

Table S2 B Up-regulated proteins (fold changes) revealed by quantitative I TRAQ proteomic a

Gene	Description	24h	48h
sll1945	1-deoxy-xylulose 5-phosphate synthase	1.59	
slr2130	3-dehydroquinate synthase	1.78	
ssl3436	50s ribosomal protein l29	1.50	
sll0480	aspartate aminotransferase related protein	1.57	
sll0208	conserved hypothetical protein	1.57	
slr0609	conserved hypothetical protein	1.61	
ssr3451	cytochrome b559 alpha chain	1.64	
smr0006	cytochrome b559 beta chain	1.79	
sll0018	fructose-bisphosphate aldolase (ec 4.1.2.13)	1.82	
slr0151	hypothetical protein	1.77	
sll1618	hypothetical protein	1.52	
slr1472	-identity	1.84	
sll1363	ketol-acid reductoisomerase (ec 1.1.1.86)	1.75	
sll1743	L11 protein	2.36	
sll0947	light repressed protein a	1.52	
sll0258	low potential cytochrome C	1.97	
sll0629	photosystem i reaction centre subunit x (psi-k)	1.77	
sll1471	phycobilisome rod-core linker polypeptide CpcG	2.67	
slr0775	protein-export membrane protein SecF, putative, putative	2.55	
slr1164	ribonucleotide reductase alpha chain	1.53	
slr0653	RNA polymerase sigma factor rpod1	1.59	
sll1931	serine hydroxymethyltransferase	1.57	
sll1688	threonine synthase	1.81	
sll0860	conserved hypothetical protein	1.53	2.14
slr0186	2-isopropylmalate synthase	1.88	1.92
sll0336	acetyl-coenzyme a carboxylase carboxyl transferase subunit beta	1.58	2.17
ssl2084	acyl carrier protein	2.78	3.61
slr0729	conserved hypothetical protein	2.18	3.51
slr2136	conserved hypothetical protein	1.72	1.70
slr1847	conserved hypothetical protein	2.46	3.05
ssl3364	conserved hypothetical protein	1.53	3.24
sll1214	conserved hypothetical protein (orf349)	2.67	2.17
slr0923	conserved hypothetical protein (orf99)	2.78	2.16
sll1185	coproporphyrinogen III oxidase, aerobic	2.00	2.02
sll1663	CpcE-related protein	1.66	2.16
sll0504	diaminopimelate decarboxylase	2.34	1.64
sll1091	geranylgeranyl hydrogenase	2.83	1.80
slr0033	glutamyl-tRNA (Gln) amidotransferase subunit C	1.88	2.48
slr0426	GTP cyclohydrolase i	1.79	2.31
sll0872	hypothetical protein	2.56	2.85
slr1853	PcaC-like protein, putative	1.67	1.89
sll1110	peptide chain release factor RF-1	1.76	1.66
sll1994	porphobilinogen synthase	2.18	2.87
sll1019	probable hydroxyacylglutathione hydrolase	4.39	3.64
sll0807	ribulose-phosphate 3-epimerase (ec 5.1.3.1)	1.67	1.72

slr1417	T10O24.11	1.85	3.62
sll1980	thiol:disulfide interchange protein txla	1.62	2.40
sll0381	hypothetical protein		2.01
slr1761	12 kDa FK506-binding protein (fkBP) (peptidyl-prolyl)		2.04
ssl3436	50s ribosomal protein l29		1.57
slr0242	bacterioferritin comigratory protein		3.34
sll1654	conserved hypothetical protein		1.74
slr0823	conserved hypothetical protein		2.56
sll1336	conserved hypothetical protein		1.69
sll1734	conserved hypothetical protein		2.19
ssl0352	conserved hypothetical protein		1.64
slr0581	conserved hypothetical protein		2.08
ssl1707	conserved hypothetical protein		2.92
ssr3122	conserved hypothetical protein		2.61
sll0634	conserved hypothetical protein		1.69
ssr2998	conserved hypothetical protein		1.50
sll0662	conserved hypothetical protein		1.85
ssl2982	conserved hypothetical protein (orf75)		1.92
slr1828	ferredoxin ii		2.43
slr0739	geranylgeranyl diphosphate synthase (SelGGPS)		1.66
sll0057	grpe protein , fragment-related		1.62
slr1600	hypothetical protein		1.92
ssr1853	hypothetical protein		4.10
slr1339	hypothetical protein		1.56
sll0630	hypothetical protein		3.45
slr0455	hypothetical protein		2.17
slr1431	hypothetical protein		2.06
slr0476	hypothetical protein		1.69
sll1620	hypothetical protein		1.75
sll1549	hypothetical protein		2.06
ssl0461	hypothetical protein		1.73
ssl0242	hypothetical protein		10.31
slr1160	hypothetical protein		2.39
slr0111	hypothetical protein		1.90
ssr3402	hypothetical protein		2.11
slr1915	hypothetical protein		2.63
sll0162	hypothetical protein		1.57
slr1970	hypothetical protein		3.77
slr1472	-identity		1.92
sll1074	leucyl-tRNA synthetase		2.73
slr1198	LsfA		2.02
slr1030	Mg-Protoporphyrin IX		1.82
sll1209	M-protein, putative		1.61
sll1732	NADH dehydrogenase subunit 5		2.18
slr0043	nrtC-like transporter protein (cmpC)		1.91
sll0199	ntss01_ORF03920		4.44
slr1887	PBG-D (aa1-344)		1.86
slr0394	phosphoglycerate kinase		2.39

ssr2831	photosystem i reaction centre subunit iv	2.39
ssr3383	phycobilisome 7.8 kd linker polypeptide, allophycocyanin-associated, core	1.57
slr2051	phycobilisome rod-core linker polypeptide cpcg	2.13
slr1783	probable transcriptional regulator ycf29	1.82
ssl0563	product binds the terminal electron accepting Fe-S centers of photosystem I	2.07
slr1846	promoter active fragment E3	1.51
slr0114	regulatory protein, putative	1.77
slr0194	ribose 5-phosphate isomerase, putative	1.64
sll0145	ribosome recycling factor (ribosome releasing factor) (rrf)	1.68
sll1594	rubisco operon transcriptional regulator	1.56
sll0039	similar to sir1042 protein of Synechocystis sp. strain PCC 6803	1.79
slr1271	teichoic acid biosynthesis protein a-related	1.77
slr1139	thioredoxin	2.61
slr1992	vitami B12 transporter protein/glutathione peroxidase	2.16

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Table S2 A Down-regulated proteins (fold changes) revealed by quantitative I TRAQ p

Gene	Description	N24	N48
sll0900	ATP phosphoribosyltransferase	0.003	
slr0769	conserved hypothetical protein	0.210	
slr0957	hypothetical protein	0.219	
sll1080	hypothetical 36.3 kd lipoprotein precursor, putative	0.295	
sll1757	conserved hypothetical protein	0.583	
sll0783	hypothetical protein	0.352	
ssl1918	hypothetical protein	0.354	
sll0172	hypothetical protein	0.369	
slr1735	glutamine transport ATP-binding protein glnq	0.373	
slr1171	BsaA	0.566	
slr0058	hypothetical protein	0.567	
slr0518	alpha-l-arabinofuranosidase b precursor b)-related	0.433	
slr0374	conserved hypothetical protein	0.459	
sll1426	hypothetical protein	0.582	
slr2101	conserved hypothetical protein	0.481	
sll1483	transforming growth factor induced protein	0.490	
slr1773	hypothetical protein	0.561	
sll0779	utilizing regulatory protein tutC	0.517	
sll1054	conserved hypothetical protein	0.527	
sll1508	UDP-3-0-acyl N-acetylglucosamine deacetylase	0.537	
slr1678	50S ribosomal protein L21	0.528	
sll0051	conserved hypothetical protein	0.533	
sll1933	DnaJ1 protein	0.534	
slr1693	pilg protein, putative	0.603	
sll0103	conserved hypothetical protein	0.613	
sll1089	hypothetical protein	0.617	
slr1958	hypothetical protein	0.623	
slr1410	putative WD-repeat protein, putative	0.623	
slr0201	succinate dehydrogenase subunit C, putative	0.628	
ssr1600	putative anti-sigma factor antagonist, putative	0.631	
slr2060	hypothetical protein	0.641	
sll1981	acetolactate synthase	0.643	
sll0753	methylenetetrahydrofolate dehydrogenase	0.646	
sll0470	hypothetical protein	0.647	
sll0923	putative transmembrane protein Wzc, putative	0.651	
sll0180	hypothetical 41.2 kd lipoprotein in hded-gada intergenic region pre	0.653	
sll1837	conserved hypothetical protein	0.654	
slr1924	Alkaline D-peptidase	0.657	
sll0272	hypothetical protein	0.663	
ssl2501	hypothetical protein	0.136	0.081
sll1330	response regulator SrrB, putative	0.295	0.253
sll1498	()	0.376	0.584
slr1830	poly-beta-hydroxybutyrate polymerase	0.398	0.348
sll1223	hoxU	0.399	0.362

slr1829	conserved hypothetical protein	0.404	0.323
sll1291	ChpA, putative	0.427	0.496
slr0469	cyanelle ribosomal protein S4	0.476	0.497
sll0499	hypothetical protein	0.512	0.623
sll1821	chloroplast ribosomal protein L13	0.527	0.617
sll1740	ribosomal protein L19	0.536	0.446
slr1276	hypothetical protein	0.539	0.509
sll0374	urea/short-chain amide ABC transporter, ATP-binding protein, putative	0.542	0.322
slr1694	appA protein	0.548	0.476
slr1289	isocitrate dehydrogenase [nadp] (ec 1.1.1.42)	0.554	0.380
sll1811	50s ribosomal protein l18	0.558	0.468
slr1258	conserved hypothetical protein	0.563	0.492
slr0369	mexF	0.568	0.466
sll1380	conserved hypothetical protein (orf238)	0.571	0.577
sll0420	urease beta subunit	0.582	0.653
sll0368	pyrimidine operon regulatory protein PyrR	0.585	0.589
sll1388	conserved hypothetical protein	0.597	0.659
ssl3437	30s ribosomal protein s17	0.608	0.444
sll1296	ChpA, putative	0.616	0.489
slr1363	conserved hypothetical protein	0.625	0.518
sll1358	conserved hypothetical protein	0.625	0.438
slr1793	transaldolase	0.625	0.621
sll1423	NtcA	0.632	0.607
slr1406	hypothetical protein	0.634	0.624
slr1275	hypothetical protein	0.641	0.502
slr1743	NADH dehydrogenase	0.647	0.449
slr1753	hypothetical protein	0.652	0.513
sll1118	conserved hypothetical protein	0.653	0.601
sll1097	30S ribosomal protein S7	0.654	0.575
sll0781	conserved hypothetical protein	0.656	0.371
slr1881	()		0.528
sll0528	(), putative		0.524
slr0250	17.3 kd protein in mura-rpon intergenic region precursor, putative		0.575
sll1817	30s ribosomal protein s11		0.520
slr0628	30S ribosomal protein S14		0.518
sll1804	30S ribosomal protein S3		0.513
sll1809	30s ribosomal protein s8		0.335
slr1994	3-oxoacyl-(acyl-carrier protein) reductase		0.235
sll1676	4-alpha-glucanotransferase (ec 2.4.1.25) (amylomaltase)		0.594
sll1819	50s ribosomal protein l17		0.377
sll1802	50s ribosomal protein l2		0.647
sll1803	50s ribosomal protein l22		0.607
sll1801	50s ribosomal protein l23		0.463
ssr2799	50S ribosomal protein L27		0.552
sll1800	50s ribosomal protein l4		0.563
sll1810	50s ribosomal protein l6		0.521
sll1082	ABC transporter, ATP-binding protein		0.275
sll1770	ABC transporter, putative		0.525

slr1993	acetyl-coa acetyltransferase	0.325
slr1898	acetylglutamate kinase (n-acetylglutama)	0.306
slr1022	acetylornithine aminotransferase	0.575
sll1085	aerobic glycerol-3-phosphate dehydrogenase, putative	0.629
sll1270	amino acid ABC transporter, permease protein	0.277
sll0224	amino-acid abc transporter binding protein	0.610
sll0108	ammonium transporter	0.234
slr0585	argininosuccinate synthase	0.433
sll1327	ATP synthase gamma chain	0.416
slr1768	B-cell receptor associated protein-related protein, putative	0.593
sll1314	c4-dicarboxylate-binding periplasmic protein precursor, putative	0.397
slr0257	carboxyl terminal protease	0.564
slr1751	carboxyl terminal protease	0.552
slr0798	cation-transporting ATPase, P-type (pacS)	0.584
sll1822	chloroplast 30s ribosomal protein s9	0.344
slr0929	chromosome partitioning protein, ParA family	0.585
sll0401	citrate synthase	0.420
sll0185	conserved hypothetical protein	0.361
sll0335	conserved hypothetical protein	0.254
sll0596	conserved hypothetical protein	0.413
sll0749	conserved hypothetical protein	0.666
sll0772	conserved hypothetical protein	0.608
sll0788	conserved hypothetical protein	0.264
sll0997	conserved hypothetical protein	0.573
sll1039	conserved hypothetical protein	0.400
sll1218	conserved hypothetical protein	0.591
sll1252	conserved hypothetical protein	0.556
sll1271	conserved hypothetical protein	0.392
sll1306	conserved hypothetical protein	0.487
sll1367	conserved hypothetical protein	0.656
sll1825	conserved hypothetical protein	0.429
slr0083	conserved hypothetical protein	0.626
slr0551	conserved hypothetical protein	0.555
slr0809	conserved hypothetical protein	0.613
slr1104	conserved hypothetical protein	0.664
slr1179	conserved hypothetical protein	0.666
slr1203	conserved hypothetical protein	0.662
slr1260	conserved hypothetical protein	0.354
slr1815	conserved hypothetical protein	0.403
slr1908	conserved hypothetical protein	0.636
slr1926	conserved hypothetical protein protein	0.595
sll1744	cyanelle ribosomal protein L1	0.606
sll1096	cyanelle ribosomal protein S12	0.456
ssr0482	cyanelle ribosomal protein S16	0.607
slr2002	cyanophycin synthetase	0.612
sll0813	cytochrome c oxidase subunit II	0.511
slr1379	cytochrome d ubiquinol oxidase subunit I	0.593
sll1258	Deoxycytidine triphosphate deaminase family protein	0.612

slr2058 DNA topoisomerase i	0.615
slr1265 DNA-directed RNA polymerase gamma chain	0.519
sll1427 DO serine protease	0.588
slr0839 ferrocyclase	0.583
slr1233 fumarate reductase flavoprotein subunit	0.484
slr1143 GGDEF family protein	0.589
slr1238 glutathione synthetase	0.563
slr0884 glyceraldehyde 3-phosphate dehydrogenase 1	0.298
sll0301 HglK	0.426
slr1259 homology to a plant EST:RICS2753A	0.569
sll1226 hoxH	0.664
sll1514 HspA	0.522
sll1221 hydrogenase subunit (hoxF)	0.465
sll1080 hypothetical 36.3 kd lipoprotein precursor, putative	0.297
sll0069 hypothetical protein	0.485
sll0172 hypothetical protein	0.397
sll0446 hypothetical protein	0.602
sll0606 hypothetical protein	0.534
sll0625 hypothetical protein	0.594
sll0854 hypothetical protein	0.598
sll0877 hypothetical protein	0.612
sll0911 hypothetical protein	0.630
sll1049 hypothetical protein	0.313
sll1217 hypothetical protein	0.451
sll1545 hypothetical protein	0.439
sll1571 hypothetical protein	0.597
sll1862 hypothetical protein	0.571
slr0226 hypothetical protein	0.595
slr0439 hypothetical protein	0.491
slr0575 hypothetical protein	0.629
slr0637 hypothetical protein	0.519
slr0645 hypothetical protein	0.565
slr0658 hypothetical protein	0.649
slr0708 hypothetical protein	0.534
slr0818 hypothetical protein	0.460
slr1178 hypothetical protein	0.644
slr1385 hypothetical protein	0.533
slr1612 hypothetical protein	0.629
slr1616 hypothetical protein	0.507
slr1681 hypothetical protein	0.318
slr1931 hypothetical protein	0.411
slr1944 hypothetical protein	0.388
slr1951 hypothetical protein	0.588
slr2004 hypothetical protein	0.577
slr2018 hypothetical protein	0.516
slr2144 hypothetical protein	0.467
ssl1918 hypothetical protein	0.310
slr0721 malate oxidoreductase	0.657

sll1053	membrane fusion protein mtrc precursor, putative	0.488
sll1294	methyl-accepting chemotaxis protein, putative	0.372
slr0904	Mg(2+) chelatase family protein	0.602
sll0080	N-acetyl-glutamate semialdehyde dehydrogenase ArgL	0.595
slr0891	N-acetylmuramoyl-L-alanine amidase, putative, putative	0.658
sll1453	nitrate transporter protein (nrtD) homolog (cmpD)	0.291
sll1452	nrtC-like transporter protein (cmpC)	0.451
sll0002	penicillin-binding protein 1	0.519
sll1679	periplasmic serine protease	0.588
sll1196	Pfk1	0.661
sll0920	phosphoenolpyruvate carboxylase	0.530
sll0395	phosphoglycerate mutase, putative	0.576
slr1254	phytoene dehydrogenase	0.650
sll1694	pilin	0.574
slr0163	pilin biogenesis protein	0.438
slr0162	pilin biogenesis protein-related	0.500
sll1581	polysaccharide export protein, putative, putative	0.637
sll2008	processing protease, putative	0.477
sll2009	processing protease, putative	0.654
slr0665	putative aconitate hydratase	0.544
slr0942	putative alcohol dehydrogenase	0.589
slr0370	putative aldehyde dehydrogenase	0.620
slr0051	putative carbonic anhydrase	0.518
sll1641	putative glutamate decarboxylase	0.615
sll0553	putative protein	0.646
sll0175	putative protein-related	0.577
sll1440	pyridoxamine 5-phosphate oxidase	0.589
sll0741	pyruvate-flavodoxin oxidoreductase	0.585
sll0569	reca protein	0.639
slr2100	response regulator	0.514
sll1284	serine esterase [Spirulina platensis, C1, Genomic, 827 nt].	0.499
sll1027	small subunit of NADH-dependent glutamate synthase	0.594
slr1841	SomA	0.392
slr2089	squalene--hopene cyclase (ec 5.4.99.-)	0.639
sll0173	streptogramin B lactonase, putative	0.335
sll0837	TprN	0.659
slr0744	translation initiation factor if-2	0.642
sll1343	Tricorn protease interacting factor F3, putative	0.621
slr0773	TRK system potassium uptake protein, putative, putative	0.494
slr1031	tyrosyl-tRNA synthetase	0.636
sll0764	urea/short-chain amide ABC transporter, ATP-binding protein, putative	0.337
sll1750	urease alpha subunit	0.657
sll0915	zinc protease, putative	0.595

proteomic analysis