TABLE S1. Expression ratios (Log_{10}) of MR-1 genes exhibiting altered mRNA expression levels in response to 180 mM $SrCl_2$ exposure in different hierarchical clustering groups.

Group I

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so1482	TonB-dependent receptor, putative	Transport and binding proteins	-0.23	1.11	1.70	1.72
so3030	siderophore biosynthesis protein	Transport and binding proteins	0.12	1.23	1.52	1.67
so3031	siderophore biosynthesis protein, putative	Transport and binding proteins	-0.02	1.31	2.12	2.70
so3032	siderophore biosynthesis protein, putative	Transport and binding proteins	-0.16	1.16	2.31	2.14
so3033	ferric alcaligin siderophore receptor	Transport and binding proteins	-0.21	0.90	1.91	2.04
so3344	hypothetical protein	Hypothetical protein	0.88	1.83	1.84	2.11
so3667	conserved hypothetical protein	Hypothetical proteins	-0.11	1.25	2.09	2.12
so3668	conserved hypothetical protein	Hypothetical proteins	-0.12	1.06	1.77	1.89
so3669	heme transport protein	Transport and binding proteins	0.11	1.58	2.24	2.30
so3670	TonB1 protein	Transport and binding proteins	0.79	1.90	2.19	2.35
so3671	TonB system transport protein ExbB1	Transport and binding proteins	0.52	2.26	2.58	2.75
so3672	TonB system transport protein ExbD1	Transport and binding proteins	0.39	1.74	2.04	2.24
so3673	hemin ABC transporter, periplasmic hemin-binding protein	Transport and binding proteins	0.18	1.54	2.02	1.92
so3674	hemin ABC transporter, permease protein	Transport and binding proteins	0.18	1.39	1.78	1.85
so3675	hemin ABC transporter, ATP-binding protein	Transport and binding proteins	0.07	1.60	2.02	2.05
so3914	TonB-dependent receptor, putative	Transport and binding proteins	-0.42	1.02	1.68	1.58
so4636	lipoprotein, putative	Cell envelope	1.14	1.73	1.88	1.79

Group II

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0101	selenium-containing formate dehydrogenase, nitrate inducible, alpha subunit	Energy metabolism	-0.29	-0.94	-0.95	-0.94
so0108	conserved hypothetical protein	Hypothetical proteins	-0.49	-0.67	-0.92	-1.42
so0403	hypothetical protein	Hypothetical protein	-0.41	-1.03	-1.24	-0.84
so0404	hypothetical protein	Hypothetical protein	-0.29	-1.03	-1.26	-1.42
so0581	hypothetical protein	Hypothetical protein	-0.79	-1.07	-1.02	-0.93
so0903	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrB	Energy metabolism	-0.44	-1.02	-1.07	-0.81
so1258	adenylosuccinate synthetase, putative	Purines, pyrimidines, nucleosides, and nucleotides	-0.72	-1.09	-0.99	-0.69
so3542	conserved hypothetical protein	Hypothetical proteins	-0.31	-1.02	-0.83	-0.73
so3627	transcriptional regulator, TetR family	Regulatory functions	-0.50	-1.71	-1.70	-1.38
so3743	transcriptional regulator, TetR family	Regulatory functions	-0.52	-0.89	-0.91	-0.89
so3774	proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase, putative	Energy metabolism	-0.51	-1.03	-0.87	-0.70
so3891	conserved hypothetical protein	Hypothetical proteins	-0.05	-1.13	-1.04	-1.18
so4407	GGDEF family protein	Unknown function	-0.34	-0.81	-1.42	-1.00
so4473	outer membrane protein, putative	Cell envelope	-0.75	-0.99	-1.10	-1.01

Group III, Subgroup A

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0150	lipoprotein, putative	Cell envelope	0.85	0.59	0.53	0.54
so0275	N-acetyl-gamma-glutamyl-phosphate reductase	Amino acid biosynthesis	0.89	0.31	0.95	1.17
so0300	lipoprotein, putative	Cell envelope	0.45	0.87	0.77	0.78
so0451	hypothetical protein	Hypothetical protein	0.06	0.92	0.56	1.29
so0583	bacterioferritin-associated ferredoxin	Transport and binding proteins	0.56	0.57	0.63	0.74
so1188	conserved hypothetical protein	Hypothetical proteins	0.10	0.83	1.17	1.17
so1193	protein-export membrane protein SecD	Protein fate	0.28	0.84	0.78	0.82
so1194	protein-export membrane protein SecF	Protein fate	0.25	0.70	0.69	0.60
so1343	sigma-E factor negative regulatory protein	Regulatory functions	0.68	0.65	0.76	0.77
so1532	hypothetical protein	Hypothetical protein	0.25	0.30	0.63	0.83
so1580	TonB-dependent heme receptor	Transport and binding proteins	0.00	0.01	0.71	1.15
so1787	conserved hypothetical protein	Hypothetical proteins	0.90	0.69	0.83	0.97
so1807	phage shock protein A	Cellular processes	0.83	0.88	1.00	0.85
so1808	phage shock protein B	Cellular processes	0.63	0.73	0.74	0.66
so1809	phage shock protein C	Cellular processes	0.60	0.68	0.72	0.55
so1963	conserved hypothetical protein	Hypothetical proteins	0.52	0.87	0.44	0.36
so1977	conserved hypothetical protein	Hypothetical proteins	0.95	0.84	0.80	0.90
so2074	ATP phosphoribosyltransferase	Amino acid biosynthesis	0.88	0.15	0.58	1.01
so2263	Rrf2 family protein	Unknown function	-0.04	0.48	0.79	0.49
so2425	hypothetical protein	Hypothetical protein	0.12	0.55	0.75	0.63
so2426	DNA-binding response regulator	Signal transduction	0.25	0.99	1.32	1.52
so2849	acetyltransferase, GNAT family	Unknown function	0.60	0.80	0.63	0.42
so2850	acetyltransferase, GNAT family	Unknown function	0.65	0.77	0.66	0.46
so2887	disulfide bond formation protein b	Protein fate	0.16	0.43	0.74	0.72
so2924	signal peptidase I family protein	Protein fate	0.38	0.65	0.80	0.83
so3025	conserved hypothetical protein	Hypothetical proteins	-0.16	0.42	0.91	1.16
so3034	ferric iron reductase protein, putative	Energy metabolism	0.34	0.71	1.44	1.56
so3062	hypothetical protein	Hypothetical protein	0.34	0.51	1.18	1.27
so3063	sodium:alanine symporter family protein	Transport and binding proteins	0.49	0.35	0.77	0.98
so3364	conserved hypothetical protein	Hypothetical proteins	0.63	0.70	0.62	0.62
so3406	hypothetical protein	Hypothetical protein	0.39	1.04	1.04	1.21
so3407	conserved hypothetical protein	Hypothetical proteins	0.10	1.00	1.17	1.21
so3408	conserved hypothetical protein	Hypothetical proteins	-0.10	0.88	0.99	1.02
so3560	peptidase, M16 family	Protein fate	0.65	0.67	0.72	0.81
so3585	azoreductase, putative	Cellular processes	0.68	0.42	0.72	0.77
so3684	transcriptional regulator, TetR family	Regulatory functions	0.68	0.43	0.50	0.45
so3885	ATPase, AAA family	Unknown function	0.02	0.70	0.76	0.64
so3913	conserved hypothetical protein	Hypothetical proteins	-0.11	0.99	1.35	1.10
so3942	serine protease, HtrA/DegQ/DegS family	Protein fate	0.65	0.56	0.54	0.50
so4312	adenylate cyclase CyaA, putative	Regulatory functions	0.70	0.58	0.56	0.40
so4476	spheroplast protein y precursor, putative	Unknown function	0.52	0.93	0.86	0.71
so4516	ferric vibriobactin receptor	Transport and binding proteins	-0.47	0.56	1.30	1.46
so4523	iron-regulated outer membrane virulence protein	Transport and binding proteins	-0.18	0.69	1.17	1.43
so4524	transcriptional regulator, LysR family	Regulatory functions	0.41	0.50	0.74	0.82
so4558	hypothetical protein	Hypothetical protein	0.72	0.93	0.85	1.13
so4639	conserved hypothetical protein	Hypothetical proteins	0.82	0.87	0.82	0.77
so4740	conserved hypothetical protein	Hypothetical proteins	0.37	0.85	1.05	1.67

Group III, Subgroup B

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0020	fatty oxidation complex, beta subunit	Fatty acid and phospholipid metabolism	0.54	0.46	0.07	0.13
so0021	fatty oxidation complex, alpha subunit	Fatty acid and phospholipid metabolism	0.71	0.41	0.12	0.11
so0022	prolidase	Protein fate	0.50	0.08	0.09	-0.01
so0023	conserved hypothetical protein TIGR00257	Hypothetical proteins	0.33	0.02	0.07	-0.18
so0056	transporter, putative	Transport and binding proteins	0.38	0.13	-0.01	0.09
so0058	potassium uptake protein, putative	Transport and binding proteins	0.37	-0.19	-0.08	-0.11
so0060	sensor histidine kinase	Signal transduction	0.61	0.20	-0.06	0.23
so0062	hypothetical protein	Hypothetical protein	0.75	0.25	0.25	0.21
so0063	conserved hypothetical protein	Hypothetical proteins	0.62	0.21	0.12	0.18
so0071	hydrolase, alpha/beta hydrolase fold family	Unknown function	0.70	0.34	0.39	0.45
so0072	transcriptional regulator, GntR family	Regulatory functions	0.41	0.05	0.03	0.08
so0073	ABC transporter, ATP-binding protein	Transport and binding proteins	0.45	0.12	0.09	0.08
so0079	conserved hypothetical protein	Hypothetical proteins	0.30	0.03	-0.02	-0.06
so0080	conserved hypothetical protein	Hypothetical proteins	0.33	0.11	0.06	0.03
so0085	hypothetical protein	Hypothetical protein	0.37	-0.01	-0.05	-0.07
so0087	hypothetical protein	Hypothetical protein	0.51	0.05	0.02	0.07
so0088	hypothetical protein	Hypothetical protein	0.46	0.02	0.01	0.00
so0092	purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	0.48	-0.02	-0.26	-0.54
so0093	NupC family protein	Transport and binding proteins	0.48	0.04	-0.14	-0.27
so0129	conserved hypothetical protein TIGR00427	Hypothetical proteins	0.33	0.09	-0.07	0.00
so0147	hypothetical protein	Hypothetical protein	0.62	0.12	0.15	-0.03
so0148	hypothetical protein	Hypothetical protein	0.77	0.33	0.07	0.01
so0156	hypothetical protein	Hypothetical protein	0.53	0.20	0.15	0.15
so0176	general secretion pathway protein N	Protein fate	0.42	0.10	0.00	0.04
so0181	hypothetical protein	Hypothetical protein	0.36	0.12	0.05	0.00
so0182	hypothetical protein	Hypothetical protein	0.44	0.27	-0.07	-0.13
so0193	transcriptional regulator, TetR family	Regulatory functions	0.43	-0.44	0.09	0.02
so0194	acyltransferase family protein	Unknown function	0.31	-0.10	-0.18	-0.03
so0201	transposase, IS3 family, degenerate	Mobile and extrachromosomal element functions	0.34	0.03	-0.05	-0.04
so0202	conserved hypothetical protein	Hypothetical proteins	0.35	0.04	0.03	-0.06
so0210	ISSo10, transposase, authentic point mutation	Mobile and extrachromosomal element functions	0.61	0.28	0.19	0.06
so0276	acetylglutamate kinase	Amino acid biosynthesis	0.44	0.07	0.06	0.12
so0279	argininosuccinate lyase	Amino acid biosynthesis	0.34	0.05	0.07	0.11
so0296	integral membrane domain protein	Unknown function	0.34	-0.15	-0.20	-0.13
so0304	conserved hypothetical protein	Hypothetical proteins	0.38	0.08	-0.09	-0.09
so0306	hypothetical protein	Hypothetical protein	0.72	0.18	0.16	0.14
so0307	hypothetical protein	Hypothetical protein	0.32	-0.02	0.00	0.02
so0316	conserved hypothetical protein TIGR00481	Hypothetical proteins	0.50	0.34	0.32	0.35
so0317	transcriptional regulator, AraC/XylS family	Regulatory functions	0.57	0.09	0.15	0.31
so0346	transcriptional regulator. GntR family	Regulatory functions	0.72	0.69	0.17	0.07
so0355	AMP-binding protein	Unknown function	0.58	0.24	0.12	-0.06
so0367	conserved hypothetical protein	Hypothetical proteins	0.32	0.09	0.02	0.15
so0369	transcriptional regulator, LysR family	Regulatory functions	0.36	0.14	0.10	0.00
so0373	site-specific recombinase, phage integrase family, truncation+B176	DNA metabolism	0.30	-0.07	0.02	-0.02
so0384	hypothetical protein	Hypothetical protein	0.42	-0.05	-0.23	-0.18
so0386	DNA-binding protein, putative	Unknown function	0.33	0.03	0.02	-0.02
so0388	site-specific recombinase, phage integrase family	DNA metabolism	1.07	0.22	-0.01	-0.09
so0389	hypothetical protein	Hypothetical protein	0.82	0.05	0.10	-0.25
so0390	hypothetical protein	Hypothetical protein	0.43	0.10	-0.23	-0.15
so0391	hypothetical protein	Hypothetical protein	0.38	-0.02	-0.09	0.00
so0402	transcriptional regulator, LysR family	Regulatory functions	0.58	-0.09	-0.21	-0.17
so0465	hypothetical protein	Hypothetical protein	0.45	0.10	0.09	-0.07
so0479	cytochrome c, putative	Energy metabolism	0.53	0.00	0.05	0.00
so0493	hypothetical protein	Hypothetical protein	0.69	0.14	0.00	-0.10
so0496	conserved hypothetical protein	Hypothetical proteins	0.64	0.06	-0.02	-0.08
so0499	hypothetical protein	Hypothetical protein	0.92	0.24	0.22	0.08
so0572	enoyl-CoA hydratase/isomerase family protein	Fatty acid and phospholipid metabolism	0.94	0.22	0.09	0.05
so0576	PhoH family protein	Unknown function	0.76	0.11	-0.18	-0.27
so0580	hypothetical protein	Hypothetical protein	0.65	-0.35	0.49	-0.35
so0584	methyl-accepting chemotaxis protein	Cellular processes	0.46	0.08	-0.01	-0.12
so0594	hypothetical protein	Hypothetical protein	0.51	-0.12	0.26	0.13
so0617	acetylornithine aminotransferase	Amino acid biosynthesis	0.45	0.07	-0.18	-0.25
so0618	arginine N-succinyltransferase	Energy metabolism	0.55	0.22	-0.12	-0.21
so0637	conserved hypothetical protein	Hypothetical proteins	0.36	-0.04	-0.02	-0.09
so0641	prophage MuSo1, transcriptional regulator, Cro/CI family	Mobile and extrachromosomal element functions	0.41	0.05	0.07	0.09
so0650	hypothetical protein	Hypothetical protein	0.37	0.22	-0.28	-0.11
so0698	fxsA protein	Unknown function	0.33	0.14	0.26	-0.07
so0699	hypothetical protein	Hypothetical protein	0.32	0.02	0.17	-0.05
so0700	hypothetical protein	Hypothetical protein	0.41	-0.02	0.13	-0.13
so0701	transcriptional regulator, LysR family	Regulatory functions	0.43	0.16	0.13	0.19
so0702	MATE efflux family protein	Transport and binding proteins	0.50	0.22	0.24	0.30
so0705	transcriptional regulator, Cro/CI family	Regulatory functions	0.59	0.13	0.13	0.35
so0706	conserved hypothetical protein	Hypothetical proteins	0.74	0.10	0.01	0.15
so0707	hypothetical protein	Hypothetical protein	0.50	0.22	0.33	0.19
so0708	transposase, mutator family	Mobile and extrachromosomal element functions	0.45	0.31	0.30	0.27
so0713	hypothetical protein	Hypothetical protein	0.90	0.26	0.19	0.03
so0724	hypothetical protein	Hypothetical protein	0.32	0.10	-0.03	-0.01
so0726	ABC transporter, ATP-binding protein	Transport and binding proteins	0.32	0.17	0.07	0.16
so0734	conserved hypothetical protein	Hypothetical proteins	0.40	0.24	0.18	0.30
so0736	conserved hypothetical protein	Hypothetical proteins	0.33	-0.06	0.00	-0.03
so0737	TonB-dependent receptor, putative	Transport and binding proteins	0.39	0.24	-0.02	0.28
so0752	hypothetical protein	Hypothetical protein	0.86	0.52	0.56	0.79
so0758	hypothetical protein	Hypothetical protein	0.35	0.11	-0.04	0.08
so0759	hypothetical protein	Hypothetical protein	0.30	0.03	0.06	0.00
so0760	ammonium transporter	Transport and binding proteins	0.34	0.12	0.17	-0.01
so0768	conserved hypothetical protein	Hypothetical proteins	0.59	0.47	0.38	0.08
so0772	oxidoreductase, short chain dehydrogenase/reductase family	Unknown function	0.35	0.12	0.05	0.20
so0782	hypothetical protein	Hypothetical protein	0.27	-0.01	-0.04	-0.74
so0783	hypothetical protein	Hypothetical protein	0.30	-0.03	-0.15	-0.36
so0785	hypothetical protein	Hypothetical protein	0.36	-0.07	-0.13	-0.07
so0786	hypothetical protein	Hypothetical protein	1.27	0.03	-0.07	-0.17
so0787	hypothetical protein	Hypothetical protein	0.66	0.00	0.04	-0.01
so0806	alkaline phosphatase, putative	Central intermediary metabolism	0.44	0.10	-0.08	-0.07
so0838	hypothetical protein	Hypothetical protein	0.40	-0.08	0.09	0.16
so0868	hypothetical protein	Hypothetical protein	0.45	-0.04	0.02	-0.20
so0871	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	Biosynthesis of cofactors, prosthetic groups, and carriers	0.35	0.20	0.14	0.04
so0877	acetyltransferase, GNAT family	Unknown function	0.32	0.18	0.16	0.06
so0894	hypothetical protein	Hypothetical protein	0.01	-0.32	0.02	0.08
so0900	oxidoreductase, aldo/keto reductase family	Unknown function	0.32	-0.16	-0.08	0.12
so0906	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE	Energy metabolism	0.33	-0.19	-0.09	-0.04
so0921	hypothetical protein	Hypothetical protein	0.35	0.01	0.00	-0.02
so0946	conserved hypothetical protein	Hypothetical proteins	0.33	0.20	0.03	0.22
so0958	alkyl hydroperoxide reductase, C subunit	Cellular processes	0.30	-0.01	0.10	-0.28
so0964	conserved hypothetical protein	Hypothetical proteins	0.35	0.06	0.08	-0.05
so0972	conserved hypothetical protein	Hypothetical proteins	0.31	0.07	-0.05	0.08
so0973	hypothetical protein	Hypothetical protein	0.40	0.10	0.12	0.12
so0997	transcriptional regulator, LysR family	Regulatory functions	0.34	-0.01	-0.10	-0.22
so1012	NADH dehydrogenase I, K subunit	Energy metabolism	0.35	-0.04	0.06	0.22
so1027	hypothetical protein	Hypothetical protein	1.17	0.34	0.32	0.21
so1028	hypothetical protein	Hypothetical protein	0.36	0.13	0.18	-0.04
so1029	hypothetical protein	Hypothetical protein	0.42	0.05	-0.17	-0.12
so1044	amino acid ABC transporter, periplasmic amino acid-binding protein	Transport and binding proteins	0.77	0.30	0.38	0.52
so1046	transcriptional regulator, LysR family	Regulatory functions	0.39	-0.02	-0.04	0.08
so1076	hypothetical protein	Hypothetical protein	0.37	0.04	0.06	-0.07
so1077	hypothetical protein	Hypothetical protein	0.49	-0.13	-0.40	-0.34
so1085	RNA pseudouridylate synthase family protein	Protein synthesis	0.41	0.15	0.14	0.16
so1086	hypothetical protein	Hypothetical protein	0.49	0.02	0.21	0.16

so1094	conserved hypothetical protein	Hypothetical proteins	1.14	0.43	0.57	0.22
so1098	conserved hypothetical protein	Hypothetical proteins	0.36	0.20	0.22	0.02
so1114	DNA-damage-inducible protein P	Unknown function	0.71	0.31	0.29	0.36
so1118	hypothetical protein	Hypothetical proteins	0.42	-0.09	0.01	-0.05
so1219	hypothetical protein	Hypothetical proteins	0.41	-0.20	-0.06	-0.01
so1236	ATP-dependent RNA helicase, DEAD box family	Transcription	0.32	-0.08	0.03	0.07
so1258	flps family protein	Cellular processes	0.66	0.14	0.07	-0.18
so1292	hypothetical protein	Hypothetical proteins	0.44	0.43	0.31	0.20
so1293	nitrobenzene cytochrome c	Energy metabolism	0.61	0.00	0.02	0.00
so1298	acyltransferase family protein	Unknown function	0.51	0.03	0.06	0.14
so1299	conserved hypothetical protein	Hypothetical proteins	0.61	0.18	0.05	0.37
so1362	hypothetical protein	Hypothetical proteins	1.06	0.38	0.34	0.31
so1364	conserved hypothetical protein	Hypothetical proteins	1.37	0.70	0.22	0.37
so1365	transcriptional regulator, putative	Regulatory functions	0.49	0.05	-0.02	0.00
so1367	conserved hypothetical protein	Hypothetical proteins	0.93	0.55	0.20	0.38
so1368	glutamine synthetase	Amino acid biosynthesis	0.84	0.35	0.11	0.15
so1373	polyamine ABC transporter, permease protein	Transport and binding proteins	0.40	0.09	0.02	-0.25
so1374	conserved hypothetical protein	Hypothetical proteins	0.61	0.29	0.10	0.17
so1379	hypothetical protein	Hypothetical proteins	0.21	0.32	-0.15	0.20
so1387	aquaporin Z	Transport and binding proteins	0.51	0.12	0.01	0.18
so1311	transcriptional regulator	Regulatory functions	0.38	0.16	0.13	0.00
so1317	hypothetical protein	Hypothetical proteins	0.43	0.19	0.29	0.30
so1325	glutamate synthase, large subunit	Amino acid biosynthesis	0.55	0.04	0.19	0.01
so1326	conserved hypothetical protein	Hypothetical proteins	0.69	0.27	0.34	0.52
so1342	RNA polymerase sigma-24 factor	Transcription	0.37	0.15	0.13	0.18
so1384	hypothetical protein	Hypothetical proteins	0.31	0.16	-0.03	-0.07
so1398	hypothetical protein	Hypothetical proteins	0.56	0.09	-0.03	-0.07
so1419	hypothetical protein	Hypothetical proteins	0.65	0.03	0.23	-0.22
so1420	outer membrane porin, putative	Transport and binding proteins	0.50	0.00	-0.25	-0.02
so1421	fumarate reductase flavoprotein subunit	Energy metabolism	0.32	-0.06	-0.03	-0.02
so1423	hypothetical protein	Hypothetical proteins	0.79	-0.06	0.03	-0.03
so1439	site-specific recombinase, phage integrase family, interruption-N	DNA metabolism	0.55	0.19	0.20	0.16
so1440	conserved hypothetical protein	Hypothetical proteins	0.48	0.11	0.01	0.00
so1441	hypothetical protein	Hypothetical proteins	0.30	0.11	0.06	-0.10
so1442	conserved hypothetical protein	Hypothetical proteins	0.67	0.12	0.11	-0.04
so1443	conserved hypothetical protein	Hypothetical proteins	0.69	0.18	0.14	0.06
so1444	conserved hypothetical protein	Hypothetical proteins	0.50	0.16	0.03	-0.03
so1445	transcriptional regulator, CopG family	Regulatory functions	0.44	0.10	0.11	0.00
so1452	hypothetical protein	Hypothetical proteins	0.36	-0.11	0.14	0.10
so1455	DNA repair protein, RadC family	DNA metabolism	0.60	0.04	0.13	0.08
so1467	conserved hypothetical protein, authentic point mutation	Hypothetical proteins	0.50	0.22	0.30	0.33
so1470	hypothetical protein	Hypothetical proteins	0.36	0.07	0.11	0.12
so1471	site-specific recombinase, phage integrase family	DNA metabolism	0.54	-0.14	-0.20	-0.43
so1472	hypothetical protein	Hypothetical proteins	0.35	-0.07	-0.12	-0.17
so1478	methylase, putative	Unknown function	0.55	0.19	0.19	0.00
so1480	GGDEF family protein	Unknown function	0.43	0.13	0.09	0.00
so1492	peptidyl-prolyl cis-trans isomerase, cyclophilin family	Protein fate	0.31	0.19	0.15	0.05
so1493	4-alpha-glucanotransferase	Energy metabolism	0.48	0.08	0.13	0.01
so1496	glycogen phosphorylase family protein	Energy metabolism	0.32	0.11	0.04	-0.13
so1504	hypothetical protein	Hypothetical proteins	0.34	0.01	0.15	-0.08
so1523	conserved hypothetical protein	Hypothetical proteins	0.39	0.20	0.20	0.25
so1528	hypothetical protein	Hypothetical proteins	0.33	0.03	-0.03	0.02
so1557	outer membrane porin, putative	Transport and binding proteins	0.68	0.19	0.12	0.28
so1558	phosphate regulon response regulator PhoB	Signal transduction	0.76	0.36	0.26	0.34
so1559	phosphate regulon sensor protein PhoR	Signal transduction	0.32	0.13	0.08	0.06
so1560	phosphate-binding protein	Transport and binding proteins	0.96	0.58	0.49	0.75
so1562	ISSo8, transposase	Mobile and extrachromosomal element functions	0.49	0.15	0.15	0.14
so1563	glutathione peroxidase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	0.59	0.05	0.17	0.20
so1567	hypothetical protein	Hypothetical proteins	0.08	-0.40	-0.01	-0.16
so1585	fumarylacetoacetase hydrolase family protein	Unknown function	0.35	-0.03	0.03	0.23
so1586	conserved hypothetical protein	Hypothetical proteins	0.31	0.07	0.00	0.06
so1593	hypothetical protein	Hypothetical proteins	0.93	0.06	-0.07	-0.11
so1594	hypothetical protein	Hypothetical proteins	0.60	0.19	0.29	0.37
so1613	hypothetical protein	Hypothetical proteins	0.46	0.10	0.09	0.25
so1614	acetyltransferase, GNAT family	Unknown function	0.60	0.44	0.36	0.10
so1615	conserved hypothetical protein	Hypothetical proteins	0.67	0.66	0.19	-0.08
so1689	cation transport ATPase, E1-E2 family	Cellular processes	0.36	-0.12	0.01	0.17
so1694	FAD-binding protein	Unknown function	0.52	0.20	0.17	0.20
so1695	sensory box/GGDEF family protein	Regulatory functions	0.65	0.03	-0.14	-0.03
so1696	hypothetical protein	Hypothetical proteins	0.45	0.01	0.22	0.10
so1697	hypothetical protein	Hypothetical proteins	0.44	0.11	0.05	0.18
so1699	transcriptional regulator	Regulatory functions	0.38	0.19	-0.10	0.16
so1701	hypothetical protein	Hypothetical proteins	0.47	0.21	0.31	0.27
so1710	hypothetical protein	Hypothetical proteins	0.38	-0.21	-0.03	-0.09
so1718	conserved hypothetical protein	Hypothetical proteins	0.51	0.20	0.21	0.09
so1720	DnrN family protein	Unknown function	0.32	0.09	0.09	0.12
so1722	ACT domain protein	Unknown function	0.38	0.14	0.19	0.21
so1723	phosphate ABC transporter, permease protein, putative	Transport and binding proteins	0.82	0.37	0.57	0.59
so1724	phosphate ABC transporter, permease protein, putative	Transport and binding proteins	0.85	0.36	0.15	0.73
so1728	hypothetical protein	Hypothetical proteins	0.44	0.10	0.17	0.02
so1748	hypothetical protein	Hypothetical proteins	0.02	-0.30	-0.04	-0.07
so1753	hypothetical protein	Hypothetical proteins	0.36	0.38	0.44	0.28
so1780	decaheme cytochrome c MtrF	Energy metabolism	0.30	0.01	-0.03	-0.09
so1782	decaheme cytochrome c MtrD	Energy metabolism	0.63	-0.04	0.03	0.10
so1806	pap operon transcriptional activator	Regulatory functions	0.32	0.18	0.10	0.01
so1822	TonB-dependent receptor, putative	Transport and binding proteins	0.47	0.20	0.08	0.07
so1838	hypothetical protein	Hypothetical proteins	0.43	0.08	-0.13	-0.09
so1839	hypothetical protein	Hypothetical proteins	0.49	0.20	0.22	0.19
so1840	conserved hypothetical protein	Hypothetical proteins	0.49	0.15	0.14	0.09
so1841	hypothetical protein	Hypothetical proteins	0.43	0.14	0.02	0.09
so1842	hypothetical protein	Hypothetical proteins	0.50	0.15	0.13	0.17
so1867	conserved hypothetical protein	Hypothetical proteins	0.35	0.15	-0.07	0.08
so1872	lipoprotein, putative	Cell envelope	0.69	0.14	0.04	0.07
so1873	conserved hypothetical protein	Hypothetical proteins	0.67	0.10	0.12	0.04
so1874	hypothetical protein	Hypothetical proteins	0.39	-0.05	-0.11	0.00
so1899	conserved hypothetical protein	Hypothetical proteins	0.31	0.06	-0.05	-0.11
so1901	tagE protein	Cellular processes	0.45	0.47	0.42	0.41
so1943	hypothetical protein	Hypothetical proteins	0.35	-0.02	-0.04	0.07
so1955	hypothetical protein	Hypothetical proteins	0.58	0.07	0.00	-0.03
so1956	conserved hypothetical protein	Hypothetical proteins	0.78	0.21	0.05	0.12
so1957	conserved hypothetical protein	Hypothetical proteins	0.57	0.03	0.02	0.01
so1959	ABC transporter, periplasmic substrate-binding protein, putative	Transport and binding proteins	0.31	0.21	0.02	-0.04
so1965	transcriptional regulator, LysR family	Regulatory functions	0.60	0.44	0.41	0.15
so1973	conserved hypothetical protein	Hypothetical proteins	0.45	0.14	0.10	0.19
so1975	Zinc carboxypeptidase-related protein	Unknown function	0.72	0.36	0.16	0.43
so1976	hydrolase, alpha/beta fold family	Unknown function	1.20	0.84	0.68	0.73
so1983	hypothetical protein	Hypothetical proteins	0.97	0.19	0.25	0.17
so1987	ATP-dependent protease La (LON) domain protein	Protein fate	0.31	0.06	0.02	0.06
so1988	conserved hypothetical protein	Hypothetical proteins	0.39	0.01	0.07	0.14
so2002	hypothetical protein	Hypothetical proteins	1.17	0.77	0.36	0.17
so2003	hypothetical protein	Hypothetical proteins	1.31	0.29	0.18	0.04
so2004	TonB-dependent receptor C-terminal region domain protein	Unknown function	1.17	0.38	0.31	0.40
so2050	conserved hypothetical protein	Hypothetical proteins	0.35	0.10	0.14	0.25
so2068	IsoF protein (cyclase)	Amino acid biosynthesis	0.47	0.18	0.19	0.31
so2069	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	Amino acid biosynthesis	0.34	0.08	0.12	0.06
so2071	imidazoleglycerol-phosphate dehydratase/histidinol-phosphatase	Amino acid biosynthesis	0.48	0.06	0.01	0.30
so2072	histidinol-phosphate aminotransferase	Amino acid biosynthesis	0.29	-0.51	0.00	0.20
so2073	histidinol dehydrogenase	Amino acid biosynthesis	0.92	0.16	0.09	0.40
so2076	hypothetical protein	Hypothetical proteins	0.49	0.23	0.04	0.05
so2077	acyltransferase domain protein	Unknown function	0.40	0.16	0.17	0.13
so2102	hypothetical protein	Hypothetical proteins	0.52	0.27	-0.14	-0.12
so2120	chemotaxis protein CheY	Cellular processes	0.74	0.40	0.09	0.14
so2121	chemotaxis protein CheA	Cellular processes	0.60	0.18	0.03	0.11
so2128	hypothetical protein	Hypothetical proteins	0.31	0.07	0.00	0.28
so2140	glutamate decarboxylase, interruption	Central intermediary metabolism	0.49	-0.17	0.33	-0.05
so2142	glutamate decarboxylase, interruption	Central intermediary metabolism	0.31	0.00	0.18	0.05
so2153	MscR protein	Unknown function	0.32	0.16	0.10	0.23
so2158	hypothetical protein	Hypothetical proteins	0.46	-0.03	0.01	0.23
so2173	hypothetical protein	Hypothetical proteins	0.41	-0.02	0.06	-0.05
so2206	hypothetical protein	Hypothetical proteins	0.52	0.04	0.02	-0.06
so2209	hypothetical protein	Hypothetical proteins	0.62	0.10	0.07	0.03
so2219	hypothetical protein	Hypothetical proteins	0.42	0.14	0.21	0.22
so2281	alkaline phosphatase	Cell envelope	0.47	0.15	0.14	0.14
so2282	transcriptional regulator, GntR family	Regulatory functions	0.31	0.04	0.13	-0.01
so2285	conserved hypothetical protein	Hypothetical proteins	0.41	0.20	0.10	0.09
so2287	hypothetical protein	Hypothetical proteins	0.41	0.04	0.28	0.37
so2319	anti-anti-sigma factor, putative	Regulatory functions	0.55	0.11	0.11	0.13
so2374	transcriptional regulator, LysR family	Regulatory functions	0.45	0.03	0.13	0.21
so2383	hypothetical protein	Hypothetical proteins	0.44	0.40	0.37	0.15
so2395	acyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	0.42	0.14	0.06	0.22
so2419	2,4-dienoyl-CoA reductase, putative	Fatty acid and phospholipid metabolism	0.62	0.38	0.10	0.18
so2427	TonB-dependent receptor, putative	Transport and binding proteins	0.38	0.17	-0.24	-0.42
so2439	srpA-related protein	Unknown function	0.31	0.07	0.09	0.13
so2443	thiF protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	0.53	0.17	0.32	0.27
so2461	surface protein, putative, truncation	Cell envelope	0.36	0.05	0.01	0.05
so2464	surface protein, putative	Cell envelope	0.30	0.08	0.02	0.16
so2487	6-phosphogluconate dehydratase	Energy metabolism	0.36	-0.11	-0.10	-0.03
so2488	6-phosphoglucono-lactonase	Energy metabolism	0.48	-0.08	-0.14	-0.02
so2489	glucose-6-phosphate 1-dehydrogenase	Energy metabolism	0.36	-0.34	-0.25	-0.19
so2492	oxidoreductase, acyl-CoA dehydrogenase family	Unknown function	0.59	0.19	0.03	0.14
so2493	transcriptional regulator, TetR family	Regulatory functions	0.77	0.21	0.05	0.17
so2496	hypothetical protein	Hypothetical proteins	0.34	0.05	0.09	0.07
so2500	conserved hypothetical protein	Hypothetical proteins	0.52	0.10	-0.03	-0.09
so2504	conserved hypothetical protein	Hypothetical proteins	0.34	0.14	0.06	0.08
so2520	GGDEF domain protein	Unknown function	0.33	0.20	0.07	0.25
so2538	response regulator	Signal transduction	0.62	0.25	0.08	-0.05
so2539	response regulator	Signal transduction	0.90	0.35	0.27	0.04
so2540	response regulator	Signal transduction	0.66	0.14	0.15	0.09
so2541	response regulator	Signal transduction	0.52	-0.12	-0.13	-0.23
so2542	conserved hypothetical protein	Hypothetical proteins	0.68	0.20	0.05	-0.04
so2543	sensor histidine kinase	Signal transduction	0.90	0.38	0.38	0.09
so2553	conserved hypothetical protein	Hypothetical proteins	0.44	0.15	0.13	0.13
so2597	conserved hypothetical protein	Hypothetical proteins	0.53	-0.03	-0.18	-0.27
so2603	conserved hypothetical protein	Hypothetical proteins	0.62	0.29	0.36	0.24
so2604	conserved hypothetical protein	Hypothetical proteins	0.55	0.27	0.32	0.25
so2639	hypothetical protein	Hypothetical proteins	0.32	-0.06	-0.04	-0.04
so2649	cys regulon transcriptional activator	Regulatory functions	0.38	0.15	0.11	0.10
so2671	conserved hypothetical protein	Hypothetical proteins	0.32	0.01	0.13	0.05
so2678	hypothetical protein	Hypothetical proteins	0.17	-0.30	0.36	0.08
so2703	conserved hypothetical protein	Hypothetical proteins	0.30	0.09	0.14	0.37
so2719	purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	0.11	-0.30	-0.11	0.02
so2754	sodium-type flagellar protein MotY, authentic frameshift	Cellular processes	0.30	-0.11	-0.21	-0.23
so2766	conserved hypothetical protein	Hypothetical proteins	0.37	0.01	0.07	-0.12
so2788	ribosomal RNA large subunit methyltransferase A	Protein synthesis	0.49	0.24	0.31	0.24
so2866	chromosome initiation inhibitor	DNA metabolism	0.36	0.13	-0.05	0.02
so2883	conserved hypothetical protein	Hypothetical proteins	0.51	0.45	0.44	0.08
so2892	hypothetical protein	Hypothetical proteins	0.37	-0.03	0.02	0.07
so2893	conserved hypothetical protein	Hypothetical proteins	0.42	0.53	0.31	0.20
so2907	TonB-dependent receptor domain protein	Unknown function	0.30	-0.04	-0.39	-0.59
so2908	conserved hypothetical protein, degenerate	Hypothetical proteins	0.43	0.10	0.18	0.06
so2914	conserved hypothetical protein	Hypothetical proteins	0.32	-0.02	0.19	0.20
so2924	conserved hypothetical protein	Hypothetical proteins	0.37	0.05	0.05	-0.22
so2939	hypothetical protein	Hypothetical proteins	0.53	0.17	0.28	0.10
so2957	conserved hypothetical protein	Hypothetical proteins	0.28	0.01	0.16	0.45
so2990	prophage LambdaSo, transcriptional regulator, Cro/CI family	Mobile and extrachromosomal element functions	0.36	0.13	0.19	-0.01
so3019	anthranilate synthase component I	Amino acid biosynthesis	0.61	0.11	0.24	0.68
so3020	glutamine amido-transferase	Amino acid biosynthesis	0.75	-0.10	-0.04	0.09
so3021	anthranilate phosphoribosyltransferase	Amino acid biosynthesis	0.69	0.05	-0.20	0.01
so3022	indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase	Amino acid biosynthesis	0.45	-0.17	-0.07	0.00
so3038	ISSo5, transposase, truncation	Mobile and extrachromosomal element functions	0.31	0.06	0.04	0.04
so3050	outer membrane porin, putative	Transport and binding proteins	0.46	0.40	0.42	0.39
so3063	DNA topoisomerase III	DNA metabolism	0.35	0.06	0.08	0.15
so3088	fatty oxidation complex, alpha subunit	Fatty acid and phospholipid metabolism	0.63	0.23	0.11	0.11
so3089	fatty oxidation complex, beta subunit	Fatty acid and phospholipid metabolism	0.83	0.21	0.15	0.23
so3132	hypothetical protein	Hypothetical proteins	0.44	0.08	0.16	0.30
so3151	conserved hypothetical protein	Hypothetical proteins	0.37	0.02	-0.05	-0.14
so3170	conserved hypothetical protein	Hypothetical proteins	0.52	0.39	0.31	0.28
so3276	hypothetical protein	Hypothetical proteins	0.73	0.30	0.11	0.09
so3277	transcriptional regulator, TetR family	Regulatory functions	0.87	0.38	0.20	0.20
so3278	conserved hypothetical protein	Hypothetical proteins	0.69	0.20	0.02	0.09
so3279	AcrR/AcrS/AcrF family protein	Cellular processes	0.44	0.14	0.14	0.02
so3280	conserved hypothetical protein	Hypothetical proteins	0.32	-0.17	-0.18	0.00
so3289	hypothetical protein	Hypothetical proteins	0.38	-0.16	-0.23	-0.62
so3290	hypothetical protein	Hypothetical proteins	0.45	0.03	-0.15	-0.39
so3291	cytidine/deoxycytidylate deaminase family protein	Unknown function	0.48	-0.16	-0.19	-0.39
so3296	ISSo812, transposase	Mobile and extrachromosomal element functions	0.76	0.09	0.16	0.25
so3298	conserved hypothetical protein	Hypothetical proteins	0.56	-0.05	-0.11	0.06

so3300	cytochrome c	Energy metabolism	0.48	-0.07	0.07	-0.17
so3301	flavocytochrome c flavin subunit	Unknown function	0.73	0.05	-0.04	-0.15
so3320	conserved hypothetical protein	Hypothetical proteins	0.36	0.10	0.21	0.01
so3322	hypothetical protein	Hypothetical protein	0.30	0.05	0.08	-0.12
so3326	conserved hypothetical protein	Hypothetical proteins	0.51	-0.05	0.09	0.09
so3327	hypothetical protein	Hypothetical protein	0.31	0.12	0.10	0.08
so3328	acetyltransferase, GNAT family	Unknown function	0.87	0.09	0.32	-0.15
so3339	OmpA family protein	Cell envelope	0.49	0.32	0.27	0.22
so3351	twitching motility protein PilT	Cellular processes	0.33	0.05	0.00	-0.15
so3362	hypothetical protein	Hypothetical protein	0.48	-0.16	-0.02	0.00
so3373	hypothetical protein	Hypothetical protein	0.30	0.03	0.23	0.19
so3378	conserved hypothetical protein	Hypothetical proteins	0.36	0.26	0.08	0.40
so3385	transcriptional regulator, MerR family	Regulatory functions	0.39	0.41	0.29	0.14
so3386	conserved hypothetical protein	Hypothetical proteins	0.73	0.49	0.30	0.36
so3402	hypothetical protein	Hypothetical protein	0.64	0.05	0.09	-0.03
so3403	ribosomal subunit interface protein	Protein synthesis	0.63	0.51	0.43	0.08
so3414	homoserine kinase	Amino acid biosynthesis	0.38	-0.12	-0.16	-0.02
so3415	aspartokinase I/homoserine dehydrogenase, threonine-sensitive	Amino acid biosynthesis	0.24	-0.36	-0.12	-0.01
so3432	RNA polymerase sigma-38 factor	Transcription	0.42	0.18	0.14	0.03
so3452	ISSo1, transposase OrfB, interruption	Mobile and extrachromosomal element functions	1.21	0.74	0.79	0.51
so3462	DNA repair protein RecN	DNA metabolism	0.48	0.17	0.14	0.05
so3485	drug resistance transporter, Bcr/CflA family protein	Cellular processes	0.35	-0.03	0.07	0.26
so3488	transcriptional regulator, AraC/XylS family	Regulatory functions	0.37	-0.15	-0.22	-0.26
so3489	GGDEF domain protein	Unknown function	0.70	0.12	-0.05	-0.13
so3496	aldehyde dehydrogenase	Energy metabolism	0.54	0.21	0.07	0.08
so3497	aminotransferase, class III	Unknown function	0.63	0.27	0.02	0.32
so3510	methyl-accepting chemotaxis protein, putative	Hypothetical proteins	0.48	-0.05	-0.06	-0.01
so3512	conserved hypothetical protein	Hypothetical proteins	0.45	-0.01	0.03	-0.11
so3513	tryptophan halogenase, putative	Central intermediary metabolism	0.34	0.13	0.01	-0.17
so3520	type IV pilus biogenesis protein, putative	Cell envelope	0.62	0.06	-0.02	-0.01
so3521	type IV pilus biogenesis protein, putative	Cell envelope	0.52	-0.04	-0.02	0.03
so3561	conserved hypothetical protein	Hypothetical proteins	0.33	0.04	-0.20	-0.06
so3586	glyoxalase family protein	Unknown function	0.56	0.42	0.39	0.35
so3588	gpr1/fun34/yaaH family protein	Cell envelope	0.34	0.13	0.20	0.21
so3608	serine/threonine protein kinase	Regulatory functions	0.35	0.19	0.13	0.07
so3620	hypothetical protein	Hypothetical protein	0.35	-0.16	0.13	-0.04
so3664	long-chain-fatty-acid--CoA ligase	Fatty acid and phospholipid metabolism	0.38	0.29	-0.25	-0.18
so3683	coniferyl aldehyde dehydrogenase	Energy metabolism	0.67	0.16	0.08	0.12
so3686	curli production assembly/transport component CsgF, putative	Cell envelope	0.39	0.19	0.27	-0.03
so3713	conserved domain protein	Hypothetical proteins	0.40	-0.10	-0.11	-0.35
so3730	phospholipase A1 family protein, interruption	Fatty acid and phospholipid metabolism	0.34	0.05	0.03	0.03
so3747	sodium/hydrogen exchanger family/TrkA domain protein	Transport and binding proteins	0.47	0.44	0.38	0.35
so3754	conserved domain protein	Hypothetical proteins	0.48	0.10	-0.21	0.18
so3757	rubisco operon transcriptional regulator	Regulatory functions	0.51	0.21	0.13	0.17
so3775	hypothetical protein	Hypothetical protein	0.41	0.10	0.12	0.06
so3786	hypothetical protein	Hypothetical protein	0.32	0.11	0.04	-0.11
so3787	hypothetical protein	Hypothetical protein	0.45	-0.13	-0.14	-0.17
so3807	sterol desaturase family protein	Unknown function	0.30	0.09	-0.03	-0.16
so3808	conserved hypothetical protein	Hypothetical proteins	0.48	0.05	-0.03	0.06
so3817	2-dehydropantoate 2-reductase	Biosynthesis of cofactors, prosthetic groups, and carriers	0.45	0.13	0.07	0.07
so3818	hypothetical protein	Hypothetical protein	0.10	0.33	-0.33	0.02
so3823	ISSo5, transposase, interruption	Mobile and extrachromosomal element functions	0.92	0.33	0.12	0.03
so3825	ISSo5, transposase, interruption	Mobile and extrachromosomal element functions	0.76	0.18	0.17	0.04
so3846	conserved hypothetical protein	Hypothetical proteins	0.84	0.17	0.13	0.22
so3869	hypothetical protein	Hypothetical protein	0.34	0.12	0.08	0.13
so3870	disulfide bond formation protein	Protein fate	0.46	0.11	0.03	0.02
so3871	thiol:disulfide interchange protein, DsbA family	Protein fate	0.90	0.12	0.07	-0.02
so3872	arylsulfate sulfotransferase	Central intermediary metabolism	0.74	0.04	-0.22	-0.06
so3873	hypothetical protein	Hypothetical protein	1.01	0.10	0.13	0.03
so3909	conserved hypothetical protein	Hypothetical proteins	0.36	0.02	0.02	-0.05
so3972	conserved hypothetical protein	Hypothetical proteins	0.45	0.00	0.01	-0.09
so3996	hypothetical protein	Hypothetical protein	0.57	0.10	-0.14	0.13
so4046	hypothetical protein	Hypothetical protein	0.43	0.05	0.08	-0.21
so4052	transcriptional regulator, MarR family	Regulatory functions, Cellular processes	0.39	0.18	0.19	0.23
so4067	hypothetical protein	Hypothetical protein	0.46	0.02	0.12	0.08
so4070	conserved hypothetical protein	Hypothetical proteins	0.41	0.56	0.31	0.34
so4126	hypothetical protein	Hypothetical protein	0.91	0.75	0.37	0.35
so4127	hypothetical protein	Hypothetical protein	0.67	-0.03	0.01	0.08
so4134	conserved hypothetical protein	Hypothetical proteins	0.04	-0.46	-0.01	-0.12
so4140	transcriptional regulator, LysR family	Regulatory functions	0.33	0.14	0.07	0.14
so4142	cytochrome c family protein	Energy metabolism	0.49	-0.18	0.14	-0.20
so4144	cytochrome c, putative	Energy metabolism	0.37	0.06	0.06	0.09
so4153	N-ethylmaleimide reductase, putative	Central intermediary metabolism	0.41	0.08	0.13	0.11
so4154	transcriptional regulator, LysR family	Regulatory functions	0.48	0.19	0.12	0.10
so4159	hypothetical protein	Hypothetical protein	0.32	-0.15	-0.09	-0.20
so4160	flagellar biosynthesis protein, putative	Cell envelope	0.33	0.09	0.02	-0.18
so4180	hypothetical protein	Hypothetical protein	0.43	0.01	-0.11	-0.03
so4186	hypothetical protein	Hypothetical protein	0.35	0.03	-0.04	0.08
so4191	DedA family protein	Unknown function	0.61	0.25	0.12	-0.02
so4194	conserved hypothetical protein	Hypothetical proteins	0.40	-0.35	-0.05	-0.03
so4195	PAP2 family protein	Unknown function	0.52	-0.20	-0.18	-0.18
so4229	hypothetical protein	Hypothetical protein	0.40	0.03	0.00	0.12
so4233	3-isopropylmalate dehydratase, small subunit	Amino acid biosynthesis	0.23	-0.20	-0.31	-0.09
so4235	3-isopropylmalate dehydrogenase	Amino acid biosynthesis	0.48	-0.15	-0.14	-0.20
so4236	2-isopropylmalate synthase	Amino acid biosynthesis	0.39	-0.24	-0.06	-0.16
so4242	conserved hypothetical protein	Hypothetical proteins	0.59	0.12	0.02	-0.07
so4245	amino-acid acetyltransferase	Amino acid biosynthesis	0.34	0.17	0.13	0.26
so4260	conserved domain protein	Hypothetical proteins	0.60	0.22	0.14	0.13
so4261	hypothetical protein	Hypothetical protein	0.43	0.09	-0.02	-0.03
so4271	site-specific recombinase, phage integrase family, authentic frameshift	DNA metabolism	0.31	0.00	-0.07	-0.14
so4273	hypothetical protein	Hypothetical protein	0.49	0.20	0.19	0.13
so4276	hypothetical protein	Hypothetical protein	0.34	-0.20	0.03	-0.04
so4281	potassium uptake protein KtrA, putative	Transport and binding proteins	0.60	0.60	0.08	-0.34
so4282	potassium uptake protein KtrB	Transport and binding proteins	0.64	0.57	0.27	-0.29
so4283	apbE family protein	Cell envelope	0.49	0.36	0.07	-0.40
so4285	hypothetical protein	Hypothetical protein	0.86	-0.04	0.07	-0.22
so4286	chemotaxis motB protein	Cellular processes	0.41	-0.19	-0.24	-0.45
so4287	chemotaxis motA protein	Transport and binding proteins	0.39	-0.20	-0.19	-0.30
so4288	exopolysaccharide synthesis protein, putative	Unknown function	0.46	0.07	-0.09	-0.09
so4291	phosphate ABC transporter, permease protein	Transport and binding proteins	0.37	0.12	-0.04	-0.08
so4292	phosphate ABC transporter, periplasmic phosphate-binding protein	Transport and binding proteins	0.52	0.49	0.32	0.30
so4345	dihydroxy-acid dehydratase	Amino acid biosynthesis	0.50	-0.19	0.13	0.04
so4346	acetolactate synthase II, small subunit	Amino acid biosynthesis	0.52	-0.07	0.01	-0.12
so4347	acetolactate synthase II, large subunit	Amino acid biosynthesis	0.78	0.04	0.22	0.48
so4349	ketol-acid reductoisomerase	Amino acid biosynthesis	0.36	0.04	-0.09	0.00
so4350	transcriptional regulator ilvY	Regulatory functions	0.38	0.02	-0.10	-0.02
so4358	anaerobic dimethyl sulfoxide reductase, A subunit	Energy metabolism	0.76	0.22	0.05	0.07
so4359	outer membrane protein, putative	Cell envelope	1.16	0.34	0.13	0.15
so4360	decaheme cytochrome c	Energy metabolism	1.17	0.27	0.16	0.04
so4361	hypothetical protein	Hypothetical protein	1.19	0.18	0.00	-0.12
so4362	conserved hypothetical protein	Hypothetical proteins	0.95	0.12	-0.08	-0.17
so4363	hypothetical protein	Hypothetical protein	0.36	0.04	0.03	0.01
so4364	ATP-dependent DNA helicase RecG	DNA metabolism	0.39	0.18	0.07	0.12
so4372	thioester dehydrase family protein	Fatty acid and phospholipid metabolism	1.33	0.47	0.52	0.31
so4387	sensor histidine kinase	Signal transduction	0.36	0.37	-0.18	-0.01
so4389	hypothetical protein	Hypothetical protein	0.43	-0.28	-0.29	-0.10
so4393	acetyltransferase, GNAT family	Unknown function	0.32	0.17	0.10	0.15
so4394	phage shock protein E	Cellular processes	0.44	0.09	0.13	0.08
so4395	hypothetical protein	Hypothetical protein	0.41	-0.04	0.05	0.08
so4428	DNA-binding response regulator	Regulatory functions	0.60	0.33	0.15	0.08
so4429	hypothetical protein	Hypothetical protein	0.78	0.44	0.37	0.22
so4431	conserved domain protein	Hypothetical proteins	0.46	0.09	-0.13	-0.03
so4433	conserved domain protein	Hypothetical proteins	0.40	-0.05	0.22	-0.10
so4434	hypothetical protein	Hypothetical protein	0.50	0.05	0.05	0.12
so4438	hypothetical protein	Hypothetical protein	0.53	0.17	0.08	-0.25
so4443	hypothetical protein	Hypothetical protein	0.56	0.10	0.09	0.00
so4463	prolyl 4-hydroxylase, alpha subunit domain protein	Unknown function	0.36	0.11	0.14	0.05
so4471	nitrogen regulation protein	Signal transduction	0.49	0.18	0.07	-0.12
so4493	conserved hypothetical protein, authentic frameshift	Hypothetical proteins	0.42	0.11	0.16	0.43
so4514	formate dehydrogenase, iron-sulfur subunit	Energy metabolism	0.60	0.08	0.04	0.18
so4527	integral membrane domain protein	Unknown function	0.46	0.17	0.07	0.01
so4530	hypothetical protein	Hypothetical protein	0.68	0.10	0.05	0.16
so4535	hypothetical protein	Hypothetical protein	0.45	0.00	-0.13	-0.14
so4547	hypothetical protein	Hypothetical protein	0.45	0.06	0.12	0.06
so4564	TonB2 protein, putative	Transport and binding proteins	0.43	0.08	0.07	0.24
so4566	hypothetical protein	Hypothetical protein	0.38	0.00	-0.23	0.03
so4568	formate-dependent nitrite reductase, nrfD protein	Central intermediary metabolism	0.76	0.24	0.08	0.18
so4569	formate-dependent nitrite reductase, nrfC protein, truncation	Central intermediary metabolism	0.89	0.24	0.08	-0.07
so4571	transcriptional regulator, LysR family	Regulatory functions	1.07	0.16	0.06	-0.21
so4572	cytochrome c, putative	Energy metabolism	0.26	-0.33	-0.21	-0.33
so4589	transcriptional regulator, AraC family	Regulatory functions	0.32	0.02	-0.04	-0.01
so4593	hypothetical protein	Hypothetical protein	0.50	0.02	0.23	0.38
so4598	heavy metal efflux pump, CzcA family	Transport and binding proteins	0.47	-0.05	-0.11	0.20
so4603	LexA repressor	DNA metabolism	0.57	0.27	0.23	0.28
so4604	conserved hypothetical protein	Hypothetical proteins	0.64	0.34	0.26	0.34
so4606	cytochrome c oxidase, subunit II	Energy metabolism	0.47	0.37	0.33	0.38
so4607	cytochrome c oxidase, subunit I	Energy metabolism	0.33	0.53	0.26	0.33
so4620	fumarate reductase, flavoprotein subunit precursor	Energy metabolism	0.30	0.07	0.02	0.01
so4621	hypothetical protein	Hypothetical protein	0.81	-0.10	0.14	-0.05
so4625	competence protein ComF	Cellular processes	0.35	0.08	0.23	0.28
so4635	methyl-accepting chemotaxis protein	Cellular processes	0.80	0.33	0.36	0.23
so4640	antioxidant, AhpC/Tsa family	Cellular processes	0.42	0.21	0.21	0.38
so4643	hypothetical protein	Hypothetical protein	0.32	0.17	0.02	-0.01
so4644	hypothetical protein	Hypothetical protein	0.67	0.10	0.10	0.12
so4668	hypothetical protein	Hypothetical protein	0.32	-0.03	-0.17	0.00
so4683	hypothetical protein	Hypothetical protein	0.30	0.05	0.12	-0.07
so4689	conserved hypothetical protein	Hypothetical proteins	0.41	0.46	0.32	0.29
so4697	glutathione S-transferase	Cellular processes	0.37	0.10	0.11	0.02
so4742	transcriptional regulator, DeoR family	Regulatory functions	0.29	0.35	-0.14	-0.09
soa0003	type II restriction endonuclease, putative	DNA metabolism	0.35	0.10	0.03	-0.10
soa0007	hypothetical protein	Hypothetical protein	0.35	0.46	0.31	0.32
soa0008	hypothetical protein	Hypothetical protein	0.31	-0.18	-0.08	0.03
soa0010	conserved hypothetical protein	Hypothetical proteins	0.39	0.15	-0.03	0.16
soa0012	umuC protein	DNA metabolism	0.31	0.04	0.01	0.13
soa0017	ISSo9, nucleotidyltransferase domain protein	Unknown function	0.85	0.30	0.23	0.23
soa0018	ISSod9, conserved hypothetical protein	Mobile and extrachromosomal element functions	0.75	0.14	0.21	0.16
soa0019	ISSod9, DNA-invertase	Mobile and extrachromosomal element functions	0.74	0.30	0.26	0.23
soa0020	transposase family protein, truncation	Mobile and extrachromosomal element functions	0.68	0.11	0.15	0.32
soa0023	proteic killer suppressor protein	Cellular processes	0.54	0.29	0.14	0.07
soa0026	site-specific recombinase, resolvase family	DNA metabolism	0.36	0.09	0.08	0.04
soa0041	transcriptional regulator, PemK family	Regulatory functions	0.66	0.05	0.05	-0.02
soa0042	hypothetical protein	Hypothetical protein	0.68	0.09	-0.06	0.17
soa0046	hypothetical protein	Hypothetical protein	1.14	-0.02	0.08	-0.17
soa0055	hypothetical protein	Hypothetical protein	0.46	0.12	0.08	0.20
soa0059	conserved hypothetical protein	Hypothetical proteins	0.86	0.36	0.40	0.27
soa0067	hypothetical protein	Hypothetical protein	0.58	0.07	0.06	0.07
soa0072	conserved hypothetical protein	Hypothetical proteins	0.65	0.13	0.09	0.14
soa0075	hypothetical protein	Hypothetical protein	0.56	0.24	0.33	0.06
soa0084	transposase, IS6 family, truncation	Mobile and extrachromosomal element functions	0.43	0.12	0.25	0.37
soa0088	plasmid stabilization protein ParE, putative	Mobile and extrachromosomal element functions	0.77	0.18	0.15	-0.05
soa0105	ISSod8, transposase	Mobile and extrachromosomal element functions	0.47	0.14	0.24	0.18
soa0108	hypothetical protein	Hypothetical protein	0.97	0.00	0.10	0.22
soa0109	hypothetical protein	Hypothetical protein	0.76	0.33	0.09	0.33
soa0116	ISSo6, transposase, truncation	Mobile and extrachromosomal element functions	0.31	0.15	0.09	0.00
soa0117	hypothetical protein	Hypothetical protein	0.74	0.23	0.45	0.59
soa0118	conserved domain protein	Hypothetical proteins	0.31	0.00	0.02	0.05
soa0124	transposase, degenerate	Mobile and extrachromosomal element functions	0.59	0.36	0.35	0.61
soa0132	conserved hypothetical protein	Hypothetical proteins	0.35	-0.33	-0.26	-0.27
soa0137	conserved domain protein	Hypothetical proteins	0.40	0.15	0.20	0.16
soa0147	hypothetical protein	Hypothetical protein	0.77	0.12	0.06	0.02
soa0149	conserved hypothetical protein	Hypothetical proteins	0.74	0.04	0.33	0.05
soa0150	hypothetical protein	Hypothetical protein	0.48	-0.01	0.01	0.08
soa0153	heavy metal efflux pump, CzcA family	Transport and binding proteins	0.44	0.01	0.09	0.04
soa0155	conserved domain protein	Hypothetical proteins	0.42	-0.21	-0.02	0.18
soa0159	multidrug efflux transporter	Cellular processes	0.37	-0.09	-0.07	-0.04
soa0163	conserved hypothetical protein, degenerate	Hypothetical proteins	0.43	0.00	0.06	-0.03
soa0164	iron-containing alcohol dehydrogenase	Unknown function	0.44	0.10	0.07	0.17
soa0172	site-specific recombinase, resolvase family	DNA metabolism	1.13	0.39	0.15	0.04
soa0173	hypothetical protein	Hypothetical protein	1.00	0.40	0.20	0.13

Sr Group IV, Subgroup C

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so2824	carbon starvation protein A, authentic point mutation	Cellular processes	-0.67	0.49	0.50	-0.19
so3599	sulfate ABC transporter, periplasmic sulfate-binding protein	Transport and binding proteins	0.09	0.55	0.54	-0.44
so3723	adenylylsulfate kinase	Central intermediary metabolism	0.07	0.56	0.59	-0.35
so3724	hypothetical protein	Hypothetical protein	0.05	0.54	0.64	-0.55
so3725	hypothetical protein	Hypothetical protein	0.06	0.58	0.58	-0.40

so3726	sulfate adenylyltransferase, subunit 1	Central intermediary metabolism	-0.05	0.44	0.54	-0.53
so3727	sulfate adenylyltransferase, subunit 2	Central intermediary metabolism	-0.04	0.52	0.53	-0.40
so3736	phosphoadenosine phosphosulfate reductase	Central intermediary metabolism	-0.08	0.52	0.51	-0.58
so3737	sulfite reductase (NADPH) hemoprotein beta-component (cysI)	Central intermediary metabolism	-0.01	0.58	0.51	-0.54
so3738	sulfite reductase (NADPH) flavoprotein alpha-component	Central intermediary metabolism	0.00	0.52	0.56	-0.40
so3819	nitrogen regulatory protein P-II	Amino acid biosynthesis	-0.35	0.08	-0.02	-1.09
so3820	ammonium transporter, degenerate	Transport and binding proteins	-0.40	0.27	-0.01	-1.24
so4026	hypothetical protein	Hypothetical protein	-0.25	0.37	0.89	-0.75
so4410	glutamine synthetase, type I	Amino acid biosynthesis	-0.51	0.14	-0.07	-1.25
so4654	sulfate ABC transporter, permease protein	Transport and binding proteins	-0.12	0.45	0.77	-0.23
so4655	sulfate ABC transporter, ATP-binding protein	Transport and binding proteins	-0.03	0.54	0.84	-0.33

Sr Group IV, Subgroup D

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0003	tRNA modification GTPase TrmE	Protein synthesis	-0.33	-0.06	-0.09	0.12
so0051	hypothetical protein	Hypothetical protein	-0.26	0.49	0.00	-0.24
so0115	hypothetical protein	Hypothetical protein	-0.13	0.01	0.36	0.09
so0124	hypothetical protein	Hypothetical protein	-0.01	-0.05	-0.15	-0.35
so0139	ferritin	Transport and binding proteins	-0.39	0.01	0.21	0.41
so0142	3,4-dihydroxy-2-butanone 4-phosphate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.24	-0.31	-0.20	0.28
so0152	conserved hypothetical protein	Hypothetical proteins	-0.35	0.01	-0.08	0.06
so0163	chaperonin HslO	Protein fate	-0.41	0.03	0.00	0.07
so0218	preprotein translocase, SecE subunit	Protein fate	-0.38	0.01	0.09	0.21
so0219	transcription antitermination protein NusG	Transcription	-0.34	0.00	0.08	0.06
so0221	ribosomal protein L1	Protein synthesis	-0.31	-0.18	0.15	0.11
so0223	ribosomal protein L7/L12	Protein synthesis	-0.43	-0.37	-0.06	0.03
so0224	DNA-directed RNA polymerase, beta subunit	Transcription	-0.33	-0.36	-0.10	0.02
so0225	DNA-directed RNA polymerase, beta' subunit	Transcription	-0.10	-0.32	-0.10	0.11
so0227	ribosomal protein S7	Protein synthesis	-0.25	-0.42	-0.10	-0.02
so0228	translation elongation factor G	Protein synthesis	-0.26	-0.33	0.00	0.09
so0230	ribosomal protein S10	Protein synthesis	-0.42	-0.12	0.05	0.16
so0232	ribosomal protein L4	Protein synthesis	-0.42	-0.04	-0.03	-0.15
so0235	ribosomal protein S19	Protein synthesis	-0.16	-0.32	-0.06	0.09
so0236	ribosomal protein L22	Protein synthesis	-0.23	-0.44	-0.10	0.11
so0237	ribosomal protein S3	Protein synthesis	-0.19	-0.41	-0.08	0.20
so0238	ribosomal protein L16	Protein synthesis	-0.17	-0.41	-0.10	0.12
so0240	ribosomal protein S17	Protein synthesis	-0.23	-0.50	-0.02	0.05
so0241	ribosomal protein L14	Protein synthesis	-0.41	-0.46	-0.09	-0.01
so0242	ribosomal protein L24	Protein synthesis	-0.48	-0.46	-0.21	-0.05
so0244	ribosomal protein S14	Protein synthesis	-0.51	-0.45	-0.20	-0.03
so0245	ribosomal protein S8	Protein synthesis	-0.42	-0.52	-0.22	-0.04
so0246	ribosomal protein L6	Protein synthesis	-0.41	-0.52	-0.23	-0.01
so0247	ribosomal protein L18	Protein synthesis	-0.33	-0.46	-0.19	-0.01
so0248	ribosomal protein S5	Protein synthesis	-0.32	-0.53	-0.13	-0.03
so0249	ribosomal protein L30	Protein synthesis	-0.26	-0.54	-0.05	0.02
so0250	ribosomal protein L15	Protein synthesis	-0.21	-0.44	-0.07	0.11
so0251	preprotein translocase, SecY subunit	Protein fate	-0.19	-0.34	-0.03	0.13
so0252	ribosomal protein L36	Protein synthesis	-0.23	-0.43	0.01	0.08
so0253	ribosomal protein S13	Protein synthesis	-0.27	-0.33	-0.06	0.10
so0254	ribosomal protein S11	Protein synthesis	-0.30	-0.37	-0.05	0.05
so0255	ribosomal protein S4	Protein synthesis	-0.30	-0.37	-0.06	0.07
so0256	DNA-directed RNA polymerase, alpha subunit	Transcription	-0.25	-0.36	-0.04	0.09
so0268	cytochrome c-type biogenesis protein CcmH	Energy metabolism	-0.33	-0.14	-0.01	-0.07
so0294	tryptophanyl-tRNA synthetase	Protein synthesis	-0.31	0.00	-0.02	0.05
so0328	hypothetical protein	Hypothetical protein	-0.33	-0.04	0.37	0.41
so0456	immunogenic-related protein	Unknown function	0.06	0.27	0.06	-0.32
so0608	ubiquinol-cytochrome c reductase, iron-sulfur subunit	Energy metabolism	-0.31	0.06	-0.12	-0.30
so0620	conserved hypothetical protein	Hypothetical proteins	-0.23	0.07	-0.15	-0.43
so0632	ATP-dependent helicase HrpB	Unknown function	-0.42	-0.10	-0.06	0.06
so0910	hypothetical protein	Hypothetical protein	0.00	0.38	0.36	-0.19
so0929	S-adenosylmethionine synthetase	Central intermediary metabolism	-0.37	-0.08	0.02	0.05
so0962	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.12	-0.04	-0.03
so0991	peptide chain release factor 2, programmed frameshift	Protein synthesis	-0.35	-0.01	0.00	0.05
so0993	hypothetical protein	Hypothetical protein	-0.37	0.02	-0.07	-0.06
so0995	hypothetical protein	Hypothetical protein	-0.30	-0.32	0.16	0.20
so0996	glyoxalase family protein	Unknown function	-0.20	-0.20	0.36	0.38
so1034	iron-compound ABC transporter, permease protein	Transport and binding proteins	-0.62	0.00	0.19	-0.18
so1065	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA	Protein fate	-0.42	-0.06	0.01	0.02
so1075	conserved hypothetical protein	Hypothetical proteins	-0.43	-0.04	0.04	0.13
so1139	peptidyl-prolyl cis-trans isomerase FklB	Protein fate	-0.37	0.06	-0.02	0.03
so1161	lipoic acid synthetase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.32	-0.04	0.01	-0.03
so1167	rod shape-determining protein RodA	Cell envelope	-0.48	-0.06	-0.06	-0.06
so1169	conserved hypothetical protein TIGR00246	Hypothetical proteins	-0.43	0.04	-0.01	0.14
so1170	iojap domain protein	Unknown function	-0.46	-0.03	0.06	0.17
so1185	conserved hypothetical protein TIGR00092	Hypothetical proteins	-0.52	-0.13	-0.07	-0.07
so1202	conserved hypothetical protein	Hypothetical proteins	-0.47	-0.13	0.06	-0.01
so1203	N utilization substance protein A	Transcription	-0.43	-0.38	-0.17	-0.05
so1217	deoxyribose-phosphate aldolase	Purines, pyrimidines, nucleosides, and nucleotides	-0.38	-0.48	-0.28	-0.07
so1287	conserved hypothetical protein	Hypothetical proteins	-0.39	-0.16	0.00	0.22
so1288	ribosomal protein S21	Protein synthesis	-0.45	-0.03	0.10	0.23
so1306	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.04	-0.03	-0.02
so1315	tyrosyl-tRNA synthetase	Protein synthesis	-0.54	-0.05	-0.05	0.02
so1346	GTP-binding protein LepA	Unknown function	-0.56	0.00	0.10	0.10
so1347	signal peptidase I	Protein fate	-0.53	-0.02	0.10	0.10
so1348	ribonuclease III	Transcription	-0.48	-0.16	0.04	-0.10
so1349	GTP-binding protein Era	Cellular processes	-0.50	-0.14	-0.06	-0.09
so1350	DNA repair protein RecO	DNA metabolism	-0.33	-0.13	-0.03	-0.13
so1351	pyridoxal phosphate biosynthetic protein PdxJ	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.41	-0.16	-0.17	0.19
so1357	ribosomal protein S16	Protein synthesis	-0.38	-0.40	-0.14	0.04
so1358	16S rRNA processing protein RimM	Transcription	-0.34	-0.29	-0.10	-0.04
so1359	tRNA (guanine-N1)-methyltransferase	Protein synthesis	-0.36	-0.51	-0.14	-0.04
so1360	ribosomal protein L19	Protein synthesis	-0.16	-0.55	-0.09	0.04
so1381	conserved hypothetical protein	Hypothetical proteins	-0.40	0.05	0.00	-0.10
so1383	ATP-dependent RNA helicase, DEAD box family	Transcription	-0.54	-0.35	-0.13	0.11
so1476	small protein A	Unknown function	-0.15	-0.13	0.29	0.33
so1525	deoxyxylulose-5-phosphate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.30	-0.05	-0.06	-0.03
so1537	hypothetical protein	Hypothetical protein	-0.33	0.02	-0.03	-0.03
so1538	isocitrate dehydrogenase, NAD-dependent	Energy metabolism	-0.38	0.02	0.14	-0.03
so1569	integral membrane domain protein	Unknown function	-0.19	0.02	0.15	-0.35
so1597	conserved hypothetical protein	Hypothetical proteins	-0.17	-0.40	-0.05	-0.04
so1601	hypothetical protein	Hypothetical protein	-0.11	-0.04	0.19	-0.56
so1625	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	Amino acid biosynthesis	-0.35	0.06	0.03	-0.09
so1629	ribosomal protein S2	Protein synthesis	-0.34	-0.39	-0.09	-0.05
so1630	translation elongation factor Ts	Protein synthesis	-0.28	-0.39	-0.11	0.02
so1690	ABC transporter, ATP-binding protein	Transport and binding proteins	-0.63	-0.08	0.01	0.21
so1737	hypothetical protein	Hypothetical protein	-0.26	0.06	0.08	-0.35
so1752	hypothetical protein	Hypothetical protein	-0.38	-0.06	-0.10	0.19
so1784	ferrous iron transport protein B	Transport and binding proteins	-0.39	0.08	0.26	0.41
so1786	glutaminyl-tRNA synthetase	Protein synthesis	-0.44	-0.10	-0.06	-0.09
so1798	peptidyl-prolyl cis-trans isomerase D	Protein fate	-0.58	-0.03	-0.02	-0.17
so1800	conserved hypothetical protein	Hypothetical proteins	-0.59	-0.08	-0.02	0.01
so1835	conserved hypothetical protein	Hypothetical proteins	-0.51	-0.05	0.19	0.36
so1836	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.07	0.09	0.24
so1868	conserved hypothetical protein	Hypothetical proteins	-0.36	-0.05	0.05	-0.04
so1869	hypothetical protein	Hypothetical protein	-0.34	0.05	0.17	0.21
so1883	acetyltransferase, GNAT family	Unknown function	-0.31	0.02	0.04	-0.28
so1910	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.43	-0.13	-0.10	0.14
so1927	succinate dehydrogenase, cytochrome b556 subunit	Energy metabolism	-0.30	0.05	-0.06	-0.26
so2006	NifR3/Smm1 family protein	Unknown function	-0.48	-0.18	-0.14	0.19
so2018	adenylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.45	0.15	0.27	0.02
so2039	conserved domain protein	Hypothetical proteins	-0.35	0.14	0.12	0.18
so2059	hypothetical protein	Hypothetical protein	-0.32	-0.08	0.03	-0.04
so2085	phenylalanyl-tRNA synthetase, alpha subunit	Protein synthesis	-0.31	-0.02	0.13	0.25
so2137	conserved hypothetical protein TIGR00427	Hypothetical proteins	-0.24	-0.03	0.27	0.43
so2189	conserved hypothetical protein	Hypothetical proteins	-0.26	-0.04	0.17	0.34
so2257	lipoprotein releasing system transmembrane protein LolE	Transport and binding proteins	-0.38	-0.07	-0.01	0.01
so2261	RNA methyltransferase, TrmH family, group 1	Protein synthesis	-0.42	-0.03	0.07	0.01
so2262	serine acetyltransferase	Amino acid biosynthesis	-0.32	-0.10	0.01	-0.15
so2264	cysteine desulfurase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.32	0.08	0.33	0.19
so2268	chaperone protein HscA	Protein fate	-0.29	-0.06	0.35	0.27
so2269	ferredoxin, 2Fe-2S	Energy metabolism	-0.39	-0.18	0.23	0.19
so2294	hypothetical protein	Hypothetical protein	-0.51	0.02	0.07	0.00
so2299	threonyl-tRNA synthetase	Protein synthesis	-0.44	-0.33	-0.27	-0.09
so2320	chemotaxis protein CheA, interruption-N	Cellular processes	-0.11	-0.11	-0.17	-0.35
so2353	hypothetical protein	Hypothetical protein	-0.33	0.02	0.08	0.17
so2360	conserved hypothetical protein	Hypothetical proteins	-0.48	-0.34	-0.17	-0.10
so2387	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.31	-0.09	0.07
so2391	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.10	0.04	0.15
so2402	ribosomal protein S1	Protein synthesis	-0.31	-0.17	0.15	0.12
so2403	cytidylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.35	-0.02	0.05	0.05
so2436	methyltransferase, putative	Unknown function	-0.34	-0.03	-0.06	0.03
so2451	conserved hypothetical protein	Hypothetical proteins	-0.39	-0.05	0.08	0.25
so2474	carbonic anhydrase family protein	Unknown function	-0.60	0.03	0.00	-0.08
so2480	hypothetical protein	Hypothetical protein	-0.31	-0.35	-0.10	-0.08
so2529	hypothetical protein	Hypothetical protein	-0.46	-0.01	0.05	0.14
so2530	polypeptide deformylase	Protein fate	-0.16	-0.01	0.07	0.30
so2581	long-chain-fatty-acid--CoA ligase	Fatty acid and phospholipid metabolism	-0.30	-0.06	-0.03	-0.06
so2587	delta-aminolevulinic acid dehydratase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.29	-0.04	0.30	0.46
so2612	DNA polymerase III, delta prime subunit	DNA metabolism	-0.34	0.03	-0.02	-0.03
so2616	deoxycytidine triphosphate deaminase	Purines, pyrimidines, nucleosides, and nucleotides	-0.31	-0.02	-0.01	0.02
so2634	conserved hypothetical protein	Hypothetical proteins	-0.40	-0.05	-0.01	-0.06
so2644	phosphoenolpyruvate synthase	Energy metabolism	-0.58	0.10	0.12	-0.17
so2645	conserved hypothetical protein	Hypothetical proteins	-0.47	0.00	-0.06	-0.06
so2646	phospho-2-dehydro-3-deoxyheptonate aldolase, trp-sensitive	Amino acid biosynthesis	-0.42	0.01	0.04	0.10
so2685	prophage MuSo2, major head subunit, putative	Mobile and extrachromosomal element functions	-0.23	-0.32	-0.08	0.18
so2688	hypothetical protein	Hypothetical protein	-0.41	-0.13	-0.09	0.21
so2691	hypothetical protein	Hypothetical protein	-0.43	-0.06	-0.02	0.06
so2746	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.05	-0.03	-0.19
so2778	3-oxoacyl-(acyl-carrier-protein) synthase III	Fatty acid and phospholipid metabolism	-0.69	-0.07	0.02	0.03
so2779	fatty acid/phospholipid synthesis protein PlsX	Fatty acid and phospholipid metabolism	-0.44	-0.11	-0.03	-0.12
so2780	ribosomal protein L32	Protein synthesis	-0.62	-0.19	0.00	-0.17
so2781	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.04	0.04	0.18
so2787	cold shock domain family protein	Cellular processes	-0.32	-0.06	0.03	0.02
so2796	conserved hypothetical protein	Hypothetical proteins	-0.30	-0.15	0.00	-0.12
so2797	conserved hypothetical protein	Hypothetical proteins	-0.30	-0.46	-0.21	-0.04
so2806	conserved hypothetical protein	Hypothetical proteins	-0.35	-0.30	-0.13	-0.06
so2858	conserved hypothetical protein	Hypothetical proteins	0.00	0.28	0.02	-0.33
so2876	hypothetical protein	Hypothetical protein	-0.07	0.26	0.35	-0.47
so2881	superoxide dismutase, Fe	Cellular processes	-0.02	-0.12	-0.23	-0.47
so2903	cysteine synthase A	Amino acid biosynthesis	-0.14	0.12	0.06	-0.32
so2911	formate transporter, putative	Transport and binding proteins	-0.27	-0.47	-0.28	-0.06
so2968	conserved hypothetical protein	Hypothetical proteins	-0.15	-0.06	0.31	0.19
so2989	prophage LambdaSo, transcriptional regulator, Cro/CI family	Mobile and extrachromosomal element functions	-0.15	-0.21	0.28	-0.37
so3007	hypothetical protein	Hypothetical protein	-0.24	-0.20	-0.15	0.36
so3037	exodeoxyribonuclease III	DNA metabolism	-0.36	-0.02	0.11	0.06
so3110	protein-export membrane protein SecF	Protein fate	-0.36	-0.08	0.07	0.00
so3111	protein-export membrane protein SecD	Protein fate	-0.32	-0.08	0.11	0.02
so3112	preprotein translocase, YajC subunit	Protein fate	-0.60	-0.19	0.09	-0.12
so3113	queuine tRNA-ribosyltransferase	Protein synthesis	-0.42	0.02	0.17	0.00
so3119	hypothetical protein	Hypothetical protein	-0.37	-0.41	-0.12	0.08
so3120	oxidoreductase, Gfo/Idh/MocA family	Unknown function	-0.32	0.01	-0.05	-0.09
so3159	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.07	-0.08	-0.10
so3193	polysaccharide biosynthesis protein	Cell envelope	-0.36	0.00	-0.04	-0.02
so3292	GMP synthase	Purines, pyrimidines, nucleosides, and nucleotides	-0.47	-0.49	-0.20	-0.13
so3306	sensor histidine kinase	Signal transduction	-0.10	-0.08	-0.12	-0.37
so3308	GTP-binding protein EngA	Unknown function	-0.39	-0.01	0.08	0.14
so3310	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.03	0.03	0.04
so3336	hypothetical protein	Hypothetical protein	-0.07	0.13	0.36	-0.13
so3361	conserved hypothetical protein	Hypothetical proteins	-0.44	0.06	0.05	-0.01
so3365	glutaminase A	Energy metabolism	-0.39	-0.03	-0.01	-0.06
so3367	conserved hypothetical protein TIGR00091	Hypothetical proteins	-0.35	-0.12	0.02	-0.05
so3420	cytochrome c'	Energy metabolism	-0.12	-0.04	-0.21	-0.40
so3441	CTP synthase	Purines, pyrimidines, nucleosides, and nucleotides	-0.38	0.02	0.02	0.04
so3464	thiamin-monophosphate kinase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.34	-0.01	-0.08	-0.03
so3537	ribosomal protein S20	Protein synthesis	-0.38	-0.03	0.13	0.19
so3595	sensor protein RstB, putative	Signal transduction	-0.36	0.04	-0.05	0.03
so3602	sulfate ABC transporter, ATP-binding protein	Transport and binding proteins	-0.06	0.00	-0.01	-0.32
so3629	expression activator-related protein	Unknown function	0.16	0.32	0.34	-0.27
so3630	hypothetical protein	Hypothetical protein	-0.13	-0.08	-0.15	-0.40
so3642	methyl-accepting chemotaxis protein	Cellular processes	-0.52	-0.16	-0.03	-0.22
so3651	ribosomal protein L27	Protein synthesis	-0.48	0.01	0.15	0.21
so3652	ribosomal protein L21	Protein synthesis	-0.45	-0.09	0.11	0.37
so3695	dihydroorotase, homodimeric type	Purines, pyrimidines, nucleosides, and nucleotides	-0.44	-0.37	-0.25	-0.03
so3739	hypothetical protein	Hypothetical protein	-0.07	0.33	0.34	-0.23
so3740	NAD(P) transhydrogenase, alpha subunit	Energy metabolism	-0.32	-0.05	-0.08	-0.48
so3741	NAD(P) transhydrogenase, beta subunit	Energy metabolism	-0.22	-0.01	0.04	-0.52
so3802	ABC transporter, ATP-binding protein	Transport and binding proteins	-0.45	0.02	0.36	-0.07

so3803	hypoxanthine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.36	-0.03	-0.04	-0.17
so3811	lipoprotein, putative	Cell envelope	-0.34	-0.02	-0.05	-0.12
so3837	ribose-phosphate pyrophosphokinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.50	0.07	0.04	0.01
so3851	hypothetical protein	Hypothetical proteins	-0.42	-0.13	-0.03	-0.15
so3852	conserved hypothetical protein	Hypothetical proteins	-0.49	-0.06	-0.03	-0.07
so3859	cyclic nucleotide phosphodiesterase, putative	DNA metabolism	0.02	-0.08	-0.23	-0.42
so3912	TIM-barrel protein, yjbN family	Unknown function	-0.50	0.05	0.15	0.21
so3937	adenylosuccinate synthetase	Purines, pyrimidines, nucleosides, and nucleotides	-0.35	-0.01	-0.01	0.04
so3989	hypothetical protein	Hypothetical proteins	-0.10	-0.47	0.03	-0.10
so4037	hypothetical protein	Hypothetical protein	-0.12	-0.43	0.18	0.16
so4095	maf protein	Cellular processes	-0.36	0.01	-0.02	-0.05
so4096	rod shape-determining protein MreD	Cell envelope	-0.55	0.18	0.10	0.07
so4097	rod shape-determining protein MreC	Cell envelope	-0.43	0.20	0.17	0.14
so4123	arginyl-tRNA synthetase	Protein synthesis	-0.35	0.07	-0.01	0.13
so4211	preprotein translocase, SecA subunit	Protein fate	-0.36	0.01	0.03	-0.10
so4220	cell division protein ftsW	Cellular processes	-0.19	-0.05	0.30	0.08
so4247	ribosomal protein L28	Protein synthesis	-0.49	-0.14	0.01	0.04
so4248	DNA repair protein RadC	DNA metabolism	-0.32	0.00	0.26	0.07
so4313	hypothetical protein	Hypothetical proteins	-0.31	0.11	0.19	0.19
so4334	inner membrane protein, putative	Cell envelope	-0.36	0.00	0.12	0.04
so4367	acyltransferase family protein	Unknown function	-0.38	-0.06	-0.04	-0.16
so4370	membrane protein, putative	Cell envelope	-0.38	-0.06	0.01	-0.14
so4371	conserved hypothetical protein	Hypothetical proteins	-0.32	0.03	0.03	-0.01
so4415	hypothetical protein	Hypothetical proteins	-0.29	-0.41	-0.07	-0.05
so4422	siderophore receptor, putative, degenerate	Transport and binding proteins	-0.51	-0.46	-0.24	-0.12
so4467	conserved hypothetical protein	Hypothetical proteins	0.00	0.05	-0.21	-0.41
so4472	nitrogen regulation protein NR(I)	Signal transduction	0.05	0.00	-0.05	-0.47
so4540	hypothetical protein	Hypothetical proteins	-0.37	0.03	-0.09	0.06
so4609	cytochrome c oxidase subunit III	Energy metabolism	-0.39	-0.02	0.09	0.03
so4618	prolyl oligopeptidase family protein	Protein fate	-0.47	-0.09	0.01	0.13
so4645	hypothetical protein	Hypothetical proteins	-0.24	-0.03	0.03	0.32
so4691	hypothetical protein	Hypothetical proteins	-0.50	0.01	-0.11	0.03
so4830	oligopeptidase A	Protein fate	-0.11	0.01	0.31	-0.18
so4717	sensor histidine kinase	Signal transduction	-0.09	-0.38	-0.08	-0.01
soa0060	acetyltransferase, GNAT family	Unknown function	-0.13	0.04	-0.07	-0.47

Sr Group IV, Subgroup E

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0050	rhodanese domain protein	Unknown function	-0.24	0.19	0.39	-0.02
so0052	protein-export protein SecB	Protein fate	-0.21	0.24	0.40	-0.05
so0053	glycerol-3-phosphate dehydrogenase (NAD(P)+)	Energy metabolism	-0.25	0.27	0.49	0.12
so0059	transcriptional regulatory protein KdpE	Regulatory functions	0.35	0.19	0.13	-0.09
so0069	transport protein, putative	Transport and binding proteins	0.23	0.25	0.23	0.38
so0070	ATP-binding transport protein NasA	Transport and binding proteins	0.45	0.33	0.37	0.44
so0082	carboxymuconolactone decarboxylase family protein	Energy metabolism	0.34	0.25	0.29	0.32
so0090	hypothetical protein	Hypothetical proteins	0.13	0.07	0.34	0.57
so0153	hypothetical protein	Hypothetical proteins	-0.09	0.13	0.18	0.35
so0154	conserved hypothetical protein	Hypothetical proteins	0.15	-0.08	0.07	0.52
so0157	proline/glutamate symporter	Transport and binding proteins	0.08	0.07	0.20	0.43
so0159	hypothetical protein	Hypothetical protein	0.11	0.21	0.28	0.35
so0164	heat shock protein 15	Protein synthesis	0.07	0.18	0.30	0.23
so0184	conserved hypothetical protein	Hypothetical proteins	0.31	0.41	0.20	0.06
so0185	conserved hypothetical protein	Hypothetical proteins	0.47	0.38	0.24	0.10
so0277	ornithine carbamoyltransferase	Amino acid biosynthesis	0.33	0.31	0.33	0.27
so0301	conserved hypothetical protein TIGR00006	Hypothetical proteins	0.14	0.20	0.06	0.34
so0313	thiol:disulfide interchange protein DsbA	Protein fate	0.04	0.16	0.20	0.37
so0334	conserved hypothetical protein	Hypothetical proteins	0.08	-0.11	0.14	0.35
so0335	conserved hypothetical protein	Hypothetical proteins	0.25	0.07	0.24	0.32
so0336	conserved hypothetical protein	Hypothetical proteins	0.45	0.29	0.35	0.54
so0342	conserved hypothetical protein	Hypothetical proteins	0.03	0.56	0.25	0.17
so0343	aconitate hydratase 1	Energy metabolism	0.20	0.60	0.34	0.18
so0344	methylcitrate synthase	Energy metabolism	0.34	0.58	0.21	-0.04
so0345	methylisocitrate lyase	Energy metabolism	0.34	0.44	0.15	-0.04
so0349	magnesium chelatase family protein	Unknown function	0.47	0.28	0.16	0.19
so0361	guanylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	0.05	0.18	0.17	0.36
so0370	conserved hypothetical protein	Hypothetical proteins	-0.01	0.30	0.32	0.31
so0371	conserved hypothetical protein	Hypothetical proteins	-0.13	0.49	0.39	0.24
so0372	HAD-superfamily hydrolase, subfamily IA, variant 1 protein family	Unknown function	0.16	0.42	0.40	0.37
so0447	hypothetical protein	Hypothetical protein	0.16	0.40	0.46	0.55
so0448	hypothetical protein	Hypothetical protein	0.08	0.32	0.38	0.52
so0449	conserved hypothetical protein	Hypothetical proteins	-0.17	0.40	0.54	0.71
so0450	major facilitator family protein	Transport and binding proteins	-0.22	0.31	0.44	0.44
so0452	thioredoxin 2	Energy metabolism	0.07	0.29	0.34	0.18
so0462	hypothetical protein	Hypothetical protein	0.23	0.25	0.33	0.27
so0512	3-dehydroquinate dehydratase, type II	Amino acid biosynthesis	0.18	0.27	0.20	0.30
so0516	hypothetical protein	Hypothetical protein	0.44	0.25	0.33	0.45
so0541	metallo-beta-lactamase family protein	Unknown function	0.08	0.17	0.21	0.48
so0602	tRNA delta(2-isopentenyl)pyrophosphate transferase	Protein synthesis	0.02	0.26	0.39	0.12
so0604	GTP-binding protein HflX	Unknown function	-0.02	0.27	0.36	0.15
so0685	MfK protein	Protein fate	-0.08	0.27	0.35	0.08
so0843	transposase, putative	Mobile and extrachromosomal element functions	0.22	0.23	0.23	0.35
so0646	hypothetical protein	Hypothetical protein	0.11	0.26	0.15	0.35
so0648	conserved hypothetical protein	Hypothetical proteins	0.14	0.29	0.29	0.40
so0651	conserved hypothetical protein	Hypothetical proteins	0.07	0.23	0.16	0.40
so0668	prophage MuSo1_F protein, putative	Mobile and extrachromosomal element functions	0.23	0.01	0.43	0.37
so0683	hypothetical protein	Hypothetical proteins	0.09	0.26	0.33	-0.04
so0687	hypothetical protein	Hypothetical protein	0.32	0.29	0.08	0.08
so0716	monoheme cytochrome c, putative	Energy metabolism	0.13	0.41	0.04	0.20
so0723	hypothetical protein	Hypothetical protein	0.21	0.23	0.35	0.29
so0735	hypothetical protein	Hypothetical protein	0.36	0.25	0.07	0.07
so0747	ferredoxin--NADP reductase	Energy metabolism	0.22	0.26	0.22	0.30
so0761	nitrogen regulatory protein P-II 1	Amino acid biosynthesis	0.15	0.35	0.31	-0.05
so0763	hypothetical protein	Hypothetical protein	0.18	0.21	0.56	0.07
so0769	arginine repressor	Regulatory functions	0.25	0.42	0.23	0.16
so0798	conserved hypothetical protein	Hypothetical proteins	0.03	0.26	0.32	0.38
so0811	inosine-uridine preferring nucleoside hydrolase family protein	Purines, pyrimidines, nucleosides, and nucleotides	-0.13	0.01	0.18	0.52
so0820	HlyD family secretion protein	Transport and binding proteins	0.07	0.23	0.43	0.60
so0821	ABC transporter, ATP-binding/permease protein	Transport and binding proteins	0.02	0.26	0.27	0.59
so0822	outer membrane efflux family protein	Transport and binding proteins	0.00	0.22	0.33	0.40
so0864	transcriptional regulator, LuxR family	Regulatory functions	0.33	0.31	0.11	0.13
so0867	serine protease, subtilase family	Protein fate	-0.05	0.14	0.33	0.15
so0916	transcriptional regulator, MarR family	Cellular processes	0.36	0.27	0.53	0.62
so0984	hypothetical protein	Hypothetical protein	0.07	0.17	0.17	0.36
so1023	hypothetical protein	Hypothetical protein	0.22	0.42	0.45	0.45
so1060	AgfH family protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	0.07	0.50	0.11	0.18
so1126	chaperone protein DnaK	Protein fate	0.04	0.07	0.44	0.07
so1127	chaperone protein DnaJ	Protein fate	-0.11	0.11	0.31	0.11
so1146	hypothetical protein	Hypothetical protein	0.33	0.21	0.34	0.57
so1164	D-alanyl-D-alanine carboxypeptidase	Cell envelope	0.34	0.37	0.44	0.51
so1189	conserved hypothetical protein	Hypothetical proteins	-0.44	0.34	0.71	0.67
so1190	conserved hypothetical protein	Hypothetical proteins	-0.76	0.20	0.71	0.64
so1195	conserved hypothetical protein TIGR00253	Hypothetical proteins	-0.23	0.37	0.11	0.25
so1196	ribosomal RNA large subunit methyltransferase J	Protein synthesis	0.21	0.39	0.55	0.18
so1245	membrane protein, putative	Cell envelope	-0.02	0.18	0.40	0.61
so1303	hypothetical protein	Hypothetical protein	0.08	-0.02	0.03	0.35
so1303	hypothetical protein	Hypothetical protein	-0.06	0.35	0.25	0.31
so1344	sigma-E factor regulatory protein RseB	Regulatory functions	0.43	0.48	0.52	0.46
so1345	sigma-E factor regulatory protein RseC	Regulatory functions	0.30	0.56	0.48	0.35
so1376	conserved hypothetical protein	Hypothetical proteins	0.08	0.45	0.33	0.15
so1450	conserved hypothetical protein	Hypothetical proteins	0.33	0.26	0.68	0.49
so1453	conserved hypothetical protein	Hypothetical proteins	0.31	0.47	0.49	0.35
so1479	hypothetical protein	Hypothetical proteins	0.15	0.27	0.38	0.04
so1483	malate synthase A	Energy metabolism	0.38	0.59	0.45	0.35
so1484	isocitrate lyase	Energy metabolism	0.24	0.55	0.49	0.43
so1524	heat shock protein GrpE	Protein fate	-0.34	0.33	0.43	0.15
so1549	exodeoxyribonuclease IX	DNA metabolism	0.34	0.22	0.23	0.12
so1550	conserved hypothetical protein	Hypothetical proteins	0.36	0.36	0.29	0.35
so1554	protease, putative, degenerate	Protein fate	0.33	0.18	0.33	0.38
so1571	hypothetical protein	Hypothetical protein	-0.12	-0.16	0.03	0.35
so1577	glutathione S-transferase family protein	Cellular processes	0.35	0.24	0.25	0.20
so1636	membrane-associated zinc metalloprotease, putative	Protein fate	0.06	0.33	0.33	0.43
so1646	GGDEF family protein	Unknown function	0.10	0.35	0.27	0.41
so1648	cold shock domain family protein	Cellular processes	-0.11	0.05	0.29	0.34
so1650	conserved hypothetical protein	Hypothetical proteins	-0.01	0.21	0.40	0.20
so1676	homoserine O-succinyltransferase	Amino acid biosynthesis	0.19	0.24	0.23	0.38
so1687	transcriptional regulator, MerR family	Regulatory functions	0.27	0.53	0.09	0.09
so1706	ABC transporter, ATP-binding protein, putative	Transport and binding proteins	0.21	0.11	0.06	0.39
so1716	transporter, LysE family	Transport and binding proteins	0.10	0.16	0.03	0.32
so1717	hypothetical protein	Hypothetical protein	0.46	0.27	0.15	0.14
so1725	phosphate ABC transporter, ATP-binding protein	Transport and binding proteins	0.12	0.18	0.20	0.32
so1755	phosphoglycoromanose/phosphomannomutase family protein	Energy metabolism	0.03	0.30	0.38	0.77
so1756	glyoxalase family protein	Unknown function	-0.02	0.28	0.36	0.47
so1757	conserved hypothetical protein	Hypothetical proteins	-0.03	0.28	0.27	0.45
so1758	conserved hypothetical protein	Hypothetical proteins	0.10	0.20	0.19	0.39
so1760	AsfC family protein	Transport and binding proteins	0.12	-0.01	0.07	0.45
so1762	transcriptional regulator, AraC/XylS family	Regulatory functions	0.23	0.20	0.17	0.32
so1764	conserved hypothetical protein	Hypothetical proteins	0.37	0.08	0.21	0.10
so1765	hypothetical protein	Hypothetical protein	0.31	0.15	0.29	0.08
so1770	glycerate kinase, putative	Hypothetical proteins	-0.06	0.07	0.00	0.30
so1773	permease, CstP family	Transport and binding proteins	-0.20	-0.03	0.58	0.69
so1773	catalase-related protein, authentic point mutation	Cellular processes	-0.40	0.44	0.39	0.56
so1783	ferrous iron transport protein A	Transport and binding proteins	-0.25	0.52	0.49	0.74
so1796	ATP-dependent protease La	Protein fate	-0.08	0.10	0.31	0.18
so1810	conserved hypothetical protein	Hypothetical proteins	0.38	0.36	0.34	0.31
so1811	conserved hypothetical protein	Hypothetical proteins	0.22	0.37	0.31	0.20
so1813	DNA-binding protein, putative	Unknown function	0.45	0.40	0.15	-0.01
so1820	DNA polymerase II	DNA metabolism	0.25	0.35	0.31	0.31
so1843	hypothetical protein	Hypothetical protein	0.44	0.24	0.19	0.13
so1863	DNA-binding protein, HU family	DNA metabolism	0.10	0.33	0.17	-0.01
so1881	HlyD family-related protein	Unknown function	-0.16	0.15	0.45	0.74
so1884	membrane protein, putative	Cell envelope	0.26	0.22	0.26	0.31
so1900	pgsE protein, putative	Fatty acid and phospholipid metabolism	0.18	0.41	0.28	-0.03
so1916	transcriptional regulator, LysR family	Regulatory functions	0.35	0.25	0.20	0.21
so1926	citrate synthase	Energy metabolism	0.01	0.37	0.32	0.10
so1937	ferric uptake regulation protein	Regulatory functions	0.09	0.25	0.29	0.32
so1939	conserved hypothetical protein	Hypothetical proteins	0.14	0.32	0.13	-0.11
so1944	hypothetical protein	Hypothetical proteins	0.48	0.27	0.21	0.21
so1961	maltose O-acetyltransferase	Cellular processes	0.05	0.37	0.39	0.10
so1962	4-hydroxyphenylpyruvate dioxygenase	Energy metabolism	0.16	0.68	0.35	0.15
so1964	hypothetical protein	Hypothetical protein	0.11	0.91	0.38	0.02
so1967	hypothetical protein	Hypothetical protein	0.11	0.05	0.11	0.31
so1980	phosphorthioyl transferase domain protein	Purines, pyrimidines, nucleosides, and nucleotides	0.36	0.38	0.31	0.40
so1981	conserved hypothetical protein	Hypothetical proteins	0.36	0.28	0.23	0.31
so2010	hypothetical protein	Hypothetical protein	-0.07	-0.01	0.16	0.50
so2016	heat shock protein HtpG	Protein fate	0.00	0.26	0.45	0.21
so2017	conserved hypothetical protein	Hypothetical proteins	-0.10	0.52	0.65	0.25
so2045	cation efflux family protein	Transport and binding proteins	-0.23	0.39	0.62	0.81
so2046	transcriptional regulator, MarR family	Regulatory functions	-0.16	0.32	0.52	0.61
so2108	periplasmic glucans biosynthesis protein MdoH	Cellular processes	0.09	0.20	0.16	0.31
so2154	transposase, IS110 family, degenerate	Mobile and extrachromosomal element functions	0.49	0.26	0.14	0.17
so2159	TonB domain protein	Unknown function	0.24	0.29	0.48	0.29
so2163	hypothetical protein	Hypothetical protein	0.35	0.29	0.17	0.10
so2188	polyphosphate kinase, truncation	Central intermediary metabolism	0.18	0.17	0.34	0.53
so2191	cystathionine beta-lyase	Amino acid biosynthesis	-0.22	0.13	0.10	0.37
so2196	LPXTG-site transpeptidase family protein	Protein fate	0.18	0.36	0.06	0.20
so2203	diacylglycerol kinase	Fatty acid and phospholipid metabolism	-0.16	-0.02	0.26	0.36
so2204	DNA ligase, ATP-dependent	DNA metabolism	0.41	0.25	0.22	0.16
so2227	hypothetical protein	Hypothetical protein	0.30	0.36	0.23	0.30
so2230	hypothetical protein	Hypothetical protein	0.34	0.35	0.41	0.57
so2277	16 kDa heat shock protein A	Protein fate	0.46	0.50	0.86	0.18
so2278	acetolactate synthase III, small subunit	Amino acid biosynthesis	0.18	0.29	0.31	0.27
so2279	acetolactate synthase III, large subunit	Amino acid biosynthesis	0.24	0.33	0.34	0.40
so2295	MATE efflux family protein	Transport and binding proteins	-0.02	0.16	0.16	0.32
so2352	hsr protein, putative	Unknown function	0.11	0.22	0.30	0.36
so2370	site-specific recombinase, phage integrase family	DNA metabolism	0.54	0.39	0.58	0.43
so2375	membrane protein, putative	Cell envelope	0.36	0.33	0.44	0.61
so2444	phosphomethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	0.18	0.44	0.49	0.48
so2445	thiamin biosynthesis protein ThiC	Biosynthesis of cofactors, prosthetic groups, and carriers	0.28	0.20	0.22	0.35
so2446	hypothetical protein	Hypothetical protein	0.37	0.43	0.46	0.54
so2501	radical activating enzyme	Protein fate	0.03	0.00	0.04	0.37
so2503	erulB protein	Unknown function	-0.10	0.06	0.05	0.32
so2508	RnfAE/NqrDE family protein	Energy metabolism	0.02	0.22	0.31	0.42
so2509	iron-sulfur cluster-binding protein	Energy metabolism	-0.02	0.38	0.36	0.45
so2511	membrane protein, putative	Cell envelope	-0.18	0.13	0.21	0.41
so2523	conserved hypothetical protein	Hypothetical proteins	0.37	0.13	0.35	0.19
so2532	methylated-DNA--protein--cysteine methyltransferase, putative	DNA metabolism	0.15	0.37	0.26	0.28
so2536	oxidoreductase, acyl-CoA dehydrogenase family	Unknown function	0.29	0.33	0.08	0.13

so2562	conserved hypothetical protein	Hypothetical proteins	0.14	0.14	0.17	0.33
so2598	conserved hypothetical protein	Hypothetical proteins	0.25	0.19	0.47	0.34
so2652	prophage MuSo2, transcriptional regulator, Cro/CI family	Mobile and extrachromosomal element functions	0.13	0.37	0.29	0.05
so2654	transposase, putative	Mobile and extrachromosomal element functions	0.20	0.08	0.20	0.38
so2655	prophage MuSo2, DNA transposition protein, putative	Mobile and extrachromosomal element functions	0.06	0.16	0.19	0.36
so2656	hypothetical protein	Hypothetical protein	0.05	0.21	0.31	0.38
so2657	hypothetical protein	Hypothetical protein	0.03	0.31	0.13	0.21
so2659	hypothetical protein	Hypothetical protein	0.03	0.15	0.17	0.31
so2660	conserved hypothetical protein	Hypothetical proteins	-0.02	0.26	0.30	0.44
so2661	hypothetical protein	Hypothetical protein	-0.05	0.23	0.20	0.42
so2663	conserved hypothetical protein	Hypothetical proteins	0.01	0.03	0.34	0.25
so2664	hypothetical protein	Hypothetical protein	0.06	0.38	0.47	0.38
so2666	hypothetical protein	Hypothetical protein	0.22	0.23	0.28	0.40
so2667	conserved hypothetical protein	Hypothetical proteins	0.19	0.36	0.38	0.33
so2682	hypothetical protein	Hypothetical protein	-0.13	-0.07	0.08	0.44
so2683	hypothetical protein	Hypothetical protein	0.18	0.21	0.33	0.31
so2711	conserved hypothetical protein	Hypothetical proteins	0.35	0.27	0.29	0.22
so2714	hypothetical protein	Hypothetical protein	0.10	0.30	0.33	0.37
so2725	transcriptional regulator, LuxR family	Regulatory functions	0.06	0.39	0.34	0.23
so2739	8-amino-7-oxononanoate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.09	0.13	0.30	0.35
so2757	membrane protein, putative	Cell envelope	-0.33	0.08	0.26	0.34
so2768	acyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	0.22	0.21	0.31	0.27
so2769	conserved hypothetical protein	Hypothetical proteins	0.31	0.34	0.24	0.06
so2785	ribonuclease E	Transcription	-0.37	0.17	0.30	0.34
so2837	hypothetical protein	Hypothetical protein	0.10	-0.06	0.02	0.39
so2841	hypothetical protein	Hypothetical protein	0.30	0.34	0.26	0.25
so2855	exonuclease	Unknown function	0.07	0.29	0.32	0.15
so2882	conserved hypothetical protein	Hypothetical proteins	0.35	0.25	0.11	0.17
so2884	conserved hypothetical protein	Hypothetical proteins	0.27	0.25	0.34	0.13
so2888	hypothetical protein	Hypothetical protein	0.11	0.28	0.41	0.45
so2923	sodium/glutamate symporter	Transport and binding proteins	0.41	0.43	0.33	0.53
so2927	ABC transporter, ATP-binding protein	Transport and binding proteins	0.09	0.27	0.40	0.48
so2928	acyl-CoA thioesterase I, putative	Fatty acid and phospholipid metabolism	0.19	0.26	0.27	0.38
so2938	hypothetical protein	Hypothetical protein	0.25	0.26	0.34	0.18
so2948	prophage LambdaSo, tail assembly protein K, putative	Mobile and extrachromosomal element functions	0.22	-0.01	0.04	0.32
so2958	conserved hypothetical protein	Hypothetical proteins	0.23	0.02	0.08	0.36
so2960	conserved hypothetical protein	Hypothetical proteins	0.13	0.04	0.06	0.41
so2967	conserved hypothetical protein	Hypothetical proteins	0.17	0.18	0.24	0.44
so2978	prophage LambdaSo, site-specific recombinase, phage integrase family	DNA metabolism	0.05	0.21	0.25	0.31
so2980	hypothetical protein	Hypothetical protein	0.10	0.21	0.21	0.35
so2983	hypothetical protein	Hypothetical protein	0.09	0.16	0.20	0.38
so2984	conserved hypothetical protein	Hypothetical proteins	0.13	0.21	0.17	0.40
so2985	prophage LambdaSo, replication protein O	Mobile and extrachromosomal element functions	0.14	0.11	0.26	0.31
so2991	conserved hypothetical protein	Hypothetical proteins	0.35	0.32	0.23	0.03
so2992	hypothetical protein	Hypothetical protein	0.34	0.34	0.31	0.11
so2997	hypothetical protein	Hypothetical protein	0.28	0.38	0.35	0.42
so2998	hypothetical protein	Hypothetical protein	0.14	0.20	0.24	0.36
so3002	conserved hypothetical protein	Hypothetical proteins	0.07	0.12	0.46	0.70
so3004	prophage LambdaSo, DNA modification methyltransferase, putative	Mobile and extrachromosomal element functions	0.10	0.34	0.41	0.44
so3009	hypothetical protein	Hypothetical protein	0.10	-0.07	0.10	0.30
so3017	TrpH family protein	Unknown function	0.04	0.15	0.33	0.21
so3027	hypothetical protein	Hypothetical protein	0.18	0.31	0.44	0.28
so3048	isoquinoline 1-oxidoreductase, beta subunit, putative	Energy metabolism	0.19	0.31	0.29	0.27
so3085	conserved domain protein	Hypothetical proteins	-0.06	0.33	0.28	0.17
so3087	conserved hypothetical protein	Hypothetical proteins	0.11	0.27	0.30	0.31
so3090	MoxR domain protein	Unknown function	0.33	0.46	0.44	0.64
so3091	conserved hypothetical protein	Hypothetical proteins	0.14	0.35	0.34	0.37
so3092	hypothetical protein	Hypothetical protein	0.02	0.30	0.37	0.35
so3093	von Willebrand factor type A domain protein	Unknown function	-0.04	0.30	0.34	0.30
so3094	TPR domain protein	Unknown function	-0.17	0.24	0.34	0.25
so3096	RNA polymerase sigma-70 factor, ECF subfamily	Transcription	-0.11	0.31	0.30	0.19
so3115	hypothetical protein	Hypothetical protein	0.23	0.24	0.35	0.25
so3161	glucose-1-phosphate thymidylyltransferase-related protein	Unknown function	0.14	0.17	0.40	0.36
so3164	conserved hypothetical protein	Hypothetical proteins	0.34	0.07	0.16	0.12
so3168	DnaJ domain protein	Protein fate	0.34	0.25	0.22	0.20
so3169	transcriptional regulator, Cro/CI family	Regulatory functions	0.39	0.21	0.22	0.10
so3240	flagellar hook-associated protein FlgK, degenerate	Cellular processes	-0.02	0.31	0.29	0.15
so3241	flagellar protein FlgJ	Cellular processes	0.22	0.38	0.28	0.23
so3245	flagellar basal-body rod protein FlgF	Cellular processes	-0.04	0.34	0.29	0.43
so3250	flagellar basal-body rod protein FlgB	Cellular processes	-0.12	0.28	0.32	0.52
so3335	conserved hypothetical protein	Hypothetical proteins	0.15	0.24	0.35	0.01
so3342	conserved hypothetical protein	Hypothetical proteins	0.10	0.20	0.55	0.59
so3343	conserved hypothetical protein	Hypothetical proteins	-0.04	0.37	0.42	0.58
so3369	conserved hypothetical protein	Hypothetical proteins	-0.11	0.47	0.49	0.36
so3377	conserved hypothetical protein	Hypothetical proteins	0.07	0.31	0.11	0.16
so3382	oxidoreductase, short-chain dehydrogenase/reductase family	Unknown function	0.16	0.31	0.23	0.17
so3383	transcriptional regulator-related protein	Unknown function	0.13	0.44	0.36	0.31
so3384	deoxyribodipyrimidine photolyase	DNA metabolism	0.30	0.42	0.30	0.30
so3395	hypothetical protein	Hypothetical protein	0.33	0.27	0.05	-0.12
so3405	hypothetical protein	Hypothetical protein	0.20	0.39	0.17	0.25
so3421	b-type cytochrome, putative	Energy metabolism	0.22	0.17	0.25	0.32
so3461	transporter, putative	Transport and binding proteins	0.42	0.25	0.21	0.17
so3483	HlyD family secretion protein	Transport and binding proteins	-0.36	0.28	0.20	0.31
so3491	HDIG domain protein	Unknown function	0.42	0.21	0.17	0.15
so3498	methylmalonic acid semialdehyde dehydrogenase, interruption	Energy metabolism	0.32	0.16	0.15	0.16
so3501	conserved hypothetical protein	Hypothetical proteins	-0.07	0.25	0.29	0.42
so3559	glutamate--cysteine ligase	Biosynthesis of cofactors, prosthetic groups, and carriers	0.04	0.39	0.50	0.21
so3562	proton/glutamate symporter, putative	Transport and binding proteins	0.01	0.52	0.44	0.02
so3577	clpB protein	Protein fate	0.25	0.35	0.51	0.17
so3583	ribosomal small subunit pseudouridine synthase A	Protein synthesis	0.16	0.29	0.36	0.37
so3587	hypothetical protein	Hypothetical protein	0.33	0.25	0.46	0.34
so3603	secretion protein, HlyD family	Protein fate	0.14	0.34	0.21	0.22
so3617	hypothetical protein	Hypothetical protein	0.32	0.40	0.44	0.39
so3643	hypothetical protein	Hypothetical protein	0.25	0.16	0.40	0.08
so3665	ABC transporter, ATP-binding/permease protein, putative	Transport and binding proteins	-0.03	0.13	0.55	0.53
so3676	hypothetical protein	Hypothetical protein	-0.29	0.15	0.63	0.53
so3687	curli production assembly/transport component CsgE, putative	Cellular processes	0.33	0.36	0.30	0.27
so3688	nitrogen regulation protein NtrY, putative	Signal transduction	0.32	0.25	0.22	0.22
so3728	uroporphyrin-III C-methyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.04	0.23	0.63	-0.07
so3758	conserved hypothetical protein	Hypothetical proteins	0.24	0.06	0.17	0.32
so3763	spermine/spermidine synthase family protein	Central intermediary metabolism	0.05	0.26	0.33	0.28
so3764	conserved hypothetical protein	Hypothetical proteins	0.49	0.56	0.50	0.48
so3765	conserved hypothetical protein	Hypothetical proteins	0.35	0.35	0.47	0.48
so3766	hypothetical protein	Hypothetical protein	0.37	0.42	0.40	0.41
so3785	hypothetical protein	Hypothetical protein	0.20	0.35	0.20	0.03
so3822	conserved hypothetical protein	Hypothetical proteins	0.25	0.24	0.25	0.39
so3854	ISSod12, transposase	Mobile and extrachromosomal element functions	0.26	0.43	0.42	0.38
so3875	ISSo2, transposase OrfB, truncation	Mobile and extrachromosomal element functions	0.26	0.27	0.33	0.20
so3884	site-specific recombinase, phage integrase family	DNA metabolism	0.25	0.21	0.22	0.38
so3886	hypothetical protein	Hypothetical protein	-0.01	0.18	0.32	0.14
so3890	methyl-accepting chemotaxis protein	Cellular processes	0.07	0.20	0.25	0.31
so3910	hypothetical protein	Hypothetical protein	0.44	0.20	0.40	0.25
so3943	protease DegS	Protein fate	0.24	0.37	0.32	0.33
so3988	aerobic respiration control protein ArcA	Regulatory functions	-0.12	-0.03	0.16	0.39
so4040	integral membrane domain protein	Unknown function	-0.06	0.07	0.24	0.31
so4043	TonB domain protein	Unknown function	0.05	0.60	0.43	0.23
so4054	5,10-methylenetetrahydrofolate reductase	Amino acid biosynthesis	-0.14	0.20	0.22	0.36
so4055	aspartokinase II/homoserine dehydrogenase, methionine-sensitive	Amino acid biosynthesis	0.23	0.31	0.40	0.55
so4056	cystathionine gamma-synthase	Amino acid biosynthesis	0.18	0.33	0.31	0.65
so4130	conserved hypothetical protein	Hypothetical proteins	0.31	0.44	0.42	0.46
so4136	decarboxylase, pyridoxal-dependent	Unknown function	0.22	0.22	0.26	0.49
so4156	hypothetical protein	Hypothetical protein	-0.04	0.32	0.17	0.03
so4161	hypothetical protein	Hypothetical protein	0.19	0.16	0.39	0.08
so4162	ATP-dependent protease HslV	Protein fate	-0.05	0.25	0.52	0.25
so4163	heat shock protein HslVU, ATPase subunit HslU	Cellular processes	-0.05	0.23	0.49	0.15
so4214	UDP-3-0-acyl N-acetylglucosamine deacetylase	Cell envelope	0.30	0.30	0.28	0.27
so4244	hypothetical protein	Hypothetical protein	0.29	0.38	0.34	0.30
so4274	undecaprenol kinase, putative	Cellular processes	0.21	0.32	0.09	-0.02
so4316	hemY protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	0.33	0.15	0.18	0.10
so4324	GGDEF domain protein	Unknown function	-0.23	0.32	0.14	0.14
so4365	hypothetical protein	Hypothetical protein	0.39	0.28	0.14	0.15
so4400	proline iminopeptidase, putative	Protein fate	0.45	0.27	0.16	0.15
so4401	ribonuclease BN	Transcription	0.37	0.22	0.16	0.17
so4427	sensor histidine kinase	Signal transduction	0.36	0.28	0.02	-0.06
so4448	molybdenum ABC transporter, periplasmic molybdenum-binding protein	Transport and binding proteins	0.28	0.17	0.10	0.32
so4466	methyl-accepting chemotaxis protein	Cellular processes	0.38	0.37	0.20	0.04
so4477	transcriptional regulatory protein CpxR	Regulatory functions	0.25	0.32	0.36	0.54
so4478	sensor protein CpxA	Signal transduction	0.08	0.16	0.12	0.31
so4483	cytochrome b, putative	Energy metabolism	0.13	0.18	0.18	0.38
so4484	cytochrome c-type protein Shp	Energy metabolism	0.03	0.12	0.22	0.38
so4539	serine protease, subtilase family	Protein fate	0.26	0.30	0.33	0.20
so4543	hypothetical protein	Hypothetical protein	0.24	0.44	0.28	0.15
so4562	conserved hypothetical protein	Hypothetical proteins	0.31	0.31	0.35	0.56
so4563	conserved hypothetical protein	Hypothetical proteins	0.23	0.26	0.26	0.39
so4567	transcriptional regulator, AsnC family	Regulatory functions	0.25	0.20	0.41	0.35
so4583	RNA polymerase sigma-32 factor	Transcription	0.53	0.41	0.48	0.48
so4592	hypothetical protein	Hypothetical protein	0.52	0.25	0.39	0.53
so4611	conserved hypothetical protein	Hypothetical proteins	0.41	0.35	0.18	0.15
so4612	conserved hypothetical protein	Hypothetical proteins	0.24	0.31	0.07	-0.06
so4624	transcriptional regulator, LuxR family	Regulatory functions	-0.07	0.16	0.47	0.76
so4627	hypothetical protein	Hypothetical protein	0.40	0.27	0.26	0.29
so4628	sulfatase	Unknown function	-0.02	0.19	0.35	0.48
so4650	conserved hypothetical protein	Hypothetical proteins	0.26	0.41	0.78	-0.02
so4651	conserved hypothetical protein	Hypothetical proteins	0.02	0.18	0.76	-0.03
so4652	sulfate ABC transporter, periplasmic sulfate-binding protein	Transport and binding proteins	0.16	0.71	0.90	0.02
so4653	sulfate ABC transporter, permease protein	Transport and binding proteins	0.12	0.29	0.54	-0.13
so4656	hypothetical protein	Hypothetical protein	0.06	0.58	0.68	-0.09
so4690	conserved hypothetical protein	Hypothetical proteins	0.26	0.41	0.28	0.39
so4698	conserved hypothetical protein	Hypothetical proteins	0.25	0.20	0.34	0.19
so4715	conserved hypothetical protein	Hypothetical proteins	0.01	-0.03	-0.09	0.37
so4734	sensory box protein	Regulatory functions	0.27	0.35	0.27	0.20
so4736	hypothetical protein	Hypothetical protein	-0.18	0.00	0.29	0.40
so4743	TonB-dependent receptor, putative	Transport and binding proteins	-0.78	0.00	0.57	0.64
soa0009	hypothetical protein	Hypothetical protein	0.25	0.35	0.16	0.32
soa0062	hypothetical protein	Hypothetical protein	0.38	0.13	0.22	0.10
soa0069	conserved hypothetical protein	Hypothetical proteins	0.44	0.25	0.23	0.19
soa0134	ISSo8, transposase, degenerate	Mobile and extrachromosomal element functions	0.44	0.34	0.20	0.16
soa0166	transposase, mutator family, truncation	Mobile and extrachromosomal element functions	0.07	0.36	0.10	-0.02

Sr Group IV, Subgroup F

Gene	Gene Product	Role Category	t=5 min	t=30 min	t=60 min	t=90 min
so0002	proton/peptide symporter family protein	Transport and binding proteins	-0.36	-0.06	-0.20	-0.30
so0004	inner membrane protein, 60 kDa	Cell envelope	-0.75	-0.17	-0.17	-0.13
so0005	conserved hypothetical protein TIGR00278	Hypothetical proteins	-0.62	-0.06	-0.14	-0.12
so0006	ribonuclease P protein component	Transcription	-0.63	-0.21	-0.11	-0.11
so0007	ribosomal protein L34	Protein synthesis	-0.39	-0.15	-0.02	0.14
so0011	DNA gyrase, B subunit	DNA metabolism	-0.33	-0.25	-0.18	-0.16
so0014	glycyl-tRNA synthetase, beta subunit	Protein synthesis	-0.34	-0.15	-0.14	0.00
so0027	protoporphyrinogen oxidase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.46	-0.54	-0.42	-0.41
so0028	potassium uptake protein TrkH	Transport and binding proteins	-0.32	-0.44	-0.41	-0.44
so0076	hypothetical protein	Hypothetical protein	-0.71	-0.50	-0.34	-0.24
so0091	hypothetical protein	Hypothetical protein	0.24	-0.27	-0.37	-0.50
so0102	formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	Energy metabolism	-0.21	-0.76	-0.91	-0.78
so0103	formate dehydrogenase, nitrate-inducible, cytochrome b556 subunit	Energy metabolism	-0.15	-0.69	-0.75	-0.72
so0104	fdhE protein	Energy metabolism	-0.13	-0.76	-0.75	-0.78
so0105	L-seryl-tRNA selenium transferase	Protein synthesis	0.00	-0.47	-0.75	-0.74
so0106	selenocysteine-specific translation elongation factor	Protein synthesis	-0.11	-0.27	-0.35	-0.39
so0107	formate dehydrogenase accessory protein FdhD	Energy metabolism	-0.19	-0.62	-0.58	-0.88
so0109	conserved hypothetical protein	Hypothetical proteins	-0.45	-0.71	-0.83	-1.07
so0110	conserved hypothetical protein	Hypothetical proteins	-0.62	-0.51	-0.39	-0.25
so0112	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.34	-0.29	-0.17
so0113	conserved hypothetical protein	Hypothetical proteins	-0.12	-0.27	-0.30	-0.32
so0120	hypothetical protein	Hypothetical protein	-0.35	-0.21	-0.16	-0.01
so0130	protease, putative	Protein fate	-0.56	-0.86	-0.76	-0.60
so0141	sensory box protein	Regulatory functions	-0.54	-0.50	-0.53	-0.47
so0145	conserved hypothetical protein	Hypothetical proteins	-0.06	-0.19	-0.30	-0.38
so0162	phosphoenolpyruvate carboxykinase (ATP)	Energy metabolism	-0.15	-0.38	-0.39	-0.20
so0204	hypothetical protein	Hypothetical protein	-0.06	-0.24	-0.30	-0.14
so0222	ribosomal protein L10	Protein synthesis	-0.36	-0.32	0.03	0.04
so0226	ribosomal protein S12	Protein synthesis	-0.23	-0.37	-0.12	-0.06
so0231	ribosomal protein L3	Protein synthesis	-0.40	-0.18	0.02	0.12
so0243	ribosomal protein L5	Protein synthesis	-0.55	-0.58	-0.08	-0.13
so0262	heme exporter protein CcmB	Protein fate	-0.02	-0.39	-0.32	-0.13
so0264	cytochrome c	Energy metabolism	-0.11	-0.38	-0.67	-0.77
so0267	thiol:disulfide interchange protein DsbE	Protein fate	-0.34	-0.11	-0.10	0.02
so0272	competence/damage-inducible protein CinA	DNA metabolism	-0.40	-0.23	-0.28	-0.22
so0282	type IV pilus biogenesis protein PilN	Cell envelope	0.15	-0.09	-0.07	-0.33

sll0289	DNA adenine methylase	DNA metabolism	-0.33	-0.07	-0.16	-0.20
sll0303	phosphoglycolate phosphatase	Energy metabolism	-0.40	-0.16	-0.25	-0.17
sll0314	ornithine decarboxylase, inducible	Central intermediary metabolism	-0.15	-0.50	-0.37	-0.24
sll0324	conserved hypothetical protein	Hypothetical proteins	-0.20	-0.35	-0.30	-0.20
sll0340	branched-chain amino acid aminotransferase	Amino acid biosynthesis	-0.43	-0.23	-0.20	-0.28
sll0350	hypothetical protein	Hypothetical protein	-0.34	-0.45	-0.52	-0.39
sll0351	DNA-binding response regulator, LuxR family	Regulatory functions	-0.02	-0.20	-0.34	-0.32
sll0358	endoribonuclease L-PSP, putative	Transcription	-0.42	-0.22	-0.20	-0.18
sll0363	hypothetical protein	Hypothetical proteins	-0.35	-0.20	-0.11	0.04
sll0364	conserved hypothetical protein	Hypothetical proteins	-0.41	-0.25	-0.32	-0.20
sll0381	death-on-curing family protein	Hypothetical proteins	-0.11	-0.19	-0.22	-0.32
sll0382	type I restriction-modification system, S subunit	DNA metabolism	-0.16	-0.35	-0.30	-0.44
sll0383	type I restriction-modification system, M subunit	DNA metabolism	-0.36	-0.35	-0.36	-0.32
sll0393	DNA-binding protein Fis	DNA metabolism	-0.92	-0.52	-0.23	-0.10
sll0394	conserved hypothetical protein	Hypothetical proteins	-0.77	-0.47	-0.11	0.14
sll0395	ribosomal protein L11 methyltransferase	Protein synthesis	-0.46	-0.11	-0.21	-0.01
sll0398	fumarate reductase flavoprotein subunit	Energy metabolism	0.09	-0.57	-0.59	-0.40
sll0409	hypothetical protein	Hypothetical protein	-0.25	-0.34	-0.24	-0.21
sll0416	type IV pilus biogenesis protein PilB	Cell envelope	-0.38	-0.08	-0.23	-0.32
sll0424	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase	Energy metabolism	-0.33	-0.22	-0.18	-0.11
sll0429	peptidase, M13 family	Cell envelope	-0.38	-0.06	-0.11	-0.19
sll0432	aconitate hydratase 2	Energy metabolism	-0.38	-0.10	-0.18	-0.33
sll0435	uroporphyrinogen decarboxylase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.71	-0.43	-0.30	-0.20
sll0437	sensory box protein	Regulatory functions	-0.38	-0.09	-0.24	-0.37
sll0441	phosphoribosylamine--glycine ligase	Purines, pyrimidines, nucleosides, and nucleotides	-0.61	-0.64	-0.66	-0.55
sll0442	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Purines, pyrimidines, nucleosides, and nucleotides	-0.58	-0.39	-0.42	-0.33
sll0486	copper ABC transporter, periplasmic copper-binding protein	Transport and binding proteins	-0.13	-0.22	-0.31	-0.16
sll0505	conserved domain protein	Hypothetical proteins	-0.41	-0.18	-0.21	-0.29
sll0518	outer membrane efflux family protein, putative	Transport and binding proteins	-0.12	-0.39	-0.31	-0.06
sll0519	cation efflux protein, putative	Cellular processes	-0.22	-0.47	-0.52	-0.38
sll0520	heavy metal efflux pump, CzcA family	Cellular processes	-0.35	-0.40	-0.16	-0.28
sll0527	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.18	-0.13	-0.03
sll0531	hypothetical protein	Hypothetical proteins	-0.45	-0.04	-0.64	-0.09
sll0543	hypothetical protein	Hypothetical proteins	-0.18	-0.55	-0.82	-0.58
sll0548	DNA-binding protein, HU family	DNA metabolism	-0.21	-0.25	-0.22	-0.51
sll0550	hypothetical protein	Hypothetical protein	-0.31	-0.15	-0.13	-0.16
sll0553	hypothetical protein	Hypothetical protein	0.02	-0.22	-0.15	-0.35
sll0556	hypothetical protein	Hypothetical protein	-0.48	-0.22	-0.20	-0.09
sll0559	MusC domain protein	Unknown function	-0.30	-0.25	-0.24	-0.04
sll0567	1-acyl-sn-glycerol-3-phosphate acyltransferase	Fatty acid and phospholipid metabolism	-0.31	-0.12	-0.08	-0.04
sll0568	conserved hypothetical protein	Hypothetical proteins	-0.41	-0.16	-0.21	-0.15
sll0575	RNA polymerase-associated protein HepA	Transcription	-0.28	-0.32	-0.38	-0.12
sll0585	D-isomer specific 2-hydroxyacid dehydrogenase family protein	Unknown function	-0.16	-0.27	-0.30	-0.30
sll0588	transporter, putative	Transport and binding proteins	-0.31	-0.13	-0.11	-0.14
sll0590	phosphatidylserine decarboxylase, authentic frameshift+IS1381	Fatty acid and phospholipid metabolism	-0.41	-0.06	-0.16	-0.09
sll0593	hypothetical protein	Hypothetical proteins	-0.03	-0.31	-0.18	-0.03
sll0595	hypothetical protein	Hypothetical proteins	-0.38	-0.44	-0.51	-0.37
sll0609	ubiquinol-cytochrome c reductase, cytochrome b	Energy metabolism	-0.25	-0.04	-0.23	-0.41
sll0610	ubiquinol-cytochrome c reductase, cytochrome c1	Energy metabolism	-0.49	-0.17	-0.24	-0.38
sll0614	dipeptidyl peptidase IV, putative	Cell envelope	-0.25	-0.30	-0.41	-0.48
sll0621	sensor histidine kinase	Signal transduction	-0.28	-0.10	-0.23	-0.37
sll0626	hypothetical protein	Hypothetical protein	0.17	0.00	-0.32	0.12
sll0629	hypothetical protein	Hypothetical protein	-0.25	-0.01	-0.30	-0.11
sll0633	penicillin-binding protein 1B	Cell envelope	-0.38	-0.29	-0.31	-0.18
sll0635	peptidyl-prolyl cis-trans isomerase C	Protein fate	-0.31	-0.45	-0.49	-0.41
sll0639	Collagenase family	Protein fate	0.05	-0.21	-0.44	-0.18
sll0672	hypothetical protein	Hypothetical proteins	-0.45	-0.13	-0.23	-0.22
sll0675	prophage MuSu1, major head subunit, putative	Mobile and extrachromosomal element functions	-0.16	-0.09	-0.38	-0.26
sll0676	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.06	-0.19	-0.17
sll0679	hypothetical protein	Hypothetical proteins	-0.25	-0.15	-0.39	-0.24
sll0682	hypothetical protein	Hypothetical proteins	-0.18	-0.18	-0.31	-0.52
sll0694	galactokinase	Energy metabolism	-0.18	-0.27	-0.31	-0.20
sll0719	TonB-dependent receptor, putative	Transport and binding proteins	-0.74	-0.42	-0.33	-0.02
sll0721	conserved hypothetical protein	Hypothetical proteins	-0.39	-0.22	-0.22	-0.15
sll0728	conserved hypothetical protein	Hypothetical proteins	-0.01	-0.42	-0.40	-0.08
sll0729	hypothetical protein	Hypothetical proteins	-0.17	-0.99	-0.41	-0.08
sll0740	melanin biosynthesis protein TyrA, putative	Cellular processes	-0.44	-0.25	-0.27	-0.11
sll0753	hypothetical protein	Hypothetical protein	-0.03	-0.52	-0.22	-0.13
sll0779	glycine cleavage system T protein	Energy metabolism	-0.66	-0.47	-0.47	-0.38
sll0780	glycine cleavage system H protein	Energy metabolism	-0.42	-0.30	-0.24	-0.13
sll0781	glycine cleavage system P protein	Energy metabolism	-0.32	-0.26	-0.30	-0.25
sll0788	conserved hypothetical protein	Hypothetical proteins	-0.56	-0.46	-0.42	-0.21
sll0795	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.24	-0.31	-0.25
sll0807	hypoxanthine-guanine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.70	-0.34	-0.29	-0.07
sll0808	conserved hypothetical protein	Hypothetical proteins	-0.35	-0.15	-0.08	-0.02
sll0814	hypothetical protein	Hypothetical protein	0.09	-0.23	-0.35	-0.25
sll0815	TonB-dependent receptor C-terminal domain protein	Unknown function	-0.33	-0.71	-0.42	-0.20
sll0816	hypothetical protein	Hypothetical protein	-0.31	-0.09	-0.11	-0.09
sll0823	conserved hypothetical protein	Hypothetical proteins	-0.35	-0.04	-0.18	-0.30
sll0827	L-lactate permease	Transport and binding proteins	-0.58	-0.58	-0.61	-0.71
sll0834	spr7 protein, putative	Unknown function	-0.02	-0.17	-0.39	-0.30
sll0842	translation elongation factor G	Protein synthesis	-0.73	-0.28	-0.16	-0.16
sll0843	transcriptional regulator, LysR family	Regulatory functions	-0.41	-0.76	-0.56	-0.54
sll0845	cytochrome c-type protein NapB	Energy metabolism	0.00	-0.44	-0.54	-0.58
sll0846	iron-sulfur cluster-binding protein napH	Energy metabolism	-0.04	-0.40	-0.32	-0.16
sll0847	iron-sulfur cluster-binding protein NapG	Energy metabolism	0.11	-0.38	-0.25	-0.05
sll0848	periplasmic nitrate reductase	Energy metabolism	-0.35	-0.93	-0.89	0.36
sll0849	napD protein	Energy metabolism	-0.52	-0.53	-0.45	0.80
sll0861	conserved hypothetical protein	Hypothetical proteins	-0.37	-0.24	-0.21	-0.03
sll0869	gamma-glutamyl-beta-alanine ligase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.58	-0.39	-0.35	-0.34
sll0870	3-methyl-2-oxobutanoate hydroxymethyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.46	-0.29	-0.19	-0.04
sll0872	poly A polymerase	Transcription	-0.61	-0.24	-0.16	-0.21
sll0876	peptidase B	Protein fate	-0.28	-0.52	-0.43	-0.23
sll0883	conserved hypothetical protein	Hypothetical proteins	-0.18	-0.21	-0.32	-0.20
sll0887	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.39	-0.38	-0.27
sll0888	amidase family protein	Unknown function	-0.20	-0.43	-0.41	-0.25
sll0902	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit	Energy metabolism	-0.33	-0.68	-0.47	-0.44
sll0904	NADH:ubiquinone oxidoreductase, Na translocating, gamma subunit	Energy metabolism	0.01	-0.73	-0.48	-0.62
sll0905	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrD	Energy metabolism	0.16	-0.37	-0.44	-0.32
sll0907	NADH:ubiquinone oxidoreductase, Na translocating, beta subunit	Energy metabolism	0.08	-0.42	-0.31	-0.56
sll0913	cell filamentation protein Fic	Cellular processes	-0.09	-0.16	-0.24	-0.42
sll0915	ankyrin domain protein	Unknown function	-0.47	-0.30	-0.20	-0.19
sll0919	serine transporter, putative	Transport and binding proteins	-0.33	-0.53	-0.53	-0.34
sll0930	transferase	Energy metabolism	-0.31	-0.17	-0.13	-0.14
sll0931	D-erythrose-4-phosphate dehydrogenase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.32	-0.09	-0.10	-0.14
sll0932	phosphoglycerate kinase	Energy metabolism	-0.45	-0.34	-0.26	-0.24
sll0933	fructose-bisphosphate aldolase, class II, Calvin cycle subtype	Energy metabolism	-0.28	-0.33	-0.28	-0.26
sll0935	Na+/H+ antiporter	Transport and binding proteins	-0.10	-0.33	-0.19	-0.09
sll0936	transcriptional regulator	Regulatory functions	-0.03	-0.47	-0.22	-0.27
sll0937	hypothetical protein	Hypothetical protein	-0.19	-0.55	-0.28	-0.35
sll0940	transcriptional regulator-related protein	Unknown function	-0.40	-0.51	-0.59	-0.45
sll0941	hypothetical protein	Hypothetical protein	-0.45	-0.73	-0.65	-0.66
sll0944	conserved hypothetical protein	Hypothetical proteins	-0.44	-0.55	-0.44	-0.14
sll0961	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.21	0.11	-0.06
sll0968	D-lactate dehydrogenase	Energy metabolism	-0.44	-0.58	-0.44	-0.44
sll0970	fumarate reductase flavoprotein subunit precursor	Energy metabolism	-0.08	-0.53	-0.37	-0.60
sll0974	hypothetical protein	Hypothetical protein	0.31	-0.11	-0.28	-0.40
sll0975	hypothetical protein	Hypothetical protein	-0.54	-0.77	-0.75	-0.59
sll0987	methyl-accepting chemotaxis protein	Cellular processes	-0.23	-0.27	-0.36	-0.40
sll0992	lysyl-tRNA synthetase	Protein synthesis	-0.58	-0.23	-0.15	-0.19
sll0994	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.35	-0.23	-0.67
sll1003	hypothetical protein	Hypothetical protein	-0.23	-0.32	-0.14	-0.17
sll1004	hypothetical protein	Hypothetical protein	-0.49	-0.32	-0.22	-0.15
sll1045	hypothetical protein	Hypothetical protein	-0.39	-0.23	-0.34	-0.16
sll1048	membrane protein, putative	Cell envelope	-0.27	-0.30	-0.33	-0.12
sll1051	periplasmic glucan biosynthesis protein, putative	Cellular processes	-0.46	-0.33	-0.24	-0.39
sll1052	low-affinity inorganic phosphate transporter	Transport and binding proteins	-0.39	-0.25	-0.08	-0.14
sll1053	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.20	-0.05	-0.12
sll1056	methyl-accepting chemotaxis protein	Cellular processes	-0.36	-0.40	-0.41	-0.49
sll1059	aminopeptidase N	Cell envelope	-0.34	-0.25	-0.27	-0.18
sll1060	conserved hypothetical protein	Hypothetical proteins	-0.49	-0.28	-0.22	-0.29
sll1061	TPR domain protein	Unknown function	-0.48	-0.27	-0.19	-0.26
sll1064	conserved hypothetical protein	Hypothetical proteins	-0.17	-0.33	-0.18	-0.09
sll1066	extracellular nuclease	DNA metabolism	-0.13	-0.45	-0.50	-0.64
sll1070	catalase	Cellular processes	0.51	-0.60	-0.44	-0.64
sll1103	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit	Energy metabolism	-0.32	-0.16	-0.07	-0.25
sll1104	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrB	Energy metabolism	-0.60	-0.30	-0.19	-0.27
sll1105	NADH:ubiquinone oxidoreductase, Na translocating, gamma subunit	Energy metabolism	-0.46	-0.23	-0.19	-0.25
sll1106	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrD	Energy metabolism	-0.47	-0.30	-0.23	-0.26
sll1107	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE	Energy metabolism	-0.41	-0.29	-0.23	-0.29
sll1108	NADH:ubiquinone oxidoreductase, Na translocating, beta subunit	Energy metabolism	-0.34	-0.36	-0.23	-0.29
sll1109	thiamin biosynthesis lipoprotein ApbE	Cell envelope	-0.31	-0.20	-0.15	-0.16
sll1111	bacterioferritin subunit 2	Transport and binding proteins	0.31	-0.31	-0.42	-0.36
sll1112	bacterioferritin subunit 1	Transport and binding proteins	0.29	-0.31	-0.43	-0.33
sll1115	aminoacyl-histidine dipeptidase	Protein fate	-0.46	-0.09	-0.18	-0.13
sll1121	glutamate 5-kinase	Amino acid biosynthesis	-0.45	-0.25	-0.17	-0.15
sll1124	conserved hypothetical protein TIGR00011	Hypothetical proteins	-0.27	-0.31	-0.30	-0.08
sll1125	integral membrane domain protein	Unknown function	-0.18	-0.25	-0.24	-0.33
sll1141	carbamoyl-phosphate synthase, small subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.43	-0.21	-0.22	-0.32
sll1142	carbamoyl-phosphate synthase, large subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.37	-0.36	-0.27	-0.22
sll1150	ribose 5-phosphate isomerase	Energy metabolism	-0.51	-0.12	-0.15	-0.12
sll1174	leucyl-tRNA synthetase	Protein synthesis	-0.48	-0.15	-0.21	-0.04
sll1181	tRNA-i(6)A37 modification enzyme MiaB	Hypothetical proteins	-0.49	-0.18	-0.09	0.04
sll1187	hypothetical protein	Hypothetical protein	-0.38	-0.17	-0.09	-0.31
sll1191	transcription elongation factor GreA	Transcription	-0.36	-0.30	-0.18	-0.09
sll1204	translation initiation factor IF-2	Protein synthesis	-0.06	-0.46	-0.16	0.02
sll1207	ribosomal protein S15	Protein synthesis	-0.31	-0.27	0.10	0.03
sll1209	polyribonucleotide nucleotidyltransferase	Transcription	-0.75	-0.28	-0.18	-0.13
sll1211	peptide chain release factor 3, authentic frameshift	Protein synthesis	-0.64	-0.24	-0.22	-0.07
sll1214	NapC family protein	Transport and binding proteins	-0.34	-0.39	-0.39	-0.42
sll1215	outer membrane protein OmpK, putative	Cell envelope	-0.35	-0.65	-0.79	-0.77
sll1218	thymidine phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	0.04	-0.49	-0.42	-0.22
sll1219	phosphopentomutase	Purines, pyrimidines, nucleosides, and nucleotides	0.13	-0.36	-0.30	-0.14
sll1221	purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	-0.07	-0.28	-0.31	-0.44
sll1236	xanthine/uracil permease family protein	Transport and binding proteins	-0.29	-0.39	-0.31	-0.39
sll1247	hypothetical protein	Hypothetical protein	-0.16	-0.21	-0.37	-0.40
sll1250	conserved hypothetical protein	Hypothetical proteins	-0.22	-0.38	-0.33	-0.19
sll1251	ferredoxin, 4Fe-4S	Energy metabolism	-0.58	-0.26	-0.46	-0.05
sll1257	hypothetical protein	Hypothetical protein	-0.35	-0.61	-0.16	-0.07
sll1277	proton-dependent oligopeptide transporter (POT) family protein	Transport and binding proteins	-0.47	-0.18	-0.22	-0.19
sll1291	dihydroneopterin aldolase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.36	-0.22	-0.19	0.06
sll1292	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.31	-0.23	-0.14	-0.07
sll1293	undecaprenol kinase, putative	Cellular processes	-0.35	-0.16	-0.25	-0.10
sll1300	glutamate-1-semialdehyde-2,1-aminomutase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.56	-0.30	-0.27	-0.21
sll1301	aspartate carbamoyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.39	-0.15	-0.16	0.00
sll1322	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase	Central intermediary metabolism	-0.42	-0.13	-0.10	0.01
sll1335	thymidylate synthase	Purines, pyrimidines, nucleosides, and nucleotides	-0.44	-0.11	-0.11	-0.14
sll1354	hemolysin protein, putative	Cellular processes	-0.17	-0.21	-0.13	-0.32
sll1363	prismane protein	Energy metabolism	0.08	-0.26	-0.40	-0.33
sll1370	conserved hypothetical protein	Hypothetical proteins	-0.30	-0.11	-0.10	-0.08
sll1380	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.24	-0.11	-0.22
sll1388	aminopeptidase P, putative	Protein fate	-0.61	-0.55	-0.48	-0.39
sll1389	ROK family protein	Unknown function	-0.14	-0.24	-0.35	-0.42
sll1403	conserved hypothetical protein	Hypothetical proteins	-0.38	-0.32	-0.40	-0.13
sll1405	transglutaminase family protein	Unknown function	-0.23	-0.28	-0.28	-0.49
sll1406	mercuric transport protein MerT, putative	Transport and binding proteins	-0.10	-0.23	-0.07	-0.32
sll1410	hypothetical protein	Hypothetical protein	-0.26	-0.50	-0.36	-0.32
sll1412	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.32	-0.29	-0.37
sll1415	transcriptional regulator, TetR family	Regulatory functions	-0.69	-0.82	-0.58	-0.53
sll1418	ompK family protein	Cell envelope	0.19	-0.80	-0.73	-0.63
sll1427	decaheme cytochrome c	Energy metabolism	0.27	-0.43	-0.48	-0.58
sll1454	hypothetical protein	Hypothetical protein	0.14	-0.61	-0.51	-0.49
sll1488	hypothetical protein	Hypothetical protein	-0.64	-0.32	-0.69	-0.23
sll1489	hypothetical protein	Hypothetical protein	-0.39	-0.46	-0.36	-0.35
sll1519	iron-sulfur cluster-binding protein	Energy metabolism	-0.23	-0.37	-0.42	-0.40
sll1539	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.26	-0.27	-0.35
sll1556	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.17	-0.12	-0.04
sll1568	hypothetical protein	Hypothetical protein	-0.42	-0.49	-0.56	-0.37
sll1572	hypothetical protein	Hypothetical protein	-0.59	-0.71	-0.34	-0.36
sll1575	NOL1/NOP2/sun family putative RNA methylase	Protein synthesis	-0.47	-0.13	-0.11	0.05
sll1608	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.04	-0.19	-0.10
sll1618	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.09	-0.03	0.02
sll1631	uridylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.47	-0.37	-0.11	-0.23
sll1632	ribosome recycling factor	Protein synthesis	-0.35	-0.19	-0.07	-0.15
sll1638	outer membrane protein OmpH	Cell envelope	-0.32	-0.23	-0.09	-0.11
sll1658	hypothetical protein	Hypothetical protein	-0.45	-0.33	-0.21	-0.18
sll1663	ferredoxin-type protein NapF	Energy metabolism	-0.03	-0.17	-0.29	-0.42

so1667	purin-4-alpha-carboxlamine dehydratase	Biosynthesis of cofactors, prosthetic groups, and carriers	0.07	-0.09	-0.28	-0.32
so1673	outer membrane protein OmpW, putative	Cell envelope	-0.10	-0.82	-0.80	-0.73
so1674	short chain dehydrogenase family protein	Unknown function	-0.31	-0.07	-0.08	0.01
so1711	hypothetical protein	Hypothetical protein	0.31	-0.07	-0.31	-0.18
so1712	transcriptional regulator, putative	Regulatory functions	-0.09	-0.30	-0.33	-0.33
so1740	hypothetical protein	Hypothetical protein	-0.22	-0.08	-0.05	-0.31
so1741	conserved hypothetical protein	Hypothetical protein	-0.32	-0.11	-0.26	-0.26
so1743	hydrolase, alpha/beta hydrolase fold family	Unknown function	-0.51	-0.07	-0.17	-0.20
so1744	AMP-binding protein	Unknown function	-0.50	-0.17	-0.19	-0.28
so1746	conserved hypothetical protein	Hypothetical proteins	-0.23	-0.33	-0.37	-0.47
so1769	glutamate decarboxylase, putative	Central intermediary metabolism	-0.64	-0.45	-0.43	-0.22
so1772	hypothetical protein	Hypothetical protein	-0.17	-0.16	-0.34	-0.16
so1776	outer membrane protein precursor MlrB	Cell envelope	0.19	-0.21	-0.37	-0.71
so1777	decaheme cytochrome c MtrA	Energy metabolism	-0.03	-0.44	-0.63	-1.00
so1778	decaheme cytochrome c	Energy metabolism	-0.41	-0.68	-0.60	-0.77
so1779	decaheme cytochrome c	Energy metabolism	-0.27	-0.66	-0.75	-0.97
so1789	conserved hypothetical protein	Hypothetical proteins	-0.72	-0.41	-0.32	-0.28
so1790	peptidyl-prolyl cis-trans isomerase B	Protein fate	-0.73	-0.58	-0.47	-0.32
so1793	trigger factor	Protein fate	-0.78	-0.38	-0.20	-0.14
so1821	outer membrane porin, putative	Transport and binding proteins	-0.49	-0.29	-0.22	-0.06
so1846	hypothetical protein	Hypothetical protein	-0.32	-0.14	-0.17	-0.13
so1856	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	Fatty acid and phospholipid metabolism	-0.89	-0.30	-0.40	-0.47
so1862	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Fatty acid and phospholipid metabolism	-0.30	-0.16	-0.01	0.09
so1870	biosynthetic arginine decarboxylase	Central intermediary metabolism	-0.75	-0.49	-0.45	-0.34
so1876	NsdD transcription activator-related protein	Unknown function	0.16	-0.50	-0.38	-0.15
so1888	conserved hypothetical protein	Hypothetical protein	-0.34	-0.23	-0.16	-0.29
so1911	oxidoreductase, short chain dehydrogenase/reductase family	Unknown function	-0.35	-0.60	-0.42	-0.27
so1917	multidrug resistance protein, putative	Cellular processes	-0.06	-0.39	-0.20	-0.14
so1928	succinate dehydrogenase, flavoprotein subunit	Energy metabolism	-0.48	-0.12	-0.16	-0.32
so1929	succinate dehydrogenase, iron-sulfur protein	Energy metabolism	-0.38	-0.11	-0.13	-0.28
so1932	succinyl-CoA synthase, beta subunit	Energy metabolism	-0.35	-0.45	-0.16	-0.16
so1934	hypothetical protein	Hypothetical protein	-0.09	-0.34	-0.23	-0.10
so1935	regulator of nucleoside diphosphate kinase	Regulatory functions	-0.18	-0.43	-0.35	-0.30
so1936	acetyltransferase, GNAT family	Unknown function	-0.17	-0.44	-0.33	-0.23
so1945	sensor protein PhoQ	Signal transduction	-0.38	-0.38	-0.39	-0.33
so1948	sodium/dicarboxylate symporter family protein	Transport and binding proteins	-0.08	-0.30	-0.32	-0.36
so1949	invasin domain protein	Unknown function	-0.05	-0.18	-0.23	-0.36
so1958	conserved hypothetical protein	Hypothetical protein	-0.18	-0.33	-0.15	-0.13
so1995	peptidyl-prolyl cis-trans isomerase, FkbP family	Protein fate	-0.57	-0.38	-0.21	0.00
so2000	hypothetical protein	Hypothetical protein	-0.11	-0.49	-0.35	-0.24
so2001	5'-nucleotidase	Purines, pyrimidines, nucleosides, and nucleotides	-0.05	-0.34	-0.53	-0.68
so2005	disA-type zinc finger protein	Unknown function	-0.50	-0.75	-0.83	-0.71
so2012	adenine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.44	-0.22	-0.13	0.03
so2014	conserved hypothetical protein TIGR00103	Hypothetical protein	-0.37	-0.13	-0.05	-0.04
so2015	recombination protein RecR	DNA metabolism	-0.38	-0.13	-0.08	-0.01
so2019	ferrochelatase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.44	-0.61	-0.53	-0.21
so2020	inosine-guanosine kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.41	-0.37	-0.31	-0.17
so2048	membrane protein, putative	Cell envelope	-0.36	-0.18	-0.13	-0.14
so2051	hypothetical protein	Hypothetical protein	-0.16	-0.10	-0.35	0.01
so2082	rod shape-determining-related protein	Unknown function	0.11	-0.16	-0.23	-0.31
so2092	hydrogenase assembly chaperone hypC/hypF	Protein fate	-0.08	-0.33	-0.29	-0.37
so2093	hydrogenase accessory protein HypB	Protein fate	-0.29	-0.62	-0.46	-0.70
so2099	quinone-reactive Ni/Fe hydrogenase, small subunit precursor	Energy metabolism	0.16	-0.63	-0.54	-0.77
so2112	ribosomal protein L25	Protein synthesis	0.05	-0.34	-0.18	-0.06
so2115	asparaginase family protein	Energy metabolism	0.04	-0.16	-0.31	-0.26
so2136	aldehyde-alcohol dehydrogenase	Energy metabolism	0.08	-0.68	-0.56	-0.29
so2167	conserved hypothetical protein	Hypothetical proteins	-0.04	-0.29	-0.23	-0.48
so2177	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.07	-0.11	0.03
so2178	cytochrome c551 peroxidase	Cellular processes	-0.38	-0.52	-0.62	-0.81
so2182	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.26	-0.40	-0.32
so2185	enolase/phosphatase	Central intermediary metabolism	-0.36	-0.46	-0.35	-0.26
so2192	sensor histidine kinase	Signal transduction	-0.34	-0.06	-0.12	-0.09
so2215	sun protein, putative	Protein synthesis	-0.39	-0.26	-0.18	0.05
so2217	D-alanine--D-alanine ligase	Cell envelope	-0.47	-0.28	-0.36	-0.30
so2218	asparagine-tRNA synthetase	Protein synthesis	-0.58	-0.09	-0.13	-0.06
so2222	fumarate hydratase, class I, anaerobic, putative	Energy metabolism	-0.31	-0.29	-0.49	-0.37
so2223	peptidase, putative	Protein fate	-0.31	-0.03	-0.14	-0.14
so2240	methyl-accepting chemotaxis protein	Cellular processes	-0.38	-0.23	-0.29	-0.23
so2251	conserved hypothetical protein	Hypothetical proteins	-0.19	-0.40	-0.25	-0.11
so2258	lipoprotein releasing system ATP-binding protein LolD	Transport and binding proteins	-0.54	-0.21	-0.13	-0.03
so2259	lipoprotein releasing system transmembrane protein LolC, putative	Transport and binding proteins	-0.38	-0.13	-0.11	-0.05
so2260	extragenic suppressor protein SuhB	Unknown function	-0.71	-0.49	-0.24	0.21
so2270	ribosomal protein S6 modification protein	Protein synthesis	-0.40	-0.33	-0.16	-0.10
so2273	hypothetical protein	Hypothetical protein	0.04	-0.41	-0.45	-0.41
so2274	nucleoside diphosphate kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.69	-0.44	-0.32	-0.39
so2280	rhodanese domain protein	Unknown function	-0.35	-0.16	-0.04	0.11
so2303	thioredoxin reductase	Energy metabolism	-0.41	-0.34	-0.23	-0.17
so2304	alanine dehydrogenase, authentic point mutation	Energy metabolism	-0.43	-0.38	-0.35	-0.34
so2313	ISSo4, transposase, interruption	Mobile and extrachromosomal element functions	-0.26	-0.31	-0.13	-0.06
so2323	methyl-accepting chemotaxis protein	Cellular processes	-0.03	-0.29	-0.38	-0.38
so2328	translation elongation factor P	Protein synthesis	-0.70	-0.25	-0.23	-0.10
so2329	conserved hypothetical protein	Hypothetical proteins	-0.55	-0.36	-0.19	-0.04
so2330	flavodoxin	Energy metabolism	-0.54	-0.28	-0.16	-0.13
so2347	glyceraldehyde 3-phosphate dehydrogenase	Energy metabolism	-0.70	-0.36	-0.43	-0.60
so2348	hypothetical protein	Hypothetical protein	-0.79	-0.10	-0.43	-0.42
so2350	aspartate aminotransferase	Amino acid biosynthesis	-0.55	-0.39	-0.28	-0.29
so2354	conserved hypothetical protein	Hypothetical proteins	-0.54	-0.23	-0.14	0.05
so2359	cation transport ATPase, E1-E2 family	Cellular processes	-0.41	-0.17	-0.15	-0.13
so2361	cytochrome c oxidase, cbb3-type, subunit III	Energy metabolism	-0.27	-0.32	-0.17	-0.16
so2362	cytochrome c oxidase, cbb3-type, CcoQ subunit	Energy metabolism	-0.35	-0.45	-0.23	-0.21
so2363	cytochrome c oxidase, cbb3-type, subunit II	Energy metabolism	-0.42	-0.40	-0.24	-0.24
so2364	cytochrome c oxidase, cbb3-type, subunit I	Energy metabolism	-0.38	-0.38	-0.28	-0.32
so2373	drug resistance transporter, BcrC/BA family protein	Cellular processes	-0.31	-0.46	-0.40	-0.25
so2382	hypothetical protein	Hypothetical protein	0.03	-0.30	-0.34	0.20
so2389	multidrug resistance protein D	Cellular processes	-0.79	-0.50	-0.36	-0.05
so2390	CDP-diacylglycerol--serine O-phosphatidyltransferase	Fatty acid and phospholipid metabolism	-0.42	-0.31	-0.23	-0.18
so2393	hypothetical protein	Hypothetical protein	-0.27	-0.43	-0.15	-0.12
so2407	conserved hypothetical protein	Hypothetical proteins	0.18	-0.13	-0.08	-0.57
so2408	radical activating enzyme	Protein fate	0.22	0.02	-0.31	-0.21
so2410	phosphoserine aminotransferase	Amino acid biosynthesis	-0.44	-0.06	-0.17	-0.27
so2415	ribonucleoside-diphosphate reductase, alpha subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.43	-0.17	-0.11	0.00
so2416	ribonucleoside-diphosphate reductase, beta subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.44	-0.22	-0.16	-0.07
so2420	signal peptide peptidase SppA, 67K type	Protein fate	-0.35	-0.08	-0.10	-0.09
so2437	hypothetical protein	Hypothetical protein	-0.38	-0.17	-0.10	-0.15
so2472	D-alanyl-D-alanine carboxypeptidase-related protein	Unknown function	-0.34	-0.14	-0.12	-0.01
so2473	hydrolase, alpha/beta fold family	Unknown function	-0.43	-0.13	-0.15	-0.16
so2475	hypothetical protein	Hypothetical protein	-0.36	0.09	-0.32	-0.06
so2476	polysaccharide biosynthesis protein	Cell envelope	-0.58	-0.41	-0.46	-0.33
so2477	alcohol dehydrogenase, iron-containing	Energy metabolism	-0.27	-0.45	-0.46	-0.36
so2481	conserved hypothetical protein	Hypothetical proteins	-0.63	-0.40	-0.27	-0.29
so2525	ABC transporter, ATP-binding protein	Transport and binding proteins	-0.63	-0.38	-0.22	0.03
so2564	transglycosylase, Slt family	Cell envelope	-0.58	-0.44	-0.33	-0.17
so2569	hypothetical protein	Hypothetical protein	0.00	-0.37	-0.33	-0.30
so2572	peptidyl-prolyl cis-trans isomerase B	Protein fate	-0.52	-0.20	-0.20	-0.17
so2589	oxidoreductase, iron/ascorbate family	Unknown function	-0.50	-0.32	-0.18	-0.16
so2592	dihydroorotate dehydrogenase	Purines, pyrimidines, nucleosides, and nucleotides	-0.46	-0.27	-0.21	-0.39
so2593	conserved hypothetical protein	Hypothetical proteins	-0.38	-0.08	-0.09	-0.20
so2610	hydrolase, TatD family	Unknown function	-0.45	-0.15	-0.12	0.03
so2617	uridine kinase	Purines, pyrimidines, nucleosides, and nucleotides	-0.34	-0.15	-0.12	-0.02
so2625	translation initiation factor IF-1	Protein synthesis	-0.64	-0.23	-0.20	-0.10
so2635	adenylosuccinate lyase	Purines, pyrimidines, nucleosides, and nucleotides	-0.61	-0.16	-0.10	-0.17
so2636	conserved hypothetical protein	Hypothetical proteins	-0.52	-0.32	-0.24	-0.12
so2637	hypothetical protein	Hypothetical protein	0.03	-0.13	-0.06	-0.33
so2638	leucine dehydrogenase	Energy metabolism	-0.36	0.07	-0.18	-0.11
so2647	cytosolic long-chain acyl-CoA thioester hydrolase family protein	Fatty acid and phospholipid metabolism	-0.30	-0.22	-0.08	0.00
so2696	hypothetical protein	Hypothetical protein	-0.12	-0.30	-0.50	-0.23
so2705	DNA topoisomerase I	DNA metabolism	-0.26	-0.26	-0.32	-0.22
so2727	cytochrome c3	Energy metabolism	-0.10	-0.10	-0.25	-0.38
so2735	hypothetical protein	Hypothetical protein	-0.01	-0.51	-0.31	-0.37
so2736	conserved hypothetical protein	Hypothetical proteins	-0.18	-0.41	-0.37	-0.40
so2747	peptidoglycan-associated lipoprotein	Cell envelope	-0.30	-0.46	-0.12	-0.33
so2752	conserved hypothetical protein TIGR00051	Hypothetical proteins	-0.40	-0.18	-0.02	0.09
so2758	GGDEF family protein	Unknown function	0.00	-0.31	-0.17	-0.23
so2759	uracil phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.35	-0.30	-0.25	-0.21
so2771	2-hydroxy-3-oxopropionate reductase	Energy metabolism	-0.50	-0.30	-0.23	-0.17
so2774	3-oxoacyl-[acyl-carrier-protein] synthase II	Fatty acid and phospholipid metabolism	-0.69	-0.35	-0.35	-0.15
so2775	acyl carrier protein	Fatty acid and phospholipid metabolism	-0.47	-0.31	-0.23	-0.36
so2776	3-oxoacyl-[acyl-carrier-protein] reductase	Fatty acid and phospholipid metabolism	-0.31	-0.35	-0.28	-0.23
so2777	malonyl CoA-acyl carrier protein transacylase	Fatty acid and phospholipid metabolism	-0.40	-0.32	-0.20	-0.17
so2783	hydrolase, haloacid dehalogenase-like family, authentic frameshift	Unknown function	-0.31	-0.10	-0.14	-0.13
so2821	conserved hypothetical protein	Hypothetical proteins	-0.28	-0.45	-0.28	-0.25
so2823	response regulator	Signal transduction	-0.53	-0.24	-0.28	-0.45
so2830	hypothetical protein	Hypothetical protein	-0.48	-0.34	-0.26	-0.35
so2831	GTP cyclohydrolase II	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.38	-0.14	-0.08	-0.03
so2852	conserved hypothetical protein	Hypothetical proteins	-0.41	-0.22	0.02	0.03
so2834	anaerobic ribonucleoside-triphosphate reductase	Purines, pyrimidines, nucleosides, and nucleotides	-0.23	-0.34	-0.33	-0.25
so2840	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.26	-0.33	-0.29
so2853	3-oxoacyl-[acyl-carrier-protein] synthase III, putative	Fatty acid and phospholipid metabolism	-0.39	-0.20	-0.08	-0.18
so2865	L-lysine exporter, putative	Transport and binding proteins	-0.43	-0.66	-0.51	-0.54
so2871	ureotate reductase, putative	Cellular processes	-0.39	-0.17	-0.03	0.04
so2872	conserved hypothetical protein	Hypothetical proteins	-0.38	-0.18	-0.19	-0.15
so2879	uracil permease	Transport and binding proteins	-0.36	-0.23	-0.23	-0.31
so2880	glutaredoxin domain protein	Unknown function	-0.40	-0.27	-0.23	-0.16
so2886	Na+/H+ antiporter	Transport and binding proteins	-0.24	-0.37	-0.38	-0.31
so2900	hypothetical protein	Hypothetical protein	-0.01	-0.12	-0.13	-0.30
so2905	O-methyltransferase, putative	Cellular processes	-0.44	-0.53	-0.51	-0.22
so2912	formate acetyltransferase	Energy metabolism	-0.02	-0.46	-0.26	-0.15
so2929	hypothetical protein	Hypothetical protein	-0.03	-0.17	-0.25	-0.31
so2933	mltB protein, peptidase U7 family	Protein fate	-0.37	-0.15	-0.03	-0.01
so2824	tryptophan synthase, alpha subunit	Amino acid biosynthesis	-0.33	-0.05	-0.17	-0.04
so3046	methyl-accepting chemotaxis protein, authentic point mutation	Cellular processes	-0.36	-0.30	-0.22	-0.24
so3053	hypothetical protein	Hypothetical protein	-0.43	-0.50	-0.33	-0.23
so3059	formate hydrogenylase transcriptional activator, putative	Regulatory functions	-0.56	-0.89	-0.72	-0.56
so3064	aminophosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.92	-0.48	-0.46	-0.55
so3072	3-oxoacyl-[acyl-carrier-protein] synthase I	Fatty acid and phospholipid metabolism	-0.83	-0.26	-0.27	-0.34
so3076	conserved hypothetical protein	Hypothetical proteins	-0.36	-0.11	-0.15	-0.03
so3077	conserved hypothetical protein	Hypothetical proteins	-0.33	-0.13	-0.14	-0.08
so3099	long-chain fatty acid transport protein, putative	Transport and binding proteins	-0.63	-0.51	-0.61	-0.74
so3107	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.13	-0.08	-0.21
so3130	glutamyl-tRNA synthetase, authentic point mutation	Protein synthesis	-0.50	-0.15	-0.14	-0.01
so3144	electron transfer flavoprotein, alpha subunit	Energy metabolism	-0.34	-0.22	-0.40	-0.45
so3145	electron transfer flavoprotein, beta subunit	Energy metabolism	-0.30	-0.26	-0.36	-0.38
so3154	prolyl-tRNA synthetase	Protein synthesis	-0.58	-0.18	-0.22	-0.07
so3195	di-tripeptide transport protein, authentic frameshift	Transport and binding proteins	0.11	-0.09	-0.15	-0.36
so3275	hypothetical protein	Hypothetical protein	0.07	-0.30	-0.22	-0.31
so3282	methyl-accepting chemotaxis protein	Cellular processes	-0.07	-0.42	-0.46	-0.47
so3284	conserved hypothetical protein	Hypothetical proteins	-0.08	-0.16	-0.04	-0.37
so3285	cytochrome d ubiquinol oxidase, subunit II	Energy metabolism	-0.24	-0.54	-0.58	-0.84
so3286	cytochrome d ubiquinol oxidase, subunit I	Energy metabolism	-0.51	-0.65	-0.55	-0.72
so3287	phosphoribosylformylglycinamidine synthase	Purines, pyrimidines, nucleosides, and nucleotides	-0.37	-0.28	-0.17	-0.20
so3295	hypothetical protein	Hypothetical protein	-0.78	-0.08	-0.24	-0.06
so3297	transcriptional regulator, LysR family	Regulatory functions	0.47	-0.56	-0.81	-0.33
so3305	DNA-binding response regulator, LuxR family	Regulatory functions	-0.31	-0.27	-0.27	-0.30
so3315	conserved hypothetical protein TIGR00048	Hypothetical proteins	-0.37	-0.21	-0.18	0.04
so3316	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.11	-0.13	-0.28
so3337	conserved domain protein	Hypothetical proteins	-0.37	-0.46	-0.52	-0.67
so3338	L-allo-threonine dehidase	Energy metabolism	-0.12	-0.23	-0.32	-0.18
so3348	ferrochelatase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.31	-0.07	-0.10	-0.17
so3359	oxygen-independent coproporphyrinogen III oxidase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.47	-0.24	-0.24	-0.08
so3366	conserved hypothetical protein	Hypothetical proteins	-0.47	-0.19	-0.23	-0.23
so3368	AG-specific adenine glycosylase	DNA metabolism	-0.48	-0.16	-0.23	-0.17
so3370	conserved hypothetical protein	Hypothetical proteins	-0.41	-0.21	-0.22	-0.23
so3401	conserved hypothetical protein TIGR01033	Hypothetical proteins	-0.75	-0.30	-0.21	-0.07
so3409	OmpC/OPn family protein	Unknown function	-0.16	-0.33	-0.44	-0.51
so3410	hypothetical protein	Hypothetical protein	0.19	-0.43	-0.33	-0.18
so3416	hypothetical protein	Hypothetical protein	-0.52	-0.80	-0.50	-0.20
so3417	peptidyl-prolyl cis-trans isomerase SlyD	Protein fate	-0.27	-0.50	-0.44	-0.34
so3422	ribosomal subunit interface protein	Protein synthesis	0.33	-0.18	-0.39	-0.36
so3424	valyl-tRNA synthetase	Protein synthesis	-0.34	-0.14	-0.07	-0.03
so3428	alanyl-tRNA synthetase	Protein synthesis	-0.36	-0.20	-0.17	-0.12
so3440	enolase	Energy metabolism	-0.38	-0.15	-0.08	-0.03
so3449	conserved domain protein	Hypothetical proteins	-0.34	-0.26	-0.25	-0.27
so3458	conserved hypothetical protein	Hypothetical proteins	-0.38	-0.17	-0.15	-0.23
so3459	hypothetical protein	Hypothetical protein	-0.22	-0.15	-0.35	-0.46
so3463	phosphatidylglycerophosphatase A	Fatty acid and phospholipid metabolism	-0.53	-0.03	-0.13	-0.04
so3465	N utilization substance protein B	Transcription	-0.48	-0.15	-0.19	-0.15
so3466	riboflavin synthase, beta subunit	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.34	-0.06	-0.06	0.00

so3471	serine hydroxymethyltransferase	Amino acid biosynthesis	-0.59	-0.29	-0.31	-0.21
so3472	ABC transporter, ATP-binding protein	Transport and binding proteins	-0.40	-0.27	-0.25	-0.10
so3479	hypothetical protein	Hypothetical protein	-0.06	-0.34	-0.60	-0.57
so3503	glucose/galactose transporter	Transport and binding proteins	0.02	-0.40	-0.14	-0.19
so3507	conserved hypothetical protein	Hypothetical proteins	-0.20	-0.49	-0.46	-0.24
so3539	peptidase, M28D family	Protein fate	-0.06	-0.20	-0.26	-0.31
so3540	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.22	-0.19	-0.17
so3549	conserved hypothetical protein	Hypothetical proteins	-0.11	-0.38	-0.29	-0.34
so3553	sulfate permease family protein	Transport and binding proteins	-0.49	-0.58	-0.47	-0.37
so3554	phosphoribosylaminoimidazole carboxylase, catalytic subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.47	-0.23	-0.29	-0.18
so3555	phosphoribosylaminoimidazole carboxylase, ATPase subunit	Purines, pyrimidines, nucleosides, and nucleotides	-0.50	-0.31	-0.46	-0.37
so3565	2,3'-cyclic-nucleotide 2'-phosphodiesterase	Purines, pyrimidines, nucleosides, and nucleotides	0.00	-0.44	-0.62	-0.40
so3613	phosphoribosylglycinamide formyltransferase 2	Purines, pyrimidines, nucleosides, and nucleotides	-0.27	-0.28	-0.35	-0.21
so3640	spaG protein	Unknown function	-0.42	-0.09	-0.18	-0.19
so3653	octaprenyl-diphosphate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.36	-0.22	-0.23	-0.13
so3656	hypothetical protein	Hypothetical protein	-0.33	-0.19	-0.13	-0.05
so3659	thiol:disulfide interchange protein, putative	Protein fate	0.06	-0.06	-0.28	-0.38
so3694	conserved hypothetical protein	Hypothetical proteins	-0.37	-0.25	-0.24	0.00
so3696	hypothetical protein	Hypothetical protein	-0.38	-0.24	-0.31	-0.52
so3697	steroid delta-isomerase domain protein	Unknown function	-0.18	-0.22	-0.26	-0.37
so3698	hypothetical protein	Hypothetical protein	-0.38	-0.23	-0.26	-0.28
so3699	hypothetical protein	Hypothetical protein	-0.47	-0.38	-0.36	-0.38
so3705	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase, putative	Central intermediary metabolism	-0.89	-0.22	-0.35	-0.23
so3706	NagC family protein	Transport and binding proteins	-0.59	-0.07	-0.08	-0.11
so3714	sugar-binding protein, putative	Unknown function	0.05	-0.31	-0.36	-0.41
so3715	oxygen-insensitive NAD(P)H nitroreductase	Unknown function	-0.45	-0.43	-0.49	-0.48
so3718	thiol:disulfide interchange protein, DsbA family	Protein fate	-0.61	-0.61	-0.48	-0.52
so3719	hypothetical protein	Hypothetical protein	-0.08	-0.39	-0.20	-0.23
so3723	hypothetical protein	Hypothetical protein	-0.54	-0.26	-0.13	-0.10
so3744	hypothetical protein	Hypothetical protein	0.07	-0.32	-0.28	-0.20
so3748	LysM domain protein	Unknown function	-0.51	-0.15	-0.16	-0.24
so3783	ATP-dependent RNA helicase, DEAD box family	Transcription	-0.59	-0.37	-0.16	0.04
so3798	ribosomal large subunit pseudouridine synthase A	Protein synthesis	-0.62	-0.39	-0.36	-0.22
so3804	phenylacrylic acid decarboxylase, 3-octaprenyl-4-hydroxybenzoate carbony-lyase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.31	-0.21	-0.22	-0.31
so3812	peptidyl-prolyl cis-trans isomerase A	Protein fate	-0.36	-0.04	-0.11	-0.27
so3827	2-dehydro-3-deoxyphosphooctonate aldolase	Cell envelope	-0.41	-0.25	-0.24	-0.26
so3828	conserved hypothetical protein	Hypothetical proteins	-0.35	-0.13	-0.16	-0.24
so3832	hemK family protein	Unknown function	-0.36	-0.14	-0.15	-0.19
so3833	peptide chain release factor 1	Protein synthesis	-0.33	-0.17	-0.11	-0.06
so3834	glutamyl-tRNA reductase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.36	-0.34	-0.23	-0.24
so3842	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.31	-0.42	-0.46
so3844	peptidase, M13 family	Protein fate	-0.42	-0.35	-0.34	-0.31
so3848	hypothetical protein	Hypothetical protein	-0.72	-0.45	-0.35	-0.33
so3856	hypothetical protein	Hypothetical protein	-0.39	-0.25	-0.36	-0.22
so3857	PAP2 family protein	Unknown function	-0.36	-0.22	-0.18	-0.07
so3863	molybdenum ABC transporter, periplasmic molybdenum-binding protein	Transport and binding proteins	-0.07	-0.32	-0.37	-0.47
so3864	molybdenum ABC transporter, permease protein	Transport and binding proteins	-0.11	-0.18	-0.41	-0.23
so3865	molybdenum ABC transporter, ATP-binding protein	Transport and binding proteins	-0.23	-0.25	-0.33	-0.38
so3874	transcriptional regulator, LysR family	Regulatory functions	0.68	-0.55	-0.42	-0.52
so3896	outer membrane porin, putative	Transport and binding proteins	-0.18	-0.17	-0.40	-0.65
so3900	conserved hypothetical protein	Hypothetical proteins	-0.28	-0.26	-0.31	-0.37
so3905	conserved hypothetical protein	Hypothetical proteins	-0.31	-0.06	-0.11	-0.19
so3918	conserved hypothetical protein	Hypothetical proteins	-0.59	-0.18	-0.22	-0.36
so3920	periplasmic Fe hydrogenase, large subunit	Energy metabolism	-0.41	-0.58	-0.63	-0.55
so3921	periplasmic Fe hydrogenase, small subunit	Energy metabolism	-0.64	-0.84	-0.79	-0.42
so3922	formate dehydrogenase, putative	Energy metabolism	-0.24	-0.35	-0.49	-0.29
so3948	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell envelope	-0.37	-0.12	-0.12	-0.08
so3967	molybdenum ABC transporter, periplasmic molybdenum-binding protein, putative	Transport and binding proteins	-0.43	-0.44	-0.40	-0.03
so3969	OmpA family protein	Cell envelope	-0.46	-0.61	-0.57	-0.42
so3978	conserved hypothetical protein	Hypothetical proteins	-0.14	-0.31	-0.33	-0.10
so3980	cytochrome c552 nitrite reductase	Energy metabolism	-0.39	-1.00	-0.99	0.03
so3981	nitrate/nitrite sensor protein NarQ	Signal transduction	-0.18	-0.33	-0.31	-0.10
so3991	fructose-1,6-bisphosphatase	Energy metabolism	-0.24	-0.31	-0.28	-0.22
so4027	hypothetical protein	Hypothetical protein	-0.42	-0.12	-0.17	-0.30
so4028	single-stranded binding protein	DNA metabolism	-0.54	-0.29	-0.28	-0.31
so4031	hypothetical protein	Hypothetical protein	-0.44	-0.05	-0.14	-0.18
so4053	methyl-accepting chemotaxis protein	Cellular processes	-0.39	-0.79	-0.73	-0.65
so4057	hypothetical protein	Regulatory functions	-0.64	-0.35	-0.38	-0.17
so4066	phosphoribosylaminoimidazole-succinocarboxamide synthase, putative	Purines, pyrimidines, nucleosides, and nucleotides	-1.05	-0.25	-0.37	-0.40
so4072	MraR-like putative RNA modifying enzyme YbG	Hypothetical proteins	-0.73	-0.46	-0.39	-0.11
so4075	hypothetical protein	Hypothetical protein	0.19	-0.11	-0.15	-0.32
so4077	TonB-dependent receptor, putative	Transport and binding proteins	-0.39	-0.74	-0.88	-0.63
so4079	conserved hypothetical protein	Hypothetical proteins	-0.32	-0.16	-0.18	-0.19
so4080	conserved hypothetical protein	Hypothetical proteins	-0.35	-0.18	-0.23	-0.31
so4081	amino acid permease	Transport and binding proteins	-0.62	-0.64	-0.61	-0.42
so4082	hypothetical protein	Hypothetical protein	-0.37	-0.66	-0.10	-0.06
so4085	chitinase A	Energy metabolism	-0.21	-0.43	-0.27	-0.30
so4086	hypothetical protein	Hypothetical protein	-0.25	-0.43	-0.29	-0.33
so4118	malate oxidoreductase, putative	Energy metabolism	-0.62	-0.45	-0.55	-0.63
so4124	cell division protein FtsN, putative	Cellular processes	-0.31	-0.09	-0.09	-0.04
so4131	conserved hypothetical protein	Hypothetical proteins	-0.42	-0.52	-0.51	-0.43
so4133	uridine phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	-0.17	-0.38	-0.29	-0.22
so4138	conserved hypothetical protein	Hypothetical proteins	-0.29	-0.31	-0.16	-0.12
so4150	transporter, putative	Transport and binding proteins	-0.62	-0.47	-0.96	-0.87
so4151	polysaccharide deacetylase family protein	Energy metabolism	-0.45	-0.45	-0.22	-0.58
so4155	sensor histidine kinase	Signal transduction	-0.40	-0.44	-0.29	-0.37
so4157	DNA-binding response regulator	Regulatory functions	-0.41	-0.72	-0.55	-0.63
so4170	C-factor, putative	Cellular processes	0.06	-0.42	-0.20	-0.29
so4171	hypothetical protein	Hypothetical protein	-0.19	-0.43	-0.23	-0.37
so4180	inorganic pyrophosphatase, manganese-dependent	Central intermediary metabolism	-0.52	-0.20	-0.17	-0.26
so4192	hypothetical protein	Hypothetical protein	-0.36	-0.51	-0.45	-0.60
so4196	conserved hypothetical protein	Hypothetical proteins	0.60	-0.42	-0.45	-0.54
so4199	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.58	-0.38	-0.41	-0.19
so4200	conserved hypothetical protein	Hypothetical proteins	-0.43	-0.31	-0.44	-0.35
so4201	ubiquinone biosynthesis protein AarF	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.44	-0.27	-0.30	-0.28
so4202	Sec-independent protein translocase protein TatA	Protein fate	-0.46	-0.36	-0.33	-0.22
so4203	Sec-independent protein translocase protein TatB	Protein fate	-0.47	-0.35	-0.46	-0.36
so4204	Sec-independent periplasmic protein translocation protein TatC	Protein fate	-0.58	-0.42	-0.51	-0.49
so4205	hypothetical protein	Hypothetical protein	-0.34	-0.24	-0.29	-0.22
so4206	hydrolase, TatD family	Unknown function	-0.41	-0.31	-0.39	-0.35
so4207	GGDEF domain protein	Unknown function	-0.36	-0.28	-0.28	-0.28
so4208	delta-aminolevulinic acid dehydratase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.54	-0.46	-0.46	-0.46
so4250	deoxyuridine 5'-triphosphate nucleotidohydrolase	Purines, pyrimidines, nucleosides, and nucleotides	-0.38	-0.27	-0.22	-0.21
so4251	transcriptional regulator, TetR family	Regulatory functions	-0.31	-0.27	-0.23	-0.27
so4255	nonane phosphotrichotransferase	Purines, pyrimidines, nucleosides, and nucleotides	-0.39	-0.12	-0.23	-0.39
so4298	cyclic nucleotide binding protein, putative	Unknown function	-0.47	-0.33	-0.41	-0.25
so4313	porphobilinogen deaminase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.63	-0.46	-0.41	-0.32
so4314	uroporphyrinogen-III synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.31	-0.41	-0.36	-0.34
so4340	conserved hypothetical protein	Hypothetical proteins	-0.57	-0.43	-0.37	-0.45
so4341	hypothetical protein	Hypothetical protein	-0.03	-0.30	-0.21	-0.38
so4355	hypothetical protein	Hypothetical protein	0.21	-0.63	-0.63	-0.77
so4368	acyl carrier protein, putative	Fatty acid and phospholipid metabolism	-0.51	-0.13	-0.19	-0.23
so4369	acyl carrier protein, putative	Fatty acid and phospholipid metabolism	-0.53	-0.04	-0.22	-0.17
so4373	glycosyl transferase, group 2 family protein	Cell envelope	-0.36	-0.08	-0.11	-0.15
so4376	hypothetical protein	Hypothetical protein	-0.33	-0.17	-0.14	-0.20
so4384	hypothetical protein	Hypothetical protein	-0.36	-0.14	-0.13	-0.19
so4408	virulence regulator BipA	Regulatory functions	-0.76	-0.53	-0.46	-0.26
so4417	anaerobic C4-dicarboxylate membrane transporter	Transport and binding proteins	0.03	-0.17	-0.32	0.02
so4420	peptidase, M23/M37 family	Protein fate	-0.42	-0.31	-0.35	-0.26
so4461	hypothetical protein	Hypothetical protein	-0.03	-0.23	-0.39	0.02
so4462	hypothetical protein	Hypothetical protein	-0.01	-0.19	-0.29	-0.36
so4502	conserved domain protein	Hypothetical proteins	0.08	-0.21	-0.29	-0.33
so4504	conserved hypothetical protein	Hypothetical proteins	-0.26	-0.54	-0.77	-0.77
so4505	conserved hypothetical protein	Hypothetical proteins	-0.27	-0.48	-0.93	-0.87
so4506	iron-sulfur cluster-binding protein	Energy metabolism	0.01	-0.03	-0.33	-0.23
so4507	TorA specific chaperone, putative	Energy metabolism	-0.08	-0.12	-0.46	-0.46
so4508	hypothetical protein	Hypothetical protein	0.11	-0.35	-1.05	-0.67
so4509	formate dehydrogenase, alpha subunit	Energy metabolism	0.01	-0.29	-0.69	-0.49
so4510	formate dehydrogenase, iron-sulfur subunit	Energy metabolism	-0.21	-0.28	-0.36	-0.35
so4512	conserved hypothetical protein	Hypothetical proteins	-0.15	-0.74	-0.95	-0.72
so4513	formate dehydrogenase, alpha subunit	Energy metabolism	-0.01	-0.49	-0.76	-0.81
so4518	hypothetical protein	Hypothetical protein	-0.05	-0.16	-0.13	-0.38
so4520	oxygen-independent coproporphyrinogen III oxidase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.34	-0.36	-0.22	-0.21
so4529	RNA methyltransferase, TrmH family, group 2	Protein synthesis	-0.42	-0.30	-0.23	0.06
so4538	peptidase, M16 family, degenerate	Protein fate	-0.41	-0.21	-0.37	-0.34
so4557	methyl-accepting chemotaxis protein	Cellular processes	-0.45	-0.33	-0.32	-0.14
so4561	tetraheme cytochrome c	Energy metabolism	-0.22	-0.31	-0.20	-0.15
so4619	ybgI protein	Unknown function	-0.36	-0.16	-0.02	0.14
so4622	sensor histidine kinase	Signal transduction	-0.21	-0.30	-0.34	-0.32
so4623	DNA-binding response regulator	Regulatory functions	-0.40	-0.54	-0.50	-0.39
so4673	threonine 3-dehydrogenase	Energy metabolism	-0.37	-0.55	-0.48	-0.45
so4674	2-amino-3-ketobutyrate coenzyme A ligase	Energy metabolism	-0.29	-0.49	-0.35	-0.34
so4681	glycosyl transferase, group 1 family protein	Cell envelope	-0.70	-0.48	-0.60	-0.57
so4712	ABC transporter, ATP-binding protein, putative	Transport and binding proteins	-0.34	-0.39	-0.51	-0.46
so4713	menaquinone-specific isochorismate synthase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.30	-0.39	-0.24	-0.18
so4719	conserved hypothetical protein	Hypothetical proteins	-0.48	-0.67	-0.73	-0.90
so4720	ABC transporter, permease protein	Transport and binding proteins	-0.48	-0.45	-0.52	-0.43
so4721	ABC transporter, ATP-binding protein	Transport and binding proteins	-0.37	-0.41	-0.42	-0.41
so4722	molybdopterin-guanine dinucleotide biosynthesis protein	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.24	-0.42	-0.37	-0.35
so4723	molybdopterin biosynthesis MoaA protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.11	-0.39	-0.42	-0.39
so4724	molybdenum cofactor biosynthesis protein A, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.03	-0.29	-0.43	-0.46
so4729	conserved hypothetical protein	Hypothetical proteins	-0.34	-0.31	-0.10	-0.17
so4730	oxygen-independent coproporphyrinogen III oxidase	Biosynthesis of cofactors, prosthetic groups, and carriers	-0.64	-0.62	-0.47	-0.36
so4741	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Central intermediary metabolism	-0.23	-0.15	-0.58	-0.34
so4745	UDP-N-acetylglucosamine pyrophosphorylase	Cell envelope	-0.39	-0.21	-0.21	-0.24
so4746	ATP synthase F1, epsilon subunit	Energy metabolism	-0.12	-0.62	-0.46	-0.23
so4747	ATP synthase F1, beta subunit	Energy metabolism	-0.17	-0.86	-0.62	-0.29
so4748	ATP synthase F1, gamma subunit	Energy metabolism	-0.27	-0.98	-0.64	-0.34
so4749	ATP synthase F1, alpha subunit	Energy metabolism	-0.34	-0.85	-0.44	-0.35
so4750	ATP synthase F1, delta subunit	Energy metabolism	-0.35	-0.80	-0.48	-0.34
so4751	ATP synthase F0, B subunit	Energy metabolism	-0.39	-0.90	-0.32	-0.29
so4752	ATP synthase F0, C subunit	Energy metabolism	-0.43	-0.78	-0.40	-0.27
so4753	ATP synthase F0, A subunit	Energy metabolism	-0.43	-0.78	-0.24	-0.21
so4754	ATP synthase protein I	Energy metabolism	-0.39	-0.70	-0.19	-0.16
so4755	FtsH family protein	Cellular processes	-0.32	-0.23	-0.10	-0.20
soa0005	hypothetical protein	Hypothetical protein	0.17	-0.06	-0.21	-0.31
soa0052	hypothetical protein	Hypothetical protein	-0.51	-0.33	-0.34	-0.48
soa0052	hypothetical protein	Hypothetical protein	-0.46	-0.33	-0.24	-0.20
soa0077	site-specific recombinase, resolvase family	DNA metabolism	-0.35	-0.13	-0.18	-0.09
soa0093	ISSo3, transposase, truncation	Mobile and extrachromosomal element functions	-0.11	-0.44	-0.29	-0.09
soa0113	site-specific recombinase, resolvase family, truncation	DNA metabolism	-0.24	-0.40	-0.14	-0.18
soa0138	hypothetical protein	Hypothetical protein	-0.48	-0.35	-0.22	-0.14
soa0149	hypothetical protein	Hypothetical protein	-0.22	-0.43	-0.43	-0.37
soa0146	hypothetical protein	Hypothetical protein	-0.13	-0.35	-0.39	-0.35