

## Supplementary Table S1: Primers used in this study.

### For mutant construction

Primer ID	Primer Sequences (5'-3')
Km-F2	AGCGAGGTATGTAGGCCGGTGCT
Km-R2	GGAAATGTGCGCGGAACCCCT
slr1588-F1	GCCACCATTGCACTGCCTTGT
slr1588-R1	ACTCTGTAGCACCGCCTACATACCTCGCTAGGGATTAATCAAATCTTTG
slr1588-F3	AAACAAATAGGGGTTCCGCGCACATTTCCCAGTTCAGTCAAGATGCGAA
slr1588-R3	CGCTCCCGCCACGTCGAAT

### For operon confirmation

Primer ID	Primer Sequences (5'-3')
Primer set 1-F	TTTTAGTGCTCGCCAAGCG
Primer set 1-R	CTGCTTAAACGCCGCTACAT
Primer set 2-F	TGACCAGGTGGAAGCTATGAC
Primer set 2-R	TTCTGTACCGGCAGGAGTTT
Primer set 3-F	TTGAGGACGGGGAGTTTTTAGT
Primer set 3-R	TCATCCATCAAAAACACAGAGGG

### For RT-PCR

Gene ID	Primer Sequences (5'-3')
<i>6803s01</i>	GTGAGGACAGTGCCACAGAA GGCAGGAAAAAGACCAACCT
<i>slr0746</i>	GCCTGGATGCCGATTATGTC CACGTGCTCCCCATTGGT
<i>slr0747</i>	GCCCCGAAAGAAATCAGTAAA CACCTGGTCATGGGTAAACGTAA
<i>sll1566</i>	AGACGGGTTGTGGTAGACCAA AACGCAACTGGGTGGTGAGT
<i>sll1085</i>	TCCCTGGTTGGGTAAATATCTGA AACCCTGTGAGGGAACCAT
<i>sll0045</i>	GACCATTGACCGTTACGATCTCT GGCGAAACAAAGCATAACATC
<i>slr0952</i>	TGCCCCATTGGTCGCTAT TGAGGTTAATGTCCACGTTGGA
<i>slr0953</i>	CCCATGGAAAATTAGCTATCATCTC CCTTCAACATCTCCGTAAATTGG

### For His<sub>6</sub>-Slr1588 overexpression and EMSAs

Primer ID	Primer Sequences (5'-3')
His6-slr1588-F	GACGACGACAAGATGAGTACTATTTTAGTTGTCGAGGA
His6-slr1588-R	GAGGAGAAGCCCGGTCAGCGCCGTAGGGGCAAATAG
slr0746-F	AGCCAGTGGCGATAAGTCCTATTTTGCCCCCTACGGC
slr0746-R	AGCCAGTGGCGATAAGCGAGGGAGAAACGTTGTTGG
slr0747-F	AGCCAGTGGCGATAAGCAGCGCCGAAGAGTCCATT
slr0747-R	AGCCAGTGGCGATAAGCTGTTCAAAACTGACACTGGC
sll1566-F	AGCCAGTGGCGATAAGGCAGAAATCTTGCCAGAAAAGC
sll1566-R	AGCCAGTGGCGATAAGGGTAAAGGATCAAAAGGATG
sll0045-F	AGCCAGTGGCGATAAGTCGGAACATTTGGGACGAAGA

sll0045-R AGCCAGTGGCGATAAGCCCGAATTAAACCATGGACAC  
sll1085-F AGCCAGTGGCGATAAGCCGATGTGGTACTGGGAGAG  
sll1085-R AGCCAGTGGCGATAAGATGGCTGGGTAATGCTCAA  
sll0689-F AGCCAGTGGCGATAAGGACGCCTTTCCAATCTTGAGC  
sll0689-R AGCCAGTGGCGATAAGGGAGGGAGCAATGGGTTCAT  
slr0953-F AGCCAGTGGCGATAAGATCAGCGACCACAAACAACG  
slr0953-R AGCCAGTGGCGATAAGAGCAATAACTGTTCGCATAGGA  
slr0952-F AGCCAGTGGCGATAAGGTTCGGCAAATCCGCCTGAA  
slr0952-R AGCCAGTGGCGATAAGGAATCTCACTAACGGTCATGGA

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Supplementary Table S2: All proteomes detected in the proteomic study.

Protein ID	Slr1588-r1 vs. Control-r1	Slr1588-r1 vs. Control-r2	Slr1588-r2 vs. Control-r1	Slr1588-r2 vs. Control-r2	Description
SI0002	0.991	0.829	0.861	0.642	penicillin-binding protein
SI0005	1.486	2.252	1.230	1.776	hypothetical protein
SI0006	0.746	0.918	0.709	0.850	putative aminotransferase
SI0007	0.847	0.954	0.623	0.678	hypothetical protein
SI0008	0.930	1.010	0.909	1.027	unknown protein
SI0016	0.868	1.236	0.636	1.318	probable membrane-bound lytic transglycosylase A
SI0017	0.873	1.056	0.912	1.131	glutamate-1-semialdehyde aminomutase
SI0017	0.873	1.056	0.912	1.131	glutamate-1-semialdehyde aminomutase
SI0018	1.391	1.698	1.325	1.524	fructose-bisphosphate aldolase, class II
SI0019	1.020	1.015	1.342	1.304	1-deoxy-d-xylulose 5-phosphate reductoisomerase
SI0020	1.117	1.389	1.144	1.333	ATP-dependent Clp protease ATPase subunit
SI0021	0.693	0.801	1.052	0.980	probable exonuclease
SI0023	0.520	0.542	0.769	0.606	hypothetical protein
SI0030	0.009		0.004		cmp operon transcriptional regulator, LysR family protein
SI0033	0.962	1.024	1.776	1.953	carotene isomerase
SI0034	1.093	1.789	0.859	1.325	putative carboxypeptidase
SI0036	0.798	1.155	0.684	1.024	hypothetical protein
SI0037	0.826	0.557	0.491	0.304	hypothetical protein
SI0038	0.838	0.845	1.015	0.923	positive phototaxis protein, two-component response regulator PatA subfamily
SI0039	0.858	0.733	1.572	1.406	positive phototaxis protein, two-component response regulator CheY subfamily
SI0040	1.340	0.987	1.043	0.758	positive phototaxis protein, homologous to chemotaxis protein CheW
SI0041	0.797	0.613	0.955	0.639	phytochrome-like photoreceptor protein for positive phototaxis
SI0042	0.876	0.750	0.806	0.611	methyl-accepting chemotaxis protein for positive phototaxis
SI0043	0.747	0.530	0.846	0.750	homologous to chemotaxis protein CheA, two-component hybrid histidine kinase
SI0044	0.686	0.415	0.487	0.378	unknown protein
SI0045	1.686	3.774	0.934	1.529	sucrose phosphate synthase
SI0048	0.746	0.727	1.134	1.089	unknown protein
SI0051	1.429	1.314	1.172	1.101	hypothetical protein
SI0053	0.717	0.812	0.977	1.124	biotin carboxylase
SI0055	1.242	1.681	1.374	1.815	processing protease
SI0057	0.996	1.057	0.658	0.694	heat shock protein GrpE
SI0058	0.714	0.647	0.782	0.622	DnaK protein 1, heat shock protein 70, molecular chaperone
SI0063	1.036	1.325	0.573	0.770	hypothetical protein
SI0064	2.179	1.898	1.538	1.783	periplasmic protein, putative polar amino acid transport system substrate-binding protein
SI0065	0.880	1.135	0.681	0.775	acetolactate synthase small subunit
SI0066	0.913	0.907	0.968	1.017	unknown protein
SI0067	0.794	1.059	0.682	0.810	glutathione S-transferase
SI0068	0.519	0.450	1.028	0.858	unknown protein
SI0069	0.717	0.799	0.641	0.734	hypothetical protein
SI0070	0.818	0.833	0.797	0.785	phosphoribosylglycinamide formyltransferase
SI0071	0.964	1.319	1.359	1.795	hypothetical protein
SI0072	0.605	0.424	0.636	0.523	hypothetical protein
SI0078	0.955	1.332	0.959	1.167	threonyl-tRNA synthetase
SI0080	0.856	1.054	0.650	0.791	N-acetyl-gamma-glutamyl-phosphate reductase
SI0085	0.881	1.515	1.186	1.171	unknown protein
SI0086	0.906	1.199	0.794	1.035	putative arsenical pump-driving ATPase
SI0088	1.120	0.841	0.614	0.372	hypothetical protein
SI0094	0.835	0.965	0.639	0.764	two-component sensor histidine kinase
SI0096	1.225	1.161	1.016	0.888	hypothetical protein
SI0098	1.001	0.821	1.289	1.119	hypothetical protein
SI0100	0.934	0.697	0.696	0.724	N-acyl-L-amino acid amidohydrolase
SI0102	1.024	1.052	1.225	1.425	hypothetical protein
SI0103	0.922	1.024	0.808	0.809	hypothetical protein
SI0108	1.190	0.931	1.312	1.174	ammonium/methylammonium permease
SI0109	1.658	0.695	1.623	0.761	chorismate mutase
SI0135	1.309	1.637	1.309	1.724	putative 5-methylthioadenosine phosphorylase
SI0136	0.962	1.346	1.089	1.613	aminopeptidase P
SI0141	1.100	0.890	0.976	0.780	hypothetical protein
SI0142	0.890	0.671	0.802	0.604	probable cation efflux system protein
SI0144	0.876	0.977	0.753	0.872	uridine monophosphate kinase
SI0145	1.093	1.203	1.089	1.280	ribosome releasing factor
SI0147	0.920	0.885	0.936	0.940	hypothetical protein
SI0148	1.064	0.964	1.362	1.215	hypothetical protein
SI0149	1.115	1.175	1.531	1.773	hypothetical protein
SI0154	0.903	1.280	1.064	1.175	hypothetical protein
SI0157	1.397	2.315	1.453	2.421	hypothetical protein
SI0158	1.046	1.332	0.870	1.072	1,4-alpha-glucan branching enzyme
SI0160	1.381	1.103	0.870	0.686	hypothetical protein
SI0162	0.941	0.868	1.274	1.376	hypothetical protein
SI0163	0.780	0.736	1.147	0.957	WD-repeat protein
SI0166	0.903	0.978	1.927	1.905	a fusion protein between uroporphyrinogen-III C-methyltransferase (CobA/CorA) and uroporphyrinogen-III synthase (HemD)
SI0167	0.735	0.992	1.220	1.285	unknown protein
SI0169	0.816	0.777	0.843	1.074	cell division protein Fm2 homolog
SI0170	1.055	1.351	0.606	0.762	DnaK protein 2, heat shock protein 70, molecular chaperone
SI0171	1.008	0.982	1.188	1.076	probable aminomethyltransferase
SI0171	1.008	0.982	1.188	1.076	probable aminomethyltransferase
SI0172	0.886	0.950	0.699	0.792	periplasmic protein, function unknown
SI0173	0.812	0.802	0.687	0.762	virginiamycin B hydrolase, periplasmic protein
SI0175	1.047	1.605	1.060	1.536	hypothetical protein
SI0176	0.739	0.796	0.792	0.694	hypothetical protein
SI0178	1.049	1.189	1.066	1.305	hypothetical protein
SI0179	0.992	1.041	0.798	0.887	glutamyl-tRNA synthetase
SI0180	0.890	0.829	0.743	0.683	hypothetical protein
SI0182	1.082	0.891	0.728	0.602	ABC transporter ATP-binding protein
SI0183	0.941	0.861	1.010	0.978	hypothetical protein
SI0184	1.012	1.739	1.135	1.786	group2 RNA polymerase sigma factor SigC
SI0185	0.842	0.983	0.772	0.979	hypothetical protein
SI0188	0.983	0.755	1.236	0.894	unknown protein
SI0191	1.484	0.893	1.742	1.035	unknown protein
SI0192	1.381	0.725	0.720	0.373	hypothetical protein
SI0195	0.896	1.890	1.486	1.949	probable ATP-dependent protease
SI0195	0.896	1.890	1.486	1.949	probable ATP-dependent protease
SI0199	1.368	1.395	2.268	2.415	plastocyanin
SI0202	0.983	1.009	1.250	1.267	glucose inhibited division protein
SI0204	0.879	1.093	0.907	0.945	glucose inhibited division protein
SI0207	1.143	1.712	0.878	1.029	glucose-1-phosphate thymidyltransferase
SI0208	1.629	1.802	1.119	0.891	hypothetical protein
SI0209	1.188	0.977	1.949	1.585	hypothetical protein
SI0216	1.110	1.316	1.114	1.362	hypothetical protein
SI0220	1.052	1.314	0.935	1.285	L-glutamine:D-fructose-6-P amidotransferase
SI0221	1.064	1.136	1.692	1.786	bacterioferritin comigratory protein
SI0222	0.824	0.742	0.863	0.861	putative purple acid phosphatase
SI0223	1.041	0.799	0.789	0.402	NADH dehydrogenase subunit 2
SI0223	1.041	0.799	0.789	0.402	NADH dehydrogenase subunit 2
SI0224	1.577	1.314	0.963	0.784	amino-acid ABC transporter binding protein
SI0226	1.032	1.309	1.595	1.590	photosystem I assembly related protein
SI0227	1.065	1.208	0.953	1.049	peptidyl-prolyl cis-trans isomerase B, periplasmic protein
SI0228	0.829	0.868	0.915	0.799	arginase
SI0230	1.185	0.649	0.453	0.324	hypothetical protein
SI0236	0.892	0.876	0.691	0.661	unknown protein
SI0237	0.979	1.357	0.694	0.951	unknown protein
SI0243	1.082		1.441		unknown protein
SI0244	1.105	1.003	0.765	0.752	UDP-glucose 4-epimerase
SI0245	1.022	1.153	1.122	1.242	probable GTP binding protein
SI0247	1.002	1.079	0.092	0.069	iron-stress chlorophyll-binding protein, homologous to psbC (CP43)
SI0248	0.362	0.208	0.310	0.170	flavodoxin
SI0250	0.891	1.418	0.684	0.988	pantothenate metabolism flavoprotein

SI0253	0.486	0.300	0.887	0.388	hypothetical protein
SI0254	0.741	1.127	0.950	1.613	probable phytoene dehydrogenase Rieske iron-sulfur component
SI0258	0.974	0.732	1.497	1.159	cytochrome c550
SI0260	1.057	1.163	0.895	0.869	hypothetical protein
SI0263	0.529	0.931	0.578	0.558	unknown protein
SI0267	0.546	0.749	0.632	0.622	unknown protein
SI0268			0.535	0.590	hypothetical protein
SI0270	0.942	1.199	0.754	1.096	primosomal protein N'
SI0271	1.083	0.988	1.179	0.885	N utilization substance protein B homolog
SI0272	1.168	1.255	0.725	0.849	hypothetical protein
SI0273	1.383	1.587	1.342	1.468	Na <sup>+</sup> /H <sup>+</sup> antiporter
SI0274	1.081	0.960	1.215	1.160	hypothetical protein
SI0281	0.539	0.729	0.626	0.806	unknown protein
SI0283	0.597	0.599	0.960	0.827	hypothetical protein
SI0284	1.357	0.587	0.951	0.406	hypothetical protein
SI0286	1.159	1.757	1.323	1.965	hypothetical protein YCF52
SI0288	0.850	1.832	0.605	1.232	septum site-determining protein MinC
SI0289	0.776	0.999	0.680	0.845	septum site-determining protein MinD
SI0290	0.946	0.962	0.832	0.847	polyphosphate kinase
SI0293	1.040	1.684	0.890	1.292	unknown protein
SI0295	0.834	1.205	1.277	1.821	hypothetical protein
SI0300	0.791	0.792	0.741	0.733	riboflavin synthase alpha chain
SI0301	0.989	1.616	1.300	1.789	hypothetical protein
SI0312	1.449	1.553	0.877	1.071	probable oligopeptides ABC transporter permease protein
SI0314	0.792	1.277	0.833	1.200	periplasmic protein, function unknown
SI0318	0.898	1.269	1.445	2.169	hypothetical protein
SI0319	1.600	2.381	1.088	1.681	periplasmic protein, function unknown
SI0320	1.163	1.248	0.791	0.866	probable ribonuclease D
SI0321	1.157	1.353	1.050	1.198	unknown protein
SI0325	1.439	2.058	1.096	1.695	hypothetical protein
SI0329	1.229	1.629	0.858	1.126	6-phosphogluconate dehydrogenase
SI0335	1.244	1.305	1.212	1.107	hypothetical protein
SI0336	0.843	0.619	1.264	0.833	acetyl-CoA carboxylase beta subunit
SI0337	0.784	0.808	0.840	0.817	phosphate sensor, two-component sensor histidine kinase
SI0350	1.104	0.934	1.013	0.788	hypothetical protein
SI0359	0.987	1.218	0.751	0.849	hypothetical protein
SI0361	1.546	2.114	1.307	1.458	hypothetical protein
SI0362	0.912	1.009	1.175	1.058	alanyl-tRNA synthetase
SI0368	1.017	1.754	1.332	2.273	uracil phosphoribosyltransferase
SI0370	1.000	1.217	1.098	1.359	carbamoyl-phosphate synthase, pyrimidine-specific, large chain
SI0373	1.080	1.247	1.080	1.208	gamma-glutamyl phosphate reductase
SI0374	0.944	1.114	1.035	1.156	urea transport system ATP-binding protein
SI0376	1.264	0.830	1.704	1.135	unknown protein
SI0377	0.864	1.025	1.037	1.401	transcription-repair coupling factor
SI0379	0.738	1.070	0.812	1.078	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine o-acyltransferase
SI0380	0.724	0.960	0.745	0.943	probable glycosyltransferase
SI0381	1.205	1.083	0.973	0.991	hypothetical protein
SI0395	0.930	1.212	0.799	1.001	phosphoglycerate mutase
SI0396	0.731	0.743	0.715	0.599	two-component response regulator OmpR subfamily
SI0400	0.748	0.708	0.712	0.608	hypothetical protein
SI0401	0.939	0.756	0.955	0.891	citrate synthase
SI0402	0.888	0.989	1.125	1.189	aspartate aminotransferase
SI0404	0.663	0.746	1.170	1.094	glycolate oxidase subunit GlcD
SI0406	0.946	1.182	0.735	0.771	unknown protein
SI0408	0.968	0.930	0.805	0.733	peptidyl-prolyl cis-trans isomerase
SI0410	1.020	1.247	1.332	1.508	hypothetical protein
SI0412	1.272	1.014	1.502	1.082	hypothetical protein
SI0413	1.048	1.495	0.959	1.078	hypothetical protein
SI0414	0.877	1.111	0.695	0.766	hypothetical protein
SI0415	0.917	1.062	1.016	0.842	ATP-binding protein of ABC transporter
SI0415	0.917	1.062	1.016	0.842	ATP-binding protein of ABC transporter
SI0416	1.120	1.439	0.678	0.814	60 kDa chaperonin 2, GroEL2, molecular chaperone
SI0418	1.200	1.244	1.166	1.282	2-methyl-6-phytylbenzoquinone methyltransferase
SI0419	0.953	1.266	0.778	1.020	unknown protein
SI0420	1.028	1.364	0.739	0.923	urease beta subunit
SI0420	1.028	1.364	0.739	0.923	urease beta subunit
SI0421	1.015	1.042	1.305	1.175	adenylosuccinate lyase
SI0422	0.899	0.710	0.773	0.661	asparaginase
SI0424	1.059	1.225	1.425	1.427	hypothetical protein
SI0427	0.929	0.876	1.582	1.464	photosystem II manganese-stabilizing polypeptide
SI0430	1.284	2.247	0.769	1.374	HtpG, heat shock protein 90, molecular chaperone
SI0441	1.277	1.302	1.946	2.049	unknown protein
SI0443	1.109	1.297	0.695	0.857	unknown protein
SI0445	0.779	0.491	1.198	0.745	unknown protein
SI0446	0.687	0.588	1.078	0.805	unknown protein
SI0454	0.928	0.756	0.867	0.760	phenylalanyl-tRNA synthetase alpha chain
SI0455	1.202	1.311	1.107	1.193	homoserine dehydrogenase
SI0456	0.857	0.796	1.136	1.013	hypothetical protein
SI0459	0.981	1.181	1.115	1.294	excinuclease ABC subunit B
SI0459	0.981	1.181	1.115	1.294	excinuclease ABC subunit B
SI0461	0.737	0.787	0.743	0.728	gamma-glutamyl phosphate reductase
SI0467	0.905	1.302	0.794	1.230	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
SI0469	1.018	1.256	1.124	1.462	ribose-phosphate pyrophosphokinase
SI0470	0.719	1.028	1.081	1.418	hypothetical protein
SI0471	1.538	1.408	1.139	1.086	hypothetical protein
SI0477	0.615	0.570	0.931	1.034	putative biopolymer transport ExbB-like protein
SI0480	1.079	1.272	1.134	1.353	probable aminotransferase
SI0480	1.079	1.272	1.134	1.353	probable aminotransferase
SI0482	1.653	0.829	0.611	0.302	unknown protein
SI0485	0.778	0.649	0.469	0.387	two-component response regulator NarL subfamily
SI0486	0.688	0.761	0.597	0.538	circadian clock protein KaiB homolog
SI0487	1.002	1.031	0.832	0.688	hypothetical protein
SI0489	1.057	0.964	1.159	1.304	ATP-binding protein of ABC transporter
SI0493	0.975	1.080	0.855	0.907	hypothetical protein
SI0495	1.182	1.550	1.441	1.527	asparaginyl-tRNA synthetase
SI0497	1.013	0.832	0.833	0.699	hypothetical protein
SI0498	1.192	1.558	1.026	1.876	hypothetical protein
SI0499	0.865	1.009	0.550	0.515	hypothetical protein
SI0501	0.758	0.808	1.018	0.954	probable glycosyltransferase
SI0502	1.015	1.335	1.082	1.326	arginyl-tRNA-synthetase
SI0504	1.042	0.890	1.669	1.366	diaminopimelate decarboxylase
SI0505	0.736	0.828	0.765	0.940	hypothetical protein
SI0506	0.845	0.494	0.903	0.160	undecaprenyl pyrophosphate synthetase
SI0507	0.644	0.472	0.569	0.393	probable cation transporter
SI0508	0.835	0.938	0.293	0.426	unknown protein
SI0509	0.974	1.063	0.860	0.937	similar to 5',5''-P-1,P-4-tetraphosphate phosphorylase II
SI0513	0.888	1.032	1.522	1.504	hypothetical protein
SI0514	1.227	1.323	0.544	0.631	hypothetical protein
SI0518	1.101	1.344	2.041	2.710	unknown protein
SI0519	1.267	1.083	0.643	0.630	NADH dehydrogenase subunit 1
SI0520	1.330	1.195	0.883	0.791	NADH dehydrogenase subunit NdhI
SI0521	1.238	0.976	0.566	0.436	NADH dehydrogenase subunit 6
SI0524	0.998	1.147	1.000	1.203	hypothetical protein
SI0525	1.357	1.592	0.668	0.779	hypothetical protein
SI0528	1.139	1.047	0.712	0.741	hypothetical protein
SI0529	0.958	0.879	0.922	0.826	hypothetical protein
SI0533	1.335	1.582	1.942	2.232	trigger factor
SI0534	1.075	1.116	1.050	1.063	ATP-dependent Clp protease proteolytic subunit 2
SI0535	1.292	1.333	0.998	1.193	ATP-dependent Clp protease ATPase subunit
SI0540	0.821	1.595	0.417	0.620	phosphate-binding protein PstS homolog
SI0541	1.481	0.941	2.584	1.621	acyl-lipid desaturase (delta 9)
SI0542	0.838	0.623	1.279	0.912	acetyl-coenzyme A synthetase
SI0543				0.029	hypothetical protein
SI0544	0.933	0.701	0.978	0.726	hypothetical protein

SI0545	0.407	0.215	0.565	0.294	hypothetical protein
SI0546	0.950	1.095	1.437	1.818	probable translation initiation factor
SI0547	0.554	0.564	0.672	0.675	unknown protein
SI0550	1.370	1.294	1.838	1.645	flavoprotein
SI0553	1.416	1.548	0.964	0.873	hypothetical protein
SI0554	1.464	1.499	1.513	1.473	ferredoxin-thioredoxin reductase, catalytic chain
SI0555	0.678	0.434	0.859	0.543	methionine aminopeptidase
SI0556	1.000	1.266	1.198	1.425	Na <sup>+</sup> /H <sup>+</sup> antiporter
SI0558	0.880	0.990	1.064	1.294	hypothetical protein YCF53
SI0563	1.368	1.567	1.295	1.198	unknown protein
SI0564	1.475	1.235	2.257	1.908	hypothetical protein
SI0567	0.995	0.935	0.992	1.025	ferric uptake regulation protein
SI0569	0.648	1.046	1.129	1.590	RecA gene product
SI0572	0.852	0.497	1.182	0.688	hypothetical protein
SI0573	1.217	0.503	1.372	0.481	carbamate kinase
SI0574	0.888	0.440	1.832	0.967	probable permease protein of lipopolysaccharide ABC transporter
SI0575	0.943	1.082	1.153	1.248	probable lipopolysaccharide ABC transporter ATP binding subunit
SI0576	0.834	1.050	0.816	0.950	putative sugar-nucleotide epimerase/dehydratase
SI0577	0.903	1.070	1.256	1.504	hypothetical protein
SI0578	1.066	1.060	1.346	1.376	phosphoribosylaminoimidazole carboxylase ATPase subunit
SI0585	0.997	1.138	0.661	0.591	hypothetical protein
SI0586	0.687	0.486	0.952	0.665	hypothetical protein
SI0587	0.898	1.087	0.675	0.879	pyruvate kinase
SI0588	0.374	0.584	0.499	0.685	unknown protein
SI0593	0.785	0.611	0.934	0.743	glucokinase
SI0596	0.796	1.332	0.346	0.422	hypothetical protein
SI0601	0.771	0.654	0.722	0.607	nitrilase homolog
SI0602	0.814	0.722	1.072	0.953	hypothetical protein
SI0603	0.726	0.741	0.954	0.962	menaquinone biosynthesis protein MenD
SI0606	1.070	1.096	0.944	0.898	hypothetical protein
SI0613	1.337	2.053	0.224	0.402	Holliday junction DNA helicase RuvB
SI0616	1.120	1.110	1.094	1.153	preprotein translocase SecA subunit
SI0617	1.022	0.834	0.936	0.641	plasma membrane protein essential for thylakoid formation
SI0622	0.959	0.567	1.350	0.803	quinolinate synthase
SI0623	1.136	1.767	0.978	1.406	unknown protein
SI0625	0.942	1.140	0.681	0.957	unknown protein
SI0626	0.815	0.892	0.872	1.036	putative neutral invertase
SI0629	0.878	0.733	3.155	2.564	alternative photosystem I reaction center subunit X
SI0630	0.528	0.518	0.433	0.256	unknown protein
SI0631	0.764	0.735	0.864	0.787	L-aspartate oxidase
SI0634	0.830	0.866	1.017	0.841	photosystem I biogenesis protein BtpA
SI0635	0.854	0.814	1.447	1.403	probable thiamine-phosphate pyrophosphorylase
SI0635	0.854	0.814	1.447	1.403	probable thiamine-phosphate pyrophosphorylase
SI0638	1.639	1.859	1.182	1.508	periplasmic protein, function unknown
SI0639	1.318	1.258	1.364	1.259	hypothetical protein
SI0640	0.789	0.784	0.849	0.806	probable sodium/sulfate symporter
SI0643	0.937	1.250	1.261	1.196	urease accessory protein G
SI0644	1.215	0.833	1.021	0.667	probable esterase
SI0645	0.883	0.917	0.678	0.576	unknown protein
SI0646	0.873	0.861	1.035	1.175	guanylyl cyclase
SI0649	0.782	1.136	1.218	1.637	two-component response regulator OmpR subfamily
SI0649	0.782	1.136	1.218	1.637	two-component response regulator OmpR subfamily
SI0654	1.089	1.490	1.086	1.179	alkaline phosphatase
SI0656	0.843	1.119	0.595	0.792	unknown protein
SI0659	0.939	0.901	0.801	0.934	hypothetical protein
SI0660	0.934	0.964	0.894	0.820	pyridoxal phosphate biosynthetic protein PdxA
SI0661	0.935	1.274	1.009	1.422	hypothetical protein YCF35
SI0672	0.728	0.730	0.818	0.764	cation-transporting p-type ATPase PacL
SI0676	0.587	0.676	0.619	0.668	hypothetical protein
SI0679	0.684	0.867	0.574	0.718	periplasmic phosphate-binding protein of ABC transporter
SI0680	1.106	1.626	1.105	1.504	phosphate-binding periplasmic protein precursor (PBP)
SI0685	0.407	0.494	0.868	0.898	hypothetical protein
SI0689	0.969	0.604	0.449	0.216	Na <sup>+</sup> /H <sup>+</sup> antiporter
SI0691	0.907	0.701	1.031	0.855	hypothetical protein
SI0698	0.698	0.803	0.937	0.966	drug sensory protein A, low temperature sensor, two-component sensor histidine kinase
SI0703	1.101	1.199	0.904	1.199	unknown protein
SI0704	0.604	0.625	0.912	0.888	cysteine desulfurase
SI0708	0.755	1.486	1.397	2.160	dimethyladenosine transferase
SI0708	0.755	1.486	1.397	2.160	dimethyladenosine transferase
SI0709	0.833	0.628	0.620	0.740	putative endonuclease
SI0711	1.018	1.239	0.803	0.998	isopentenyl monophosphate kinase
SI0712	1.319	1.007	1.647	1.073	cysteine synthase
SI0716	0.606	0.577	0.563	0.597	leader peptidase I (signal peptidase I)
SI0721	1.395	1.294	0.741	0.765	unknown protein
SI0723	3.021	2.451	3.215	2.660	unknown protein
SI0726	1.028	1.314	0.986	1.238	phosphoglucomutase
SI0728	0.900	0.859	1.244	1.186	acetyl-CoA carboxylase alpha subunit
SI0729	1.064	1.259	1.230	1.570	probable DNA methyltransferase
SI0735	0.781	0.782	0.953	0.887	hypothetical protein
SI0736	0.713	0.853	0.513	0.560	hypothetical protein
SI0737	0.734	0.746	0.887	0.730	hypothetical protein
SI0740	0.978	1.202	0.696	0.772	hypothetical protein
SI0741	1.000	0.816	1.033	0.943	pyruvate flavodoxin oxidoreductase
SI0742	1.748	1.608	1.116	1.271	hypothetical protein
SI0744	0.994	0.725	0.954	0.889	hypothetical protein
SI0745	0.760	0.798	0.730	1.003	phosphofructokinase
SI0749	1.049	1.053	0.875	0.989	hypothetical protein
SI0750	0.938	0.979	0.833	0.907	two-component sensor histidine kinase, KaiC-interacting protein, involved in circadian rhythm
SI0751	1.080	1.256	0.597	0.465	hypothetical protein YCF22
SI0752	1.212	1.188	0.882	0.814	hypothetical protein
SI0753	0.943	0.929	1.104	1.147	FoD bifunctional protein
SI0754	1.138	1.362	1.127	1.376	ribosome binding factor A
SI0755	0.858	1.081	0.962	1.316	thioredoxin peroxidase
SI0756	0.722	0.592	0.800	0.554	unknown protein
SI0757	0.853	0.975	0.906	1.016	amidophosphoribosyltransferase
SI0759	1.179	1.610	1.200	1.647	ABC transporter ATP-binding protein
SI0759	1.179	1.610	1.200	1.647	ABC transporter ATP-binding protein
SI0760	1.290	1.182	1.068	1.040	hypothetical protein YCF38
SI0764	0.984	1.120	1.466	1.292	urea transport system ATP-binding protein
SI0766	0.829	1.153	0.684	0.695	DNA repair protein RadC
SI0767	1.017	0.611	1.441	1.013	50S ribosomal protein L20
SI0771	0.912	0.737	1.366	0.920	glucose transport protein
SI0772	1.267	0.667	1.280	0.938	probable porin; major outer membrane protein
SI0781	0.945	1.036	0.594	0.724	hypothetical protein
SI0783	1.493	1.101	1.111	0.847	unknown protein
SI0788	0.176	0.193	0.356	0.293	hypothetical protein
SI0789	0.240	0.218	0.341	0.354	two-component response regulator OmpR subfamily
SI0790	0.418	0.489	0.454	0.415	two-component sensor histidine kinase
SI0802	1.021	0.485	0.796	0.373	hypothetical protein
SI0804	0.685	0.789	1.056	1.200	hypothetical protein
SI0807	1.099	1.181	1.072	1.134	pentose-5-phosphate-3-epimerase
SI0813	0.819	0.912	0.700	0.665	cytochrome c oxidase subunit II
SI0814	1.203	1.517	1.253	1.560	hypothetical protein
SI0815	1.247	1.404	1.397	1.284	unknown protein
SI0816	1.105	1.085	1.085	0.990	probable oxidoreductase
SI0818	0.846	0.901	0.663	0.727	tetrapyrrole methylase family protein
SI0819	0.975	0.765	1.661	1.456	photosystem I reaction center subunit III precursor (PSI-F), plastocyanin (cyt c553) docking protein
SI0821	1.058	0.921	1.250	0.867	phytochrome-like protein
SI0822	1.004	1.385	1.085	1.712	hypothetical protein
SI0823	0.904	0.890	1.172	1.022	probable succinate dehydrogenase iron-sulfur protein
SI0827	1.553	0.456	0.733	0.212	hypothetical protein
SI0828	1.582	1.658	1.170	1.263	putative amidase
SI0829	0.926	0.949	0.822	0.832	probable methyltransferase
SI0830	0.889	0.646	0.999	0.788	elongation factor EF-G

SI10832	0.730	1.337	0.824	0.945	hypothetical protein
SI10833	0.841	0.649	0.832	0.633	probable oligopeptides ABC transporter permease protein
SI10834	1.294	0.530	1.996	0.907	low affinity sulfate transporter
SI10837	0.654	0.755	0.481	0.560	periplasmic protein, function unknown
SI10838	0.930	0.937	0.729	0.749	orotidine 5' monophosphate decarboxylase
SI10842	1.100	1.161	1.167	1.263	neopullulanase
SI10844	1.195	1.105	1.309	1.087	tRNA (5-methylaminomethyl-2-thiouridylylate)-methyltransferase
SI10846	0.912	0.454	0.378	0.186	hypothetical protein
SI10848	0.799	0.984	0.676	1.280	chromosomal replication initiator protein DnaA
SI10849	0.926	0.703	1.901	1.600	photosystem II reaction center D2 protein
SI10851	1.013	0.879	1.672	1.037	photosystem II CP43 protein
SI10853	1.420	1.391	1.350	1.311	hypothetical protein
SI10854	0.846	0.912	1.091	0.975	hypothetical protein
SI10858	2.278	0.551	2.247	0.687	hypothetical protein
SI10860	0.824	0.639	0.906	0.660	hypothetical protein
SI10861	0.983	1.062	1.151	1.121	hypothetical protein
SI10867	1.460	1.282	1.364	1.447	hypothetical protein
SI10872	0.569	0.342	0.553	0.333	unknown protein
SI10873	1.063	1.209	1.050	1.199	carboxynorspermidine decarboxylase
SI10876	1.431	2.008	0.466	0.645	Holliday junction DNA helicase RuvA
SI10877	1.074	1.418	0.876	1.059	hypothetical protein
SI10886	0.987	0.967	0.969	0.880	hypothetical protein
SI10887	1.248	1.269	1.616	1.894	putative modulator of DNA gyrase; PmbA homolog
SI10888	1.218	1.166	0.636	0.836	hypothetical protein
SI10891	0.868	0.739	0.707	0.554	malate dehydrogenase
SI10895	0.868	0.824	0.964	0.898	CysQ protein homolog
SI10897	1.157	1.190	1.475	1.546	DnaJ protein, heat shock protein 40, molecular chaperone
SI10898	0.975	1.096	0.989	1.239	hypothetical protein
SI10899	1.030	0.954	0.967	0.928	UDP-N-acetylglucosamine pyrophosphorylase
SI10900	0.930	1.008	0.718	0.712	ATP phosphoribosyltransferase
SI10901	1.377	1.136	1.379	1.309	phosphoribosylaminoimidazole carboxylase
SI10902	1.003	0.953	0.969	0.925	ornithine carbamoyltransferase
SI10905	0.668	0.620	0.951	0.873	hypothetical protein
SI10909	0.595	0.411	0.549	0.374	unknown protein
SI10912	1.082	1.083	1.565	1.449	ABC transporter ATP binding protein
SI10915	0.917	1.126	0.697	0.852	periplasmic protease
SI10916	0.497	0.623	0.785	0.973	precorrin isomerase, precorrin-8X methylmutase
SI10920	0.965	1.145	1.399	1.477	phosphoenolpyruvate carboxylase
SI10921	0.689	0.675	0.754	0.679	two-component response regulator NarL subfamily
SI10921	0.689	0.675	0.754	0.679	two-component response regulator NarL subfamily
SI10923	0.683	0.532	0.714	0.609	unknown protein
SI10925	0.706	1.093	0.544	0.875	hypothetical protein
SI10927	0.917	1.208	0.622	0.817	S-adenosylmethionine synthetase
SI10928	0.842	0.628	1.289	1.003	allophycocyanin-B
SI10931	1.033	1.036	1.047	0.993	hypothetical protein
SI10934	1.230	1.333	1.052	1.145	carboxysome formation protein CcmA
SI10936	1.155	1.202	1.261	1.245	putative oxidoreductase
SI10938	1.071	0.853	1.259	0.993	aspartate transaminase
SI10945	0.796	0.811	0.932	0.847	glycogen synthase
SI10947	1.355	1.006	2.273	1.919	light repressed protein A homolog
SI10981	0.895	0.880	1.116	1.038	unknown protein
SI10982	1.626	2.066	0.929	1.235	unknown protein
SI10992	1.100	1.148	0.784	0.654	putative esterase
SI10995	1.048	1.595	0.730	0.997	hypothetical protein
SI10996	1.182	1.229	1.232	1.357	hypothetical protein
SI10997	1.339	1.346	1.148	1.263	hypothetical protein
SI10998	0.703	0.769	1.361	1.079	LysR family transcriptional regulator
SI11002	1.946	1.225	0.859	0.708	hypothetical protein YCF22
SI11004	0.812	0.880	1.046	1.070	hypothetical protein
SI11005	1.314	0.651	1.675	0.820	MazG protein homolog
SI11017	0.839	1.233	1.030	1.416	ammonium/methylammonium permease
SI11018	1.045	1.266	1.028	1.406	dihydroorotase
SI11019	0.659	0.606	0.767	0.580	hydroxyacylglutathione hydrolase
SI11020	0.873	0.991	0.925	1.135	probable glycosyltransferase
SI11021	0.840	0.873	0.907	0.954	hypothetical protein
SI11023	0.970	0.823	1.014	0.911	succinyl-CoA synthetase beta chain
SI11025	0.982	1.027	0.887	1.050	hypothetical protein
SI11027	1.106	0.983	2.849	2.688	NADH-dependent glutamate synthase small subunit
SI11028	0.892	0.703	0.960	0.681	carbon dioxide concentrating mechanism protein CcmK
SI11029	0.865	0.720	0.935	0.727	carbon dioxide concentrating mechanism protein CcmK
SI11030	0.759	0.723	0.542	0.556	carbon dioxide concentrating mechanism protein CcmL, putative carboxysome assembly protein
SI11031	0.896	0.820	1.524	1.427	carbon dioxide concentrating mechanism protein CcmM, putative carboxysome structural protein
SI11032	0.673	0.580	0.458	0.235	carbon dioxide concentrating mechanism protein CcmN, putative carboxysome assembly protein
SI11033	0.880	0.833	0.790	0.754	probable protein phosphatase
SI11035	1.007	1.290	0.959	1.164	uracil phosphoribosyltransferase
SI11036	0.914	0.921	0.852	0.800	hypothetical protein
SI11037	1.178	1.603	1.056	1.418	unknown protein
SI11039	1.003	1.017	1.006	1.032	hypothetical protein
SI11040	1.335	1.658	0.567	0.655	unknown protein
SI11041	1.171	1.120	1.019	1.028	similar to sulfate transport ATP-binding protein CysA
SI11043	0.913	1.033	0.818	0.954	polyribonucleotide nucleotidyltransferase
SI11045	1.056	1.582	1.063	1.650	mutator MutI protein
SI11049	0.820	0.852	0.924	0.916	hypothetical protein
SI11051	1.332	1.326	0.990	0.976	phycoerythrin alpha-subunit phycoerythrin lyase
SI11051	1.332	1.326	0.990	0.976	phycoerythrin alpha-subunit phycoerythrin lyase
SI11053	1.451	1.675	0.816	0.916	hypothetical protein
SI11054	0.957	0.962	0.754	0.657	hypothetical protein
SI11056	0.885	0.937	1.015	1.149	phosphoribosylformyl glycylamide synthetase II
SI11057	1.033	0.809	1.709	1.639	thioredoxin M
SI11058	1.115	1.008	0.992	0.884	dihydrodipicolinate reductase
SI11059	0.895	0.801	0.966	0.712	adenylate kinase
SI11060	0.818	0.781	0.769	0.497	hypothetical protein
SI11064	0.781	0.883	0.689	0.726	hypothetical protein
SI11069	1.002	0.851	1.499	0.988	3-oxoacyl-[acyl-carrier-protein] synthase II
SI11070	1.418	1.595	1.527	1.949	transketolase
SI11071	0.948	0.912	1.332	1.183	hypothetical protein
SI11072	0.719	1.206	0.436	0.722	hypothetical protein
SI11074	0.951	1.135	0.955	0.945	leucyl-tRNA synthetase
SI11077	0.996	1.112	0.898	0.932	agmatinase
SI11080	0.964	0.978	0.855	0.907	ABC transport system substrate-binding protein
SI11082	0.990	0.932	0.821	0.763	ABC transport system ATP-binding protein
SI11082	0.990	0.932	0.821	0.763	ABC transport system ATP-binding protein
SI11084	1.120	0.969	1.786	1.057	hypothetical protein
SI11085	2.725	3.891	2.169	2.545	glycerol-3-phosphate dehydrogenase
SI11089	1.016	0.926	0.811	0.765	periplasmic protein, function unknown
SI11091	1.495	1.499	2.558	2.358	geranylgeranyl hydrogenase
SI11092	0.740	0.904	0.668	0.665	hypothetical protein
SI11096	1.880	1.414	1.427	1.060	30S ribosomal protein S12
SI11097	1.541	1.672	1.792	1.748	30S ribosomal protein S7
SI11098	0.947	1.089	0.904	1.010	elongation factor EF-G
SI11099	0.943	0.929	0.964	0.951	elongation factor Tu
SI11101	1.071	1.131	2.445	3.040	30S ribosomal protein S10
SI11104	0.919	0.623	0.862	0.681	periplasmic substrate-binding protein of a TRAP-type permease
SI11106	1.119	1.008	1.258	1.087	hypothetical protein
SI11107	0.776	0.428	0.739	0.454	type IV pilus biogenesis protein Pill homolog
SI11108	1.012	1.031	0.834	1.072	stationary-phase survival protein SurE homolog
SI11109	0.649	0.800	0.706	0.841	hypothetical protein
SI11110	1.071	1.264	1.030	1.183	peptide chain release factor 1
SI11112	1.036	1.198	0.968	0.958	3-dehydroquinate dehydratase
SI11118	1.083	1.321	0.739	0.745	hypothetical protein
SI11120	0.754	0.826	0.586	0.592	chromosome segregation protein SMC1
SI11121	0.741	0.896	0.824	0.984	hypothetical protein
SI11123	0.965	0.733	0.707	0.567	hypothetical protein
SI11124	0.712	0.688	1.056	1.076	two-component sensor histidine kinase, phytochrome-like protein

SII1127	1.337	1.114	1.565	1.412	1,4-dihydroxy-2-naphthoate synthase
SII1130	1.221	1.506	0.948	1.129	unknown protein
SII1138	1.057	1.230	1.093	1.066	hypothetical protein
SII1142	0.891	1.114	0.785	1.032	hypothetical protein
SII1143	1.451	1.862	1.675	2.415	ATP-dependent helicase PcrA
SII1144	1.073	1.538	1.658	2.198	hypothetical protein
SII1147	0.668	0.835	1.034	1.267	glutathione S-transferase
SII1150	0.915	0.704	2.398	1.689	hypothetical protein
SII1151	0.823	0.758	0.854	0.678	unknown protein
SII1159	0.934	1.046	1.272	1.493	probable bacterioferritin comigratory protein
SII1165	1.269	1.560	1.506	1.692	DNA mismatch repair protein
SII1172	1.067	1.081	1.179	1.427	threonine synthase
SII1173	0.677	0.901	0.670	0.971	hypothetical protein
SII1174	0.992	0.998	1.299	1.284	unknown protein
SII1178	0.768	0.899	0.655	0.763	probable carbamoyl transferase
SII1180	1.074	1.253	1.003	1.130	toxin secretion ABC transporter ATP-binding protein
SII1181	1.397	1.256	1.422	1.368	similar to hemolysin secretion protein
SII1182	1.170	1.709	1.174	1.695	cytochrome b6-f complex alternative iron-sulfur subunit (Rieske iron sulfur protein)
SII1184	0.849	0.894	2.288	2.119	heme oxygenase
SII1185	0.945	0.957	1.689	1.597	coproporphyrinogen III oxidase, aerobic (oxygen-dependent)
SII1186	1.289	1.721	1.524	2.146	hypothetical protein
SII1188	1.156	1.067	1.517	1.433	hypothetical protein
SII1189	0.930	0.945	1.289	1.093	glycolate oxidase subunit GlcE
SII1193	0.910	0.980	0.504	0.536	hypothetical protein
SII1194	1.222	0.965	2.532	2.151	photosystem II 12 kDa extrinsic protein
SII1196	0.730	0.622	1.277	0.946	phosphofructokinase
SII1198	0.794	0.635	1.135	0.562	tRNA (guanine-N1)-methyltransferase
SII1201	0.729	0.743	0.561	0.656	hypothetical protein
SII1209	0.944	1.115	0.790	0.913	DNA ligase
SII1212	1.107	1.307	0.909	1.005	GDP-mannose 4,6-dehydratase
SII1213	0.867	1.036	0.782	0.919	GDP-fucose synthetase
SII1214	1.443	1.346	2.513	2.404	hypothetical protein YCF59
SII1217	1.259	1.192	1.618	1.675	unknown protein
SII1218	0.929	0.912	0.767	0.683	hypothetical protein YCF39
SII1220	1.351	1.558	1.376	1.488	putative diaphorase subunit of the bidirectional hydrogenase
SII1221	1.208	1.311	1.290	1.351	diaphorase subunit of the bidirectional hydrogenase
SII1222	1.112	1.282	0.909	1.060	hypothetical protein
SII1223	1.368	1.211	1.144	1.065	diaphorase subunit of the bidirectional hydrogenase
SII1224	0.746	0.543	0.984	0.540	hydrogenase subunit of the bidirectional hydrogenase
SII1226	1.109	1.058	1.042	0.878	hydrogenase subunit of the bidirectional hydrogenase
SII1228	0.758	0.781	0.863	0.629	two-component hybrid sensor and regulator
SII1229	0.689	0.519	0.689	0.838	two-component hybrid sensor and regulator
SII1231	0.883	1.271	0.291	0.484	mannosyltransferase
SII1232	0.938	0.496	1.011	0.527	hypothetical protein
SII1233	0.870	0.795	0.705	0.699	hypothetical protein
SII1234	1.235	1.466	1.271	1.590	adenosylhomocysteinase
SII1237	0.813	0.827	0.473	0.476	N(5)-glutamine methyltransferase
SII1239	0.697	0.537	0.470	0.326	unknown protein
SII1242	0.772	0.558	0.632	0.623	hypothetical protein
SII1244	1.099	1.350	1.961	2.457	50S ribosomal protein L9
SII1249	0.957	1.239	0.944	1.361	pantothenate synthetase/cytidylate kinase
SII1252	1.403	1.357	1.361	1.597	hypothetical protein
SII1253	0.832	0.898	0.836	0.816	similar to polyA polymerase
SII1254	0.778	1.004	0.705	1.054	hypothetical protein
SII1258	1.010	1.043	0.749	0.915	dCTP deaminase
SII1260	1.093	1.135	2.188	2.105	30S ribosomal protein S2
SII1261	1.153	1.130	1.062	1.022	elongation factor TS
SII1262	0.876	0.742	0.973	1.071	hypothetical protein
SII1265	1.456	1.126	0.932	0.661	unknown protein
SII1267	0.972	0.997	0.680	0.689	unknown protein
SII1270	0.641	0.517	0.921	0.668	periplasmic substrate-binding and integral membrane protein of the ABC-type
SII1271	1.054	0.661	0.781	0.519	probable porin; major outer membrane protein
SII1272	1.130	1.449	0.749	1.157	unknown protein
SII1273	0.886	1.037	1.170	1.203	unknown protein
SII1275	0.887	0.880	1.063	0.953	pyruvate kinase 2
SII1276	0.885	0.942	0.867	1.055	ATP-binding protein of ABC transporter
SII1280	1.072	1.164	0.999	1.271	hypothetical protein
SII1282	1.083	1.052	0.939	0.858	riboflavin synthase beta subunit
SII1284	0.786	0.936	0.728	0.864	esterase
SII1286	0.640	0.509	1.259	1.175	transcriptional regulator
SII1289	1.416	0.962	1.224	0.601	hypothetical protein
SII1290	0.941	1.148	1.129	1.466	probable ribonuclease II
SII1291	1.016	0.816	1.575	0.914	two-component response regulator PatA subfamily
SII1291	1.016	0.816	1.575	0.914	two-component response regulator PatA subfamily
SII1292	0.692	0.715	0.691	0.881	two-component response regulator CheY subfamily
SII1293	0.493	0.462	0.260	0.304	unknown protein
SII1296	0.514	0.617	0.661	0.396	two-component hybrid sensor and regulator
SII1298	0.881	0.869	0.847	0.886	putative carboxymethylglutaminylase
SII1299	1.092	0.881	0.860	0.936	acetate kinase
SII1304	0.814	0.861	0.733	0.726	unknown protein
SII1305	0.678	0.503	0.898	0.449	probable hydrolase
SII1306	0.737	0.673	0.515	0.462	periplasmic protein, function unknown
SII1307	1.437	1.389	1.006	0.986	periplasmic protein, function unknown
SII1308	0.848	0.769	0.805	0.825	probable oxidoreductase
SII1314	0.907	0.796	0.706	0.708	putative C4-dicarboxylase binding protein, periplasmic protein
SII1315	0.806	0.995	0.565	0.723	unknown protein
SII1316	1.167	0.968	1.066	0.850	cytochrome b6-f complex iron-sulfur subunit (Rieske iron sulfur protein)
SII1317	0.989	0.814	1.255	1.233	apocytochrome f, component of cytochrome b6/f complex
SII1318	0.770	0.966	0.894	1.107	hypothetical protein
SII1322	1.025	0.306	0.942	0.282	ATP synthase A chain of CF(0)
SII1323	0.983	0.540	1.052	0.534	ATP synthase subunit b' of CF(0)
SII1324	1.175	0.961	0.893	0.654	ATP synthase B chain (subunit I) of CF(0)
SII1325	0.924	0.754	0.934	0.675	ATP synthase delta chain of CF(1)
SII1326	0.923	0.880	1.029	0.988	ATP synthase alpha chain
SII1327	1.245	1.456	3.509	3.788	ATP synthase gamma chain
SII1329	0.867	0.792	0.959	0.935	inositol monophosphate family protein
SII1330	1.139	1.704	0.722	1.106	two-component system response regulator OmpR subfamily
SII1334	0.386	0.391	1.208	1.043	two-component sensor histidine kinase
SII1336	0.959	1.115	0.998	1.157	hypothetical protein
SII1338	0.732	0.667	0.739	0.688	unknown protein
SII1341	0.952	1.074	0.858	0.990	bacterioferritin
SII1342	0.951	1.043	0.873	0.973	NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase
SII1343	1.170	1.385	0.921	1.067	aminopeptidase
SII1349	0.579	0.571	0.819	0.686	phosphoglycolate phosphatase
SII1350	0.801	0.340	1.233	0.502	hypothetical protein
SII1354	0.970	0.864	0.769	0.815	single-strand-DNA-specific exonuclease RecJ
SII1355	0.727	0.776	0.600	0.534	hypothetical protein
SII1356	1.138	0.893	1.183	0.913	glycogen phosphorylase
SII1358	0.753	0.845	0.512	0.597	putative oxalate decarboxylase, periplasmic protein
SII1359	0.759	1.115	0.541	0.822	unknown protein
SII1360	0.828	1.101	0.814	0.834	DNA polymerase III subunit gamma/tau [Contains: Ssp dnaX intein]
SII1362	1.188	1.309	1.321	1.555	isoleucyl-tRNA synthetase
SII1363	0.970	1.125	0.769	0.890	ketol-acid reductoisomerase
SII1365	0.822	0.877	0.847	1.101	unknown protein
SII1366	1.110	1.121	1.189	1.117	putative SNF2 helicase
SII1367	0.868	0.826	0.883	0.967	hypothetical protein
SII1369	0.678	1.119	1.199	2.033	putative peptidase
SII1370	0.994	1.292	0.685	0.930	mannose-1-phosphate guanylyltransferase
SII1371	0.888	1.119	0.985	1.063	cAMP receptor protein, essential for motility
SII1374	0.860	1.101	0.869	1.099	probable sugar transporter
SII1376	0.936	1.451	1.024	1.348	hypothetical protein
SII1377	0.791	1.247	0.677	0.802	probable glycosyltransferase
SII1378	1.372	1.531	0.984	1.161	periplasmic protein, function unknown
SII1380	1.185	1.577	0.805	0.970	periplasmic protein, function unknown

Sl11381	0.881	0.905	1.212	0.990	hypothetical protein
Sl11382	1.062	0.894	1.174	1.172	ferredoxin, petF-like protein
Sl11383	1.304	1.435	0.962	1.092	probable myo-inositol-1(or 4)-monophosphatase
Sl11384	0.960	1.094	1.383	1.805	similar to DnaJ protein
Sl11387	0.843	0.850	0.485	0.483	serine/threonine protein phosphatase PppA
Sl11388	1.302	1.071	0.885	0.888	hypothetical protein
Sl11390	0.978	0.978	1.017	0.849	hypothetical protein
Sl11392	1.776	2.066	1.225	1.406	transcriptional regulator
Sl11393	1.037	0.982	1.127	1.086	glycogen (starch) synthase
Sl11394	1.477	1.560	1.437	1.783	peptide methionine sulfoxide reductase
Sl11395	1.042	1.590	0.925	1.403	dTDP-6-deoxy-L-mannose-dehydrogenase
Sl11396	1.120	1.577	1.229	1.176	unknown protein
Sl11398	1.222	0.948	1.202	0.917	photosystem II reaction center 13 kDa protein
Sl11399	1.001	1.003	1.047	1.019	hypothetical protein
Sl11400	1.060	0.788	0.848	0.622	hypothetical protein
Sl11414	1.151	0.983	1.014	1.073	hypothetical protein
Sl11415	0.889	0.694	0.769	0.628	hypothetical protein
Sl11418	0.846	0.597	1.242	1.073	photosystem II oxygen-evolving complex 23K protein PsbP homolog
Sl11423	0.858	0.825	0.770	1.000	global nitrogen regulator
Sl11424	1.037	0.810	1.188	0.754	hypothetical protein
Sl11425	0.982	1.030	1.182	1.297	proline-tRNA ligase
Sl11427	1.076	1.513	0.797	1.172	protease
Sl11430	1.241	1.316	1.174	1.100	adenine phosphoribosyltransferase
Sl11432	0.423	0.670	0.385	0.625	putative hydrogenase expression/formation protein HypB
Sl11432	0.423	0.670	0.385	0.625	putative hydrogenase expression/formation protein HypB
Sl11433	0.797	0.769	0.818	0.907	hypothetical protein
Sl11434	0.700	0.964	1.086	1.109	penicillin-binding protein
Sl11435	0.929	1.056	1.043	1.163	glutamyl-tRNA(Gln) amidotransferase subunit B
Sl11440	0.799	0.921	0.904	1.140	pyridoxamine 5'-phosphate oxidase
Sl11443	1.101	1.176	2.174	2.020	CTP synthetase
Sl11444	0.877	0.761	1.066	0.815	3-isopropylmalate dehydratase small subunit
Sl11446	0.670	0.901	0.509	0.707	hypothetical protein
Sl11447	1.156	0.876	0.779	0.583	hypothetical protein
Sl11450	1.344	1.176	1.351	1.107	nitrate/nitrite transport system substrate-binding protein
Sl11451	1.477	1.036	1.488	1.031	nitrate/nitrite transport system permease protein
Sl11452	1.287	1.178	1.825	1.484	nitrate/nitrite transport system ATP-binding protein
Sl11453	1.709	1.307	1.996	1.642	nitrate/nitrite transport system ATP-binding protein
Sl11454	1.616	1.205	0.951	0.861	ferredoxin-nitrate reductase
Sl11455	1.416	1.898	0.555	0.913	hypothetical protein
Sl11456	0.844	0.902	0.790	0.814	unknown protein
Sl11457	0.816	0.770	0.798	0.778	probable glycosyltransferase
Sl11459	1.330	1.350	2.203	2.890	stationary-phase survival protein SurE homolog
Sl11461	1.033	1.362	0.662	0.862	hypothetical protein
Sl11462	1.005	1.381	0.807	1.063	putative hydrogenase expression/formation protein HypE
Sl11463	1.242	1.087	1.786	1.600	cell division protein FtsH
Sl11464	1.104	0.741	1.508	0.999	hypothetical protein
Sl11466	0.916	1.209	0.927	1.133	probable glycosyltransferase
Sl11470	0.948	0.968	1.499	1.490	3-isopropylmalate dehydratase large subunit
Sl11471	1.008	1.017	1.198	1.266	phycobilisome rod-core linker polypeptide
Sl11473	2.083	1.138			a part of phytochrome-like sensor histidine kinase gene (disrupted by insertion of IS)
Sl11475	1.054	0.935	1.276	1.520	a part of phytochrome-like sensor histidine kinase gene (disrupted by insertion of IS)
Sl11479	0.753	1.198	0.599	1.076	6-phosphogluconolactonase
Sl11481	1.148	1.580	0.905	1.239	ABC-transporter membrane fusion protein
Sl11483	3.937	12.821	3.040	9.346	periplasmic protein, similar to transforming growth factor induced protein
Sl11484	0.919	1.229	0.958	1.269	type 2 NADH dehydrogenase
Sl11486	1.284	1.119	0.737	0.634	hypothetical protein
Sl11489	0.696	0.704	1.099	0.739	circadian phase modifier CpmA homolog
Sl11491	1.157	1.339	1.042	1.199	periplasmic WD-repeat protein
Sl11495	0.660	0.826	0.911	1.011	hypothetical protein
Sl11496	0.846	1.018	1.361	1.597	mannose-1-phosphate guanyltansferase
Sl11498	1.142	1.232	0.958	1.193	carbamoyl-phosphate synthase small chain
Sl11499	1.045	0.981	1.271	1.176	ferredoxin-dependent glutamate synthase
Sl11500	0.746	1.508	0.281	0.561	hypothetical protein
Sl11502	1.050	0.942	1.965	1.639	NADH-dependent glutamate synthase large subunit
Sl11504	1.222	0.939	0.750	0.569	hypothetical protein
Sl11505	0.887	0.692	0.780	0.601	hypothetical protein
Sl11507	0.502	0.667	1.089	1.072	salt-induced periplasmic protein
Sl11508	1.006	1.267	0.815	0.912	UDP-3-0-acyl N-acetylglucosamine deacetylase
Sl11514	1.368	2.865	0.214	0.535	16.6 kDa small heat shock protein, molecular chaperone
Sl11516	0.611	0.903	0.534	0.686	hypothetical protein
Sl11520	0.619	0.691	0.555	0.460	DNA repair protein RecN
Sl11521	1.047	0.937	1.321	1.297	flavoprotein
Sl11524	0.881	1.147	0.701	0.835	hypothetical protein
Sl11525	0.922	0.818	0.935	0.838	phosphoribulokinase
Sl11526	0.929	1.080	1.065	1.188	hypothetical protein
Sl11528	1.010	1.175	1.381	1.563	unknown protein
Sl11530	0.998	1.178	0.919	1.111	unknown protein
Sl11532	0.960	1.167	0.820	0.773	hypothetical protein
Sl11533	0.586	0.459	0.868	0.615	probable glycosyltransferase
Sl11534	0.765	0.560	1.292	0.935	probable glycosyltransferase
Sl11536	0.914	1.208	0.889	1.056	molybdopterin biosynthesis MoeB protein
Sl11537	0.823	0.829	0.627	0.601	similar to mutator MutI protein
Sl11538	1.174	0.945	0.907	0.907	similar to beta-hexosaminidase a precursor
Sl11541	1.464	2.198	1.229	2.208	hypothetical protein
Sl11542	0.867	1.001	0.742	0.845	hypothetical protein
Sl11545	1.068	1.264	0.840	1.032	glutathione S-transferase
Sl11546	1.075	1.091	1.736	1.838	exopolyphosphatase
Sl11546	1.075	1.091	1.736	1.838	exopolyphosphatase
Sl11549	0.383	0.270	1.000	0.616	salt-enhanced periplasmic protein
Sl11550	0.743	0.530	0.525	0.430	probable porin; major outer membrane protein
Sl11553	0.914	0.942	1.038	1.058	phenylalanyl-tRNA synthetase
Sl11555	0.688	0.797	0.596	0.680	two-component hybrid sensor and regulator
Sl11556	0.706	1.107	0.612	0.894	isopentenyl-diphosphate delta-isomerase
Sl11557	0.770	0.560	0.789	0.476	succinyl-CoA synthetase alpha chain
Sl11558	0.727	0.937	0.471	0.587	mannose-1-phosphate guanyltansferase
Sl11559	0.962	1.355	0.679	0.962	soluble hydrogenase 42 kD subunit
Sl11561	0.805	0.975	0.896	1.012	proline oxidase
Sl11563	0.781	0.998	0.697	0.926	unknown protein
Sl11564	0.978	0.933	0.634	0.873	putative lyase
Sl11566	2.392	3.401	1.631	2.392	glucosylglycerolphosphate synthase
Sl11568	1.033	1.277	0.788	0.744	fibrillin
Sl11570	1.456	1.873	1.366	1.377	unknown protein
Sl11571	1.182	0.918	0.880	0.766	hypothetical protein
Sl11577	1.018	0.895	1.139	1.033	phycocyanin beta subunit
Sl11578	0.989	0.691	1.277	0.880	phycocyanin alpha subunit
Sl11579	1.093	1.167	1.828	1.919	phycobilisome rod linker polypeptide
Sl11580	0.998	1.044	1.957	2.273	phycobilisome rod linker polypeptide
Sl11581	0.614	0.588	0.665	0.613	hypothetical protein
Sl11582	0.793	1.178	0.835	1.224	unknown protein
Sl11583	0.973	0.660	1.215	0.847	unknown protein
Sl11584	0.833	0.657	1.218	0.948	ferredoxin like protein
Sl11590	1.166	1.475	1.037	1.050	two-component sensor histidine kinase
Sl11592	1.272	1.961	0.959	1.675	two-component response regulator NarL subfamily
Sl11594	1.295	1.048	1.431	1.106	ndhF3 operon transcriptional regulator, LysR family protein
Sl11595	0.808	1.326	0.831	1.603	circadian clock protein KaiC homolog
Sl11596	0.769	0.656	0.702	0.517	circadian clock protein KaiB homolog
Sl11598	2.857	1.563	1.425	0.917	Mn transporter MntC
Sl11600	0.239	0.290	0.331	0.404	manganese transport system membrane protein MntB
Sl11605	0.835	0.719	0.784	0.603	(3R)-hydroxymyristoyl acyl carrier protein dehydrase
Sl11606	1.082	1.161	0.984	0.873	hypothetical protein
Sl11608	0.812	1.004	1.121	1.412	hypothetical protein
Sl11612	0.555	0.332	0.484	0.286	folylpolyglutamate synthase
Sl11613	0.864	0.699	0.595	0.476	unknown protein
Sl11614	1.326	1.279	1.142	1.125	cation-transporting P-type ATPase



SH1615	0.775	0.944	0.816	0.889	thiophen and furan oxidation protein
SH1618	1.188	1.209	1.055	0.973	hypothetical protein
SH1620	2.058	1.311	1.082	0.709	hypothetical protein
SH1621	1.560	1.244	0.659	0.552	AhpC/TSA family protein
SH1623	0.747	0.655	0.758	0.723	ABC transporter ATP-binding protein
SH1624	1.238	1.631	1.370	1.786	two-component response regulator
SH1625	1.289	1.340	0.903	0.849	succinate dehydrogenase iron- sulphur protein subunit
SH1626	1.323	1.629	1.575	1.880	LexA repressor
SH1628	0.855	1.174	0.695	0.894	hypothetical protein
SH1629	1.764	1.869	1.188	1.245	bacterial cryptochrome
SH1632	0.944	0.812	1.107	0.940	hypothetical protein
SH1633	1.066	0.919	0.905	0.668	cell division protein FtsZ
SH1634	0.999	1.522	0.961	1.381	hypothetical protein
SH1635	1.217	1.393	1.129	1.364	Thy1 protein homolog
SH1636	0.980	0.974	0.780	0.787	ferrityochelin binding protein
SH1638	1.148	1.045	1.178	1.018	hypothetical protein
SH1640	0.856	0.917	0.594	0.689	hypothetical protein
SH1641	1.134	1.332	1.075	1.227	glutamate decarboxylase
SH1647	0.878	1.221	0.831	1.143	probable phosphinothricin N-acetyltransferase
SH1652	1.104	1.414	1.214	3.717	hypothetical protein
SH1653	0.896	1.000	0.949	1.050	2-phytyl-1,4-benzoquinone methyltransferase
SH1654	0.969	0.844	1.178	1.034	hypothetical protein
SH1656	0.838	0.930	1.189	1.164	hypothetical protein
SH1659	0.672	0.816	0.855	1.025	hypothetical protein
SH1660	1.160	0.824	0.544	0.382	hypothetical protein
SH1662	0.621	0.886	0.792	1.035	probable prephenate dehydratase
SH1663	1.151	1.217	1.176	1.175	phycocyanin alpha phycocyanobilin lyase related protein
SH1663	1.151	1.217	1.176	1.175	phycocyanin alpha phycocyanobilin lyase related protein
SH1664	0.831	0.911	0.651	0.881	probable glycosyl transferase
SH1665	0.632	0.682	0.723	0.847	unknown protein
SH1667	1.337	1.792	1.282	1.511	periplasmic protein, similar to mitochondrial outer membrane 72K protein
SH1669	0.919	0.839	0.811	0.520	shikimate kinase
SH1672	0.819	0.991	0.521	0.725	two-component hybrid sensor and regulator
SH1673	0.890	1.072	0.640	0.783	two-component response regulator
SH1676	0.952	0.842	0.912	0.918	4-alpha-glucanotransferase
SH1679	0.705	0.819	0.625	0.706	periplasmic protease HhoA
SH1680	1.242	1.420	1.311	1.447	hypothetical protein
SH1682	0.962	1.238	0.654	0.834	alanine dehydrogenase
SH1683	0.625	0.996	0.589	0.811	lysine decarboxylase
SH1687	0.540	0.645	0.650	0.767	unknown protein
SH1688	1.385	1.669	1.233	1.447	threonine synthase
SH1689	1.130	2.119	0.975	1.805	group2 RNA polymerase sigma factor SigE
SH1692	0.675	0.493	0.946	0.519	hypothetical protein
SH1693	0.672	0.645	0.907	0.659	hypothetical protein
SH1694	0.822	0.822	1.479	1.689	pilin polypeptide PilA1
SH1696	0.982	1.179	0.842	0.999	hypothetical protein
SH1697	0.931	0.873	0.574	0.448	hypothetical protein
SH1699	1.036	0.896	0.750	0.704	oligopeptide-binding protein of oligopeptide ABC transporter
SH1703	0.806	0.721	0.662	0.628	protease IV
SH1704	0.708	0.902	0.596	0.852	probable short chain dehydrogenase
SH1708	0.650	0.733	0.460	0.451	two-component response regulator NarL, subfamily
SH1709	0.902	0.538	0.818	0.641	3-ketoacyl-acyl carrier protein reductase
SH1712	0.770	1.064	0.498	0.583	DNA binding protein HU
SH1713	0.838	1.032	0.583	0.612	histidinol-phosphate aminotransferase
SH1721	0.971	0.990	1.325	1.337	pyruvate dehydrogenase E1 component, beta subunit
SH1723	1.124	1.071	0.898	0.848	probable glycosyltransferase
SH1730		1.479	0.784		unknown protein
SH1732	0.929	0.560	0.074	0.044	NADH dehydrogenase subunit 5 (involved in low CO2-inducible, high affinity CO2 uptake)
SH1732	0.929	0.560	0.074	0.044	NADH dehydrogenase subunit 5 (involved in low CO2-inducible, high affinity CO2 uptake)
SH1734	1.282	1.901	0.263	0.353	protein involved in low CO2-inducible, high affinity CO2 uptake
SH1735	0.713	0.692	0.274	0.290	hypothetical protein
SH1737	0.819	1.130	0.957	1.193	hypothetical protein YCF60
SH1738	1.178	0.824	0.725	0.693	hypothetical protein
SH1739	1.009	1.418	1.522	2.336	unknown protein
SH1740	1.203	1.387	2.793	3.012	50S ribosomal protein L19
SH1742	0.938	0.943	0.786	0.850	transcription antitermination protein NusG
SH1743	1.802	1.667	1.587	1.305	50S ribosomal protein L11
SH1744	1.160	1.353	1.603	1.838	50S ribosomal protein L1
SH1745	1.062	0.925	1.119	1.041	50S ribosomal protein L10
SH1746	0.946	0.725	0.985	0.697	50S ribosomal protein L12
SH1747	0.968	0.833	0.797	0.696	chorismate synthase
SH1750	0.929	1.058	1.003	1.168	urease alpha subunit
SH1750	0.929	1.058	1.003	1.168	urease alpha subunit
SH1752	1.658	1.546	1.106	1.087	hypothetical protein
SH1757	1.081	1.314	0.655	0.669	hypothetical protein
SH1758	1.031	1.056	1.898	2.033	MrsA protein homolog
SH1760	0.665	0.399	0.664	0.296	homoserine kinase
SH1762	1.036	1.333	0.644	0.787	periplasmic protein, putative polar amino acid transport system substrate-binding protein
SH1767	0.975	1.115	0.578	0.607	30S ribosomal protein S6
SH1768	0.844	0.313	0.763	0.326	probable oligopeptides ABC transporter permease protein
SH1769	1.153	1.420	0.783	0.873	hypothetical protein
SH1770	1.143	1.531	1.280	1.645	hypothetical protein
SH1771	0.820	0.894	0.798	0.958	protein serin-threonin phosphatase
SH1772	1.083	1.563	0.952	1.447	DNA mismatch repair protein MutS
SH1773	1.451	1.972	0.949	1.239	hypothetical protein
SH1774	0.963	1.408	0.870	1.256	hypothetical protein
SH1775	0.829	0.975	1.122	1.179	hypothetical protein
SH1776	0.883	0.989	0.689	0.729	deoxyribose-phosphate aldolase
SH1776	0.883	0.989	0.689	0.729	deoxyribose-phosphate aldolase
SH1783	0.835	0.540	1.019	0.591	hypothetical protein
SH1784	0.617	0.508	0.591	0.512	periplasmic protein, function unknown
SH1785	0.611	0.716	0.546	0.617	periplasmic protein, function unknown
SH1786	0.756	0.859	0.693	0.722	putative deoxyribonuclease, tatD homolog
SH1787	0.975	1.080	1.695	1.764	RNA polymerase beta subunit
SH1789	0.952	1.002	1.220	1.355	RNA polymerase beta prime subunit
SH1796	0.510	0.352	0.850	0.636	cytochrome c553
SH1797	1.016	1.418	0.888	1.236	hypothetical protein YCF21
SH1799	1.193	1.661	1.852	2.660	50S ribosomal protein L3
SH1800	1.033	1.441	4.587	6.849	50S ribosomal protein L4
SH1801	1.575	1.698	5.618	5.650	50S ribosomal protein L23
SH1802	1.484	0.761	2.101	1.105	50S ribosomal protein L2
SH1803	0.980	1.279	2.681	3.289	50S ribosomal protein L22
SH1804	1.318	1.359	2.532	2.381	30S ribosomal protein S3
SH1805	1.062	1.192	1.036	1.148	50S ribosomal protein L16
SH1806	1.092	0.837	1.821	1.541	50S ribosomal protein L14
SH1807	1.121	1.949	0.968	1.330	50S ribosomal protein L24
SH1808	1.119	1.238	3.135	3.268	50S ribosomal protein L5
SH1809	1.143	1.443	2.151	2.950	30S ribosomal protein S8
SH1810	1.639	1.761	2.045	1.776	50S ribosomal protein L6
SH1811	1.637	1.908	2.513	3.021	50S ribosomal protein L18
SH1812	1.418	2.101	1.727	2.545	30S ribosomal protein S5
SH1813	1.189	1.269	2.439	3.436	50S ribosomal protein L15
SH1814	0.880	0.661	0.712	0.628	preprotein translocase SecY subunit
SH1815	0.895	0.901	0.985	0.917	adenylate kinase
SH1816	0.958	1.372	1.684	2.217	30S ribosomal protein S13
SH1817	1.479	1.976	1.443	1.506	30S ribosomal protein S11
SH1818	0.960	1.143	1.025	1.117	RNA polymerase alpha subunit
SH1819	0.912	0.970	0.927	0.964	50S ribosomal protein L17
SH1820	0.951	1.045	0.692	0.782	tRNA pseudouridine synthase 1
SH1821	1.103	1.422	2.703	3.175	50S ribosomal protein L13
SH1822	1.330	2.062	2.370	3.077	30S ribosomal protein S9
SH1823	1.022	1.529	1.300	2.222	adenylosuccinate synthetase
SH1825	1.110	1.312	0.625	0.908	hypothetical protein
SH1830	0.834	0.901	0.728	0.652	unknown protein

SlI1831	0.800	0.392	1.318	0.476	glycolate oxidase subunit, (Fe-S)protein
SlI1833	0.833	1.247	0.616	0.950	penicillin-binding protein
SlI1835	0.797	0.769	0.943	0.970	periplasmic protein, function unknown
SlI1837	1.319	1.168	1.229	1.136	periplasmic protein, function unknown
SlI1841	1.100	0.902	1.385	1.196	pyruvate dehydrogenase dihydrolipoamide acetyltransferase component (E2)
SlI1848	1.124	1.079			putative acyltransferase
SlI1852	1.302	1.934	0.496	0.676	nucleoside diphosphate kinase
SlI1852	1.302	1.934	0.496	0.676	nucleoside diphosphate kinase
SlI1854	0.905	0.932	0.639	0.783	exodeoxyribonuclease III
SlI1862	3.774	2.392	2.674	1.792	unknown protein
SlI1863	6.757	3.425	3.788	2.309	unknown protein
SlI1865	1.238	1.486	0.574	0.892	peptide chain release factor 2
SlI1866	0.803	0.968	1.754	2.119	hypothetical protein
SlI1870	0.730	0.743	0.687	0.719	ATP-binding protein of ABC transporter
SlI1871	0.896	1.013	0.922	0.692	two-component system sensory histidine kinase
SlI1872	0.978	1.439	1.224	1.441	transcriptional regulator
SlI1873	1.189	1.957	1.449	2.762	unknown protein
SlI1878	0.563	0.686	0.912	0.947	iron(III)-transport ATP-binding protein
SlI1879	0.716	0.597	0.922	0.503	two-component response regulator
SlI1882	0.447	0.316	1.172	0.818	unknown protein
SlI1883	1.057	0.870	1.305	1.057	arginine biosynthesis bifunctional protein ArgJ
SlI1884	1.437	2.833	0.850	1.538	hypothetical protein
SlI1885	1.075	0.845	0.874	0.699	unknown protein
SlI1888	0.887	1.044	0.741	1.092	two-component sensor histidine kinase
SlI1891	1.255	2.227	1.949	3.378	unknown protein
SlI1892	0.993	1.205	0.775	1.250	unknown protein
SlI1893	0.657	0.792	0.702	0.864	cyclase
SlI1894	1.188	1.156	1.081	1.171	riboflavin biosynthesis protein RibA
SlI1895	1.202	1.524	0.914	1.252	hypothetical protein
SlI1897	0.690	1.269	0.534	0.969	hypothetical protein
SlI1902	0.884	1.015	0.946	0.911	hypothetical protein
SlI1905	0.792	0.887	0.919	0.933	two-component hybrid sensor and regulator
SlI1908	0.948	0.840	1.017	0.852	D-3-phosphoglycerate dehydrogenase
SlI1909	0.661	0.610	0.775	0.547	probable methyltransferase
SlI1910	0.980	1.036	0.993	1.005	protein conferring resistance to acetazolamide Zam
SlI1911	1.497	1.486	0.799	1.153	hypothetical protein
SlI1913	0.805	0.788	0.680	0.483	hypothetical protein
SlI1917	1.192	0.965	2.012	1.610	coproporphyrinogen III oxidase, anaerobic (oxygen-independent)
SlI1920	1.134	1.340	0.999	1.091	copper-transporting P-type ATPase PacS
SlI1925	0.988	0.737	1.203	0.887	hypothetical protein
SlI1927	0.880	0.957	0.943	1.035	ABC transporter ATP-binding protein
SlI1931	0.986	0.974	1.312	1.253	serine hydroxymethyltransferase
SlI1932	0.933	1.139	1.033	1.359	DnaK protein
SlI1933	1.098	1.406	1.170	1.626	DnaJ protein, heat shock protein 40, molecular chaperone
SlI1934	1.189	1.876	0.894	1.335	hypothetical protein
SlI1937	0.756	1.131	0.732	0.947	ferric uptake regulation protein
SlI1938	0.807	0.991	0.681	0.728	hypothetical protein
SlI1940	0.620	0.978	0.518	0.793	hypothetical protein
SlI1941	0.990	1.119	0.991	1.259	DNA gyrase A subunit
SlI1945	0.889	1.043	1.119	1.122	1-deoxyxylulose-5-phosphate synthase
SlI1946	0.594	0.612	0.453	0.413	hypothetical protein
SlI1949	0.763	0.746	0.608	0.589	unknown protein
SlI1950	0.847	0.955	0.760	0.805	unknown protein
SlI1951	1.062	0.600	0.582	0.394	unknown protein
SlI1956	0.718	1.094	0.689	1.183	hypothetical protein
SlI1957	0.835	0.691	1.212	1.142	transcriptional regulator
SlI1958	0.825	0.916	0.890	1.014	histidinol phosphate aminotransferase
SlI1959	0.786	0.732	0.750	0.689	probable inositol monophosphatase
SlI1961	0.978	0.848	0.886	0.841	hypothetical protein
SlI1967	1.015	1.414	1.490	1.942	probable RNA methyltransferase
SlI1971	1.274	0.771	0.917	0.548	probable hexosyltransferase
SlI1971	1.274	0.771	0.917	0.548	probable hexosyltransferase
SlI1973	0.695	0.870	1.130	1.395	hypothetical protein
SlI1979	1.065	0.730	0.786	0.528	hypothetical protein
SlI1980	0.847	1.110	0.961	1.134	thiol:disulfide interchange protein TrxA
SlI1981	0.804	0.951	0.850	0.973	acetolactate synthase
SlI1981	0.804	0.951	0.850	0.973	acetolactate synthase
SlI1987	0.879	0.732	1.050	0.868	catalase peroxidase
SlI1988	1.558	1.799	1.543	1.637	33 kDa chaperonin
SlI1994	0.858	0.896	0.968	1.022	porphobilinogen synthase (5-aminolevulinic acid dehydratase)
SlI2001	1.178	1.321	0.978	0.908	leucine aminopeptidase
SlI2002	0.845	0.734	1.043	0.881	hypothetical protein
SlI2003	1.011	0.981	0.837	0.767	hypothetical protein
SlI2005	1.003	1.025	1.071	1.104	DNA gyrase B subunit [Contains: Ssp gyrB intein]
SlI2006	0.935	0.622	0.797	0.524	hypothetical protein
SlI2009	1.174	1.580	1.139	1.623	processing protease
SlI2010	0.775	0.853	0.974	0.987	UDP-N-acetylmuramoylalanine--D-glutamate ligase
SlI2014	1.049	0.959	0.789	0.681	sugar fermentation stimulation protein
Slr0001	1.475	1.418	1.961	2.237	hypothetical protein
Slr0006	1.013	0.870	0.431	0.433	unknown protein
Slr0007	0.836	1.007	0.615	0.731	probable sugar-phosphate nucleotidyltransferase
Slr0008	0.705	0.668	0.709	0.617	carboxyl-terminal processing protease
Slr0009	0.922	0.760	0.755	0.677	ribulose biphosphate carboxylase large subunit
Slr0012	0.792	0.686	0.539	0.457	ribulose biphosphate carboxylase small subunit
Slr0013	0.878	0.927	0.913	0.801	hypothetical protein
Slr0015	0.676	0.869	0.648	0.752	lipid A disaccharide synthase
Slr0016	0.907	0.650	1.021	0.723	hypothetical protein
Slr0017	1.025	1.103	0.920	1.136	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
Slr0018	0.932	1.019	0.730	0.791	fumarase
Slr0020	1.028	1.364	1.279	1.675	DNA recombinase
Slr0021	1.299	1.905	1.527	2.283	protease
Slr0023	1.073	1.008			unknown protein
Slr0031	1.181	1.156	0.899	0.876	hypothetical protein
Slr0032	0.858	0.885	1.005	0.960	probable branched-chain amino acid aminotransferase
Slr0033	1.297	1.005	1.212	1.060	glutamyl-tRNA(Gln) amidotransferase subunit C
Slr0038	0.870	0.767	0.812	0.679	hypothetical protein
Slr0039	0.814	0.801	0.836	0.935	hypothetical protein
Slr0040	0.659	0.475	0.561	0.388	bicarbonate transport system substrate-binding protein
Slr0042	0.852	0.648	0.501	0.373	probable porin; major outer membrane protein
Slr0043	0.362	0.484	0.817	0.501	bicarbonate transport system ATP-binding protein
Slr0049	1.000	1.445	1.653	2.632	hypothetical protein
Slr0050	0.579	0.542	0.829	0.645	hypothetical protein YCF56
Slr0051	0.678	0.880	0.644	0.805	periplasmic beta-type carbonic anhydrase
Slr0055	0.864	0.855	0.503	0.483	anthranilate synthase component II
Slr0056	1.205	1.333	0.931	0.935	chlorophyll a synthase
Slr0058	1.285	1.044	1.215	1.060	hypothetical protein
Slr0063	0.931	1.064	1.218	1.441	pilus biogenesis protein homologous to general secretion pathway protein E
Slr0064	1.070	0.999	1.435	1.321	hypothetical protein
Slr0065	0.829	0.786	1.037	0.970	hypothetical protein
Slr0066	0.641	0.739	0.717	0.815	riboflavin biosynthesis protein RibD
Slr0067	0.962	0.728	0.842	0.563	MRP protein homolog
Slr0070	0.814	0.962	0.972	1.124	methionyl-tRNA formyltransferase
Slr0072	0.898	1.057	1.088	1.272	glucose inhibited division protein B
Slr0073	0.796	0.801	0.898	0.907	two-component sensor histidine kinase
Slr0074	1.114	1.057	0.948	1.068	ABC transporter subunit
Slr0075	1.451	1.718	0.722	0.803	ABC transporter ATP-binding protein
Slr0076	1.171	1.129	0.929	0.849	hypothetical protein
Slr0077	0.951	1.075	0.974	0.917	cysteine desulfurase
Slr0078	0.924	2.525	0.887	1.736	putative 6-pyruvoyl tetrahydrobiopterin synthase
Slr0079	0.705	0.653	0.887	0.765	probable general secretion pathway protein E
Slr0080	1.346	1.381	2.119	1.427	ribonuclease H
Slr0081	0.785	0.847	0.788	0.855	two-component response regulator OmpR subfamily
Slr0082	1.119	0.889	1.020	0.826	hypothetical protein
Slr0083	0.880	0.846	2.062	1.757	RNA helicase Light

Slr0084	0.774	0.759	0.858	0.709	amidotransferase HisH
Slr0086	0.911	1.120	0.864	1.176	similar to DnaK protein
Slr0088	0.747	0.641	0.563	0.536	beta-carotene ketolase
Slr0089	1.656	1.582	1.721	1.621	gamma-tocopherol methyltransferase
Slr0091	1.570	1.927	1.883	1.812	aldehyde dehydrogenase
Slr0093	1.342	1.667	0.870	1.043	DnaJ protein, heat shock protein 40, molecular chaperone
Slr0095	0.810	0.707	0.493	0.579	O-methyltransferase
Slr0104	0.792	0.904	1.110	1.241	hypothetical protein
Slr0106	0.873	0.290	1.299	0.242	unknown protein
Slr0110	0.898	0.911	0.892	0.875	hypothetical protein
Slr0111	0.399	0.297	0.569	0.538	unknown protein
Slr0112	0.840	0.807	0.995	0.944	unknown protein
Slr0115	0.935	0.929	0.741	0.747	response regulator for energy transfer from phycobilisomes to photosystems
Slr0116	0.993	0.990	0.743	0.617	phycocyanobilin:ferredoxin oxidoreductase
Slr0118	0.921	1.016	1.350	1.239	thiamine biosynthesis protein ThiC
Slr0120	0.982	0.971	0.573	0.668	probable tRNA/rRNA methyltransferase
Slr0121	0.990	1.114	1.232	1.368	hypothetical protein
Slr0144	0.929	0.691	2.278	1.661	hypothetical protein
Slr0145	0.759	0.441	1.093	0.744	unknown protein
Slr0146	0.615	0.340	0.892	0.345	hypothetical protein
Slr0147	0.839	0.595	3.215	2.000	hypothetical protein
Slr0148	1.103	1.195	1.078	1.189	hypothetical protein
Slr0149	0.813	0.510	1.144	0.733	hypothetical protein
Slr0151	0.825	0.656	1.416	0.974	unknown protein
Slr0152	0.775	0.858	0.686	0.750	serine/threonine protein kinase
Slr0156	0.853	0.894	0.825	0.865	CtpB protein
Slr0161	0.931	1.065	1.005	1.030	twitching motility protein PilT
Slr0163	0.883	1.016	1.374	1.376	a part of pilC, pilin biogenesis protein, required for twitching motility
Slr0164	0.963	1.024	0.887	1.074	ATP-dependent Clp protease proteolytic subunit
Slr0165	0.967	1.012	0.602	0.680	ATP-dependent Clp protease proteolytic subunit
Slr0168	0.824	1.217	0.692	0.862	unknown protein
Slr0169	1.181	1.056	0.952	0.912	hypothetical protein
Slr0171	1.125	1.515	2.710	2.717	photosystem I assembly related protein Ycf37
Slr0172	1.020	0.809	1.256	0.993	hypothetical protein
Slr0181	1.007	2.488	0.524	1.276	hypothetical protein
Slr0184	0.727	0.581	0.611	0.648	unknown protein
Slr0185	1.054	2.336	0.578	1.222	orotate phosphoribosyltransferase
Slr0186	0.840	1.021	0.820	0.914	2-isopropylmalate synthase
Slr0191	1.066	1.136	1.318	1.164	amidase enhancer, periplasmic protein
Slr0192	1.477	1.757	0.865	1.555	hypothetical protein
Slr0193	0.998	1.148	2.183	2.353	RNA-binding protein
Slr0194	1.115	1.125	1.003	1.050	ribose 5-phosphate isomerase
Slr0201	1.176	1.229	1.350	1.168	heterodisulfide reductase subunit B
Slr0207	1.195	1.147	1.018	1.193	hypothetical protein
Slr0208	0.853	1.000	0.806	0.946	hypothetical protein
Slr0209	0.891	0.838	0.845	0.840	unknown protein
Slr0211	1.567	1.610	1.351	1.370	hypothetical protein
Slr0212	0.939	0.949	1.060	1.107	5-methyltetrahydrofolate--homocysteine methyltransferase
Slr0213	0.705	0.964	1.065	1.279	GMP synthetase
Slr0217	0.688	0.838	0.551	0.557	hypothetical protein
Slr0220	1.050	1.050	1.112	1.103	glycyl-tRNA synthetase beta chain
Slr0222	1.040	0.705	1.019	0.693	two-component hybrid sensor and regulator
Slr0226	0.827	1.029	0.746	1.188	unknown protein
Slr0228	1.124	0.849	1.193	1.082	cell division protein FisH
Slr0229	0.615	0.675	0.980	1.121	3-hydroxyisobutyrate dehydrogenase
Slr0233	0.826	0.709	0.582	0.490	thioredoxin M
Slr0236	0.867	0.968	0.759	0.763	similar to glutathione S-transferase
Slr0237	1.145	1.401	1.054	1.074	glycogen operon protein GlgX homolog
Slr0238	0.915	0.620	0.658	0.382	hypothetical protein
Slr0239	0.867	1.155	1.029	1.121	precorrin-4 C11-methyltransferase
Slr0239	0.867	1.155	1.029	1.121	precorrin-4 C11-methyltransferase
Slr0242	0.912	0.582	1.558	1.232	bacterioferritin comigratory protein homolog
Slr0244	0.932	0.887	1.575	1.346	hypothetical protein
Slr0245	0.646	0.671	0.661	0.615	Histone deacetylase family protein
Slr0249	0.555	0.438	0.677	0.527	hypothetical protein
Slr0250	0.961	0.819	1.116	1.046	hypothetical protein
Slr0251	1.143	1.151	0.813	0.880	ATP-binding protein of ABC transporter
Slr0254	0.777	0.634	0.641	0.555	hypothetical protein
Slr0257	0.737	0.671	0.995	0.843	periplasmic carboxyl-terminal protease
Slr0260	1.112	1.464	1.718	2.193	cob(J)alamin adenosyltransferase
Slr0261	1.064	1.185	0.711	0.737	NADH dehydrogenase subunit 7
Slr0261	1.064	1.185	0.711	0.737	NADH dehydrogenase subunit 7
Slr0262	0.759	0.870	1.175	1.350	unknown protein
Slr0267	1.208	1.135	1.149	1.124	hypothetical protein
Slr0280	1.057	1.130	1.047	1.007	hypothetical protein
Slr0287	1.109	1.499	2.012	2.681	hypothetical protein
Slr0288	1.139	1.167	1.916	1.876	glutamate--ammonia ligase
Slr0288	1.139	1.167	1.916	1.876	glutamate--ammonia ligase
Slr0291	1.022	0.773	0.744	0.556	hypothetical protein
Slr0293	1.116	1.495	0.853	1.152	glycine dehydrogenase
Slr0298	0.908	0.651	0.646	0.444	FraH protein homolog
Slr0300	1.176	1.160	0.985	1.043	hypothetical protein
Slr0301	0.633	0.610	0.820	0.723	phosphoenolpyruvate synthase
Slr0302	0.785	0.791	0.565	0.450	unknown protein
Slr0303	1.259	1.399	1.488	1.727	hypothetical protein
Slr0306	0.792	0.781	0.644	0.628	unknown protein
Slr0312	1.170	1.218	0.938	1.082	two-component response regulator NarL subfamily
Slr0315	1.543	1.675	1.054	1.131	probable oxidoreductase
Slr0317	1.020	0.853	0.867	0.920	hypothetical protein
Slr0319	2.193	1.912	1.462	1.312	beta-lactamase
Slr0320	1.096	1.229	1.143	1.264	hypothetical protein
Slr0321	0.927	0.887	1.179	0.943	GTP-binding protein ERA homolog
Slr0322	0.842	0.786	1.195	1.318	two-component hybrid sensor and regulator
Slr0322	0.842	0.786	1.195	1.318	two-component hybrid sensor and regulator
Slr0323	0.944	1.088	0.701	0.805	putative alpha-mannosidase
Slr0326	1.238	0.915	1.355	1.091	hypothetical protein
Slr0329	0.790	0.691	0.739	0.637	glucokinase
Slr0331	0.943	1.122	0.496	0.675	NADH dehydrogenase subunit 4 (involved in photosystem-1 cyclic electron flow)
Slr0331	0.943	1.122	0.496	0.675	NADH dehydrogenase subunit 4 (involved in photosystem-1 cyclic electron flow)
Slr0333	0.474	0.584	0.649	0.623	unknown protein
Slr0335	1.063	1.139	2.375	2.653	phycobilisome core-membrane linker polypeptide
Slr0338	0.894	0.071	0.715	0.990	probable oxidoreductase
Slr0342	1.105	0.796	1.176	0.887	cytochrome b6
Slr0343	1.550	1.295	2.469	1.587	cytochrome b6-f complex subunit 4
Slr0346	0.830	0.700	0.804	0.661	ribonuclease III
Slr0348	1.072	1.041	1.167	1.091	hypothetical protein
Slr0348	1.072	1.041	1.167	1.091	hypothetical protein
Slr0348	1.072	1.041	1.167	1.091	hypothetical protein
Slr0351	0.661	0.678	0.835	0.733	hypothetical protein
Slr0354	0.745	0.537	0.750	0.512	ATP-binding protein of ABC transporter
Slr0355	1.215	0.995	1.416	1.138	hypothetical protein
Slr0357	1.166	1.082	1.067	1.038	histidyl-tRNA synthetase
Slr0361	1.269	1.199	1.058	0.912	probable ribosomal large subunit pseudouridine synthase B
Slr0362	0.911	0.928	1.129	0.878	hypothetical protein
Slr0366	1.938	2.801	0.464	0.845	unknown protein
Slr0369	0.825	0.829	0.821	0.879	RND multidrug efflux transporter
Slr0370	0.923	1.082	0.949	1.067	succinate-semialdehyde dehydrogenase (NADP+)
Slr0373	1.209	1.230	1.600	1.266	hypothetical protein
Slr0374	1.016	1.267	0.818	1.048	hypothetical protein
Slr0376	0.997	1.842	1.290	2.967	hypothetical protein
Slr0377	0.995	0.906	1.140	1.026	unknown protein
Slr0378	0.824	0.915	0.739	0.737	similar to 7-beta-(4-carboxybutanamido)cephalosporanic acid acylase
Slr0379	0.801	1.168	0.781	1.224	thymidylate kinase
Slr0380	0.805	0.905	1.149	1.681	hypothetical protein

Slr0381	1.266	1.280	0.950	0.928	lactoylglutathione lyase
Slr0384	1.247	1.052	1.244	1.138	sulfoquinovosyldiacylglycerol biosynthesis protein SqdX
Slr0386	1.269	1.580	1.199	1.387	unknown protein
Slr0387	0.640	1.065	0.580	0.733	cysteine desulfurase NiS
Slr0394	1.515	2.000	1.058	1.488	phosphoglycerate kinase
Slr0397	0.781	0.683	0.674	0.631	hypothetical protein
Slr0398	1.122	1.041	0.808	0.811	unknown protein
Slr0399	1.389	1.536	1.372	1.558	chaperon-like protein for quinone binding in photosystem II
Slr0400	0.719	0.825	0.576	0.665	hypothetical protein
Slr0401	0.614	0.666	0.741	0.876	periplasmic polyamine-binding protein of ABC transporter
Slr0402	0.759	1.073	1.029	1.335	hypothetical protein
Slr0404	1.387	1.267	2.033	1.546	hypothetical protein
Slr0406	0.876	0.943	0.777	0.779	dihydroorotase
Slr0415	1.395	1.534	1.412	1.435	Na <sup>+</sup> /H <sup>+</sup> antiporter
Slr0416	1.038	1.287	0.833	0.948	unknown protein
Slr0417	0.944	0.974	1.245	1.115	DNA gyrase subunit A
Slr0418	1.120	1.107	1.258	1.227	putative transcription factor DevT homolog
Slr0420	1.250	0.907	0.844	0.634	hypothetical protein
Slr0423	1.825	1.321	1.427	1.020	hypothetical protein
Slr0426	0.819	0.816	0.654	0.637	GTP cyclohydrolase I
Slr0427	0.854	0.661	0.869	0.639	putative competence-damage protein
Slr0431	1.044	1.068	0.489	0.542	hypothetical protein
Slr0434	1.143	0.700	1.538	1.049	elongation factor P
Slr0435	0.897	0.890	0.982	0.985	biotin carboxyl carrier protein of acetyl-CoA carboxylase
Slr0436	1.005	0.889	0.972	0.504	carbon dioxide concentrating mechanism protein CcmO
Slr0439	0.601	0.590	0.772	0.660	unknown protein
Slr0440	0.722	0.747	0.668	0.688	hypothetical protein
Slr0442	1.145	1.443	1.119	1.348	unknown protein
Slr0443	0.944	0.685	0.745	0.552	hypothetical protein
Slr0444	1.000	1.114	0.960	1.062	3-phosphoshikimate 1-carboxyvinyltransferase
Slr0446	0.698	0.816	0.876	0.554	DNA polymerase III delta' subunit
Slr0447	0.733	0.853	0.760	0.823	periplasmic protein, ABC-type urea transport system substrate-binding protein
Slr0448	0.865	0.547	1.362	0.749	DNA repair protein RadA
Slr0451	0.790	0.914	1.238	1.239	putative helicase
Slr0452	0.851	0.793	1.099	0.940	dihydroxyacid dehydratase
Slr0453	1.041	1.701	0.633	1.020	hypothetical protein
Slr0454	1.052	0.749	0.977	0.681	RND multidrug efflux transporter
Slr0455	1.233	0.972	1.115	0.929	hypothetical protein
Slr0457	1.140	1.253	0.920	0.961	tRNA pseudouridine synthase B
Slr0458	1.330	1.284	0.801	0.781	unknown protein
Slr0467	0.654	0.701	0.608	1.117	conserved component of ABC transporter for natural amino acids
Slr0468	0.809	1.080	1.259	1.894	unknown protein
Slr0469	1.050	0.862	2.532	1.515	30S ribosomal protein S4
Slr0473	0.519	0.548	0.818	0.772	cyanobacterial phytochrome 1, two-component sensor histidine kinase
Slr0474	0.777	0.552	0.680	0.497	two-component response regulator CheY subfamily, regulator for phytochrome 1 (Cph1)
Slr0476	1.085	1.211	0.939	0.805	unknown protein
Slr0477	0.808	0.743	0.533	0.675	phosphoribosylglycinamide formyltransferase
Slr0479	0.666	0.895	0.457	0.587	hypothetical protein
Slr0480	0.856	1.172	0.916	0.805	hypothetical protein YCF46
Slr0482	1.015	0.967	0.752	0.708	unknown protein
Slr0483	1.195	0.967	1.209	1.008	hypothetical protein
Slr0484	0.831	0.862	1.266	1.205	two-component sensor histidine kinase
Slr0493	1.332	1.582	0.992	1.163	similar to mannose-1-phosphate guanylyltransferase
Slr0502	1.425	1.431	1.821	2.336	cobalamin synthesis protein cobW homolog
Slr0503	0.742	0.738	0.859	0.356	hypothetical protein YCF66
Slr0506	1.079	1.037	2.532	2.123	light-dependent NADPH-protochlorophyllide oxidoreductase
Slr0506	1.079	1.037	2.532	2.123	light-dependent NADPH-protochlorophyllide oxidoreductase
Slr0513	0.281	0.201	0.589	0.405	iron transport system substrate-binding protein, periplasmic protein
Slr0516	1.852	1.488	1.383	1.179	hypothetical protein
Slr0518	1.014	1.053	1.095	1.075	similar to alpha-L-arabinofuranosidase B
Slr0519	0.697	0.886	0.688	0.864	hypothetical protein
Slr0520	0.921	0.939	0.911	0.796	phosphoribosyl formylglycinamide synthase
Slr0523	1.139	0.983	1.170	0.934	similar to dethiobiotin synthetase
Slr0525	1.074	1.279	1.348	1.504	Mg-protoporphyrin IX methyl transferase
Slr0526	0.826	0.971	0.951	0.657	3-methyl-2-oxobutanoate hydroxymethyltransferase
Slr0527	0.935	1.050	0.831	0.806	transcription regulator ExsB homolog
Slr0528	0.941	1.092	1.408	1.374	UDP-N-acetylmuramoylalanine-D-glutamate--2, 6-diaminopimelate ligase
Slr0529	1.848	1.745	1.456	1.451	glucosylglycerol transport system substrate-binding protein
Slr0534	0.999	1.202	1.063	0.994	probable transglycosylase
Slr0535	0.833	0.924	1.099	1.307	protease
Slr0536	0.998	0.985	0.917	0.790	uroporphyrinogen decarboxylase
Slr0537	1.167	1.142	1.992	2.110	putative sugar kinase
Slr0541	1.011	1.435	0.702	1.104	probable amidotransferase
Slr0542	1.047	1.027	0.927	0.863	ATP-dependent protease ClpP
Slr0543	1.001	1.057	1.425	1.174	tryptophan synthase beta subunit
Slr0546	1.048	1.164	0.952	1.147	indole-3-glycerol phosphate synthase
Slr0549	1.082	1.095	1.035	1.050	aspartate beta-semialdehyde dehydrogenase
Slr0550	1.020	0.985	1.065	0.806	dihydropicolinate synthase
Slr0551	1.285	1.348	1.592	1.631	hypothetical protein
Slr0552	1.203	1.385	1.075	1.245	hypothetical protein
Slr0553	0.782	0.765	0.806	0.746	hypothetical protein
Slr0556	1.037	0.962	0.804	0.584	hypothetical protein
Slr0557	1.058	1.055	1.217	1.233	valyl-tRNA synthetase
Slr0559	1.479	1.953	0.876	1.026	periplasmic binding protein of ABC transporter for natural amino acids
Slr0565	1.271	1.422	1.504	1.783	hypothetical protein
Slr0569	0.973	0.611	1.136	0.704	unknown protein
Slr0574	0.864	0.821	0.951	0.932	cytochrome P450
Slr0575	1.016	0.921	0.810	0.719	hypothetical protein
Slr0580	0.918	0.711	0.913	0.794	aluminum resistance protein homolog
Slr0581	1.019	0.887	0.787	0.676	unknown protein
Slr0583	0.814	1.002	0.815	0.939	similar to GDP-fucose synthetase
Slr0585	0.945	1.082	0.899	1.082	argininosuccinate synthetase
Slr0586	1.140	1.055	1.414	1.339	hypothetical protein
Slr0588	0.927	0.940	0.778	0.831	hypothetical protein
Slr0590	1.153	1.427	1.032	1.256	hypothetical protein
Slr0591	0.973	0.871	1.149	0.932	ribonucleoside-diphosphate reductase beta chain
Slr0592	0.839	1.092	0.671	0.779	hypothetical protein
Slr0594	0.838	0.851	0.984	1.043	hypothetical protein
Slr0596	0.779	0.601	0.612	0.434	hypothetical protein
Slr0597	1.073	0.907	1.186	1.130	phosphoribosyl aminoimidazole carboxy formyl formyltransferase
Slr0598	1.010	1.064	0.953	0.879	hypothetical protein
Slr0599	0.873	0.808	0.749	0.637	serine/threonine kinase
Slr0600	1.144	1.425	1.107	1.376	NADP-thioredoxin reductase
Slr0600	1.144	1.425	1.107	1.376	NADP-thioredoxin reductase
Slr0601		0.691		1.912	unknown protein
Slr0603	0.709	0.945	0.858	0.820	DNA polymerase III alpha subunit [Contains: Ssp dnaE intein]
Slr0604	1.196	1.404	1.372	1.590	GTP-binding protein
Slr0605	0.920	1.070	0.857	1.046	hypothetical protein
Slr0606	0.971	1.287	0.859	1.232	hypothetical protein
Slr0607	1.147	1.020	1.144	0.943	hypothetical protein
Slr0608	1.018	1.101	1.080	1.193	histidine biosynthesis bifunctional protein HisIE
Slr0609	1.473	1.410	1.988	2.012	hypothetical protein
Slr0613	1.217	1.129	1.684	1.645	hypothetical protein
Slr0615	0.534	0.637	0.621	0.389	ATP-binding protein of ABC transporter
Slr0619	1.020	1.060	0.931	0.739	hypothetical protein
Slr0623	0.810	0.801	1.159	1.263	thioredoxin
Slr0624	0.975	0.954	0.897	0.998	UDP-N-acetylglucosamine 2-epimerase
Slr0625	0.693	0.719	0.886	0.907	hypothetical protein
Slr0626	1.024	1.179	1.047	0.970	probable glycosyltransferase
Slr0628	1.802	2.381	2.114	2.899	30S ribosomal protein S14
Slr0630	1.175	0.960	1.055	0.850	hypothetical protein
Slr0633	1.235	1.261	0.938	1.156	thiamine biosynthesis protein ThiG
Slr0634	0.879	0.963	0.627	0.706	unknown protein
Slr0635	0.905	0.997	0.577	0.566	hypothetical protein

Slr0637	0.963	0.966	0.782	0.692	hypothetical protein
Slr0638	0.951	0.935	0.994	0.883	glycyl-tRNA synthetase alpha chain
Slr0643	2.024	1.040	2.174	1.103	hypothetical protein
Slr0645	1.114	1.704	0.728	1.037	hypothetical protein
Slr0646	0.789	1.030	0.568	0.633	probable D-alanyl-D-alanine carboxypeptidase
Slr0649	0.845	1.224	0.921	1.190	methionyl-tRNA synthetase
Slr0650	0.884	0.877	0.985	1.029	hypothetical protein
Slr0651	1.050	1.307	1.109	1.025	hypothetical protein
Slr0652	0.919	1.344	0.805	1.028	phosphorylformimino-5-amino- phosphorybosal-4-imidazolecarboxamideisomerase
Slr0653	1.044	0.995	2.242	2.604	principal RNA polymerase sigma factor SigA
Slr0654	0.763	0.359	1.422	0.660	unknown protein
Slr0657	0.937	1.106	0.935	1.085	aspartate kinase
Slr0658	0.782	0.876	0.991	0.922	unknown protein
Slr0659	0.980	1.060	0.954	1.059	oligopeptidase A
Slr0661	1.036	1.055	0.980	0.922	pyrroline-5-carboxylate reductase
Slr0662	0.894	0.858	0.758	0.799	arginine decarboxylase
Slr0664	1.319	2.315	1.848	3.165	hypothetical protein
Slr0665	1.078	1.112	2.008	2.141	aconitate hydratase
Slr0666	0.954	0.907	0.938	0.902	unknown protein
Slr0667	0.962	1.325	0.407	0.491	unknown protein
Slr0670	0.907	0.720	1.004	0.735	hypothetical protein
Slr0676	1.082	1.342	0.894	1.015	adenylsulfate kinase
Slr0677	1.106	1.285	0.894	1.155	biopolymer transport ExbB like protein
Slr0678	1.041	1.425	1.429	1.931	biopolymer transport ExbD like protein
Slr0679	1.300	1.522	1.263	1.414	sun protein
Slr0681	0.982	0.642	0.787	0.635	probable sodium/calcium exchanger protein
Slr0682	0.853	1.124	0.628	0.631	histidinol dehydrogenase
Slr0688	1.399	1.672	1.645	2.198	hypothetical protein
Slr0689	1.174	1.475	0.550	0.479	hypothetical protein
Slr0692	0.958	1.305	0.949	1.464	hypothetical protein YCF45
Slr0695	0.961	0.955	0.947	1.259	hypothetical protein
Slr0697	0.895	0.754	0.953	0.940	5-oxoprolinase homolog
Slr0698	1.127	1.250	0.793	0.869	hypothetical protein
Slr0699	0.765	0.784	0.664	0.664	unknown protein
Slr0707	0.852	1.106	1.130	1.335	DNA polymerase I
Slr0708	0.585	0.748	0.419	0.492	periplasmic protein, function unknown
Slr0709	1.088	0.970	0.786	0.923	hypothetical protein
Slr0710	0.958	0.897	1.020	0.867	glutamate dehydrogenase (NADP+)
Slr0711	0.816	1.600	0.769	1.385	hypothetical protein
Slr0713	0.882	0.936	0.755	0.853	tRNA-guanine transglycosylase
Slr0719	0.959	0.786	1.143	1.044	unknown protein
Slr0721	0.669	0.845	0.641	0.753	malic enzyme
Slr0722	0.789	0.728	0.627	0.575	hypothetical protein
Slr0723	0.786	0.719	0.840	0.786	hypothetical protein
Slr0727	0.984	1.181	1.404	1.715	unknown protein
Slr0729	1.517	0.722	1.905	0.765	hypothetical protein
Slr0730	0.861	0.675	0.775	0.600	hypothetical protein
Slr0731	1.058	1.289	0.950	1.038	hypothetical protein
Slr0737	1.253	1.100	1.585	1.779	photosystem I subunit II
Slr0738	0.845	0.769	1.163	0.928	anthranilate synthetase alpha-subunit
Slr0739	1.337	1.582	1.575	1.972	geranylgeranyl pyrophosphate synthase
Slr0739	1.337	1.582	1.575	1.972	geranylgeranyl pyrophosphate synthase
Slr0740	1.209	1.835	0.951	1.406	hypothetical protein
Slr0741	0.538	0.386	0.341	0.366	transcriptional regulator
Slr0742	1.093	1.212	0.984	1.143	hypothetical protein
Slr0743	1.239	1.192	1.006	1.062	similar to N utilization substance protein
Slr0744	1.709	2.123	1.613	2.062	translation initiation factor IF-2
Slr0746	2.169	0.485	3.367	0.641	glucosylglycerolphosphate phosphatase
Slr0747	1.639	1.299	1.212	0.945	glucosylglycerol transport system ATP-binding protein
Slr0748	1.316	1.179	1.043	0.951	hypothetical protein
Slr0750	1.019	1.139	1.464	1.692	light-independent protochlorophyllide reductase subunit ChIN
Slr0752	1.045	1.259	0.636	0.736	enolase
Slr0755	0.944	1.035	0.908	0.983	hypothetical protein
Slr0756	1.048	1.706	1.232	2.028	circadian clock protein KaiA homolog
Slr0757	0.944	1.855	0.614	1.266	circadian clock protein KaiB homolog
Slr0758	1.074	1.550	0.856	1.176	circadian clock protein KaiC homolog
Slr0765	1.931	2.857	1.675	1.364	hypothetical protein
Slr0769	0.490	0.771	1.522	2.564	hypothetical protein
Slr0770	0.786	0.887	0.759	0.847	hypothetical protein
Slr0771	0.705	1.072	0.667	1.001	hypothetical protein
Slr0772	1.179	1.527	1.585	2.075	light-independent protochlorophyllide reductase subunit ChIB
Slr0773	1.168	1.183	0.705	0.738	hypothetical protein
Slr0774	1.031	0.976	1.443	1.408	protein-export membrane protein SecD
Slr0775	1.148	0.740	0.938	0.438	protein-export membrane protein SecF
Slr0776	1.168	1.212	1.115	1.192	UDP-3-o-[3-hydroxymristoyl] glucosamine n-acyltransferase
Slr0780	0.758	0.835	0.730	0.671	hypothetical protein
Slr0782	0.734	0.736	0.659	0.677	putative flavin-containing monoamine oxidase
Slr0783	1.078	1.174	0.957	0.986	triosephosphate isomerase
Slr0798	0.148	0.165	0.316	0.317	zinc-transporting P-type ATPase (zinc efflux pump) involved in zinc tolerance
Slr0804	0.357	0.348	1.276	1.145	hypothetical protein
Slr0806	0.776	0.963	0.636	0.963	probable D-alanyl-D-alanine carboxypeptidase
Slr0807	0.890	0.812	0.850	0.936	probable o-sialoglycoprotein endopeptidase
Slr0808	0.847	0.751	0.911	1.007	16S rRNA processing protein RimM homolog
Slr0809	0.910	1.200	0.940	1.081	dTDP-glucose 4,6-dehydratase
Slr0812	1.094	1.111	0.534	0.561	hypothetical protein
Slr0816	0.752	0.662	0.781	0.678	hypothetical protein
Slr0818	0.687	0.789	0.739	0.850	hypothetical protein
Slr0821	1.618	1.443	1.608	1.326	hypothetical protein
Slr0823	1.040	0.975	1.284	1.176	photosystem I assembly related protein
Slr0825	0.730	1.074	0.818	1.115	probable peptidase
Slr0833	1.030	1.081	1.049	0.966	replicative DNA helicase [Contains: Ssp dnaB intein]
Slr0835	0.837	1.420	0.805	1.357	MoxR protein homolog
Slr0836	1.111	1.198	0.866	1.086	dTDP-glucose 4,6-dehydratase
Slr0838	1.095	0.656	1.010	0.532	phosphoribosyl formylglycinamide cyclo-ligase
Slr0839	0.959	0.800	1.425	0.943	ferrochelatase
Slr0841	1.274	1.684	1.307	1.603	periplasmic protein, function unknown
Slr0842	0.722	0.905	0.767	0.962	hypothetical protein
Slr0844	1.011	0.952	0.935	0.715	NADH dehydrogenase subunit 5
Slr0844	1.011	0.952	0.935	0.715	NADH dehydrogenase subunit 5
Slr0848	0.845	0.951	1.024	1.093	hypothetical protein
Slr0854	0.993	1.292	1.028	1.280	DNA photolyase
Slr0861	0.746	0.646	0.833	0.822	glycinamide ribonucleotide transformylase
Slr0862	0.777	0.664	0.838	0.708	probable sugar kinase
Slr0863	1.033	0.985	0.942	0.929	hypothetical protein
Slr0864	0.983	1.553	1.277	1.838	ATP-binding protein of ABC transporter
Slr0865	0.563	0.712	1.045	0.926	hypothetical protein
Slr0867	0.855	0.922	0.733	0.694	unknown protein
Slr0869	0.503	0.438	0.707	0.546	hypothetical protein
Slr0872	0.808	1.473	0.964	1.669	hypothetical protein
Slr0875	1.028	0.750	0.678	0.435	large-conductance mechanosensitive channel
Slr0876	1.377	1.062	2.242	1.695	hypothetical protein
Slr0877	1.045	0.968	1.264	1.111	glutamyl-tRNA(Gln) amidotransferase subunit A
Slr0878	1.178	1.845	0.881	1.399	hypothetical protein
Slr0879	0.842	0.941	1.004	0.872	glycine decarboxylase complex H-protein
Slr0882	1.339	1.280	1.404	1.364	hypothetical protein YCF84
Slr0882	1.339	1.280	1.404	1.364	hypothetical protein YCF84
Slr0884	1.105	1.344	0.956	1.274	glyceraldehyde 3-phosphate dehydrogenase 1 (NAD+)
Slr0885	0.821	1.134	0.578	1.621	hypothetical protein
Slr0886	0.936	1.075	0.705	0.862	3-oxoacyl-[acyl-carrier protein] reductase
Slr0889	1.427	1.623	0.919	1.059	hypothetical protein
Slr0891	1.052	0.881	0.767	0.741	N-acetylmuramoyl-L-alanine amidase
Slr0897	0.842	1.170	0.339	0.496	probable endoglucanase
Slr0898	1.006	0.786	1.307	0.980	ferredoxin-nitrite reductase
Slr0899	1.020	0.703	1.092	0.756	cyanate lyase

Slr0900	1.021	0.781	1.196	0.917	molybdopterin biosynthesis MoeA protein
Slr0903	1.074	0.809	1.142	0.849	molybdopterin (MPT) converting factor, subunit 2
Slr0904	0.681	0.805	1.166	1.055	competence protein ComM homolog
Slr0906	0.896	0.879	1.269	1.215	photosystem II core light harvesting protein
Slr0907	0.870	0.964	0.749	0.903	unknown protein
Slr0909	0.874	1.420	0.965	1.258	unknown protein
Slr0912	0.893	1.018	0.637	0.685	unknown protein
Slr0913	0.803	0.845	0.600	0.623	unknown protein
Slr0914	0.734	0.888	0.661	0.803	unknown protein
Slr0917	0.895	0.726	0.537	0.476	7-keto-8-aminopelargonic acid synthetase
Slr0918	1.025	1.011	1.543	1.675	methionine aminopeptidase
Slr0920	1.030	1.094	0.705	0.656	mutator MutT protein
Slr0921	0.765	0.841	0.705	0.826	hypothetical protein
Slr0922	0.912	1.035	0.939	1.312	peptidyl-tRNA hydrolase
Slr0923	1.000	0.802	1.376	1.099	hypothetical protein YCF65
Slr0924	0.670	1.058	1.022	1.653	periplasmic protein, function unknown
Slr0925	1.056	0.931	0.908	0.889	single-stranded DNA-binding protein
Slr0929	1.122	1.340	0.589	0.784	chromosome partitioning protein, ParA family
Slr0930	0.999	1.387	1.420	2.016	hypothetical protein
Slr0936	1.056	0.978	0.964	0.651	nicotinate-nucleotide pyrophosphorylase
Slr0937	0.881	0.671	1.289	1.200	unknown protein
Slr0938	1.036	1.063	1.140	1.127	probable UDP-N-acetylmuramyl tripeptide synthetase
Slr0940	1.190	1.190	1.451	1.427	zeta-carotene desaturase
Slr0941	0.841	0.923	0.690	0.770	hypothetical protein
Slr0942	1.043	1.018	1.057	1.000	alcohol dehydrogenase [NADP+]
Slr0943	0.994	1.117	1.134	1.124	fructose-bisphosphate aldolase, class I
Slr0944	0.708	0.364	0.148	0.075	multidrug-e-flux transporter
Slr0945	0.696	0.786	0.131	0.065	arsenical resistance protein ArsH homolog
Slr0946	0.858	0.749	0.325	0.308	arsenate reductase
Slr0947	0.813	0.873	0.615	0.706	response regulator for energy transfer from phycobilisomes to photosystems
Slr0948	0.750	0.823	0.938	0.887	hypothetical protein
Slr0950	0.829	1.073	0.742	0.857	hemolysin-like protein
Slr0951	0.971	1.148	0.791	0.923	4-diphosphocytidyl-2C-methyl-D-erythritol synthase
Slr0952	1.468	1.953	1.117	1.730	fructose-1,6-bisphosphatase
Slr0954	0.574	0.671	0.546	0.769	hypothetical protein
Slr0955	0.741	1.050	0.950	1.389	probable tRNA/rRNA methyltransferase
Slr0958	1.121	1.149	1.340	1.277	cysteinyI-tRNA synthetase
Slr0959	0.894	0.959	1.054	1.115	hypothetical protein
Slr0962	2.012	1.957	1.431	1.406	unknown protein
Slr0963	1.171	1.414	2.155	2.463	ferredoxin-sulfite reductase
Slr0965	0.975	1.121	0.935	1.012	DNA polymerase III beta subunit
Slr0966	0.843	0.853	0.906	0.956	tryptophan synthase alpha chain
Slr0969	0.905	1.244	0.788	1.058	precorrin methylase
Slr0971	0.830	0.714	1.020	0.778	hypothetical protein
Slr0974	1.453	2.075	1.560	2.825	initiation factor IF-3
Slr0983	0.817	0.677	0.989	0.625	glucose-1-phosphate cytidylyltransferase
Slr0984	0.779	0.906	0.749	0.673	CDP-glucose 4,6-dehydratase
Slr0985	0.705	0.800	0.669	0.672	dTDP-4-dehydrorhamnose 3,5-epimerase
Slr0989	0.919	1.126	1.129	1.536	hypothetical protein
Slr0990	0.916	0.806	1.174	1.031	hypothetical protein
Slr0992	1.183	1.353	1.299	1.538	probable tRNA/rRNA methyltransferase
Slr0993	0.421	0.303	0.790	0.883	putative peptidase
Slr1020	0.902	0.794	0.808	0.759	sulfolipid biosynthesis protein SqdB
Slr1022	0.728	0.819	0.810	1.059	N-acetylornithine aminotransferase
Slr1024	1.242	1.789	1.139	1.667	fibrillin
Slr1030	1.745	1.887	2.012	2.004	magnesium protoporphyrin IX chelatase subunit I
Slr1031	1.209	1.302	1.274	1.395	tyrosyl tRNA synthetase
Slr1033	0.961	0.575	0.964	0.617	unknown protein
Slr1034	1.017	0.772	0.885	0.759	hypothetical protein YCF41
Slr1035	1.502	1.114	1.170	0.633	hypothetical protein
Slr1037	0.657	1.002	0.509	0.842	two-component response regulator CheY subfamily
Slr1037	0.657	1.002	0.509	0.842	two-component response regulator CheY subfamily
Slr1039	1.232	1.531	0.785	0.964	hypothetical protein
Slr1041	1.031	1.004	0.965	1.078	two-component response regulator PatA subfamily
Slr1042	1.004	0.873	1.185	1.107	two-component response regulator CheY subfamily
Slr1043	0.769	0.823	0.784	0.692	similar to chemotaxis protein CheW
Slr1044	0.773	0.799	0.778	0.721	methyl-accepting chemotaxis protein, required for the biogenesis of thick pili
Slr1048	0.841	0.923	1.250	1.337	hypothetical protein
Slr1056	0.736	0.911	1.698	1.664	unknown protein
Slr1063	0.822	0.753	0.687	0.431	probable glycosyltransferase
Slr1064	0.934	1.099	1.289	1.637	probable glycosyltransferase
Slr1065	0.865	0.839	0.856	0.855	probable glycosyltransferase
Slr1066	0.790	1.156	0.984	1.225	unknown protein
Slr1067	0.861	0.974	0.840	0.995	UDP-glucose 4-epimerase
Slr1073	0.890	0.631	0.659	0.612	unknown protein
Slr1076	0.844	0.861	0.606	0.758	probable glycosyltransferase
Slr1087	0.919	1.572	0.363	0.613	hypothetical protein
Slr1090	0.719	0.795	0.806	0.951	GTP-binding protein
Slr1096	1.110	1.066	1.167	1.107	dihydroipoamide dehydrogenase
Slr1097	1.083	0.969	1.040	1.007	hypothetical protein
Slr1098	0.792	0.664	0.882	1.022	hypothetical protein
Slr1098	0.792	0.664	0.882	1.022	hypothetical protein
Slr1099	0.864	0.841	0.669	0.644	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
Slr1100	1.130	1.022	1.147	1.316	hypothetical protein
Slr1101	0.737	0.767	1.050	0.833	hypothetical protein
Slr1102	0.727	0.699	0.983	0.903	hypothetical protein
Slr1103	0.727	0.677	0.929	0.786	hypothetical protein
Slr1104	0.679	0.701	0.742	0.638	hypothetical protein
Slr1105	1.548	1.832	1.802	2.212	GTP-binding protein TypA/BipA homolog
Slr1106	1.266	1.495	0.847	1.056	prohibitin
Slr1109	0.751	0.840	0.694	0.738	similar to ankyrin
Slr1110	0.469	0.521	0.574	0.486	hypothetical protein
Slr1116	0.871	1.075	0.543	0.561	hypothetical protein
Slr1117	0.890	0.888	0.876	0.999	hypothetical protein
Slr1123	0.881	0.900	0.804	0.649	guanylate kinase
Slr1124	0.985	0.806	0.896	0.729	phosphoglycerate mutase
Slr1125	0.726	0.675	0.649	0.680	probable glucosyl transferase
Slr1127	0.787	1.046	0.221	0.307	unknown protein
Slr1128	0.932	1.010	1.043	1.209	hypothetical protein
Slr1129	0.832	0.850	1.282	1.328	ribonuclease E
Slr1133	0.880	1.119	0.723	0.891	L-argininosuccinate lyase
Slr1139	0.983	0.840	1.101	1.049	thioredoxin
Slr1140	0.903	0.934	0.982	1.008	DegT/DnrJ/EryC1/StrS family protein
Slr1142	0.668	0.795	0.637	0.749	hypothetical protein
Slr1143	0.779	0.939	0.732	0.826	hypothetical protein
Slr1149	0.857	0.833	0.987	1.029	ATP-binding protein of ABC transporter
Slr1150	1.786	1.949	1.078	1.038	unknown protein
Slr1159	0.894	0.915	1.047	1.126	glycinamide ribonucleotide synthetase
Slr1160	0.872	0.876	0.606	0.625	periplasmic protein, function unknown
Slr1161	2.169	2.062	1.667	1.706	hypothetical protein
Slr1162	1.208	1.255	1.287	1.404	unknown protein
Slr1164	0.838	0.872	0.598	0.766	ribonucleotide reductase subunit alpha
Slr1165	1.110	1.115	1.225	1.339	sulfate adenyltransferase
Slr1166	1.019	1.198	1.420	1.351	UDP-glucose:tetrahydrobiopterin glucosyltransferase
Slr1167	0.687	0.550	0.403	0.301	glycerol dehydrogenase
Slr1171	1.321	2.725	0.847	2.179	glutathione peroxidase-like NADPH peroxidase:glutathione peroxidase
Slr1173	0.708	0.763	0.791	0.813	hypothetical protein
Slr1176	1.136	1.364	1.263	1.639	glucose-1-phosphate adenyltransferase
Slr1177	0.847	0.999	1.067	1.242	hypothetical protein
Slr1179	0.963	0.867	1.218	1.190	hypothetical protein
Slr1185	0.442	0.407	0.507	0.551	cytochrome b6-f complex alternative iron-sulfur subunit (Rieske iron sulfur protein)
Slr1185	0.442	0.407	0.507	0.551	cytochrome b6-f complex alternative iron-sulfur subunit (Rieske iron sulfur protein)
Slr1188	0.800	1.004	0.706	0.883	hypothetical protein
Slr1189	0.781	0.743	0.907	0.793	unknown protein

Slr1192	1.000	0.863	0.800	0.659	probable alcohol dehydrogenase
Slr1194	0.657	0.617	0.919	0.818	hypothetical protein
Slr1195	1.022	1.290	0.944	1.513	hypothetical protein
Slr1196	1.015	1.065	0.813	0.901	periplasmic protein, function unknown
Slr1197	1.081	0.992	0.646	0.844	SMF protein
Slr1198	1.054	1.067	1.592	1.748	antioxidant protein
Slr1200	0.995	1.033	1.179	1.225	urea transport system permease protein
Slr1201	0.770	0.915	0.749	0.736	urea transport system permease protein
Slr1203	1.538	1.678	0.795	0.728	hypothetical protein
Slr1204	0.308	0.245	0.794	0.499	protease
Slr1205	1.049	1.131	1.156	1.081	similar to chlorobenzene dioxygenase, ferredoxin component
Slr1206	1.011	0.948	0.797	1.274	hypothetical protein
Slr1207	0.812	0.789	1.218	1.080	hypothetical protein
Slr1208	0.934	1.095	0.999	1.110	probable oxidoreductase
Slr1210	0.656	1.029	0.711	1.101	unknown protein
Slr1211	0.993	0.983	0.888	0.929	cobalt-chelatase subunit CobN
Slr1214	0.725	0.471	0.829	0.532	two-component response regulator PatA subfamily
Slr1216	1.019	1.637	0.720	1.149	Mg2+ transport protein
Slr1218	0.847	0.972	0.606	0.544	hypothetical protein YCF39
Slr1219	0.797	0.543	0.706	0.509	urease accessory protein E
Slr1220	1.157	1.189	0.840	0.880	hypothetical protein
Slr1223	0.853	1.125	0.919	1.076	hypothetical protein
Slr1224	0.832	0.932	0.918	1.048	ATP-binding protein of sugar ABC transporter
Slr1225	0.912	1.074	0.812	1.122	serine/threonine kinase
Slr1226	0.764	0.825	0.907	0.924	phosphoribosyl aminodazole succinocarboxamide synthetase
Slr1227	1.200	0.915	0.826	0.623	chloroplastic outer envelope membrane protein homolog
Slr1228	1.529	1.414	1.439	1.362	peptide-chain-release factor 3
Slr1230	1.359	0.935	1.100	0.979	hypothetical protein
Slr1233	0.968	0.866	1.109	0.789	succinate dehydrogenase flavoprotein subunit
Slr1234	0.894	0.934	0.838	0.984	protein kinase C inhibitor
Slr1235	1.222	1.151	0.966	1.096	hypothetical protein
Slr1236	0.944	1.233	0.733	0.891	hypothetical protein
Slr1238	1.056	1.290	0.976	1.233	glutathione synthetase
Slr1239	1.148	1.038	1.661	1.414	pyridine nucleotide transhydrogenase alpha subunit
Slr1239	1.148	1.038	1.661	1.414	pyridine nucleotide transhydrogenase alpha subunit
Slr1240	1.241	1.045	3.049	3.311	unknown protein
Slr1243	0.916	1.056	1.587	1.805	unknown protein
Slr1251	1.103	1.508	0.917	1.144	peptidyl-prolyl cis-trans isomerase
Slr1253	0.728	0.438	0.288	0.149	unknown protein
Slr1254	1.176	1.100	1.229	1.250	phytoene dehydrogenase (phytoene desaturase)
Slr1255	0.854	0.625	1.403	0.911	phytoene synthase
Slr1256	1.124	1.183	0.775	0.902	urease gamma subunit
Slr1256	1.124	1.183	0.775	0.902	urease gamma subunit
Slr1257	1.333	2.041	1.236	1.862	unknown protein
Slr1258	1.131	0.817	1.092	0.843	unknown protein
Slr1259	1.188	2.660	0.797	1.792	hypothetical protein
Slr1260	1.127	2.786	0.597	1.600	hypothetical protein
Slr1261	1.350	4.016	0.822	2.212	hypothetical protein
Slr1263	0.814	0.851	1.003	1.049	hypothetical protein
Slr1265	1.104	1.256	1.447	1.541	RNA polymerase gamma-subunit
Slr1266	0.717	0.807	0.647	0.639	hypothetical protein
Slr1269	0.644	0.507	0.787	0.623	gamma-glutamyltranspeptidase
Slr1270	1.105	0.915	0.903	0.701	periplasmic protein, function unknown
Slr1271	0.676	0.591	0.633	0.670	probable UDP-N-acetyl-D-mannosaminuronic acid transferase
Slr1272	1.130	0.983	0.746	0.578	probable porin; major outer membrane protein
Slr1273	0.823	0.726	0.890	0.758	hypothetical protein
Slr1274	0.752	0.887	0.611	0.636	probable fimbrial assembly protein PilM, required for motility
Slr1275	0.698	0.766	0.358	0.326	hypothetical protein
Slr1276	0.655	0.886	0.445	0.505	hypothetical protein
Slr1277	0.898	0.838	0.639	0.637	pilus assembly protein homologous to general secretion pathway protein D
Slr1280	0.977	1.091	0.585	0.633	NADH dehydrogenase subunit NdhK
Slr1280	0.977	1.091	0.585	0.633	NADH dehydrogenase subunit NdhK
Slr1281	0.881	0.781	0.521	0.409	NADH dehydrogenase subunit I
Slr1287	0.947	1.066	0.826	0.649	hypothetical protein
Slr1289	0.992	1.229	1.242	1.414	isocitrate dehydrogenase (NADP+)
Slr1293	1.161	1.036	0.907	0.799	similar to phytoene dehydrogenase
Slr1295	0.517	0.427	0.820	0.677	iron transport system substrate-binding protein
Slr1298	0.938	0.984	0.969	1.021	unknown protein
Slr1299	0.985	0.982	0.820	0.875	UDP-glucose dehydrogenase
Slr1301	0.993	1.092	0.728	0.832	hypothetical protein
Slr1302	1.209	0.882	1.305	0.903	protein involved in constitutive low affinity CO2 uptake
Slr1305	0.689	0.955	0.718	0.874	two-component response regulator
Slr1306	0.660	0.608	0.965	0.877	hypothetical protein
Slr1311	1.067	1.001	2.165	1.969	photosystem II D1 protein
Slr1312	0.778	1.043	1.081	1.330	arginine decarboxylase
Slr1315	0.786	0.892	0.760	0.853	hypothetical protein
Slr1318	0.439	0.370	0.453	0.561	iron(III) dicitrate transport system ATP-binding protein
Slr1322	1.370	1.395	1.351	1.456	putative modulator of DNA gyrase; TldD
Slr1324	0.965	1.302	0.929	1.053	two-component hybrid sensor and regulator
Slr1325	0.720	0.851	0.918	1.086	GTP pyrophosphokinase
Slr1329	0.894	0.796	0.863	0.815	ATP synthase beta subunit
Slr1330	0.941	0.730	0.897	0.663	ATP synthase epsilon chain of CF(1)
Slr1331	0.866	0.889	0.820	0.850	periplasmic processing protease
Slr1334	1.073	1.066	1.030	0.996	phosphoglucosyltransferase/phosphomannosyltransferase
Slr1338	1.012	1.252	0.783	0.942	hypothetical protein
Slr1340	0.968	1.004	0.923	0.976	unknown protein
Slr1342	0.741	0.818	0.691	0.824	hypothetical protein
Slr1343	0.576	0.705	0.572	0.481	hypothetical protein
Slr1347	0.731	0.835	0.945	0.907	beta-type carbonic anhydrase localized in the carboxysome
Slr1348	0.656	0.577	0.664	0.559	serine acetyltransferase
Slr1349	1.050	1.214	0.989	1.179	glucose-6-phosphate isomerase
Slr1351	1.181	0.967	1.012	0.865	UDP-N-acetylmuramoylalanine-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase
Slr1353	1.271	2.119	1.357	2.033	hypothetical protein
Slr1356	1.025	0.875	1.024	0.915	30S ribosomal protein S1
Slr1362	1.272	1.010	1.042	0.863	hypothetical protein
Slr1363	1.026	1.117	1.427	2.024	hypothetical protein
Slr1364	0.952	0.928	1.181	1.460	biotin synthetase
Slr1367	1.319	1.701	1.570	1.912	glycogen phosphorylase
Slr1367	1.319	1.701	1.570	1.912	glycogen phosphorylase
Slr1368	0.955	0.848	0.920	0.789	precorrin decarboxylase
Slr1377	0.745	0.613	0.684	0.483	leader peptidase I (signal peptidase I)
Slr1378	0.907	1.397	0.499	0.797	hypothetical protein
Slr1379	1.190	1.724	0.786	1.034	quinol oxidase subunit I
Slr1384	1.057	1.230	1.309	1.504	hypothetical protein
Slr1385	0.818	0.990	0.758	0.808	unknown protein
Slr1390	0.923	1.048	0.763	0.873	cell division protein FisH
Slr1391	1.302	2.020	2.151	3.077	unknown protein
Slr1392	0.423	0.520	0.475	0.576	ferrous iron transport protein B
Slr1393	0.698	0.622	1.241	0.992	phytochrome-like protein, two-component sensor histidine kinase
Slr1395	0.620	0.775	0.650	0.811	hypothetical protein
Slr1397	0.929	1.134	0.929	1.053	unknown protein
Slr1398	0.901	1.016	0.808	0.936	unknown protein
Slr1403	0.736	1.366	0.172	0.258	unknown protein
Slr1406	0.659	0.905	0.445	0.588	periplasmic protein, function unknown
Slr1407	0.521	0.571	0.393	0.438	unknown protein
Slr1409	0.661	0.913	0.537	0.608	periplasmic WD-repeat protein
Slr1410	0.536	0.673	0.504	0.561	periplasmic WD-repeat protein
Slr1411	0.756	1.021	0.686	0.833	hypothetical protein
Slr1413	0.940	0.980	0.621	0.635	hypothetical protein
Slr1414	0.797	0.870	0.822	1.047	two-component sensor histidine kinase
Slr1416	0.840	0.805	0.708	0.649	similar to MorR protein
Slr1417	0.900	0.632	0.376	0.254	hypothetical protein YCF57
Slr1418	0.996	1.101	1.175	1.401	dihydroorotate dehydrogenase
Slr1419	1.103	1.161	1.133	1.096	hypothetical protein

Slr1420	0.720	0.892	0.674	0.894	probable sugar kinase
Slr1423	0.763	0.767	1.264	1.389	UDP-N-acetylmuramate-alanine ligase
Slr1424	0.664	0.694	1.009	1.125	UDP-N-acetylenolpyruvoylglucosamine reductase
Slr1424	0.664	0.694	1.009	1.125	UDP-N-acetylenolpyruvoylglucosamine reductase
Slr1425	0.731	0.789	0.675	0.571	hypothetical protein
Slr1426	0.796	1.050	0.633	0.937	recombination protein RecK
Slr1428	0.892	0.903	0.783	0.633	hypothetical protein
Slr1431	0.415	0.489	0.779	0.905	hypothetical protein
Slr1434	1.600	1.095	2.375	1.603	pyridine nucleotide transhydrogenase beta subunit
Slr1434	1.600	1.095	2.375	1.603	pyridine nucleotide transhydrogenase beta subunit
Slr1435	1.330	1.403	1.484	1.555	PmbA protein homolog
Slr1436	1.264	1.339	1.312	1.515	unknown protein
Slr1437	0.889	0.620	0.990	0.762	unknown protein
Slr1438	0.672	0.622	0.990	0.808	hypothetical protein
Slr1444	0.832	1.071	0.894	1.339	hypothetical protein
Slr1448	1.035	1.116	0.992	1.295	fructokinase
Slr1452	6.410	1.645	5.952	1.709	sulfate transport system substrate-binding protein
Slr1455	2.882	1.152	3.135	1.304	sulfate transport system ATP-binding protein
Slr1459	0.987	0.940	0.894	0.808	phycobilisome core component
Slr1462	0.934	1.279	1.017	1.342	hypothetical protein
Slr1463	1.189	1.227	1.292	1.235	elongation factor EF-G
Slr1464	0.871	0.986	0.658	0.736	hypothetical protein
Slr1467	0.664	0.740	0.668	0.652	precorrin isomerase
Slr1468	0.844	0.864	0.663	0.767	hypothetical protein
Slr1470	1.284	1.125	1.610	1.427	hypothetical protein
Slr1471	1.163	1.196	1.192	1.289	hypothetical protein
Slr1472	0.887	0.375	0.852	0.406	hypothetical protein
Slr1476	1.028	1.152	0.881	0.893	aspartate carbamoyltransferase
Slr1485	1.351	0.964	0.972	0.870	putative phosphatidylinositol phosphate kinase, salt-induced periplasmic protein
Slr1498	1.080	1.026	0.703	0.699	putative hydrogenase expression/formation protein HypD
Slr1501	1.179	1.285	1.045	0.983	probable acetyltransferase
Slr1503	0.853	1.025	0.755	0.897	hypothetical protein
Slr1505	0.534	0.422	0.579	0.440	unknown protein
Slr1506	0.734	0.832	0.602	0.672	hypothetical protein
Slr1507	1.127	1.067	1.550	1.316	hypothetical protein
Slr1508	0.778	0.962	1.024	1.312	probable glycosyltransferase
Slr1510	1.026	0.909	1.122	1.064	fatty acid/phospholipid synthesis protein PlsX
Slr1511	0.910	1.318	0.994	1.464	3-oxoacyl-[acyl-carrier-protein] synthase III
Slr1512	0.540	0.355	0.255	0.180	sodium-dependent bicarbonate transporter
Slr1513	0.705	0.614	0.298	0.226	periplasmic protein, function unknown
Slr1516	0.798	0.589	0.985	0.723	superoxide dismutase
Slr1517	1.089	0.845	0.879	0.556	3-isopropylmalate dehydrogenase
Slr1519	1.013	1.253	0.756	0.869	hypothetical protein
Slr1521	1.202	1.560	1.490	1.770	GTP-binding protein
Slr1529	0.786	0.815	1.214	1.133	nitrogen assimilation regulatory protein
Slr1531	1.033	1.242	1.590	1.733	signal recognition particle protein
Slr1533	1.203	1.815	1.600	2.088	hypothetical protein
Slr1534	1.004	1.052	1.224	1.255	hypothetical protein
Slr1535	1.087	3.676	1.431	2.681	hypothetical protein
Slr1537	0.813	0.833	0.776	0.858	unknown protein
Slr1540	1.014	0.970	1.109	1.131	mRNA-binding protein
Slr1541	1.136	0.946	0.880	0.797	hypothetical protein
Slr1542	0.892	0.835	0.923	0.720	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Slr1544	1.799	1.066	1.096	0.642	unknown protein
Slr1545	1.353	1.285	1.629	1.527	RNA polymerase ECF-type (group 3) sigma-E factor
Slr1549	1.167	1.055	0.744	0.645	polypeptide deformylase
Slr1550	0.903	0.936	0.902	1.078	lysyl-tRNA synthetase
Slr1552	0.559	0.499	0.510	0.415	unknown protein
Slr1556	0.535	0.847	0.743	1.161	2-hydroxyacid dehydrogenase homolog
Slr1557	0.952	0.972	1.595	1.541	hypothetical protein
Slr1559	0.748	0.878	0.600	0.700	shikimate 5-dehydrogenase
Slr1560	0.847	0.724	0.810	0.692	histidyl tRNA synthetase
Slr1562	0.697	0.615	0.648	0.605	glutaredoxin
Slr1564	1.199	0.898	1.100	1.010	group 3 RNA polymerase sigma factor
Slr1565	0.920	0.784	1.513	1.117	hypothetical protein
Slr1566	0.813	1.046	1.984	2.188	hypothetical protein
Slr1567	0.732	0.732	0.462	0.487	unknown protein
Slr1572	0.467	0.611	0.444	0.573	hypothetical protein
Slr1573	0.943	1.196	0.782	0.935	hypothetical protein
Slr1575	0.655	0.495	0.573	0.427	probable potassium efflux system
Slr1577	0.824	1.143	0.574	0.747	hypothetical protein
Slr1579	0.863	0.866	1.151	1.297	hypothetical protein
Slr1583	1.052	0.623	0.466	0.273	hypothetical protein
Slr1584	0.945	1.337	1.043	1.458	two-component transcription regulator OmpR subfamily
Slr1588	0.656	0.167	0.797	0.247	two-component transcription regulator
Slr1590	1.053	1.109	1.295	1.229	hypothetical protein
Slr1596	0.879	0.772	1.441	1.199	a protein in the cytoplasmic membrane involved in light-induced proton extrusion.
Slr1597	0.835	0.890	0.955	1.159	chromosome partitioning ATPase, ParA family
Slr1598	1.808	0.966	1.026	0.541	lipic acid synthetase
Slr1600	1.065	1.342	0.937	1.236	hypothetical protein
Slr1603	1.124	1.142	0.810	0.976	hypothetical protein
Slr1604	1.060	1.015	1.181	1.163	cell division protein FtsH
Slr1608	1.534	1.639	2.092	1.669	putative glucose dehydrogenase-B, periplasmic protein
Slr1609	0.992	0.942	0.985	0.835	long-chain-fatty-acid CoA ligase
Slr1610	0.520	0.502	0.461	0.447	putative C-3 methyl transferase
Slr1612	0.696	1.721	0.348	0.661	hypothetical protein
Slr1613	0.725	1.035	0.363	0.446	hypothetical protein
Slr1615	0.897	1.071	0.545	0.739	perosamine synthetase
Slr1616	0.691	0.924	0.630	0.885	unknown protein
Slr1617	1.037	1.139	1.464	1.712	similar to UDP-glucose 4-epimerase
Slr1618	0.707	0.720	0.923	0.967	unknown protein
Slr1619	1.015	1.215	0.947	1.156	hypothetical protein
Slr1622	0.908	0.662	0.879	0.615	soluble inorganic pyrophosphatase
Slr1622	0.908	0.662	0.879	0.615	soluble inorganic pyrophosphatase
Slr1623	1.125	1.067	0.742	0.631	hypothetical protein
Slr1624	0.908	0.975	0.944	0.929	hypothetical protein
Slr1626	0.969	0.708	0.560	0.449	dihydroneopterin aldolase
Slr1629	0.706	1.052	1.109	1.661	ribosomal large subunit pseudouridine synthase D
Slr1639	2.415	2.262	2.347	2.169	SsrA-binding protein
Slr1641	1.196	1.362	0.372	0.375	ClpB protein
Slr1643	1.078	0.877	1.225	0.983	ferredoxin-NADP oxidoreductase
Slr1644	0.978	0.890	1.437	1.252	hypothetical protein
Slr1645	0.956	1.134	1.302	1.468	photosystem II 11 kD protein
Slr1646	1.372	1.318	1.080	1.821	ribonuclease III
Slr1648	1.135	1.420	0.929	1.167	hypothetical protein
Slr1649	1.255	1.140	1.238	1.017	hypothetical protein
Slr1653	0.737	1.065	0.790	0.943	N-acyl-L-amino acid amidohydrolase
Slr1655	1.091	1.105	1.241	1.374	photosystem I subunit XI
Slr1656	1.112	0.923	1.730	1.416	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl -undecaprenol N-acetylglucosamine transferase
Slr1657	0.930	0.858	0.703	0.641	hypothetical protein
Slr1658	0.928	1.241	0.663	0.958	unknown protein
Slr1659	1.129	1.105	0.557	0.596	hypothetical protein
Slr1661	1.082	0.760	0.661	0.513	hypothetical protein
Slr1665	0.642	0.753	1.115	1.282	diaminopimelate epimerase
Slr1666	1.035	1.011	0.930	0.985	pleiotropic regulatory protein homolog
Slr1668	0.627	0.704	0.919	1.122	periplasmic protein, function unknown (target gene of sycrp1)
Slr1670	2.294	2.506	1.600	1.721	unknown protein
Slr1672	1.206	1.587	1.063	1.565	glycerol kinase
Slr1673	1.742	2.146	0.736	0.769	probable tRNA/rRNA methyltransferase
Slr1674	1.425	1.186	0.568	0.467	hypothetical protein
Slr1677	0.849	1.637	0.827	1.374	hypothetical protein
Slr1678	1.055	1.412	1.393	1.783	50S ribosomal protein L21
Slr1679	1.129	0.843	0.922	0.762	hypothetical protein
Slr1681	0.499	0.607	0.603	0.680	unknown protein



Slr1686	0.677	0.787	0.502	0.569	hypothetical protein
Slr1687	1.675	1.229	1.235	0.741	hypothetical protein
Slr1689	0.915	1.391	1.031	1.517	formamidopyrimidine-DNA glycosylase
Slr1690	1.208	2.049	0.611	1.399	hypothetical protein
Slr1691	0.716	0.803	0.878	0.993	glutamine-dependent NAD(+) synthetase
Slr1692	0.878	1.018	0.986	1.335	hypothetical protein
Slr1693	0.825	0.879	0.943	1.012	two-component response regulator PatA subfamily
Slr1693	0.825	0.879	0.943	1.012	two-component response regulator PatA subfamily
Slr1694	0.709	0.855	0.818	0.880	expression activator appA homolog
Slr1697	1.007	0.978	1.695	2.000	serine/threonine kinase
Slr1699	1.124	1.091	0.971	0.931	hypothetical protein
Slr1702	0.891	0.898	0.895	0.787	hypothetical protein
Slr1703	0.855	0.980	1.033	1.199	seryl-tRNA synthetase
Slr1704	1.647	0.838	1.055	0.481	hypothetical protein
Slr1706	0.950	1.374	0.637	0.908	dihydroflavonol 4-reductase
Slr1712	0.625	0.931	0.519	0.345	hypothetical protein
Slr1717	1.114	1.531	0.714	1.088	hypothetical protein
Slr1718	0.943	0.991	0.989	1.093	hypothetical protein
Slr1719	0.840	0.852	0.710	0.765	DrgA protein homolog
Slr1720	0.986	1.148	0.822	0.935	aspartyl-tRNA synthetase
Slr1721	0.955	0.915	0.766	0.821	hypothetical protein
Slr1722	0.897	0.813	0.977	0.877	inosine-5'-monophosphate dehydrogenase
Slr1723	1.103	0.844	0.660	0.550	permease protein of sugar ABC transporter
Slr1724	0.735	0.754	0.822	1.008	hypothetical protein
Slr1727	1.083	1.441	0.691	1.026	Na <sup>+</sup> /H <sup>+</sup> antiporter
Slr1728	3.289	2.088	2.564	1.667	potassium-transporting P-type ATPase A chain
Slr1729	3.745	3.021	2.959	2.625	potassium-transporting P-type ATPase B chain
Slr1730	1.739	1.698	1.919	1.626	potassium-transporting P-type ATPase C chain
Slr1731	2.967	3.003	1.786	1.786	potassium-transporting P-type ATPase D chain
Slr1732	1.289	1.269	2.315	2.273	hypothetical protein
Slr1734	0.988	1.087	0.891	1.030	glucose 6-phosphate dehydrogenase assembly protein
Slr1735	1.041	1.218	1.418	1.678	ATP-binding subunit of the ABC-type Bgt permease for basic amino acids and glutamine
Slr1739	1.862	2.045	1.082	1.151	photosystem II 13 kDa protein homolog
Slr1740	1.121	1.256	0.978	1.034	oligopeptide binding protein of ABC transporter
Slr1742	0.935	1.056	1.020	1.198	probable cobryic acid synthase
Slr1743	1.163	1.529	0.750	1.133	type 2 NADH dehydrogenase NdbB
Slr1743	1.163	1.529	0.750	1.133	type 2 NADH dehydrogenase NdbB
Slr1744	1.096	1.157	1.453	1.504	N-acetylmuramoyl-L-alanine amidase, periplasmic protein
Slr1748	0.664	1.151	1.351	1.199	probable phosphoglycerate mutase
Slr1751	0.685	0.822	0.855	0.948	periplasmic carboxyl-terminal protease
Slr1752	0.887	0.766	0.584	0.506	hypothetical protein
Slr1753	0.990	0.739	0.705	0.622	hypothetical protein
Slr1755	1.091	1.590	0.943	1.098	NAD <sup>+</sup> dependent glycerol-3-phosphate dehydrogenase
Slr1756	0.995	0.987	1.214	1.138	glutamate--ammonia ligase
Slr1756	0.995	0.987	1.214	1.138	glutamate--ammonia ligase
Slr1761	0.910	1.101	0.829	0.983	FKBP-type peptidyl-prolyl cis-trans isomerase, periplasmic protein
Slr1762	0.943	1.011	0.807	0.926	hypothetical protein
Slr1763	1.190	1.242	1.404	1.294	probable methyltransferase
Slr1768	0.644	0.675	0.643	0.591	unknown protein
Slr1772	1.727	1.642	1.645	1.484	probable hydrolase, periplasmic protein
Slr1773	0.911	0.990	0.664	0.643	unknown protein
Slr1777	1.502	1.580	1.603	1.592	magnesium protoporphyrin IX chelatase subunit D
Slr1779	0.856	1.088	0.601	0.703	pyridoxal phosphate biosynthetic protein PdxJ
Slr1780	0.911	1.174	1.038	1.056	hypothetical protein YCF54
Slr1783	0.988	0.977	1.038	0.894	two-component response regulator NarL subfamily
Slr1784	1.063	0.990	0.945	1.114	biliverdin reductase
Slr1790	1.477	1.515	1.447	1.299	hypothetical protein
Slr1791	0.873	0.894	0.947	1.038	phosphoadenosine phosphosulfate reductase
Slr1793	1.330	1.504	1.295	1.399	transaldolase
Slr1794	1.232	1.218	0.911	0.894	probable anion transporting ATPase
Slr1795	0.806	0.799	1.366	1.238	peptide methionine sulfoxide reductase
Slr1796	0.967	0.963	1.110	1.091	hypothetical protein
Slr1799	0.903	1.151	1.033	1.284	hypothetical protein
Slr1800	0.983	1.125	0.710	1.005	hypothetical protein
Slr1805	1.678	1.161	0.761	0.520	two-component sensor histidine kinase
Slr1808	0.928	1.026	0.824	1.144	transfer RNA-Gln reductase
Slr1809	0.723	0.974	0.464	0.704	unknown protein
Slr1811	1.267	1.704	1.189	1.357	hypothetical protein
Slr1814	1.715	2.500	1.105	1.348	hypothetical protein
Slr1815	0.979	1.024	1.055	0.909	hypothetical protein
Slr1816	0.702	0.747	0.867	0.820	hypothetical protein
Slr1818	1.105	1.195	0.935	1.049	hypothetical protein
Slr1819	0.983	0.999	0.806	0.682	hypothetical protein
Slr1821	1.172	1.350	0.772	0.956	hypothetical protein
Slr1822	0.791	1.538	0.991	1.401	endonuclease III
Slr1826	0.986	0.690	1.182	0.656	hypothetical protein
Slr1828	1.250	1.495	1.681	1.988	ferredoxin, petF-like protein
Slr1829	0.890	1.727	1.001	1.869	putative poly(3-hydroxyalkanoate) synthase component
Slr1830	0.912	0.847	1.018	1.202	poly(3-hydroxyalkanoate) synthase
Slr1834	1.255	1.217	1.410	1.248	P700 apoprotein subunit Ia
Slr1835	1.104	0.758	1.727	1.148	P700 apoprotein subunit Ib
Slr1837	0.502	0.556	0.505	0.533	two-component system response regulator OmpR subfamily
Slr1838	0.896	0.756	0.753	0.656	carbon dioxide concentrating mechanism protein CcmK homolog 3, putative carboxysome assembly protein
Slr1839	0.670	0.788	0.577	0.630	carbon dioxide concentrating mechanism protein CcmK homolog 4, putative carboxysome assembly protein
Slr1840	1.040	1.100	0.858	0.895	hypothetical protein
Slr1841	1.114	1.109	0.825	0.782	probable porin; major outer membrane protein
Slr1842	0.899	1.087	0.601	0.712	cysteine synthase
Slr1843	0.828	0.999	0.957	1.319	glucose 6-phosphate dehydrogenase
Slr1844	1.016	1.414	1.136	1.379	excinuclease ABC subunit A
Slr1846	1.608	1.217	0.695	0.512	hypothetical protein YCF64
Slr1847	1.074	0.693	0.942	0.829	hypothetical protein
Slr1848	0.978	1.193	1.021	1.148	histidinol dehydrogenase
Slr1848	0.978	1.193	1.021	1.148	histidinol dehydrogenase
Slr1852	0.674	0.988	0.628	0.886	unknown protein
Slr1853	0.701	1.083	0.556	0.818	carboxymuconolactone decarboxylase
Slr1854	0.689	0.953	1.058	1.344	unknown protein
Slr1855	0.629	0.781	0.526	0.668	unknown protein
Slr1856	0.625	0.953	0.693	0.937	phosphoprotein substrate of icfG gene cluster
Slr1857	0.528	0.672	0.627	0.658	isoamylase
Slr1859	0.587	0.801	0.460	0.693	anti-sigma f factor antagonist
Slr1860	0.903	1.206	0.556	0.815	carbon metabolisms regulatory protein lcfG
Slr1861	0.871	0.963	0.586	0.655	probable sigma regulatory factor
Slr1865	1.248	1.332	0.857	1.058	unknown protein
Slr1867	0.939	0.876	0.794	0.765	anthranilate phosphoribosyltransferase
Slr1870	0.778	0.810	0.689	1.832	hypothetical protein
Slr1874	0.745	1.001	0.799	0.977	D-alanine--D-alanine ligase
Slr1875	1.209	0.833	0.978	0.936	hypothetical protein
Slr1877	0.903	1.053	0.789	0.914	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
Slr1878	1.073	1.225	1.160	1.147	phycocyanin alpha-subunit phycocyanobilin lyase
Slr1878	1.073	1.225	1.160	1.147	phycocyanin alpha-subunit phycocyanobilin lyase
Slr1879	1.060	1.318	0.916	1.124	precorrin-2 methyltransferase
Slr1880	0.829	1.351	0.896	1.441	hypothetical protein
Slr1881	1.055	1.125	0.868	0.869	ATP-binding subunit of the ABC-type Nat permease for neutral amino acids
Slr1882	1.200	1.140	0.746	0.839	riboflavin biosynthesis protein RibF
Slr1884	0.918	0.962	0.784	0.797	tryptophanyl-tRNA synthetase
Slr1885	0.671	0.572	0.489	0.437	hypothetical protein
Slr1887	1.076	1.032	1.314	1.238	porphobilinogen deaminase (hydroxymethylbilan synthase, preuroporphyrinogen synthase)
Slr1888	0.479	0.803	0.565	0.936	4-hydroxybutyrate coenzyme A transferase
Slr1890	0.898	0.911	0.683	0.720	bacterioferritin
Slr1890	0.898	0.911	0.683	0.720	bacterioferritin
Slr1894	3.003	3.731	2.381	2.695	probable DNA-binding stress protein
Slr1895	1.094	1.222	0.753	0.793	hypothetical protein
Slr1897	0.889	0.926	0.898	0.747	periplasmic sugar-binding protein of ABC transporter
Slr1898	1.190	1.049	1.289	1.143	N-acetylglutamate kinase

Slr1899	0.848	0.911	0.652	0.732	urease accessory protein F
Slr1900	0.968	1.122	0.824	0.898	hypothetical protein
Slr1901	1.131	1.560	0.999	1.339	ATP-binding protein of ABC transporter
Slr1907	1.174	0.746	0.607	0.381	hypothetical protein
Slr1908	1.111	0.997	1.200	1.058	probable porin; major outer membrane protein
Slr1909	0.681	0.654	0.741	0.709	two-component response regulator NarL subfamily
Slr1911	1.048	0.917	0.524	0.452	hypothetical protein
Slr1915	0.781	0.616	0.604	0.457	hypothetical protein
Slr1916	0.555	1.779	0.494	1.340	probable esterase
Slr1919	1.672	2.268	0.981	1.582	hypothetical protein
Slr1923	1.285	0.963	1.342	1.088	hypothetical protein
Slr1924	1.953	1.555	1.988	1.645	D-alanyl-D-alanine carboxypeptidase, periplasmic protein
Slr1926	0.976	1.376	0.728	0.890	hypothetical protein
Slr1927	0.791	1.318	1.297	1.232	hypothetical protein
Slr1928	0.956	0.985	0.964	0.935	type 4 pilin-like protein
Slr1931	0.793	0.810	1.078	1.000	type 4 pilin-like protein
Slr1932	0.910	1.481	0.541	0.762	unknown protein
Slr1933	1.239	1.355	0.772	0.830	dTDP-4-dehydrohamnose 3,5-epimerase
Slr1934	0.951	0.784	1.020	0.836	pyruvate dehydrogenase E1 component, alpha subunit
Slr1938	1.037	1.408	1.139	1.395	putative translation initiation factor EIF-2b subunit 1
Slr1939	0.812	0.692	0.758	0.883	unknown protein
Slr1940	0.909	0.866	0.907	0.794	periplasmic protein, function unknown
Slr1942	0.863	0.918	0.985	0.974	circadian clock protein KaiC homolog
Slr1943	0.955	0.593	0.921	1.082	probable glycosyltransferase
Slr1944	0.721	0.858	0.638	0.693	periplasmic protein, function unknown
Slr1945	0.857	1.037	0.957	1.300	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Slr1949	1.449	1.890	1.499	1.845	hypothetical protein
Slr1950	0.812	0.724	0.786	0.674	copper-transporting P-type ATPase CtaA
Slr1951	0.582	0.833	0.454	0.654	hypothetical protein
Slr1958	0.614	0.714	0.440	0.436	unknown protein
Slr1962	0.905	0.960	0.815	0.912	probable extracellular solute-binding protein
Slr1963	1.316	2.304	0.696	1.274	water-soluble carotenoid protein
Slr1964	1.199	2.137	3.115	6.579	hypothetical protein
Slr1968	1.364	1.522	0.693	0.797	unknown protein
Slr1969	0.663	0.524	0.740	0.694	two-component sensor histidine kinase
Slr1970	0.824	0.838	0.953	0.743	hypothetical protein
Slr1971	0.942	1.215	1.105	1.323	hypothetical protein
Slr1972	0.847	0.875	1.100	1.085	hypothetical protein YCF81
Slr1974	0.840	0.912	1.664	1.916	GTP binding protein
Slr1975	0.969	0.990	0.816	0.904	N-acetylglucosamine 2-epimerase
Slr1977	0.726	0.767	0.876	0.936	hypothetical protein
Slr1979	1.111	0.938	0.833	0.694	anthranilate synthase component I
Slr1982	0.604	0.727	0.587	0.737	two-component response regulator CheY subfamily
Slr1983	0.824	1.041	1.062	1.536	two-component hybrid sensor and regulator
Slr1984	1.080	1.241	1.227	1.247	nucleic acid-binding protein, 30S ribosomal protein S1 homolog
Slr1986	0.996	0.829	1.333	1.092	allophycocyanin beta subunit
Slr1991	0.814	0.774	0.681	0.652	adenylate cyclase
Slr1992	1.266	1.721	1.103	1.395	glutathione peroxidase-like NADPH peroxidase
Slr1993	0.784	1.068	0.810	1.036	PHA-specific beta-ketothiolase
Slr1994	1.054	1.148	0.644	0.633	PHA-specific acetoacetyl-CoA reductase
Slr1998	1.027	1.224	0.660	0.898	hypothetical protein
Slr2000	1.114	1.156	0.844	0.803	hypothetical protein
Slr2001	0.923	1.017	0.874	0.886	cyanophycinase
Slr2002	0.864	0.850	1.209	1.190	cyanophycin synthetase
Slr2004	0.845	0.910	0.576	0.656	periplasmic protein, function unknown
Slr2005	0.981	1.140	0.691	0.825	periplasmic protein, function unknown
Slr2011	1.133	1.011	1.517	1.285	hypothetical protein
Slr2017	0.396	0.408	0.365	0.262	type 4 pilin-like protein, essential for motility
Slr2018	0.613	0.604	0.704	0.702	unknown protein
Slr2019	1.122	1.247	1.377	1.927	ATP-binding protein of ABC transporter
Slr2023	1.188	1.045	1.037	0.950	malonyl coenzyme A-acyl carrier protein transacylase
Slr2024	0.890	0.855	1.138	1.075	two-component response regulator CheY subfamily
Slr2024	0.890	0.855	1.138	1.075	two-component response regulator CheY subfamily
Slr2025	0.903	0.771	0.986	0.749	hypothetical protein
Slr2030	1.412	1.412	0.858	0.970	hypothetical protein
Slr2032	0.404	0.325	0.352	0.225	hypothetical protein YCF23
Slr2033	0.975	0.913	2.463	2.309	membrane-associated rubredoxin, essential for photosystem I assembly
Slr2034	1.287	1.126	1.724	1.821	putative homolog of plant HCF136, which is essential for stability or assembly of photosystem II
Slr2035	1.022	1.468	1.080	1.211	glutamate 5-kinase
Slr2041	1.059	0.977	1.389	1.471	probable two-component response regulator
Slr2043	1.010	0.845	1.233	1.017	zinc transport system substrate-binding protein
Slr2046	0.702	0.708	0.717	0.787	unknown protein
Slr2047	1.412	1.381	1.248	1.418	PhoH like protein
Slr2048	0.792	1.107	0.830	0.921	periplasmic protein, function unknown
Slr2049	1.114	1.475	1.695	1.949	hypothetical protein YCF58
Slr2051	0.990	0.995	1.284	1.339	phycobilisome rod-core linker polypeptide
Slr2052	1.280	2.151	0.904	1.541	hypothetical protein
Slr2053	0.769	0.694	0.724	0.731	putative hydrolase
Slr2058	1.580	1.927	1.835	2.283	DNA topoisomerase I
Slr2059	1.387	2.353	1.086	1.818	iron-sulfur cluster binding protein homolog
Slr2060	0.716	0.962	0.559	0.530	hypothetical protein
Slr2067	0.803	0.792	1.125	1.088	allophycocyanin alpha subunit
Slr2070	0.701	0.692	0.855	0.923	hypothetical protein
Slr2071	2.132	3.096	3.247	4.785	unknown protein
Slr2072	0.948	1.082	0.814	0.929	L-threonine deaminase
Slr2073	1.225	1.453	1.353	1.289	hypothetical protein YCF50
Slr2074	0.698	0.751	0.613	0.737	similar to mannose-1-phosphate guanylyltransferase
Slr2074	0.698	0.751	0.613	0.737	similar to mannose-1-phosphate guanylyltransferase
Slr2074	0.698	0.751	0.613	0.737	similar to mannose-1-phosphate guanylyltransferase
Slr2075	1.095	1.393	0.572	0.658	10kD chaperonin
Slr2076	1.018	1.221	0.648	0.765	60kD chaperonin
Slr2079	1.017	0.960	0.801	0.778	putative glutaminase
Slr2080	1.120	1.208	0.616	0.656	hypothetical protein
Slr2081	0.951	0.715	0.885	0.663	prephenate dehydrogenase
Slr2084	1.000	1.086	0.661	0.746	hypothetical protein
Slr2087	1.368	1.344	1.355	1.261	c-type cytochrome biogenesis protein Ccs1
Slr2088	0.884	0.887	1.159	1.185	acetohydroxy acid synthase
Slr2089	1.013	1.321	0.952	1.120	squalene-hopene-cyclase
Slr2094	1.024	1.229	0.997	1.199	fructose-1,6-/sedoheptulose-1,7-bisphosphatase
Slr2097	0.797	0.656	0.993	0.779	cyanoglobin
Slr2098	0.545	0.372	0.734	0.495	two-component hybrid sensor and regulator
Slr2099	1.052	0.997	0.794	1.156	two-component hybrid sensor and regulator
Slr2100	0.833	1.083	0.648	0.837	two-component response regulator
Slr2101	0.958	0.784	0.679	0.683	hypothetical protein
Slr2102	0.899	0.917	1.290	1.044	cell division protein FtsY
Slr2105	0.978	1.140	0.931	0.955	hypothetical protein
Slr2122	1.087	1.135	1.098	1.292	hypothetical protein
Slr2123	0.825	1.385	0.933	1.279	similar to D-3-phosphoglycerate dehydrogenase
Slr2124	0.826	0.885	0.511	0.609	3-oxoacyl-[acyl-carrier protein] reductase
Slr2125	0.680	0.804	0.206	0.333	hypothetical protein
Slr2130	0.620	0.703	0.826	0.838	3-dehydroquinate synthase
Slr2131	1.292	1.931	0.923	1.104	RND multidrug efflux transporter
Slr2132	0.894	0.791	0.730	0.637	phosphotransacetylase
Slr2136	0.924	1.089	0.890	1.085	GepE protein homolog
Slr2141	1.220	1.333	1.144	1.284	hypothetical protein
Slr2143	1.067	1.264	0.994	1.067	L-cysteine/cystine lyase
Slr2144	0.690	0.949	0.527	0.684	periplasmic protein, function unknown
Sml0008	1.859	0.957	1.255	1.072	photosystem I subunit IX
Smr0005	1.484	0.850	1.333	0.754	photosystem I subunit XII
Smr0006	1.011	0.622	0.934	0.584	cytochrome b559 b subunit
Smr0010	3.436	0.331	1.795	0.168	cytochrome b6-f complex subunit 5
Ssl0020	0.934	0.937	0.250	0.287	ferredoxin I, essential for growth
Ssl0242	0.975	0.745	2.618	2.024	hypothetical protein
Ssl0294	1.224	1.277	1.536	1.852	hypothetical protein

Ssl0352	1.284	1.529	1.008	1.119	hypothetical protein
Ssl0353	1.323	0.874	1.071	0.591	hypothetical protein
Ssl0461	1.451	1.271	1.152	0.644	hypothetical protein
Ssl0467	0.778	0.464	0.488	0.289	unknown protein
Ssl0483	0.890	0.866	0.917	0.626	hypothetical protein
Ssl0511	1.266	0.919	0.684	0.490	hypothetical protein
Ssl0546	0.917	1.059	1.475	1.642	septum site-determining protein MinE
Ssl0563	1.082	0.830	1.742	1.364	photosystem I subunit VII
Ssl0564	1.016	0.935	1.206	1.196	transcriptional regulator
Ssl0707	0.918	1.192	0.627	0.708	nitrogen regulatory protein P-II
Ssl0787	1.104	1.101	1.060	0.950	unknown protein
Ssl0788	0.826	1.238	0.859	1.658	hypothetical protein
Ssl0832	1.259	0.880	0.835	0.631	hypothetical protein
Ssl1426	1.217	1.010	1.443	1.058	50S ribosomal protein L35
Ssl1498	1.263	0.890	1.229	0.856	hypothetical protein
Ssl1533	1.065	0.971	1.272	1.247	unknown protein
Ssl1690	1.672	1.616	1.414	1.658	hypothetical protein
Ssl1707	1.284	1.616	1.818	2.257	hypothetical protein
Ssl1784	1.555	2.513	2.198	3.704	30S ribosomal protein S15
Ssl1918	0.920	1.174	0.419	0.532	hypothetical protein
Ssl1972	1.005	0.896	1.099	1.136	hypothetical protein
Ssl2009	0.634	0.581	0.778	0.687	hypothetical protein
Ssl2084	0.724	0.246	0.649	0.269	acyl carrier protein
Ssl2233	1.325	1.681	2.217	2.439	30S ribosomal protein S20
Ssl2245	1.008	0.772	0.741	0.558	unknown protein
Ssl2296	1.233	2.222	0.812	1.295	pterin-4 $\alpha$ -carbinolamine dehydratase
Ssl2501	1.658	2.532	0.741	0.987	unknown protein
Ssl2595	1.057	1.152	1.114	1.252	hypothetical protein
Ssl2598	2.475	2.004	2.299	1.838	photosystem II PsbH protein
Ssl2667	1.504	1.013	0.721	0.697	an assembly factor for iron-sulfur clusters
Ssl2717	1.284	1.105	2.331	1.996	hypothetical protein
Ssl2733	0.883	0.968	0.657	0.568	hypothetical protein
Ssl2781	0.815	1.099	0.625	0.800	hypothetical protein
Ssl2874	0.808	1.021	0.452	0.514	hypothetical protein
Ssl2982	0.815	0.850	1.277	1.351	probable DNA-directed RNA polymerase omega subunit
Ssl3044	1.385	1.563	0.763	0.809	probable ferredoxin
Ssl3093	0.906	0.882	1.435	1.290	phycobilisome small rod linker polypeptide
Ssl3291	1.486	1.318	1.255	1.096	hypothetical protein
Ssl3335	1.401	1.445	2.740	2.924	preprotein translocase SecE subunit
Ssl3364	1.272	0.583	0.338	0.146	CP12 polypeptide
Ssl3379	1.054	0.968	0.959	0.774	hypothetical protein
Ssl3432	0.846	0.875	1.119	1.148	30S ribosomal protein S19
Ssl3436	1.040	0.936	0.935	0.883	50S ribosomal protein L29
Ssl3437	0.801	1.272	1.420	2.137	30S ribosomal protein S17
Ssl3441	1.269	1.621	1.862	2.833	initiation factor IF-1
Ssl3451	0.828	0.838	1.082	0.924	hypothetical protein
Ssl3829	0.781	0.655	0.868	0.719	hypothetical protein
Ssr0102	1.101	1.122	0.978	0.983	hypothetical protein YCF40
Ssr0330	1.845	2.717	1.650	2.294	ferredoxin-thioredoxin reductase, variable chain
Ssr0332	1.383	1.876	1.901	2.381	hypothetical protein
Ssr0482	1.458	1.608	2.410	2.252	30S ribosomal protein S16
Ssr0657	1.361	0.999	1.205	0.819	hypothetical protein
Ssr0692	1.712	0.654	0.482	0.181	hypothetical protein
Ssr0693	0.298	0.286	0.395	0.375	unknown protein
Ssr1114	1.040	1.250	1.011	1.119	hypothetical protein
Ssr1256	0.898	0.765	1.408	1.183	hypothetical protein
Ssr1399	1.511	2.141	2.037	2.639	30S ribosomal protein S18
Ssr1407	1.038	0.695	0.997	0.659	hypothetical protein
Ssr1425	0.878	0.970	0.715	0.781	hypothetical protein YCF34
Ssr1480	0.816	0.663	1.312	0.923	putative RNA-binding protein
Ssr1528	0.759	0.633	0.538	0.617	hypothetical protein
Ssr1600	0.921	1.255	0.650	0.881	similar to anti-sigma f factor antagonist
Ssr1604	1.445	1.795	1.672	2.053	50S ribosomal protein L28
Ssr1765	2.208	3.185	1.957	2.114	hypothetical protein
Ssr1789	2.506	1.946	2.632	2.066	CAB/ELIP/HLIP-related protein HliD
Ssr1853	1.092	1.335	1.218	1.272	unknown protein
Ssr1951	0.945	1.531	0.803	0.657	hypothetical protein
Ssr2047	1.522	1.151	1.093	0.816	hypothetical protein
Ssr2049	1.294	1.724	1.054	1.377	unknown protein
Ssr2061	1.406	1.698	1.060	1.178	glutaredoxin
Ssr2067	1.490	0.543	1.305	0.469	hypothetical protein
Ssr2201	0.811	0.653	0.576	0.654	unknown protein
Ssr2406	2.304	2.950	0.760	0.959	unknown protein
Ssr2422	0.922	1.577	0.493	0.772	unknown protein
Ssr2554	1.142	1.527	1.397	1.799	hypothetical protein
Ssr2799	1.570	2.364	1.757	1.887	50S ribosomal protein L27
Ssr2831	1.048	1.037	1.684	1.541	photosystem I subunit IV
Ssr2857	0.955	1.307	1.374	1.590	mercuric transport protein periplasmic component precursor
Ssr2998	1.222	1.109	1.050	1.138	hypothetical protein
Ssr3000	1.147	1.131	1.124	1.095	hypothetical protein
Ssr3122	0.983	1.033	0.947	0.951	hypothetical protein
Ssr3188	1.062	0.953			hypothetical protein
Ssr3304	0.725	0.494	0.873	0.520	hypothetical protein
Ssr3341	0.956	1.004	0.511	0.551	hypothetical protein
Ssr3383	1.495	1.621	2.882	3.460	phycobilisome small core linker polypeptide
Ssr3402	1.107	1.071	1.704	1.372	unknown protein
Ssr3451	1.233	1.181	0.938	0.923	cytochrome b559 alpha subunit
Ssr3532	0.966	0.852	1.309	2.000	unknown protein

**Supplementary Table S3: Proteins up-regulated in the *Δslr1588* mutant upon salt exposure.**

Protein ID	Slr1588-r1 vs. Control-r1		Slr1588-r2 vs. Control-r1		Slr1588-r1 vs. Control-r2		Slr1588-r2 vs. Control-r2		Description
	Ratio	Sequence coverage	Ratio	Sequence coverage	Ratio	Sequence coverage	Ratio	Sequence coverage	
Slr1027			2.85	54.30					NADH-dependent glutamate synthase small subunit
Slr0394					2.00	52.20			phosphoglycerate kinase
Slr0260							2.19	21.30	cob(I)alamin adenosyltransferase
Slr0502							2.34	26.70	cobalamin synthesis protein cobW homolog
Slr1483	3.94	17.80	3.04	17.80	12.82	17.80	9.35	17.80	periplasmic protein, similar to transforming growth factor induced protein
Slr1566					3.40	34.30	2.39	34.30	glucosylglycerolphosphate synthase
Slr0319	2.19	24.00							beta-lactamase
Slr0746			3.37	15.40					glucosylglycerolphosphate phosphatase
Slr1894			2.38	66.00	3.73	66.00			probable DNA-binding stress protein
Slr0045					3.77	4.60			sucrose phosphate synthase
Slr0963			2.16	50.70			2.46	50.70	ferredoxin-sulfite reductase
Slr1608			2.09	13.30					putative glucose dehydrogenase-B, periplasmic protein
Slr0629			3.15	7.80			2.56	7.80	alternative photosystem I reaction center subunit X
Slr1085			2.17	32.60	3.89	32.60	2.54	32.60	glycerol-3-phosphate dehydrogenase
Slr1091			2.56	43.70			2.36	43.70	geranylgeranyl hydrogenase
Slr1214			2.51	36.90			2.40	36.90	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase 1;
Slr0171			2.71	34.90					photosystem I assembly related protein Ycf37
Slr0343			2.47	14.40					cytochrome b6-f complex subunit 4
Slr0506							2.12	52.80	light-dependent NADPH-protochlorophyllide oxidoreductase
Slr0772							2.07	14.20	light-independent protochlorophyllide reductase subunit ChlB
Slr1311			2.16	18.30					photosystem II D1 protein
Slr1434			2.38	8.80					pyridine nucleotide transhydrogenase beta subunit
Slr1739					2.04	37.70			photosystem II 13 kDa protein homolog
Slr2033			2.46	27.00			2.31	27.00	membrane-associated rubredoxin, essential for photosystem I assembly
Smr0010	3.44	18.40							cytochrome b6-f complex subunit 5
Ss12598	2.48	16.10			2.00	16.10			photosystem II PsbH protein
Ssr0330					2.72	17.30			ferredoxin-thioredoxin reductase, variable chain
Slr0157					2.31	35.70	2.42	35.70	hypothetical protein
Slr0325					2.06	16.30			hypothetical protein
Slr0723					2.45	28.30	2.66	28.30	hypothetical protein
Slr0982					2.07	82.00			hypothetical protein
Slr1541					2.20	15.70	2.21	15.70	hypothetical protein
Slr1652							3.72	12.10	hypothetical protein
Slr1739							2.34	7.20	hypothetical protein
Slr1862			2.67	25.70					hypothetical protein
Slr1863	6.76	57.00			3.42	57.00			hypothetical protein
Slr1873					2.83	18.10	2.76	66.10	hypothetical protein
Slr1884									hypothetical protein
Slr0147			3.22	20.50					hypothetical protein
Slr0664					2.31	9.90	3.16	9.90	hypothetical protein
Slr0765					2.86	20.10			hypothetical protein
Slr0876			2.24	46.90					hypothetical protein
Slr0962	2.01	11.30							hypothetical protein
Slr1161					2.06	46.20			hypothetical protein
Slr1240			3.05	13.40			3.31	13.40	hypothetical protein
Slr1259					2.66	44.80			hypothetical protein
Slr1353					2.12	9.90	2.03	9.90	hypothetical protein
Slr1391			2.15	22.40	2.02	22.40			hypothetical protein
Slr1535					3.68	11.50	2.68	11.50	hypothetical protein
Slr1732			2.31	48.30			2.27	48.30	hypothetical protein
Slr2071	2.13	19.60			3.10	19.60			hypothetical protein
Ss10242							2.02	28.90	hypothetical protein
Ss12501					2.53	36.00			hypothetical protein
Ss12717			2.33	43.60			2.00	43.60	hypothetical protein
Ssr3532							2.00	30.00	hypothetical protein
Slr0064	2.18	18.00							putative polar amino acid transport system substrate-binding protein
Slr0361					2.11	10.30			hypothetical protein
Slr1866							2.12	31.70	hypothetical protein
Slr1891					2.23	42.90	3.38	42.90	hypothetical protein
Slr0001							2.24	48.80	hypothetical protein
Slr0144			2.28	11.50					hypothetical protein
Slr0688							2.20	8.20	hypothetical protein
Slr1257					2.04	17.40			hypothetical proteins
Slr1261					4.02	44.70	2.21	44.70	hypothetical protein
Slr1363							2.02	34.60	hypothetical protein
Ss11707							2.26	26.20	Hypothetical proteins
Ssr1765	2.21	44.00			3.18	44.00			Hypothetical proteins
Slr0021							2.28	13.50	protease
Slr0708							2.16	9.20	dimethyladenosine transferase
Slr1101			2.44	42.90			3.04	42.90	30S ribosomal protein S10
Slr1740			2.79	41.70			3.01	41.70	50S ribosomal protein L19
Slr1799							2.66	60.60	50S ribosomal protein L3
Slr1800			4.59	33.80			6.85	33.80	50S ribosomal protein L4
Slr1803			2.68	41.30					50S ribosomal protein L22
Slr1804							2.38	55.00	30S ribosomal protein S3
Slr1808			3.13	63.00			3.27	63.00	50S ribosomal protein L5
Slr1810			2.04	54.70					50S ribosomal protein L6
Slr1811			2.51	54.20			3.02	54.20	50S ribosomal protein L18
Slr1813			2.44	76.90			3.44	76.90	50S ribosomal protein L15
Slr1816							2.22	54.30	30S ribosomal protein S13
Slr1822			2.37	61.30			3.08	61.30	30S ribosomal protein S9
Slr0628			2.11	19.00	2.38	19.00	2.90	19.00	30S ribosomal protein S14
Slr0744							2.06	26.20	translation initiation factor IF-2
Slr0974							2.82	47.50	initiation factor IF-3
Ss11784			2.20	25.80	2.51	25.80	3.70	25.80	30S ribosomal protein S15
Ss12233			2.22	41.20			2.44	41.20	30S ribosomal protein S20
Ss13437							2.14	30.10	30S ribosomal protein S17
Ss13441							2.83	37.30	initiation factor IF-1
Ssr0482			2.41	59.80			2.25	59.80	30S ribosomal protein S16
Ssr1399			2.04	43.70			2.64	43.70	30S ribosomal protein S18
Ssr2799					2.36	46.00			50S ribosomal protein L27
Slr1443			2.17	33.90			2.02	33.90	CTP synthetase
Slr0185					2.34	18.00			orotate phosphoribosyltransferase
Slr0537							2.11	46.80	putative sugar kinase
Slr0083			2.06	35.20					RNA helicase Light
Slr0080			2.12	38.20					ribonuclease H
Slr0653			2.24	27.30			2.60	27.30	principal RNA polymerase sigma factor SigA
Slr0005					2.25	16.30			ABC1-like
Slr1598	2.86	14.80							Mn transporter MntC

Slr0376							2.97	55.20	hypothetical protein	
Slr1105							2.21	37.30	GTP-binding protein TypA/BipA homolog	
Slr1452	6.41	39.80	5.95	39.80					sulfate transport system substrate-binding protein	
Slr1455	2.88	14.60	3.13	14.60					sulfate transport system ATP-binding protein	
Slr1919						2.27	16.80		ABC1-like	
Slr0199			2.27	57.90				2.42	57.90	plastocyanin
Slr0541			2.58	2.80						acyl-lipid desaturase (delta 9)
Slr1143								2.42	25.50	ATP-dependent helicase PerA
Slr1150			2.40	4.40						putative receptor-associated protein-related
Slr1171						2.72	85.20			glutathione peroxidase-like NADPH peroxidase, glutathione peroxidase
Slr1728	3.29	6.80	2.56	6.80		2.09	6.80			potassium-transporting P-type ATPase A chain
Slr1729			2.96	35.20						potassium-transporting P-type ATPase B chain
Ssl2296								2.22	77.10	pterin-4a-carbinolamine dehydratase
Ssr1789	2.51	43.90								CAB/ELIP/HLIP-related protein HliD

**Supplementary Table S4: Proteins down-regulated in the *Δslr1588* mutant upon salt exposure.**

Protein ID	Slr1588-r1 vs. Control-r1		Slr1588-r2 vs. Control-r1		Slr1588-r1 vs. Control-r2		Slr1588-r2 vs. Control-r2		Description
	Ratio	Sequence coverage	Ratio	Sequence coverage	Ratio	Sequence coverage	Ratio	Sequence coverage	
Slr1760					-2.51	21.90	-3.38	21.90	homoserine kinase
Slr1626							-2.23	24.00	dihydroneopterin aldolase
Slr1231			-3.44	9.80			-2.07	9.80	mannosyltransferase
Slr1306							-2.16	54.90	periplasmic protein, function unknown
Slr1533					-2.18	51.40			twitching mobility protein
Slr1550							-2.33	16.20	probable porin; major outer membrane protein
Slr0042			-2.00	23.10					probable porin; major outer membrane protein
Slr0804	-2.80	21.00			-2.88	21.00			probable D-alanyl-D-alanine carboxypeptidase
Slr0993	-2.38	10.20			-3.30	10.20			putative peptidase
Slr1063							-2.32	5.40	probable glycosyltransferase
Slr1293	-2.03	19.40	-3.84	19.40	-2.16	19.40	-3.29	19.40	chemotaxis protein CheW
Slr0945			-7.66	25.80					arsenical resistance protein ArsH homolog
Slr0946			-3.07	11.50			-3.25	11.50	arsenate reductase
Slr2017	-2.53	3.80			-2.45	3.80			type 4 pilin-like protein, essential for motility
Slr1432	-2.36	14.70							putative hydrogenase expression/formation protein HypB
Slr0596							-2.31	24.50	creatinine amidohydrolase
Slr1167			-2.48	13.50			-3.32	13.50	glycerol dehydrogenase
Slr0247							-14.55	5.30	iron-stress chlorophyll-binding protein, homologous to psbC (CP43)
Slr0248	-2.76	22.90	-3.22	22.90	-4.81	22.90	-5.89	22.90	flavodoxin
Slr0521							-2.29	12.10	NADH dehydrogenase subunit 6
Slr0685	-2.45	27.20			-2.02	27.20			thioredoxin-m, putative
Slr1322					-3.27	12.00	-3.55	12.00	ATP synthase A chain of CF0
Slr1732			-13.56	3.00					NADH dehydrogenase subunit 5
Slr1796					-2.84	14.60			cytochrome c553
Slr0331			-2.02	5.00					NADH dehydrogenase subunit 4
Slr0897			-2.95	9.90			-2.02	9.90	endo-1,4-beta-glucanase
Slr1185	-2.26	22.90			-2.46	22.90			cytochrome b6-f complex alternative iron-sulfur subunit
Ssl0020			-4.01	47.40			-3.49	47.40	ferredoxin I, essential for growth
Ssl2084							-3.72	22.80	acyl carrier protein
Slr0088							-2.69	5.80	hypothetical protein
Slr0230			-2.21	24.00					hypothetical protein
Slr0545	-2.46	4.90					-3.40	4.90	hypothetical protein
Slr0572					-2.01	5.30			hypothetical protein
Slr0596			-2.89	23.40			-2.37	23.40	hypothetical protein
Slr1735			-3.65	53.40			-3.45	53.40	hypothetical protein
Slr1882	-2.24	13.90			-3.17	13.90			hypothetical protein
Slr1913							-2.07	20.40	hypothetical protein
Slr1946			-2.21	4.20			-2.42	4.20	hypothetical protein
Slr0111	-2.51	19.70			-3.36	19.70			hypothetical protein
Slr0146					-2.94	11.20			hypothetical protein
Slr0238							-2.62	17.10	hypothetical protein
Slr0333	-2.11	44.30							hypothetical protein
Slr0479			-2.19	7.50					hypothetical protein
Slr0667			-2.45	12.70					hypothetical protein
Slr0708			-2.38	44.50					hypothetical protein
Slr0869					-2.28	15.30			hypothetical protein
Slr1110	-2.13	26.60							hypothetical protein
Slr1127			-4.52	1.90			-3.26	1.90	hypothetical protein
Slr1253			-3.48	14.40			-6.69	14.40	hypothetical protein
Slr1275			-2.79	27.50			-3.07	27.50	hypothetical protein
Slr1276			-2.25	26.90					hypothetical protein
Slr1378			-2.01	13.50					hypothetical protein
Slr1403			-5.80	2.70			-3.87	2.70	hypothetical protein
Slr1406			-2.25	42.50					hypothetical protein
Slr1407							-2.28	42.90	hypothetical protein
Slr1505					-2.37	37.40	-2.28	37.40	hypothetical protein
Slr1567			-2.16	8.10			-2.06	8.10	hypothetical protein
Slr1681	-2.01	15.30							hypothetical protein
Slr1704							-2.08	22.30	hypothetical protein
Slr1907							-2.63	10.60	hypothetical protein
Slr1915							-2.19	40.90	hypothetical protein
Slr1958			-2.27	40.00			-2.30	40.00	hypothetical protein
Slr2125			-4.85	8.30			-3.01	8.30	hypothetical protein
Ssl0467			-2.05	62.00	-2.16	62.00	-3.46	62.00	hypothetical protein
Ssl1918			-2.39	50.50					hypothetical protein
Ssr0693					-3.50	13.70			hypothetical protein
Ssr3304					-2.02	51.70			hypothetical protein
Slr1417			-2.66	7.90			-3.94	7.90	hypothetical protein
Slr1472					-2.67	18.70			hypothetical protein
Slr0044			-2.06	32.30	-2.41	32.30	-2.65	32.30	hypothetical protein
Slr0068					-2.22	6.90			hypothetical protein

SI0072					-2.36	9.30			hypothetical protein
SI0253	-2.06	15.60			-3.33	15.60			hypothetical protein
SI0445					-2.04	7.70			hypothetical protein
SI0508			-3.41	9.60					hypothetical protein
SI0588	-2.68	5.20	-2.00	5.20					hypothetical protein
SI0630			-2.31	26.20					hypothetical protein
SI0788					-5.17	20.90	-3.41	20.90	hypothetical protein
SI0827							-4.71	3.40	hypothetical protein
SI0846							-5.38	19.00	hypothetical protein
SI0872					-2.93	28.00	-3.00	28.00	hypothetical protein
SI1060							-2.01	5.20	hypothetical protein
SI1072			-2.29	6.70					hypothetical protein
SI1239			-2.13	28.10					hypothetical protein
SI1350					-2.94	1.50			hypothetical protein
SI1660							-2.62	9.00	hypothetical protein
SI1697							-2.23	10.00	hypothetical protein
Slr0006							-2.31	21.70	hypothetical protein
Slr0302							-2.22	3.10	unknown protein
Slr0431			-2.05	46.00					hypothetical protein
Slr0503							-2.81	11.60	hypothetical protein YCF66
Slr1572	-2.14	4.20							hypothetical protein
Slr1674							-2.14	6.90	hypothetical protein
Slr1885			-2.04	14.60					hypothetical protein
Slr2032	-2.47	34.30	-2.84	34.30	-3.07	34.30	-4.44	34.30	hypothetical protein
Ssl2874			-2.21	79.80					hypothetical protein
Ssl3364							-6.87	43.20	hypothetical protein
SI1549	-2.61	31.20			-3.71	31.20			salt-enhanced periplasmic protein
Slr1204	-3.24	25.20			-4.09	25.20	-2.01	25.20	protease
Slr1641							-2.66	55.80	ClpB protein
Slr0689							-2.09	25.90	hypothetical protein
SI0789					-4.59	29.70	-2.82	29.70	two-component response regulator OmpR subfamily
SI0790	-2.39	14.20	-2.20	14.20	-2.05	14.20	-2.41	14.20	two-component sensor histidine kinase
SI1296							-2.53	9.60	two-component hybrid sensor and regulator
SI1334					-2.56	10.20			two-component sensor histidine kinase
SI1708			-2.17	33.60					two-component response regulator NarL subfamily
Slr0474							-2.01	6.10	two-component response regulator CheY subfamily, regulator for phytochrome 1
Slr1588					-5.99	7.40	-4.04	7.40	two-component transcription regulator
SI0507					-2.12	14.50	-2.55	14.50	probable cation transporter
SI0689			-2.23	11.90			-4.64	11.90	Na <sup>+</sup> /H <sup>+</sup> antiporter
SI1600	-4.19	4.20	-3.02	4.20					manganese transport system membrane protein MntB
Slr0615							-2.57	7.40	ATP-binding protein of ABC transporter
Slr0875							-2.30	28.30	large-conductance mechanosensitive channel
Slr0944					-2.75	1.80			multidrug-efflux transporter
Slr1295					-2.34	63.30			iron transport system substrate-binding protein
Slr1392			-2.11	1.80					ferrous iron transport protein B
Slr1512							-5.56	22.70	sodium-dependent bicarbonate transporter
SI0037							-3.29	18.80	Sirohydrochlorin cobaltochelatase;
SI0837			-2.08	42.50					periplasmic protein, function unknown
SI1032			-2.18	14.90			-4.25	14.90	carbon dioxide concentrating mechanism protein CcmN
SI1305							-2.23	27.80	probable hydrolase
SI1558			-2.13	7.20					mannose-1-phosphate guanylyltransferase
SI1831					-2.55	8.90			glycolate oxidase subunit, (Fe-S)protein
Slr0095			-2.03	20.00					O-methyltransferase
Slr0298							-2.25	27.60	FraH protein homolog
Slr0798					-6.05	25.30	-3.16	25.30	zinc-transporting P-type ATPase (zinc efflux pump) involved in zinc tolerance
Slr1610							-2.24	18.50	putative C-3 methyl transferase