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Table S4 Comparison of mRNA and protein levels of responsive genes under nitrogen starvation.

gene	Protein 24h	Protein 48h	RNA 24h	RNA 48h	RNA 72h	description
sll0002	**0.7987**	**0.5187**	1.2541	0.5387	0.5609	penicillin-binding protein 1
sll0051	**0.5330**	**0.6925**	0.8954	0.8302	1.2293	conserved hypothetical protein
sll0069	**0.9001**	**0.4852**	0.7512	0.5240	0.3971	hypothetical protein
sll0080	**0.7107**	**0.5952**	0.7629	0.8458	0.9997	N-acetyl-glutamate semialdehyde dehydrogenase ArgL
sll0103	**0.6131**	**0.7686**	0.8457	0.3853	0.3979	conserved hypothetical protein
sll0108	**0.2910**	**0.2340**	0.2507	0.2994	0.4374	ammonium transporter
sll0172	**0.3690**	**0.3970**	0.8526	0.1584	0.2515	hypothetical protein
sll0173	**0.4490**	**0.3347**	0.5248	0.2104	0.2320	streptogramin B lactonase, putative
sll0175	**0.5963**	**0.5770**	2.0978	3.0558	2.8759	putative protein-related
sll0180	**0.6527**	**0.5348**	0.5708	0.3157	0.2567	hypothetical 41.2 kd lipoprotein in hded-gada intergenic region precursor, putative
sll0185	**0.4423**	**0.3608**	2.2689	0.2604	0.2930	conserved hypothetical protein
sll0224	**0.6068**	**0.6098**	0.1797	0.1905	0.2455	amino-acid abc transporter binding protein in gltj-cute intergenic region precursor, putative
sll0272	**0.6627**	**1.4025**	1.1957	0.0789	0.1278	hypothetical protein
sll0301	**0.6766**	**0.4264**	1.0128	1.5701	1.5990	HglK
sll0335	**0.3289**	**0.2537**	10.1929	1.6426	2.0160	conserved hypothetical protein
sll0368	**0.5855**	**0.5889**	1.2892	1.1195	1.9542	pyrimidine operon regulatory protein PyrR
sll0374	**0.5423**	**0.3215**	0.8381	1.1386	1.7156	urea/short-chain amide ABC transporter, ATP-binding protein, putative
sll0395	**0.7605**	**0.5764**	1.7559	1.5088	1.5862	phosphoglycerate mutase, putative
sll0401	**0.6246**	**0.4203**	0.8722	0.5846	0.6274	citrate synthase
sll0420	**0.5824**	**0.9488**	0.6208	1.4102	0.7886	urease beta subunit
sll0446	**0.7837**	**0.6017**	0.5626	1.4848	1.1401	hypothetical protein
sll0470	**0.6468**	**1.1574**	0.1885	0.1470	0.1458	hypothetical protein
sll0495	**1.2005**	**0.9268**	3.0971	5.9691	7.8992	asparaginyl-trna synthetase (ec 6.1.1.22) (asparagine--trna ligase) (asnrs)
sll0528	**0.7849**	**0.5241**	0.5715	0.7293	0.5353	(), putative
sll0553	**0.5402**	**0.6464**	0.5225	0.4588	0.3275	putative protein

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sll0569	**0.8803**	**0.6386**	2.3691	2.1921	1.4865	reca protein
sll0596	**0.6845**	**0.4131**	0.9126	0.4173	0.4810	conserved hypothetical protein
sll0606	**0.7337**	**0.5339**	7.6548	3.0739	3.9002	hypothetical protein
sll0625	**0.9116**	**0.5938**	0.8332	1.2263	1.9927	hypothetical protein
sll0741	**0.4869**	**0.5851**	0.8566	0.8624	0.8952	pyruvate-flavodoxin oxidoreductase
sll0749	**1.0001**	**0.6658**	1.5335	0.2513	0.4130	conserved hypothetical protein
sll0753	**0.6460**	**0.8271**	2.4212	1.7733	3.0440	methylenetetrahydrofolate dehydrogenase
sll0764	**0.4941**	**0.3368**	0.9025	0.8326	0.9071	urea/short-chain amide ABC transporter, ATP-binding protein, putative
sll0772	**0.7728**	**0.6079**	0.1643	0.2397	0.2976	conserved hypothetical protein
sll0779	**0.5171**	**1.1364**	2.2503	2.6133	2.9334	utilizing regulatory protein tutC
sll0781	**0.6562**	**0.3713**	0.5296	0.3356	0.3999	conserved hypothetical protein
sll0783	**0.3516**	**0.2860**	14.8254	2.8332	8.2162	hypothetical protein
sll0788	**0.4272**	**0.2641**	0.2436	0.5686	0.4538	conserved hypothetical protein
sll0813	**0.7605**	**0.5107**	0.8849	0.3861	0.4841	cytochrome c oxidase subunit II
sll0837	**0.8084**	**0.6592**	0.7081	0.3172	0.3797	TprN
sll0854	**0.8681**	**0.5977**	0.4400	0.4133	0.5315	hypothetical protein
sll0877	**0.8299**	**0.6120**	1.1330	1.5441	2.8490	hypothetical protein
sll0900	**0.0003**	**1.0870**	0.9759	0.8696	1.0857	ATP phosphoribosyltransferase
sll0911	**1.0471**	**0.6297**	0.6457	1.6585	1.0231	hypothetical protein
sll0915	**0.5770**	**0.5945**	1.1576	0.7821	0.5254	zinc protease, putative
sll0920	**0.5211**	**0.5302**	0.7115	0.2667	0.2728	phosphoenolpyruvate carboxylase
sll0923	**0.6510**	**0.4864**	1.1532	1.1069	1.5306	putative transmembrane protein Wzc, putative
sll0997	**0.7042**	**0.5734**	0.3526	0.3619	0.6626	conserved hypothetical protein
sll1027	**0.7107**	**0.5938**	1.1490	0.2960	0.3225	small subunit of NADH-dependent glutamate synthase
sll1039	**0.3319**	**0.4000**	2.6256	3.0262	3.4520	conserved hypothetical protein
sll1049	**0.4496**	**0.3131**	2.0830	0.7169	0.6822	hypothetical protein
sll1053	**0.6519**	**0.4883**	4.7421	2.3715	3.5722	membrane fusion protein mtrc precursor, putative
sll1054	**0.5266**	**0.5238**	2.1080	2.3922	1.5491	conserved hypothetical protein
sll1080	**0.2949**	**0.2970**	1.6686	2.0195	1.9212	hypothetical 36.3 kd lipoprotein precursor, putative
sll1082	**0.4686**	**0.2751**	3.2069	2.4704	5.4634	ABC transporter, ATP-binding protein
sll1085	**1.0173**	**0.6293**	2.6251	2.9436	3.8101	aerobic glycerol-3-phosphate dehydrogenase, putative
sll1089	**0.6165**	**0.8803**	0.5251	0.1458	0.1444	hypothetical protein

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sll1096	**0.8889**	**0.4564**	0.6352	0.2389	0.3668	cyanelle ribosomal protein S12
sll1097	**0.6545**	**0.5747**	1.3589	0.4637	0.1912	30S ribosomal protein S7
sll1118	**0.6527**	**0.6010**	3.2567	2.9757	1.9325	conserved hypothetical protein
sll1196	**0.8110**	**0.6605**	0.7621	0.3177	0.3137	Pfk1
sll1217	**1.1933**	**0.4511**	0.5690	2.1101	2.3114	hypothetical protein
sll1218	**0.7283**	**0.5907**	2.6447	2.4308	2.8860	conserved hypothetical protein
sll1221	**0.5368**	**0.4647**	0.4324	0.3122	0.3265	hydrogenase subunit
sll1223	**0.3992**	**0.3618**	0.6067	0.5828	0.3353	hoxU
sll1226	**0.7348**	**0.6636**	0.6612	1.2965	1.1975	hoxH
sll1252	**0.7246**	**0.5562**	1.5924	2.8863	2.1936	conserved hypothetical protein
sll1258	**0.9407**	**0.6120**	0.3488	1.0625	0.9562	Deoxycytidine triphosphate deaminase family protein
sll1270	**0.2891**	**0.2766**	1.6125	0.5005	0.4277	amino acid ABC transporter, permease protein
sll1271	**0.2904**	**0.3915**	1.0594	1.2410	0.8080	conserved hypothetical protein
sll1284	**0.9461**	**0.4993**	3.6008	0.9670	1.0515	serine esterase [Spirulina platensis, C1, Genomic, 827 nt].
sll1291	**0.4270**	**0.4958**	0.7553	0.4006	0.5590	ChpA, putative
sll1292	**1.0152**	**1.4388**	0.5119	0.2252	0.4811	similar to sir1042 protein of Synechocystis sp. strain PCC 6803
sll1296	**0.6158**	**0.4885**	3.0689	1.1200	1.0284	ChpA, putative
sll1306	**0.7143**	**0.4866**	0.0804	0.0376	0.0452	conserved hypothetical protein
sll1314	**0.6949**	**0.3967**	0.7898	0.7502	0.7466	c4-dicarboxylate-binding periplasmic protein precursor, putative
sll1327	**0.7278**	**0.4160**	0.1304	0.0698	0.0518	ATP synthase gamma chain
sll1330	**0.2954**	**0.2533**	2.3081	0.6252	0.7123	response regulator SrrB, putative
sll1343	**0.7806**	**0.6207**	0.9212	1.1881	0.8700	Tricorn protease interacting factor F3, putative
sll1358	**0.6250**	**0.4380**	0.1872	0.1150	0.1175	conserved hypothetical protein
sll1367	**0.7813**	**0.6557**	0.9650	1.0580	1.0735	conserved hypothetical protein
sll1378	**0.9479**	**1.5601**	0.8417	1.2729	1.3466	()
sll1388	**0.5974**	**0.6588**	2.4585	1.7688	2.0320	conserved hypothetical protein
sll1423	**0.6317**	**0.6072**	0.1242	0.2560	0.2987	NtcA
sll1426	**0.5817**	**0.9940**	0.1970	0.1875	0.2339	hypothetical protein
sll1427	**0.7800**	**0.5882**	1.5348	0.9015	0.6291	DO serine protease
sll1440	**0.7364**	**0.5889**	2.3654	4.3068	11.3786	pyridoxamine 5-phosphate oxidase
sll1452	**0.7639**	**0.4507**	0.5504	0.2073	0.3132	nrtC-like transporter protein
sll1453	**0.7651**	**0.2910**	0.1324	0.1491	0.1702	nitrate transporter protein (nrtD) homolog
sll1483	**0.4897**	**1.3850**	9.4180	7.5426	10.5554	transforming growth factor induced protein

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sll1498	**0.3761**	**0.5845**	1.2662	0.7001	0.9258	()
sll1508	**0.5368**	**1.1013**	0.7718	1.0025	0.8693	UDP-3-0-acyl N-acetylglucosamine deacetylase
sll1514	**1.0395**	**0.5216**	0.2608	0.4401	0.3832	HspA
sll1545	**0.9074**	**0.7710**	0.6428	0.9109	0.7682	gstA protein, putative
sll1571	**0.6775**	**0.5970**	0.2003	0.2199	0.1783	hypothetical protein
sll1581	**0.7018**	**0.6365**	0.8899	0.5346	0.4191	polysaccharide export protein, putative, putative
sll1641	**0.7937**	**0.6150**	0.4845	0.8225	0.6800	putative glutamate decarboxylase
sll1676	**0.8237**	**0.5938**	1.2532	0.6974	0.6497	4-alpha-glucanotransferase (ec 2.4.1.25) (amylomaltase) (disproportionating enzyme) (d-enzyme)
sll1679	**0.7205**	**0.5882**	2.7300	0.4756	0.3595	periplasmic serine protease
sll1694	**0.7315**	**0.5741**	0.0145	0.0298	0.0242	pilin
sll1740	**0.5356**	**0.4464**	0.1698	0.3225	0.2693	ribosomal protein L19
sll1744	**1.0246**	**0.6061**	0.0330	0.0142	0.0170	cyanelle ribosomal protein L1
sll1750	**0.8636**	**0.6575**	1.0650	0.4414	0.5018	urease alpha subunit
sll1757	**0.5834**	**0.7524**	0.9041	0.5363	0.3343	conserved hypothetical protein
sll1770	**0.3360**	**0.5255**	0.5764	1.0843	0.7539	ABC transporter, putative
sll1800	**0.5528**	**0.5634**	0.1768	0.0455	0.0365	50s ribosomal protein l4
sll1801	**0.7241**	**0.4634**	0.0475	0.0168	0.0181	50s ribosomal protein l23
sll1802	**0.9166**	**0.6472**	0.1910	0.0404	0.0482	50s ribosomal protein l2
sll1803	**0.8826**	**0.6072**	0.3798	0.0577	0.0577	50s ribosomal protein l22
sll1804	**0.8741**	**0.5131**	0.4815	0.0515	0.0397	30S ribosomal protein S3
sll1809	**0.7639**	**0.3347**	0.2035	0.0270	0.0255	30s ribosomal protein s8
sll1810	**0.9091**	**0.5208**	0.2929	0.0295	0.0358	50s ribosomal protein l6
sll1811	**0.5580**	**0.4679**	0.6091	0.1009	0.0897	50s ribosomal protein l18
sll1817	**0.7776**	**0.5200**	0.4176	0.0719	0.0898	30s ribosomal protein s11
sll1819	**0.5507**	**0.3768**	0.2927	0.1254	0.1671	50s ribosomal protein l17
sll1821	**0.5269**	**0.6173**	0.1462	0.0364	0.0340	chloroplast ribosomal protein L13
sll1822	**0.7102**	**0.3445**	0.0993	0.0396	0.0412	chloroplast 30s ribosomal protein s9
sll1825	**0.6803**	**0.4292**	0.2740	0.3739	0.6064	conserved hypothetical protein
sll1837	**0.6540**	**0.6954**	0.6446	0.5358	0.7050	conserved hypothetical protein
sll1862	**1.2970**	**0.5708**	0.0498	0.1994	0.1499	hypothetical protein
sll1933	**0.5336**	**0.9980**	2.4461	2.6846	2.6928	DnaJ1 protein
sll1981	**0.6431**	**0.7536**	0.5109	0.1848	0.1934	acetolactate synthase

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sll2008	**1.0001**	**0.4771**	1.0451	0.5225	0.6482	processing protease, putative
sll2009	**1.0235**	**0.6536**	1.1283	0.7776	0.8630	processing protease, putative
slr0051	**0.7452**	**0.5179**	0.4812	0.8471	0.6663	putative carbonic anhydrase
slr0058	**0.5672**	**0.8525**	1.1516	0.9699	2.1791	hypothetical protein
slr0083	**0.9823**	**0.6262**	0.4678	0.1048	0.1679	conserved hypothetical protein
slr0162	**0.6739**	**0.4998**	0.3194	0.3670	0.2637	pilin biogenesis protein-related
slr0163	**0.6349**	**0.4382**	0.3890	0.5674	0.4646	pilin biogenesis protein
slr0201	**0.6277**	**0.8203**	1.8036	0.8440	1.2990	succinate dehydrogenase subunit C, putative
slr0226	**0.6667**	**0.5952**	0.1422	0.0277	0.0434	hypothetical protein
slr0250	**0.9033**	**0.5750**	1.0551	0.4714	0.6041	17.3 kd protein in mura-rpon intergenic region precursor, putative
slr0257	**0.0150**	**0.5643**	0.6792	0.1953	0.2080	carboxyl terminal protease
slr0369	**0.5675**	**0.4658**	0.6884	0.1475	0.1513	mexF
slr0370	**0.7364**	**0.6196**	0.9575	0.3559	0.2916	putative aldehyde dehydrogenase
slr0374	**0.4587**	**0.5417**	0.2712	0.0197	0.0145	conserved hypothetical protein
slr0439	**0.9381**	**0.4914**	1.1055	0.7785	0.4872	hypothetical protein
slr0469	**0.4757**	**0.4968**	0.2769	0.4827	0.2749	cyanelle ribosomal protein S4
slr0518	**0.4335**	**0.6006**	0.8931	0.8477	1.2806	alpha-l-arabinofuranosidase b precursor b)-related
slr0551	**0.9569**	**0.5546**	0.3333	0.0631	0.0738	conserved hypothetical protein
slr0575	**0.7072**	**0.6289**	0.3356	0.1887	0.2401	hypothetical protein
slr0585	**0.6341**	**0.4329**	1.6937	0.7496	0.8353	argininosuccinate synthase
slr0628	**0.5141**	**0.5184**	0.1667	0.2762	0.4971	30S ribosomal protein S14
slr0637	**0.6739**	**0.5192**	0.9681	0.2563	0.2195	hypothetical protein
slr0645	**0.5938**	**0.5647**	0.5287	0.4924	0.6907	hypothetical protein
slr0658	**0.6916**	**0.6489**	0.6601	0.9956	0.5824	hypothetical protein
slr0665	**0.5385**	**0.5444**	2.1348	0.2758	0.2904	putative aconitate hydratase
slr0708	**0.7479**	**0.5342**	0.3620	0.0805	0.0622	hypothetical protein
slr0721	**0.8475**	**0.6566**	3.0084	2.6195	2.2589	malate oxidoreductase
slr0744	**1.1494**	**0.6423**	1.1325	0.1501	0.1303	translation initiation factor if-2
slr0769	**0.2102**	**0.7123**	0.7195	0.5347	0.7880	conserved hypothetical protein
slr0773	**0.5800**	**0.4941**	0.4495	0.7738	0.4791	TRK system potassium uptake protein, putative, putative
slr0798	**0.9251**	**0.5838**	0.1888	0.2989	0.2040	cation-transporting ATPase, P-type
slr0809	**0.8203**	**1.3405**	0.4125	0.4779	0.4672	putative dTDP-glucose 4-6-dehydratase
slr0818	**0.6321**	**0.4602**	1.4798	1.5363	3.2060	hypothetical protein

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slr0839	**0.8439**	**0.5834**	0.7623	0.5358	0.4829	ferrochelatase
slr0884	**0.4125**	**0.2977**	0.5937	0.5223	0.6480	glyceraldehyde 3-phosphate dehydrogenase 1 (ec 1.2.1.12) (gapdh 1) (gap-1)
slr0891	**0.8143**	**0.6579**	2.1468	1.4389	1.3159	N-acetylmuramoyl-L-alanine amidase, putative, putative
slr0904	**1.0020**	**0.6017**	6.5042	3.5683	4.0381	Mg(2+) chelatase family protein
slr0929	**0.7782**	**0.5851**	0.8179	0.4944	0.6750	chromosome partitioning protein, ParA family
slr0942	**0.7364**	**0.5886**	0.8361	0.3894	0.5995	putative alcohol dehydrogenase
slr0957	**0.2191**	**0.2362**	0.8307	0.4347	0.3524	hypothetical protein
slr1022	**0.5931**	**0.5754**	1.2543	0.2174	0.2610	acetylornithine aminotransferase
slr1031	**0.8696**	**0.6357**	1.0101	2.2217	2.3017	tyrosyl-tRNA synthetase
slr1104	**0.8425**	**0.6636**	0.7152	2.3919	2.6185	conserved hypothetical protein
slr1143	**0.7570**	**0.5889**	1.6442	1.7831	1.0445	GGDEF family protein
slr1171	**0.5656**	**0.9479**	0.3673	1.2062	1.2599	BsaA
slr1178	**0.4577**	**0.6435**	0.2946	0.3393	0.3005	hypothetical protein
slr1179	**0.8052**	**0.6662**	0.8640	0.8135	0.9526	conserved hypothetical protein
slr1203	**0.0005**	**0.6623**	0.4586	0.5041	0.4875	conserved hypothetical protein
slr1233	**0.7153**	**0.4836**	0.6943	0.5034	0.6562	fumarate reductase flavoprotein subunit
slr1238	**0.8584**	**0.5631**	0.5110	0.7139	0.6328	glutathione synthetase
slr1254	**0.8130**	**0.6498**	1.7863	1.1290	1.0104	phytoene dehydrogenase
slr1258	**0.5634**	**0.4924**	0.8534	0.9361	0.7884	conserved hypothetical protein
slr1259	**0.9718**	**0.5695**	0.5479	0.8302	0.8844	homology to a plant EST:RICS2753A
slr1260	**0.7955**	**0.3536**	0.5819	0.6621	0.5876	conserved hypothetical protein
slr1265	**0.6169**	**0.5189**	0.4263	0.2368	0.2099	DNA-directed RNA polymerase gamma chain
slr1275	**0.6410**	**0.5020**	0.2083	0.1430	0.1701	hypothetical protein
slr1276	**0.5385**	**0.5089**	0.2333	0.1568	0.1241	hypothetical protein
slr1289	**0.5540**	**0.3799**	0.9133	0.5569	0.3979	isocitrate dehydrogenase [nadp] (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh)
slr1363	**0.6250**	**0.5181**	2.8576	2.0172	1.8537	conserved hypothetical protein
slr1379	**0.6398**	**0.5931**	0.7858	0.2764	0.3044	cytochrome d ubiquinol oxidase subunit I
slr1385	**0.8718**	**0.5330**	1.0227	2.0822	3.5235	hypothetical protein
slr1406	**0.6337**	**0.6238**	0.2516	0.3065	0.3141	hypothetical protein
slr1410	**0.6231**	**0.7032**	0.2850	0.3062	0.3239	putative WD-repeat protein, putative
slr1612	**0.6716**	**0.6289**	0.2396	0.2733	0.3119	hypothetical protein

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slr1616	**0.9149**	**0.5066**	0.5253	0.8434	0.7156	hypothetical protein
slr1678	**0.5277**	**0.6882**	0.0790	0.0716	0.0559	50S ribosomal protein L21
slr1681	**0.3114**	**0.3179**	3.3551	4.7564	4.4173	hypothetical protein
slr1693	**0.6031**	**0.5482**	0.1895	0.3477	0.4386	pilg protein, putative
slr1694	**0.5476**	**0.4762**	0.2691	0.2762	0.3325	appA protein
slr1735	**0.3730**	**0.2365**	1.0352	1.0382	0.8385	glutamine transport ATP-binding protein glnq
slr1743	**0.6472**	**0.4486**	6.0717	3.3722	2.8839	NADH dehydrogenase
slr1751	**0.6105**	**0.5519**	0.2267	0.1138	0.1289	carboxyl terminal protease
slr1753	**0.6523**	**0.5126**	1.1555	0.6132	0.3014	hypothetical protein
slr1768	**0.6527**	**0.5931**	0.3270	0.4238	0.6309	B-cell receptor associated protein-related protein, putative
slr1773	**0.5609**	**0.5297**	0.2878	0.3554	0.3738	hypothetical protein
slr1793	**0.6254**	**0.6207**	0.2589	0.2572	0.3051	transaldolase
slr1815	**0.6180**	**0.4034**	0.2007	0.2955	0.5082	conserved hypothetical protein
slr1829	**0.4042**	**0.3234**	1.1533	0.7381	0.6689	conserved hypothetical protein
slr1830	**0.3984**	**0.3479**	0.4542	0.4444	0.4662	poly-beta-hydroxybutyrate polymerase
slr1841	**0.6357**	**0.3920**	0.0405	0.0071	0.0082	SomA
slr1881	**0.7407**	**0.5283**	1.1138	1.8463	1.2776	()
slr1898	**0.4581**	**0.3064**	2.9255	1.3113	1.1047	acetylglutamate kinase
slr1908	**1.0707**	**0.6357**	0.0294	0.0363	0.0527	conserved hypothetical protein
slr1924	**0.6575**	**0.8091**	0.3208	0.4728	0.4895	Alkaline D-peptidase
slr1926	**0.8143**	**0.5952**	0.4389	0.4759	1.1318	conserved hypothetical protein protein
slr1931	**0.8658**	**0.4114**	0.2881	0.3957	0.3299	hypothetical protein
slr1944	**0.7072**	**0.3876**	0.8821	0.4360	0.5174	hypothetical protein
slr1951	**0.9960**	**0.5882**	0.5846	0.9329	1.0896	hypothetical protein
slr1958	**0.6231**	**0.6964**	0.1034	0.1237	0.1069	hypothetical protein
slr1993	**0.3609**	**0.3249**	7.9454	2.8094	4.5535	acetyl-coa acetyltransferase
slr1994	**0.3324**	**0.2353**	36.2813	1.7976	2.2452	3-oxoacyl-(acyl-carrier protein) reductase
slr2002	**0.6365**	**0.6116**	3.6634	0.6859	0.6150	cyanophycin synthetase
slr2004	**0.9756**	**0.5774**	0.3327	0.6191	0.9117	hypothetical protein
slr2018	**0.9091**	**0.5163**	0.4457	0.5879	0.4674	hypothetical protein
slr2058	**0.8576**	**0.6146**	1.4499	0.3115	0.2736	DNA topoisomerase i
slr2060	**0.6414**	**0.7174**	0.4419	0.4802	0.5446	hypothetical protein
slr2089	**0.8598**	**0.6386**	4.0659	3.1985	2.9948	squalene--hopene cyclase (ec 5.4.99.-)

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slr2100	**0.7634**	**0.5139**	1.1248	1.0344	0.9597	response regulator
slr2101	**0.4805**	**1.0277**	2.2926	0.7383	0.5095	conserved hypothetical protein
slr2144	**0.6892**	**0.4673**	1.1376	0.6134	0.3952	hypothetical protein
ssl1918	**0.3541**	**0.3099**	0.6017	1.3653	2.1090	hypothetical protein
ssl2501	**0.1364**	**0.0810**	0.2246	0.1279	0.1759	hypothetical protein
ssl3437	**0.6083**	**0.4442**	0.1098	0.0324	0.0404	30s ribosomal protein s17
ssr0482	**0.6382**	**0.6072**	0.1488	0.0354	0.0569	cyanelle ribosomal protein S16
ssr1600	**0.6309**	**1.1521**	0.1551	0.0453	0.0420	putative anti-sigma factor antagonist, putative
ssr2799	**0.6072**	**0.5522**	0.0935	0.0771	0.0549	50S ribosomal protein L27