i>	1.42	0.72	0.21	0.60	0.66	-0.19	-0.66	0.08	-0.09	0.05	Biosynthesis of cofactors, prosthetic groups, and carriers; glutathione peroxidase-like NADPH peroxidase	
<i>slr2076</i>	<i>groEL1</i>	-1.99	-3.26	-2.99	-1.72	-1.01	-0.09	-0.44	0.13	-0.23	-0.06	Cellular processes; 60kD chaperonin	
<i>sll0416</i>	<i>groEL-2</i>	-1.67	-2.75	-2.70	-1.38	-0.76	-0.02	-0.22	0.33	-0.03	0.02	Cellular processes; 60 kDa chaperonin 2, GroEL2, molecular chaperone	
<i>slr2075</i>	<i>groES</i>	-1.87	-3.25	-2.94	-1.63	-0.95	-0.09	-0.47	0.03	-0.21	0.01	Cellular processes; 10kD chaperonin	
<i>ssr2595</i>	<i>hliB,</i> <i>scpD</i>	3.31	2.57	2.12	1.55	2.26	-0.01	0.25	0.41	0.11	0.10	Other categories; adaptations and atypical conditions; high light-inducible polypeptide HliB	Promnares et al. 2006; Yao et al. 2007
<i>ssl1633</i>	<i>hliC,</i> <i>scpB</i>	1.52	1.18	0.93	0.52	0.72	0.04	-0.16	0.27	-0.09	-0.09	Hypothetical; high light-inducible polypeptide HliC	Promnares et al. 2006; Yao et al. 2007

<i>sll0576</i>	<i>HrEpiB</i>	-1.22	-1.83	-1.84	-1.28	-0.73	-0.11	-0.28	-0.12	-0.34	-0.42	Other categories; putative sugar-nucleotide epimerase/dehydratase
<i>sll1514</i>	<i>hspA</i>	0.84	1.40	2.13	1.41	0.99	-0.86	0.25	0.15	-0.13	-0.45	Cellular processes; 16.6 kDa small heat shock protein, molecular chaperone
<i>sll0430</i>	<i>htpG</i>	-1.06	-1.59	-0.91	-1.02	-0.47	0.03	-0.19	0.02	-0.11	-0.02	Cellular processes; heat shock protein 90, molecular chaperone
<i>slr1544</i>	<i>lilA</i>	3.08	2.56	1.95	1.48	2.00	0.18	0.11	0.55	0.20	0.10	Unknown protein; member of the extended light-harvesting-like (Lil) protein family Kufryk et al. 2008
<i>slr1165</i>	<i>met3</i>	-1.35	-1.86	-1.73	-1.30	-0.67	-0.17	-0.59	0.21	-0.06	0.14	Amino acid biosynthesis; serine family/sulfur assimilation; sulfate adenylyltransferase
<i>sll0657</i>	<i>mraY</i>	-1.30	-1.40	-1.42	-0.87	-0.81	-0.06	-0.42	-0.08	0.00	-0.42	Cell envelope; murein sacculus and peptidoglycan; phospho-N-acetylmuramoyl-pentapeptide-transferase
<i>sll1450</i>	<i>nrtA</i>	-0.30	-0.69	-1.55	-1.06	-1.32	0.28	-0.03	0.39	0.25	-0.23	Transport and binding proteins; nitrate/nitrite transport system substrate-binding protein
<i>slr0743</i>	<i>nusA</i>	-0.75	-1.16	-1.45	-1.22	-0.54	-0.05	-0.57	0.16	-0.10	0.34	Transcription; RNA synthesis, modification, and DNA transcription; similar to N utilization substance protein
<i>slr1734</i>	<i>opcA</i>	1.01	1.43	0.75	0.36	0.12	0.11	0.42	0.00	0.46	-0.03	Energy metabolism; pentose phosphate pathway; glucose 6-phosphate dehydrogenase assembly protein
<i>sll1694</i>	<i>pilA1</i>	2.66	2.74	2.85	1.60	1.13	0.44	1.28	-0.26	0.73	0.49	Cellular processes; pilin polypeptide PilA1
<i>sll1695</i>	<i>pilA2</i>	2.28	1.95	2.56	0.67	0.85	0.51	1.01	0.03	0.50	0.87	Cellular processes; chemotaxis; pilin polypeptide PilA2
<i>sll1696</i>		1.46	0.84	1.55	0.39	0.60	0.50	0.62	0.13	0.29	1.29	Hypothetical; part of <i>pilA1,2</i> operon Bhaya et al. 2000
<i>slr2015</i>	<i>pilA9</i>	1.11	1.23	1.67	1.31	1.13	0.15	0.04	0.18	0.36	0.44	Unknown protein; type 4 pilin-like protein, essential for motility Chandra et al. 2015
<i>slr2016</i>	<i>pilA10</i>	1.46	1.64	2.38	2.00	1.55	0.34	0.31	0.17	0.52	0.59	Unknown protein; type 4 pilin-like protein, essential for motility Chandra et al. 2015
<i>slr2017</i>	<i>pilA11</i>	1.38	1.75	2.63	2.08	1.60	0.43	0.53	0.28	0.50	0.84	Unknown protein; type 4 pilin-like protein, essential for motility Chandra et al. 2015
<i>slr2018</i>		1.22	1.53	2.09	1.88	1.38	0.29	0.36	0.26	0.53	0.47	Unknown protein; part of <i>pilA</i> operon <i>sll2015-2019</i> Chandra et al. 2015
<i>slr1622</i>	<i>ppa</i>	-1.11	-1.68	-1.40	-0.86	-0.63	-0.19	-0.45	-0.10	-0.07	-0.28	Central intermediary metabolism; Phosphorus compounds; soluble inorganic pyrophosphatase
<i>sll0680</i>	<i>pstS</i>	-0.98	-1.69	-1.62	-1.12	-0.79	-0.39	-0.31	-0.63	0.00	-0.23	Transport and binding proteins; phosphate-binding periplasmic protein precursor (PBP)
<i>slr2132</i>	<i>pta</i>	0.61	1.18	1.43	0.48	0.62	-0.16	0.15	-0.30	-0.25	0.26	Energy metabolism; pyruvate and acetyl-CoA metabolism; phosphotransacetylase
<i>sll0144</i>	<i>pyrH</i>	-0.96	-1.07	-1.42	-0.97	-0.76	-0.08	-0.38	-0.11	-0.17	-0.52	Purines, pyrimidines, nucleosides, and nucleotides; uridine monophosphate kinase
<i>sll1744</i>	<i>rpl1</i>	-0.60	-1.64	-1.68	-1.74	-0.65	0.08	-0.36	0.12	-0.17	0.21	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L1
<i>sll1745</i>	<i>rpl10</i>	-0.04	-1.52	-1.73	-1.59	-0.67	0.04	-0.19	0.01	-0.21	0.12	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L10
<i>sll1746</i>	<i>rpl12</i>	-0.45	-1.61	-1.93	-1.78	-0.75	0.16	-0.18	0.09	-0.09	0.04	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L12

<i>sll1806</i>	<i>rpl14</i>	-1.21	-2.53	-2.39	-1.76	-0.77	-0.09	-0.41	0.05	-0.18	0.30	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L14
<i>sll1813</i>	<i>rpl15</i>	-0.86	-1.88	-1.87	-1.23	-0.72	-0.04	-0.28	0.22	-0.02	0.40	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L15
<i>sll1805</i>	<i>rpl16</i>	-1.31	-2.45	-2.37	-1.74	-0.71	-0.08	-0.44	0.19	-0.14	0.41	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L16
<i>sll1811</i>	<i>rpl18</i>	-0.89	-2.03	-1.89	-1.32	-0.68	-0.09	-0.30	0.08	-0.15	0.28	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L18
<i>sll1802</i>	<i>rpl2</i>	-1.60	-2.52	-2.58	-1.81	-0.89	-0.04	-0.38	0.17	-0.06	0.42	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L2
<i>sll1803</i>	<i>rpl22</i>	-1.34	-2.38	-2.40	-1.59	-0.72	-0.12	-0.41	0.12	-0.19	0.38	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L22
<i>sll1801</i>	<i>rpl23</i>	-1.45	-2.42	-2.37	-1.78	-0.79	-0.02	-0.39	0.14	-0.07	0.38	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L23
<i>sll1807</i>	<i>rpl24</i>	-1.16	-2.47	-2.30	-1.67	-0.65	-0.07	-0.43	0.09	-0.19	0.34	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L24
<i>ssl3436</i>	<i>rpl29</i>	-1.22	-2.48	-2.25	-1.66	-0.67	-0.08	-0.41	0.10	-0.17	0.35	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L29
<i>sll1799</i>	<i>rpl3</i>	-1.49	-2.28	-2.34	-1.72	-0.71	0.08	-0.31	0.27	-0.01	0.40	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L3
<i>sll1800</i>	<i>rpl4</i>	-1.42	-2.31	-2.42	-1.66	-0.81	-0.03	-0.41	0.21	-0.12	0.28	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L4
<i>sll1808</i>	<i>rpl5</i>	-1.08	-2.38	-2.20	-1.74	-0.65	-0.04	-0.39	0.12	-0.18	0.37	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L5
<i>sll1810</i>	<i>rpl6</i>	-0.87	-2.07	-1.91	-1.33	-0.61	-0.08	-0.27	0.19	-0.17	0.34	Translation; ribosomal proteins: synthesis and modification; 50S ribosomal protein L6
<i>sll1818</i>	<i>rpoA</i>	-0.85	-1.59	-1.51	-1.14	-0.54	0.00	-0.35	0.23	-0.03	0.38	Transcription; RNA synthesis, modification, and DNA transcription; RNA polymerase alpha subunit
<i>sll1101</i>	<i>rps10</i>	-0.85	-1.44	-0.89	-1.26	-0.34	0.16	-0.31	0.29	-0.04	0.20	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S10
<i>ssl3437</i>	<i>rps17</i>	-1.18	-2.46	-2.30	-1.69	-0.67	-0.05	-0.43	0.12	-0.16	0.37	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S17
<i>ssl3432</i>	<i>rps19</i>	-1.45	-2.46	-2.56	-1.67	-0.83	-0.09	-0.38	0.11	-0.14	0.39	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S19
<i>sll1260</i>	<i>rps2</i>	-0.59	-1.78	-1.42	-1.17	-0.60	0.04	-0.30	0.19	-0.08	0.15	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S2
<i>sll1804</i>	<i>rps3</i>	-1.41	-2.48	-2.52	-1.69	-0.82	-0.11	-0.44	0.13	-0.17	0.40	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S3
<i>sll1812</i>	<i>rps5</i>	-0.86	-1.89	-1.72	-1.44	-0.70	-0.04	-0.19	0.12	-0.10	0.25	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S5
<i>sll1767</i>	<i>rps6</i>	-0.70	-1.44	-1.15	-1.02	-0.41	0.00	-0.09	-0.05	0.01	-0.16	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S6

<i>sll1809</i>	<i>rps8</i>	-0.97	-2.28	-2.04	-1.59	-0.63	-0.10	-0.32	0.11	-0.16	0.41	Translation; ribosomal proteins: synthesis and modification; 30S ribosomal protein S8
<i>sll1688</i>	<i>thrC</i>	0.65	1.41	1.59	0.63	0.26	0.28	-0.50	0.50	-0.13	-0.87	Amino acid biosynthesis; aspartate family; threonine synthase
<i>sll1261</i>	<i>tsf</i>	-0.72	-1.37	-1.51	-1.33	-0.71	0.29	-0.34	0.40	0.07	0.04	Translation; protein modification and translation factors; elongation factor TS
<i>slr0798</i>	<i>ziaA</i>	0.72	1.08	1.41	0.53	0.43	0.24	0.20	0.09	-0.02	-0.02	Transport and binding proteins; zinc-transporting P-type ATPase (zinc efflux pump) involved in zinc tolerance
<i>slr0915</i>		1.33	1.73	1.97	1.91	1.35	0.20	0.43	-0.25	0.08	-0.34	DNA replication, restriction, modification, recombination, and repair; putative endonuclease
<i>slr1166</i>		-1.19	-1.57	-1.34	-0.79	-0.31	-0.08	-0.45	0.09	-0.04	0.37	Energy metabolism; sugars; UDP-glucose:tetrahydrobiopterin glucosyltransferase
<i>slr1853</i>		-1.04	-1.33	-1.55	-1.57	-1.41	0.04	0.04	0.01	-0.01	-0.31	Other categories; carboxymuconolactone decarboxylase
<i>sll1255</i>		-0.04	0.68	1.52	-0.37	-0.45	0.42	0.61	0.59	0.16	0.12	Putative transposase [ISY203_c]
<i>slr1635</i>		-0.02	0.59	1.41	-0.38	-0.47	0.36	0.57	0.53	0.11	0.14	Putative transposase [ISY203_e]
<i>slr0180</i>		-0.04	0.65	1.48	-0.35	-0.48	0.35	0.60	0.56	0.08	0.10	Putative transposase [ISY203_f]
<i>sll1474</i>		-0.06	0.60	1.45	-0.39	-0.47	0.37	0.60	0.55	0.09	0.16	Putative transposase [ISY203_g]
<i>slr1682</i>		0.11	0.78	1.83	-0.03	-0.42	0.49	0.55	0.56	-0.12	0.07	Putative transposase [ISY391_b1]
<i>slr1859</i>		-1.09	-1.49	-1.18	-1.48	-0.96	-0.05	0.12	-0.49	-0.19	-0.12	Transcription; RNA synthesis, modification, and DNA transcription; anti-sigma f factor antagonist
<i>sll0224</i>		-0.83	-1.44	-1.71	-1.27	-0.89	-0.01	-0.02	-0.10	-0.13	-0.43	Transport and binding proteins; amino-acid ABC transporter binding protein

Hypothetical and unknown proteins

<i>sll0263</i>		-1.04	-1.55	-0.83	-1.31	-0.28	0.00	-0.84	0.27	-0.02	0.27	Unknown protein
<i>sll0473</i>		0.82	1.09	1.37	1.42	0.60	0.02	0.29	-0.39	-0.04	0.12	Unknown protein; NitT/TauT family transport system substrate-binding protein
<i>sll0661</i>		1.08	1.90	1.73	1.66	1.04	0.10	0.37	-0.01	0.21	-0.80	Hypothetical protein; YCF35
<i>sll0685</i>		1.06	1.12	1.46	0.79	0.57	0.02	0.01	-0.03	0.13	0.07	Hypothetical protein; thioredoxin-like protein
<i>sll1109</i>		-0.85	-1.45	-1.26	-1.15	-0.66	0.09	-0.24	-0.09	-0.12	-0.12	Hypothetical protein
<i>sll1158</i>		1.34	1.75	2.29	2.11	1.38	0.07	0.60	-0.06	-0.03	-0.53	Hypothetical protein
<i>sll1193</i>		1.17	1.64	1.64	0.94	0.84	0.04	0.43	-0.12	-0.19	-0.04	Hypothetical protein
<i>sll1338</i>		1.20	1.67	1.16	0.52	0.78	0.12	0.85	-0.13	0.10	-0.28	Unknown protein
<i>sll1472</i>		3.31	2.78	3.54	2.53	2.57	3.29	2.36	2.87	1.80	2.93	Unknown protein; part of <i>ccaS</i> gene cluster
<i>sll1526</i>		-1.17	-1.67	-1.50	-0.80	-0.74	-0.22	-0.48	-0.52	-0.47	-0.73	Hypothetical protein; methyltransferase
<i>sll1722</i>		-1.35	-1.50	-0.74	0.01	-0.16	-0.49	-0.55	0.72	-0.22	0.29	Hypothetical protein
<i>sll1862</i>		1.00	1.05	2.99	2.27	2.47	0.18	0.50	-0.13	-0.19	0.17	Unknown protein

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<i>slI1863</i>	1.31	1.68	3.64	2.17	2.90	0.53	0.47	0.14	0.25	0.06	Unknown protein	
<i>slr0082</i>	1.56	0.98	2.24	1.27	1.83	0.50	0.34	0.04	-0.24	1.08	Hypothetical protein; ribosomal protein S12; methylthiotransferase	
<i>slr0144</i>	0.55	1.79	1.67	0.68	0.50	-0.31	0.50	-0.61	0.08	-0.19	Hypothetical protein; L-myo -inositol 1-phosphate synthase	
<i>slr0179</i>	1.07	1.57	1.82	1.05	0.88	-0.26	0.34	-0.31	0.12	-0.25	Hypothetical protein	
<i>slr0364</i>	1.93	2.07	2.41	1.43	1.25	-0.63	-0.68	-0.44	-0.54	0.99	Hypothetical protein	
<i>slr0366</i>	1.66	1.96	1.95	1.21	1.01	-0.77	-0.66	-0.42	-0.63	1.08	Unknown protein	
<i>slr0373</i>	4.40	5.37	4.97	4.28	2.52	0.24	1.25	0.04	0.66	-0.21	Hypothetical protein; part of operon <i>slr0373-slr0374-slr0376</i>	Singh and Sherman 2002
<i>slr0374</i>	4.11	5.01	4.56	3.85	2.34	0.30	1.17	0.22	0.62	0.03	Hypothetical protein; cell division cycle protein; part of operon <i>slr0373-slr0364-slr0376</i>	Singh and Sherman 2002
<i>slr0376</i>	3.36	4.57	5.04	3.81	3.09	0.63	1.66	0.50	0.95	-0.03	Hypothetical protein; part of operon <i>slr0373-slr0374-slr0376</i>	Singh and Sherman 2002
<i>slr0404</i>	0.85	1.50	1.20	1.26	0.84	-0.04	0.15	0.12	0.21	0.27	Hypothetical protein	
<i>slr0442</i>	2.19	1.99	2.64	0.88	1.00	0.35	1.10	-0.23	0.43	0.88	Unknown protein	
<i>slr0443</i>	-1.09	-1.46	-1.09	-1.04	-0.35	-0.03	-0.43	0.10	-0.07	-0.65	Hypothetical protein	
<i>slr0587</i>	0.82	2.54	2.02	1.79	1.19	-0.49	-0.30	-0.43	-0.20	-0.04	Unknown protein	
<i>slr0607</i>	-1.11	-1.58	-1.76	-1.47	-1.03	-0.12	-0.59	-0.09	0.07	-0.31	Hypothetical protein	
<i>slr0888</i>	0.26	2.00	2.37	1.75	1.04	-0.62	0.83	-1.08	-0.26	-0.06	Hypothetical protein	
<i>slr1152</i>	0.49	2.08	2.41	1.08	1.18	-0.54	0.32	-0.68	-0.28	-0.51	Hypothetical protein	
<i>slr1436</i>	-1.29	-1.93	-1.19	-1.43	-0.56	-0.28	-0.70	-0.54	-0.22	0.39	Unknown protein	
<i>slr1583</i>	0.96	1.89	1.73	0.77	0.93	-0.12	0.08	-0.43	0.00	-0.34	Hypothetical protein	
<i>slr1634</i>	2.02	2.97	3.23	3.29	2.20	-0.10	1.11	-0.74	0.13	-0.77	Hypothetical protein	
<i>slr1674</i>	1.40	1.81	1.90	0.53	1.11	0.18	0.38	0.54	0.39	-0.24	Hypothetical protein	
<i>slr1770</i>	1.21	2.03	1.88	1.76	0.99	0.23	0.72	-0.04	0.18	-0.35	Hypothetical protein	
<i>slr1851</i>	1.45	2.68	3.04	1.23	1.63	-0.18	0.15	-0.49	-0.05	0.03	Hypothetical protein	
<i>slr1852</i>	-0.28	-0.33	-0.80	-1.46	-1.15	0.14	0.15	0.00	0.06	-0.28	Unknown protein	
<i>slr1917</i>	1.41	1.96	1.52	0.96	0.78	-0.03	0.35	-0.18	0.25	0.36	Hypothetical protein	
<i>slr1957</i>	0.77	1.73	1.85	1.04	0.64	-0.39	0.55	-0.99	-0.43	-0.32	Hypothetical protein	
<i>slr1958</i>	0.41	0.88	1.58	0.89	0.76	-0.13	0.51	-0.32	-0.21	-0.07	Unknown protein	
<i>ssl1263</i>	1.23	2.05	1.91	1.74	1.12	0.09	0.37	-0.05	0.25	-0.77	Unknown protein	
<i>ssl1533</i>	1.05	1.44	0.84	0.25	0.35	0.02	0.44	-0.32	0.22	-0.08	Unknown protein	
<i>ssl1762</i>	1.63	2.26	1.92	1.15	0.74	0.18	0.45	0.03	0.13	-0.31	Hypothetical protein	
<i>ssl2874</i>	-0.68	-1.07	-1.45	-1.54	-0.94	0.11	-0.80	0.25	-0.23	-0.21	Hypothetical protein	

<i>ssr0692</i>	1.18	1.71	2.02	1.25	1.30	-0.32	-0.35	-0.61	-0.15	-0.35	Hypothetical protein
<i>ssr1038</i>	0.65	1.83	1.66	1.94	1.41	-0.16	-0.30	-0.75	-0.63	-0.86	Unknown protein
<i>ssr1375</i>	0.70	1.58	1.03	0.01	0.20	0.09	0.18	-0.06	0.08	-0.90	Hypothetical protein
<i>ssr1562</i>	1.09	2.03	1.76	1.11	0.89	-0.29	-0.08	-0.71	-0.29	-0.54	Hypothetical protein
<i>ssr1853</i>	-0.79	-1.25	-1.51	-0.98	-0.63	-0.17	-0.48	0.46	0.11	-0.18	Unknown protein
<i>ssr2153</i>	0.58	1.43	2.64	2.88	1.23	-0.30	0.66	0.67	0.18	-1.22	Unknown protein
<i>ssr2848</i>	1.12	1.50	1.46	1.22	0.60	0.25	-0.01	0.09	0.00	0.16	Unknown protein
<i>ssr3129</i>	1.20	2.08	2.38	0.63	0.89	-0.17	0.21	-0.32	-0.01	-0.04	Unknown protein

¹Marteyn B, Domain F, Legrain P, Chauvat F, Cassier-Chauvat C (2009) The thioredoxin reductase-glutaredoxins-ferredoxin crossroad pathway for selenate tolerance in *Synechocystis* PCC6803. Mol Microbiol 71:520-532

²García-Domínguez M, Reyes JC, Florencio FJ (1999) Glutamine synthetase inactivation by protein-protein interaction. Proc Natl Acad Sci USA 96:7161-7166