Table S1. *Gene* expression profile of *S. typhimurium* LT2 and *S. typhimurium* JH4000 grown at 25 and 37°C

Complete gene expression profile data set of *S. Typhimurium* LT2 and S. Typhimurium JH4000 grown at 25 and 37°C. RNA was extracted from exponential phase cultures of *S. Typhimurium* LT2a and JH4000 grown at 25 and 37°C, cDNA labelled and co-hybridised with labelled genomic DNA from *S. Typhimurium* LT2 on microarrays comprising the 4451 *S. Typhimurium* LT2 open reading frames. The table shows the mean fluorescence ratio between the labelled cDNA and reference genomic DNA for each gene, standard deviation and ratio of expression for each strain between 37 and 25°C.

Strain / temperature					LT2a 25°C		LT2a 37°C			JH4000 25°C		JH4000 37°C		
Common name	Systematic Name	Genbank number	Map position	Mean ratio	SD	Mean ratio	SD	LT2a 37°C/25°C	Mean ratio	SD	Mean ratio	SD	JH4000 37°C/25°C	Description
thrL	STM0001	AAL18965	190..255			5.321	1.175	N/A			2.617	0.341	N/A	thr operon leader peptide
thrA	STM0002	AAL18966	337..2799	0.997	0.060	0.491	0.062	0.492	0.516	0.030	0.514	0.065	0.995	aspartokinase I , bifunctional enxyme N-terminal is aspartokinaseI and C-terminal is homoserine dehydrogenase I
thrB	STM0003	AAL18967	2801..3730	3.161	0.311	1.545	0.204	0.489	6.204	1.107	7.655	0.411	1.234	homoserine kinase
thrC	STM0004	AAL18968	3734..5020					N/A					N/A	threonine synthase
yaaA	STM0005	AAL18969	(5114..5887)	2.257	0.108	1.616	0.302	0.716	1.841	0.076	2.156	0.061	1.171	putative cytoplasmic protein
yaaJ	STM0006	AAL18970	(5966..7396)	0.705	0.066	0.782	0.179	1.108	1.342	0.215	1.413	0.034	1.053	putative AGCS family, alanine/glycine transport protein
talB	STM0007	AAL18971	7665..8618	1.837	0.267	21.026	2.219	11.447	0.929	0.066	4.793	0.103	5.158	transaldolase B
mog	STM0008	AAL18972	8729..9319	3.133	0.349	2.470	0.350	0.789	0.782	0.020	0.916	0.022	1.171	putative molybdochetalase in molybdopterine biosynthesis
yaaH	STM0009	AAL18973	(9376..9942)	0.825	0.151	0.762	0.048	0.923	0.477	0.039	0.393	0.057	0.823	putative regulator
htgA	STM0010	AAL18974	(10092..10805)	0.346	0.122	0.413	0.062	1.196	0.299	0.061	0.607	0.202	2.031	positive regulator for sigma H (sigma 32) promoters, permitting growth at high temperature
yaaI	STM0011	AAL18975	(10841..11245)	0.730	0.050	0.611	0.073	0.836	0.486	0.003	0.913	0.264	1.878	putative periplasmic protein
dnaK	STM0012	AAL18976	11593..13509	1.764	0.446	9.148	0.512	5.185	3.865	0.525	25.177	2.918	6.514	chaperone Hsp70 in DNA biosynthesis/cell division
dnaJ	STM0013	AAL18977	13595..14734	0.949	0.125	2.503	0.198	2.637	3.371	0.133	10.505	1.006	3.117	heat shock protein, DnaJ and GrpE stimulates ATPase activity of DnaK
STM0014	STM0014	AAL18978	15014..15961	0.206	0.112	0.165	0.031	0.800	1.038	0.029	1.167	0.161	1.125	putative transcriptional regulator, LysR family
STM0015	STM0015	AAL18979	16088..16432	0.279	0.095	0.189	0.040	0.675	0.606	0.057	0.570	0.026	0.941	putative bacteriophage protein
STM0016	STM0016	AAL18980	(16493..17026)	0.151	0.108	0.127	0.076	0.846	0.369	0.038	0.464	0.022	1.259	putative protein
STM0017	STM0017	AAL18981	(17043..17486)	0.565	0.096	0.534	0.249	0.945	0.677	0.042	0.670	0.049	0.990	putative protein
STM0018	STM0018	AAL18982	17867..19966	0.307	0.125	0.146	0.021	0.476	0.243	0.008	0.366	0.030	1.510	putative exochitinase
STM0019	STM0019	AAL18983	20058..23054	0.223	0.113	0.111	0.021	0.500	0.169	0.024	0.212	0.031	1.257	putative hydroxymethyltransferase
STM0020	STM0020	AAL18984	23335..24039	0.205	0.127	0.130	0.031	0.632	1.091	0.200	0.987	0.027	0.905	putative cytoplasmic protein
bcfA	STM0021	AAL18985	24469..25011	0.204	0.148	0.228	0.091	1.115	1.634	0.103	2.522	0.082	1.543	fimbrial subunit
bcfB	STM0022	AAL18986	25112..25798	0.247	0.130	0.168	0.014	0.682	0.606	0.017	0.829	0.020	1.367	fimbrial chaparone
bcfC	STM0023	AAL18987	25803..28424	0.214	0.136	0.117	0.002	0.546	0.279	0.017	0.497	0.052	1.783	fimbrial usher
bcfD	STM0024	AAL18988	28425..29432	0.225	0.139	0.106	0.007	0.470	0.266	0.072	0.427	0.027	1.604	fimbrial subunit
bcfE	STM0025	AAL18989	29433..29978	0.201	0.161	0.144	0.016	0.715	0.224	0.086	0.409	0.019	1.828	fimbrial subunit
bcfF	STM0026	AAL18990	29994..30512	0.293	0.186	0.204	0.016	0.698	0.190	0.006	0.348	0.066	1.831	fimbrial subunit
bcfG	STM0027	AAL18991	30478..31209	0.281	0.124	0.196	0.054	0.696	0.244	0.058	0.403	0.044	1.652	fimbrial chaparone

bcfH	STM0028	AAL18992	31274..32119	0.292	0.145	0.172	0.031	0.587	0.394	0.075	0.604	0.048	1.535	putative thiol-disulfide isomerase
STM0029	STM0029	AAL18993	(32545..32994)	0.363	0.082	0.300	0.046	0.828	0.323	0.065	0.310	0.041	0.959	putative transcription regulator
STM0030	STM0030	AAL18994	33364..34368	0.178	0.103	0.104	0.031	0.584	0.328	0.041	0.249	0.027	0.760	putative transcriptional regulator, LysR family
STM0031	STM0031	AAL18995	(34376..34816)	0.206	0.093	0.143	0.022	0.694	0.281	0.053	0.193	0.039	0.685	putative transcription regulator
STM0032	STM0032	AAL18996	35339..37057	0.241	0.123	0.179	0.038	0.742	0.170	0.001	0.254	0.025	1.494	putative arylsulfatase
STM0033	STM0033	AAL18997	(37103..38674)	0.161	0.100	0.175	0.056	1.088	0.272	0.034	0.551	0.025	2.024	putative 5'-nucleotidase
STM0034	STM0034	AAL18998	(38773..39534)	0.180	0.101	0.097	0.030	0.537	0.315	0.063	0.263	0.015	0.835	putative outer membrane or exported protein
STM0035	STM0035	AAL18999	40131..41624	0.348	0.095	0.394	0.056	1.131	2.001	0.152	2.427	0.326	1.213	putative arylsulfatase
STM0036	STM0036	AAL19000	41723..42913	0.503	0.096	0.201	0.020	0.401	0.494	0.029	0.450	0.039	0.911	putative arylsulfatase regulatory protein
STM0037	STM0037	AAL19001	42932..44185	0.180	0.111	0.089	0.005	0.496	0.342	0.026	0.292	0.003	0.854	putative cytoplasmic protein
STM0038	STM0038	AAL19002	44312..46027	0.305	0.078	0.176	0.009	0.576	0.280	0.025	0.485	0.030	1.730	putative arylsulfatase
nhaA	STM0039	AAL19003	46190..47356	3.058	0.218	1.418	0.183	0.464	1.670	0.222	1.686	0.128	1.009	NhaA familiy of transport protein, Na+/H antiporter, pH dependent
nhaR	STM0040	AAL19004	47418..48317	2.506	0.262	1.304	0.114	0.520	1.291	0.162	1.076	0.048	0.833	transcriptional activator of nhaA (LysR family)
STM0041	STM0041	AAL19005	(48372..50411)	0.332	0.133	0.294	0.030	0.885	0.477	0.054	1.237	0.184	2.593	putative glycosyl hydrolase
STM0042	STM0042	AAL19006	(50451..51824)	0.284	0.136	0.222	0.062	0.781	1.063	0.198	1.328	0.134	1.250	putative sodium galactoside symporter
rpsT	STM0043	AAL19007	(52280..52543)	6.574	1.657	7.325	1.020	1.114	3.370	0.126	2.487	0.747	0.738	30S ribosomal subunit protein S20
yaaY	STM0044	AAL19008	52649..52864	2.070	0.397	1.367	0.137	0.660	1.118	0.072	0.752	0.174	0.673	putative cytoplasmic protein
ribF	STM0045	AAL19009	52872..53810	2.435	0.083	3.491	0.584	1.434	1.675	0.177	1.910	0.093	1.140	flavokinase and FAD synthetase
ileS	STM0046	AAL19010	53855..56689	3.426	0.177	4.718	0.814	1.377	2.097	0.188	2.614	0.319	1.246	isoleucine tRNA synthetase
lspA	STM0047	AAL19011	56689..57189	6.716	0.897	4.886	0.641	0.727	4.234	0.148	4.649	0.749	1.098	prolipoprotein signal peptidase (SPase II)
slpA	STM0048	AAL19012	57344..57793	6.694	1.107	3.773	0.198	0.564	3.182	0.267	2.418	0.312	0.760	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
lytB	STM0049	AAL19013	57796..58746	4.543	0.761	2.387	0.194	0.525	2.675	0.531	1.621	0.072	0.606	regulates the activity of guanosine 3',5'-bispyrophosphate synthetase I (RelA)
STM0050	STM0050	AAL19014	58946..60148	0.670	0.024	0.736	0.049	1.099	0.259	0.086	0.304	0.033	1.172	putative nitrite reductase
rihC	STM0051	AAL19015	60164..61084	1.371	0.041	2.353	0.400	1.716	1.063	0.144	1.171	0.013	1.101	putative purine nucleoside hydrolase
STM0052	STM0052	AAL19016	(61106..61792)	0.531	0.050	0.434	0.059	0.817	0.668	0.074	0.862	0.064	1.291	putative transcription regulator sensor for citrate
STM0053	STM0053	AAL19017	(61794..63413)	0.205	0.071	0.237	0.041	1.158	0.319	0.047	0.489	0.044	1.532	putative transcription regulator, histidine kinase for citrate
STM0054	STM0054	AAL19018	(63548..64849)					N/A					N/A	putative oxalacetate decarboxylase, subunit beta
STM0055	STM0055	AAL19019	(64862..66637)	0.731	0.069	0.621	0.109	0.849	0.562	0.053	0.783	0.048	1.393	putative oxalacetate decarboxylase, subunit alpha
STM0056	STM0056	AAL19020	(66654..66893)	0.348	0.207	0.221	0.052	0.635	1.340	0.258	0.458	0.019	0.342	putative oxalacetate decarboxylase, subunit gamma
STM0057	STM0057	AAL19021	(67052..68392)	0.272	0.146	0.118	0.014	0.435	2.178	0.239	0.347	0.028	0.159	putative citrate-sodium symport
citC2	STM0058	AAL19022	68637..69680	0.216	0.121	0.182	0.021	0.843	2.264	0.155	0.434	0.088	0.192	putative citrate lyase synthetase (citrate (pro-3S)-lyase ligase
citD2	STM0059	AAL19023	69710..70003	0.347	0.070	0.394	0.049	1.134	2.413	0.069	0.792	0.097	0.328	putative citrate lyase acyl carrier protein (gamma chain)
citE2	STM0060	AAL19024	70000..70869	0.294	0.170	0.298	0.066	1.016	2.542	0.444	0.525	0.073	0.207	putative citrate lyase beta chain (acyl lyase subunit)
citF2	STM0061	AAL19025	70880..72400	0.226	0.147	0.326	0.056	1.445	1.415	0.161	0.388	0.014	0.274	putativ bifunctional citrate lyase alpha chain/citrate-A transferase
citX2	STM0062	AAL19026	72400..72951	0.217	0.129	0.265	0.107	1.217	1.325	0.176	0.384	0.009	0.290	putative cytoplasmic protein
citG2	STM0063	AAL19027	72929..73837	0.322	0.154	0.217	0.042	0.675	0.841	0.125	0.238	0.019	0.283	putative modifier of citrate lyase protein

dapB	STM0064	AAL19028	74017..74838	2.599	0.354	0.993	0.086	0.382	2.276	0.582	2.570	0.243	1.129	dihydrodipicolinate reductase
STM0065	STM0065	AAL19029	75088..75435	0.379	0.143	0.195	0.079	0.514	0.270	0.059	0.158	0.032	0.586	putative viral protein
carA	STM0066	AAL19030	75880..77028	1.332	0.250	1.031	0.154	0.774	0.425	0.017	0.559	0.052	1.316	carbamoyl-phosphate synthetase, glutamine-hydrolysing small subunit
carB	STM0067	AAL19031	77047..80274					N/A					N/A	carbamoyl-phosphate synthase, large subunit
caiF	STM0068	AAL19032	80548..80943	0.453	0.087	0.721	0.320	1.590	0.428	0.014	0.362	0.013	0.846	transcriptional regulator of cai and fix operon
caiE	STM0069	AAL19033	(81020..81616)	0.237	0.126	0.320	0.009	1.353	0.201	0.030	0.372	0.041	1.849	stimulates carnitine racemase activity of CaiD and CaiB activity
caiD	STM0070	AAL19034	(81725..82510)	0.410	0.160	0.911	0.050	2.224	0.403	0.065	0.953	0.048	2.363	carnitine racemase
caiC	STM0071	AAL19035	(82564..84117)	0.303	0.126	0.298	0.051	0.983	0.254	0.024	0.208	0.006	0.817	crotonobetaine/carnitine-CoA ligase
caiB	STM0072	AAL19036	(84180..85397)	0.258	0.146	0.362	0.036	1.404	0.125	0.036	0.330	0.035	2.643	l-carnitine dehydratase
caiA	STM0073	AAL19037	(85509..86651)					N/A					N/A	putative acyl-CoA dehydrogenase, carnitine metabolism
caiT	STM0074	AAL19038	(86686..88203)	0.160	0.151	0.077	0.014	0.485	0.090	0.013	0.169	0.007	1.876	putative BCCT family, betaine/carnitine/choline transport protein
fixA	STM0075	AAL19039	88684..89454	0.206	0.167	0.165	0.046	0.801	0.171	0.015	0.190	0.046	1.113	putative flavoprotein reductase, carnitine metabolism
fixB	STM0076	AAL19040	89470..90411	0.252	0.153	0.168	0.041	0.667	0.216	0.054	0.340	0.023	1.570	putative electron transfer flavoprotein, carnitine metabolism
fixC	STM0077	AAL19041	90461..91747	0.247	0.188	0.176	0.024	0.711	0.174	0.036	0.261	0.032	1.499	related to carnitine metabolism
fixX	STM0078	AAL19042	91744..92031	0.375	0.299	0.177	0.017	0.471	0.550	0.531	0.280	0.016	0.509	putative ferredoxin, carnitine metabolism
yaaU	STM0079	AAL19043	92178..93518	0.394	0.153	0.205	0.016	0.519	0.279	0.041	0.318	0.025	1.137	putative MFS family transport protein
STM0080	STM0080	AAL19044	93607..93837	0.675	0.031	0.298	0.058	0.442	1.127	0.032	0.843	0.195	0.748	putative outer membrane lipoprotein
STM0081	STM0081	AAL19045	94131..94547	0.348	0.115	0.199	0.019	0.573	1.685	0.037	1.457	0.130	0.865	putative secreted protein
STM0082	STM0082	AAL19046	(94771..95061)	0.843	0.087	0.293	0.050	0.348	7.507	0.887	3.652	0.205	0.486	putative secreted protein
STM0083	STM0083	AAL19047	95271..95465	0.708	0.127	0.412	0.050	0.581	1.882	0.044	1.129	0.067	0.600	putative inner membrane protein
STM0084	STM0084	AAL19048	95959..97848	0.248	0.142	0.174	0.018	0.700	1.264	0.069	1.481	0.109	1.172	putative sulfatase
yabF	STM0085	AAL19049	98255..98785	0.596	0.051	0.255	0.062	0.428	0.724	0.112	0.809	0.048	1.117	putative NAD(P)H oxidoreductase
kefC	STM0086	AAL19050	98778..100640	0.596	0.109	0.228	0.030	0.383	0.590	0.108	0.425	0.041	0.721	A2 family, K+ efflux antiporter, glutathione-regulated
folA	STM0087	AAL19051	100839..101318	2.098	0.259	0.708	0.071	0.337	2.622	0.539	0.953	0.067	0.364	dihydrofolate reductase type I; trimethoprim resistance
apaH	STM0088	AAL19052	(101424..102272)					N/A					N/A	diadenosine tetraphosphatase
apaG	STM0089	AAL19053	(102283..102660)	3.955	0.726	2.333	0.233	0.590	2.585	0.680	2.144	0.704	0.829	putative cytoplasmic protein
ksgA	STM0090	AAL19054	(102663..103484)	6.838	0.601	3.723	0.728	0.544	5.017	1.300	3.610	0.425	0.719	S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase; kasugamycin resistance
pdxA	STM0091	AAL19055	(103481..104470)	3.236	0.312	2.754	0.279	0.851	2.775	0.358	1.816	0.054	0.655	NAD-dependent dehydrogenase/carboxylase; pyridoxine phosphate biosynthetic protein PdxJ-PdxA subunit
surA	STM0092	AAL19056	(104470..105756)	7.109	1.492	7.667	0.713	1.078	4.891	0.586	5.149	0.251	1.053	peptidyl-prolyl cis-trans isomerase, survival protein
imp	STM0093	AAL19057	(105810..108170)	3.128	0.214	4.108	0.367	1.313	2.009	0.085	2.282	0.071	1.136	Organic solvent tolerance protein
djlA	STM0094	AAL19058	108424..109236	2.168	0.258	0.953	0.084	0.440	1.357	0.253	1.042	0.031	0.768	DnaJ like chaperone protein
rluA	STM0095	AAL19059	(109331..109990)	1.224	0.045	1.051	0.142	0.859	0.662	0.011	0.632	0.068	0.955	23S rRNA pseudouridylate 746 synthase

hepA	STM0096	AAL19060	(110002..112908)					N/A					N/A	RNA polymerase associated protein, putative SNF2 family RNA helicase
polB	STM0097	AAL19061	(113082..115433)	0.672	0.109	0.229	0.025	0.341	0.925	0.163	0.397	0.031	0.429	DNA polymerase II and and 3' --> 5' exonuclease
STM0098	STM0098	AAL19062	(115477..116097)	0.416	0.081	0.226	0.019	0.543	0.647	0.008	0.404	0.023	0.625	putative secreted protein
STM0099	STM0099	AAL19063	116299..116601	0.642	0.078	0.396	0.067	0.616	1.283	0.055	0.706	0.091	0.551	putative inner membrane protein
STM0100	STM0100	AAL19064	116816..117235	0.264	0.061	0.159	0.044	0.601	1.067	0.057	0.539	0.061	0.505	putative cytoplasmic protein
araD	STM0101	AAL19065	(117241..117936)	0.332	0.160	0.191	0.016	0.577	0.510	0.031	0.313	0.029	0.614	L-ribulose-5-phosphate 4-epimerase
araA	STM0102	AAL19066	(118077..119579)					N/A					N/A	L-arabinose isomerase
araB	STM0103	AAL19067	(119590..121299)					N/A					N/A	L-ribulokinase
araC	STM0104	AAL19068	121640..122485	0.676	0.092	2.088	0.360	3.090	0.266	0.065	1.130	0.044	4.254	transcriptional regulator (AraC/XylS family) for ara operon
yabI	STM0105	AAL19069	122604..123371	1.922	0.153	1.351	0.104	0.703	1.911	0.319	0.768	0.066	0.402	putative DedA family, membrane protein
yabJ	STM0106	AAL19070	(123410..124117)	1.066	0.078	0.538	0.053	0.504	0.726	0.071	0.410	0.027	0.565	putative ABC-transport protein
yabK	STM0107	AAL19071	(124101..125711)	1.400	0.174	0.426	0.010	0.304	1.250	0.824	0.441	0.037	0.353	putative binding-protein-dependent transport system inner membrane onent
tbpA	STM0108	AAL19072	(125687..126670)					N/A					N/A	thiamine-binding periplasmic protein
yabN	STM0109	AAL19073	(126848..128506)	0.464	0.099	0.444	0.072	0.955	0.217	0.027	0.417	0.033	1.923	paral putative periplasmic binding protein of transport system
leuD	STM0110	AAL19074	(129057..129662)	0.558	0.038	0.465	0.057	0.833	0.601	0.014	0.883	0.212	1.469	3-isopropylmalate isomerase (dehydratase), subunit with LeuC
leuC	STM0111	AAL19075	(129673..131073)	0.569	0.121	0.484	0.038	0.851	0.703	0.341	0.863	0.015	1.228	3-isopropylmalate isomerase (dehydratase), subunit with LeuD
leuB	STM0112	AAL19076	(131076..132167)	0.516	0.125	0.350	0.047	0.679	0.617	0.031	0.770	0.028	1.247	3-isopropylmalate dehydrogenase
leuA	STM0113	AAL19077	(132167..133738)	0.579	0.047	0.190	0.017	0.328	0.536	0.034	0.599	0.069	1.118	2-isopropylmalate synthase
leuL	STM0114	AAL19078	(133826..133912)	4.151		4.517	1.838	1.088	1.348	0.316			0.000	leu operon leader peptide
leuO	STM0115	AAL19079	134569..135513	0.282	0.145	0.165	0.019	0.584	3.409	0.199	2.651	0.262	0.778	putative transcriptional regulator (LysR family)
ilvI	STM0116	AAL19080	135898..137559	0.369	0.118	0.181	0.019	0.491	0.185	0.019	0.197	0.015	1.062	acetolactate synthase III, valine sensitive, large subunit
ilvH	STM0117	AAL19081	137562..138053	0.734	0.102	0.683	0.053	0.931	0.389	0.140	0.588	0.161	1.513	acetolactate synthase III, small subunit
fruR	STM0118	AAL19082	138337..139341	7.200	1.983	4.948	0.712	0.687	1.622	0.055	1.587	0.548	0.979	transcriptional repressor of fru operon and others (GlaR/LacI family)
yabB	STM0119	AAL19083	139947..140405	5.219	0.748	3.676	0.321	0.704	4.557	0.523	4.184	0.255	0.918	putative cytoplasmic protein
yabC	STM0120	AAL19084	140407..141348	2.911	0.335	3.464	0.256	1.190	3.551	0.029	4.112	0.192	1.158	putative S-adenosyl methionine adenyltransferase
ftsL	STM0121	AAL19085	141345..141710	2.850	0.432	3.292	0.393	1.155	2.818	0.033	4.222	0.263	1.498	cell division protein; ingrowth of wall at septum
ftsI	STM0122	AAL19086	141726..143492	1.862	0.211	1.146	0.157	0.615	1.891	0.052	1.686	0.060	0.892	division specific transpeptidase, penicillin-binding protein 3 re

murE	STM0123	AAL19087	143479..144966	5.841	1.218	3.980	0.344	0.681	5.820	2.111	6.400	0.247	1.100	UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate ligase
murF	STM0124	AAL19088	144963..146321	4.330	1.010	3.949	0.519	0.912	5.036	0.998	4.551	0.234	0.904	D-alanine:D-alanine-adding enzyme
mraY	STM0125	AAL19089	146315..147397	3.090	0.393	1.466	0.173	0.474	4.365	0.754	3.159	0.187	0.724	phospho-N-acetylmuramoyl-pentapeptide transferase
murD	STM0126	AAL19090	147400..148716	3.670	0.394			0.000	4.439	0.855			0.000	UDP-N-acetylmuramoylalanine-D-glutamate ligase
ftsW	STM0127	AAL19091	148716..149960	1.545	0.047	1.117	0.123	0.723	2.268	0.226	1.364	0.148	0.601	essential cell division gene, stablilzes FtsZ ring, cytoplasmic membrane required for PBP2 expression
murG	STM0128	AAL19092	149957..151024	5.968	0.757	4.041	0.536	0.677	6.747	2.018	5.469	0.326	0.811	UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
murC	STM0129	AAL19093	151143..152618	2.634	0.246	2.417	0.289	0.918	3.432	0.513	3.281	0.057	0.956	L-alanine adding enzyme, UDP-N-acetyl-muramate:alanine ligase
ddlB	STM0130	AAL19094	152611..153531	3.648	0.155	2.134	0.214	0.585	4.363	0.983	3.555	0.213	0.815	D-alanine-D-alanine ligase B, affects cell division
ftsQ	STM0131	AAL19095	153533..154363	3.083	0.154	1.874	0.261	0.608	3.030	0.438	2.395	0.341	0.790	cell division protein; ingrowth of wall at septum
ftsA	STM0132	AAL19096	154360..155622	6.979	1.002	4.060	0.650	0.582	5.369	0.936	4.972	0.222	0.926	ATP-binding cell division protein, septation process, lexes with FtsZ, associated with junctions of inner and outer membranes
ftsZ	STM0133	AAL19097	155683..156834	12.909	1.473	16.468	0.852	1.276	12.045	1.277	15.231	0.484	1.265	tubulin-like GTP-binding protein and GTPase, forms circumferential ring in cell division
lpxC	STM0134	AAL19098	156935..157852	7.369	0.704	13.046	0.805	1.771	6.024	0.600	7.436	0.179	1.234	UDP-3-O-acyl N-acetylglucosamine deacetylase
yacA	STM0135	AAL19099	158199..158627	4.043	0.328	5.440	0.501	1.345	3.324	0.121	3.175	0.189	0.955	putative inner membrane protein
secA	STM0136	AAL19100	158689..161394	1.826	0.220	5.727	0.632	3.136	1.596	0.200	3.561	0.233	2.231	preprotein translocase; secretion protein of IISP family
mutT	STM0137	AAL19101	161546..161941	1.130	0.105	0.958	0.137	0.848	1.062	0.178	0.933	0.022	0.878	7,8-dihydro-8-oxoguanine-triphosphatase, prefers dGTP
yacG	STM0138	AAL19102	(162263..162454)					N/A					N/A	putative cytoplasmic protein
yacF	STM0139	AAL19103	(162464..163207)	1.241	0.057	1.945	0.133	1.567	0.596	0.034	1.651	0.111	2.771	putative cytoplasmic protein
yacE	STM0140	AAL19104	(163207..163827)	1.594	0.122	2.584	0.451	1.622	0.651	0.109	1.301	0.085	1.999	putative nucleotide kinase
guaC	STM0141	AAL19105	164053..165096	9.092	0.908	5.088	0.671	0.560	1.998	0.118	3.025	0.222	1.514	GMP reductase
hofC	STM0142	AAL19106	(165127..166329)	0.457	0.068	0.347	0.021	0.758	0.193	0.024	0.352	0.073	1.823	putative onent in type IV pilin biogenesis
hofB	STM0143	AAL19107	(166319..167704)	0.291	0.144	0.395	0.110	1.359	0.116	0.034	0.459	0.018	3.943	putative integral membrane protein involved in biogenesis of fimbriae (type IV pilin), protein transport, DNA uptake
ppdD	STM0144	AAL19108	(167714..168151)	0.358	0.109	0.200	0.057	0.559	0.163	0.028	0.252	0.024	1.544	putative major onent of type IV pilin, prelipin peptidase dependent protein
nadC	STM0145	AAL19109	(168373..169266)	2.718	0.440	0.959	0.073	0.353	1.219	0.217	1.132	0.101	0.928	quinolinate phosphoribosyltransferase
ampD	STM0146	AAL19110	169354..169917	2.276	0.112	1.032	0.098	0.453	1.223	0.232	0.788	0.076	0.645	N-acetyl-anhydromuramyl-L-alanine amidase
ampE	STM0147	AAL19111	169914..170768	1.742	0.056	0.833	0.068	0.478	0.887	0.038	0.794	0.074	0.895	putative transmembrane protein

STM0148	STM0148	AAL19112	(170860..171810)	0.420	0.109			0.000	0.254	0.062			0.000	putative cytoplasmic protein
STM0149	STM0149	AAL19113	(171810..173216)	0.281	0.136	0.139	0.041	0.494	0.153	0.119	0.206	0.004	1.346	putative permease of the Na+:galactoside symporter family
aroP	STM0150	AAL19114	(173380..174753)	0.765	0.028	0.373	0.044	0.488	0.364	0.024	0.473	0.041	1.301	APC family, aromatic amino acid transporter
pdhR	STM0151	AAL19115	175316..176080	0.437	0.049	3.116	0.426	7.125	0.362	0.014	1.031	0.074	2.844	transcriptional repressor for pyruvate dehydrogenase lex (GntR family)
aceE	STM0152	AAL19116	176240..178903	1.269	0.134	13.620	2.370	10.729	1.247	0.018	5.270	0.210	4.226	pyruvate dehydrogenase, decarboxylase onent
aceF	STM0153	AAL19117	178918..180807	1.521	0.234	10.050	1.441	6.607	1.029	0.294	4.047	0.185	3.931	pyruvate dehydrogenase, dihydrolipoyltransacetylase onent
lpdA	STM0154	AAL19118	181007..182431	36.045	5.875	33.634	1.445	0.933	10.418	0.488	17.536	1.269	1.683	lipoamide dehydrogenase (NADH); onent of 2-oxodehydrogenase and pyruvate lexes; L protein of glycine cleavage lex second part
STM0155	STM0155	AAL19119	182720..183004	1.199	0.082	1.264	0.156	1.055	0.620	0.200	0.704	0.082	1.136	putative outer membrane protein
STM0156	STM0156	AAL19120	(183042..183833)	0.475	0.079	0.438	0.064	0.922	0.323	0.015	0.480	0.080	1.483	putative periplasmic protein
yacH	STM0157	AAL19121	(183846..185468)	0.595	0.105	0.523	0.062	0.879	0.339	0.053	0.538	0.021	1.589	putative outer membrane protein
acnB	STM0158	AAL19122	185857..188454	7.541	2.248	26.529	4.203	3.518	3.116	0.131	8.434	0.795	2.707	aconitate hydratase 2
STM0159	STM0159	AAL19123	(188515..189357)	2.315	0.544	1.613	0.218	0.697	1.187	0.087	0.756	0.050	0.637	putative restriction endonuclease
yacL	STM0160	AAL19124	189603..189965	0.812	0.006	1.442	0.137	1.776	0.420	0.079	0.397	0.039	0.943	putative cytoplasmic protein
kdgT	STM0161	AAL19125	190200..191153	0.766	0.146	0.705	0.077	0.920	0.382	0.137	0.457	0.011	1.196	2-keto-3-deoxygluconate permease
STM0162	STM0162	AAL19126	191150..192421	0.524	0.092	0.871	0.086	1.662	0.234	0.006	0.480	0.048	2.055	putative inner membrane protein
STM0163	STM0163	AAL19127	192411..193394	0.555	0.085	1.123	0.179	2.022	0.290	0.069	0.423	0.015	1.459	pyridoxine phosphate biosynthetic protein
STM0164	STM0164	AAL19128	193404..194171	1.850	0.140	1.173	0.163	0.634	0.615	0.015	0.872	0.033	1.417	putative transcriptional regulator (LysR family)
speD	STM0165	AAL19129	(194201..194995)	1.550	0.059	1.394	0.110	0.899	0.889	0.039	1.354	0.109	1.522	S-adenosylmethionine decarboxylase, proenzyme
speE	STM0166	AAL19130	(195016..195876)	2.169	0.063	1.414	0.165	0.652	2.142	0.159	1.976	0.231	0.923	spermidine synthase (putrescine aminopropyltransferase)
yacC	STM0167	AAL19131	(195983..196330)	3.814	0.697	0.683	0.110	0.179	1.480	0.151	0.639	0.093	0.432	putative periplasmic protein
cueO	STM0168	AAL19132	196532..198142	0.830	0.080	1.368	0.248	1.648	0.867	0.095	1.246	0.111	1.437	putative multicopper oxidase
gcd	STM0169	AAL19133	(198220..200610)	1.286	0.045	0.336	0.018	0.262	1.244	0.230	1.444	0.041	1.161	glucose dehydrogenase
hpt	STM0170	AAL19134	200816..201352	10.680	0.813	1.560	0.287	0.146	3.938	0.831	1.443	0.066	0.366	hypoxanthine phosphoribosyltransferase
yadF	STM0171	AAL19135	(201410..202072)	3.351	0.178	3.449	0.347	1.029	1.216	0.036	1.715	0.063	1.410	putative carbonic anhydrase
yadG	STM0172	AAL19136	202181..203107	0.797	0.075	0.621	0.122	0.779	0.515	0.021	0.436	0.026	0.845	putative ABC-type multidrug transport system, ATPase onent
yadH	STM0173	AAL19137	203104..203874	1.046	0.067	0.519	0.091	0.496	0.660	0.120	0.528	0.049	0.800	putative ABC superfamily (membrane) transport protein
stiH	STM0174	AAL19138	(203991..205070)	0.464	0.101	0.196	0.036	0.423	0.270	0.037	0.269	0.023	0.997	putative fimbriae
stiC	STM0175	AAL19139	(205079..207625)	0.545	0.188	0.947	0.245	1.737	0.541	0.261	0.697	0.056	1.289	putativie fimbrial usher
stiB	STM0176	AAL19140	(207652..208335)	0.223	0.116	0.127	0.012	0.573	0.182	0.020	0.280	0.016	1.541	putative fimbrial chaparone
stiA	STM0177	AAL19141	(208383..208922)	0.319	0.103	0.171	0.021	0.535	0.322	0.022	0.547	0.046	1.698	putative fimbrial subunit

yadI	STM0178	AAL19142	209293..209733	0.344	0.138	0.200	0.021	0.581	0.568	0.053	0.411	0.020	0.724	putative PTS enzyme
yadE	STM0179	AAL19143	209795..211024					N/A					N/A	putative xylanase/chitin deacetylase
panD	STM0180	AAL19144	(211031..211411)	2.727	0.518	2.058	0.169	0.754	2.225	0.112	1.967	0.095	0.884	aspartate 1-decarboxylase
panC	STM0181	AAL19145	(211506..212360)	2.127	0.095	1.932	0.123	0.909	1.217	0.140	1.435	0.094	1.180	pantothenate synthetase
panB	STM0182	AAL19146	(212486..213277)	0.887	0.071	1.053	0.174	1.188	0.545	0.005	0.575	0.042	1.055	3-methyl-2-oxobutanoate hydroxymethyltransferase
folK	STM0183	AAL19147	(213398..213877)	0.793	0.072	0.924	0.116	1.164	0.605	0.009	0.721	0.060	1.193	7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase, PPPK
pcnB	STM0184	AAL19148	(213874..215292)	2.694	2.559	1.575	0.322	0.585	3.090	1.101	1.356	0.433	0.439	poly(A) polymerase I
yadB	STM0185	AAL19149	(215433..216374)	1.101	0.096	1.622	0.259	1.473	0.612	0.066	0.958	0.091	1.566	putative glutamyl t-RNA synthetase
dksA	STM0186	AAL19150	(216398..216853)	8.191	1.730	12.539	2.510	1.531	4.207	0.505	7.615	1.572	1.810	dnaK suppressor protein
sfsA	STM0187	AAL19151	(217030..217734)	1.862	0.204	2.454	0.206	1.318	1.137	0.395	1.517	0.075	1.334	regulator for maltose metabolism
ligT	STM0188	AAL19152	(217751..218281)	2.472	0.138	1.647	0.184	0.666	1.042	0.201	1.418	0.100	1.360	2'-5' RNA ligase
hrpB	STM0189	AAL19153	218309..220783	2.301	0.182	1.250	0.636	0.543	1.270	0.243	1.051	0.092	0.827	helicase, ATP-dependent
mrcB	STM0190	AAL19154	220923..223445	2.545	0.107	1.405	0.159	0.552	1.608	0.321	1.633	0.083	1.015	transpeptidase of penicillin-binding protein 1b (peptidoglycan synthetase)
fhuA	STM0191	AAL19155	223738..225927	0.514	0.050	0.126	0.012	0.245	0.148	0.022	0.274	0.017	1.846	outer membrane protein receptor / transporter for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuC	STM0192	AAL19156	225976..226773	0.621	0.031	0.135	0.017	0.218	0.176	0.003	0.279	0.024	1.589	ABC superfamily (atp_bind), hydroxymate-dependent iron transport
fhuD	STM0193	AAL19157	226773..227663	0.634	0.031	0.109	0.024	0.173	0.192	0.087	0.295	0.044	1.538	ABC superfamily (bind _prot), hydroxamate-dependent iron uptake
fhuB	STM0194	AAL19158	227660..229717	0.717	0.068	0.227	0.066	0.316	0.206	0.037	0.304	0.076	1.475	ABC superfamily (membrane), hydroxamate-dependent iron uptake
stfA	STM0195	AAL19159	230657..231217	0.272	0.117	0.146	0.047	0.536	0.835	0.136	0.517	0.012	0.620	putative fimbrial subunit
stfC	STM0196	AAL19160	231303..233960	0.349	0.218	0.100	0.019	0.287	0.282	0.054	0.243	0.014	0.862	putative fimbrial outer membrane usher
stfD	STM0197	AAL19161	233978..234730	0.228	0.143	0.130	0.012	0.567	0.287	0.091	0.304	0.019	1.059	putative periplasmic fimbrial chaperone
stfE	STM0198	AAL19162	234749..235261	0.300	0.177	0.154	0.043	0.515	0.218	0.074	0.247	0.016	1.134	putaive minor fimbrial subunit
stfF	STM0199	AAL19163	235258..235734	0.302	0.096	0.106	0.011	0.351	0.157	0.030	0.190	0.010	1.205	putative minor fimbrial subunit
stfG	STM0200	AAL19164	235734..236264	0.386	0.095	0.113	0.004	0.293	0.308	0.369	0.226	0.008	0.733	putative minor fimbrial subunit; putative adhesin
STM0201	STM0201	AAL19165	236264..237103	0.342	0.085	0.202	0.029	0.591	0.202	0.018	0.240	0.033	1.188	putative outer membrane protein
hemL	STM0202	AAL19166	(237211..238491)	5.680	0.915	3.057	0.188	0.538	2.462	0.507	2.201	0.144	0.894	glutamate-1-semialdehyde aminotransferase (aminomutase)
yadQ	STM0203	AAL19167	238661..240082	1.898	0.140	0.672	0.050	0.354	1.366	0.309	0.912	0.068	0.667	putative ClC family, chlorine transport protein
yadR	STM0204	AAL19168	240119..240508	7.781	1.818	1.084	0.066	0.139	4.888	0.107	2.878	0.441	0.589	putative HesB-like domain
yadS	STM0205	AAL19169	(240609..241232)	1.756	0.130	0.659	0.088	0.375	1.048	0.151	0.714	0.060	0.681	putative inner membrane protein
btuF	STM0206	AAL19170	(241269..242069)	1.680	0.118	1.079	0.107	0.642	1.016	0.079	0.683	0.011	0.672	putative cobalamin periplasmic binding protein

pfs	STM0207	AAL19171	(242062..242760)	3.639	0.169	2.179	0.201	0.599	2.313	0.353	1.887	0.082	0.816	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
dgt	STM0208	AAL19172	242845..244362	1.129	0.082	0.778	0.069	0.689	1.336	0.036	1.174	0.148	0.879	deoxyguanosine triphosphate triphosphohydrolase
htrA	STM0209	AAL19173	244492..245919	5.230	1.918	10.227	1.494	1.956	34.979	3.256	35.959	2.052	1.028	periplasmic serine protease Do, heat shock protein
cdaR	STM0210	AAL19174	246072..247229	0.984	0.064	2.251	2.109	2.287	1.171	0.094	0.831	0.068	0.709	putative inner membrane protein
yaeH	STM0211	AAL19175	(247318..247704)	4.019	0.986	6.536	0.854	1.626	1.228	0.123	1.409	0.119	1.147	putative cytoplasmic protein
STM0212	STM0212	AAL19176	247951..249252	1.765	0.184	0.992	0.085	0.562	5.837	1.875	2.727	0.431	0.467	putative inner membrane protein
dapD	STM0213	AAL19177	(249289..250113)					N/A					N/A	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
glnD	STM0214	AAL19178	(250143..252815)	0.856	0.081	0.932	0.230	1.089	0.601	0.126	0.746	0.016	1.242	uridylyltransferase
map	STM0215	AAL19179	(253052..253846)	2.486	0.045	2.161	0.223	0.869	1.175	0.046	1.039	0.110	0.884	methionine aminopeptidase
rpsB	STM0216	AAL19180	254297..255022	47.373	1.535	37.018	3.164	0.781	20.562	0.674	18.368	1.042	0.893	30S ribosomal subunit protein S2
tsf	STM0217	AAL19181	255280..256131	27.443	1.134	19.615	2.928	0.715	11.189	0.087	9.198	0.566	0.822	protein chain elongation factor EF-Ts
pyrH	STM0218	AAL19182	256276..257001	7.883	0.491	8.726	0.572	1.107	3.725	0.191	3.705	0.144	0.995	uridylate kinase
frr	STM0219	AAL19183	257148..257705	11.450	0.982	8.132	0.625	0.710	6.018	0.338	3.584	0.278	0.596	ribosome releasing factor
dxr	STM0220	AAL19184	257846..259042	3.106	0.302	1.649	0.088	0.531	1.621	0.140	1.111	0.070	0.685	1-deoxy-D-xylulose 5-phosphate reductoisomerase
uppS	STM0221	AAL19185	259355..260113	7.139	0.267	2.453	0.386	0.344	3.221	0.429	1.049	0.059	0.326	undecaprenyl pyrophosphate synthetase (di-trans,poly-cis-decaprenylcistransferase)
cdsA	STM0222	AAL19186	260126..260983	2.495	0.085	1.376	0.131	0.551	1.498	0.154	0.776	0.072	0.518	CDP-diglyceride synthase
yaeL	STM0223	AAL19187	260995..262347	5.223	0.092	6.179	1.299	1.183	4.049	0.311	1.976	0.116	0.488	putative membrane-associated Zn-dependent protease
yaeT	STM0224	AAL19188	262379..264793	3.257	0.649	11.769	1.107	3.613	3.016	0.120	3.373	0.182	1.118	putative outer membrane antigen
hlpA	STM0225	AAL19189	264916..265401	12.949	2.311	20.082	2.258	1.551	9.401	1.557	9.549	0.294	1.016	histone-like protein, located in outer membrane
lpxD	STM0226	AAL19190	265405..266430	3.211	0.457	8.422	1.083	2.623	2.515	0.147	3.971	0.347	1.579	UDP-3-O-(3-hydroxymyristoyl)-glucosamine n-acyltransferase
fabZ	STM0227	AAL19191	266536..266991	4.305	0.261	6.525	0.314	1.516	2.927	0.097	3.416	0.306	1.167	(3R)-hydroxymyristol acyl carrier protein dehydratase
lpxA	STM0228	AAL19192	266995..267783	5.953	0.784	7.547	0.512	1.268	4.429	0.646	4.347	0.439	0.981	UDP-N-acetylglucosamine acetyltransferase
lpxB	STM0229	AAL19193	267783..268931	3.445	0.306	2.347	0.320	0.681	2.508	0.222	1.832	0.125	0.730	tetraacyldisaccharide-1-P
rnhB	STM0230	AAL19194	268928..269524	5.186	0.613	2.008	0.215	0.387	3.359	0.532	2.304	0.228	0.686	RNAse HII
dnaE	STM0231	AAL19195	269548..273030					N/A					N/A	DNA polymerase III, alpha subunit
accA	STM0232	AAL19196	273043..274002	18.923	2.507	8.729	0.432	0.461	7.504	1.630	4.621	0.189	0.616	acetylCoA carboxylase, carboxytransferase onent, alpha subunit
STM0233	STM0233	AAL19197	274183..275946	0.493	0.075	0.337	0.046	0.683	0.275	0.117	0.301	0.028	1.097	putative endochitinase
ldcC	STM0234	AAL19198	276022..278163	0.487	0.038	0.825	0.039	1.693	0.307	0.010	0.512	0.051	1.668	lysine decarboxylase 2, constitutive

yaeR	STM0235	AAL19199	278219..278608	0.884	0.060	1.178	0.038	1.332	0.581	0.044	0.814	0.052	1.401	putative lactoylglutathione lyase
mesJ	STM0236	AAL19200	278671..279963	1.634	0.089	1.182	0.114	0.724	1.045	0.038	1.043	0.048	0.998	cell cycle protein
rof	STM0237	AAL19201	(280047..280307)					N/A					N/A	modulator of Rho-dependent transcription termination
yaeP	STM0238	AAL19202	(280294..280512)	4.391	1.117	2.307	0.265	0.525	1.974	0.096	1.989	0.353	1.008	putative cytoplasmic protein
yaeQ	STM0239	AAL19203	280692..281237	2.303	0.058	1.130	0.142	0.491	1.821	0.163	2.253	0.179	1.237	putative cytoplasmic protein
yaeJ	STM0240	AAL19204	281234..281656	1.705	0.145	1.140	0.224	0.669	1.348	0.098	1.506	0.060	1.117	putative-tRNA hydrolase domain
cutF	STM0241; pseudogene; frameshift relative to E. coli					1.782	0.174	1.454	0.149	0.816	1.433	0.222	1.609	0.678 1.123
proS	STM0242	AAL19205	(282467..284185)	1.301	0.060	4.276	0.230	3.288	0.793	0.105	1.694	0.087	2.136	proline tRNA synthetase
yaeB	STM0243	AAL19206	(284296..285003)	0.826	0.032	1.539	0.229	1.864	0.642	0.070	0.884	0.029	1.378	paral putative regulator
rcsF	STM0244	AAL19207	(285000..285404)	1.881	0.109	2.872	0.384	1.527	1.528	0.194	2.714	0.216	1.776	regulator in colanic acid synthesis; overexpression confers mucoid phenotype, increases capsule synthesis
yaeC	STM0245	AAL19208	(285523..286338)	2.852	0.167	2.639	0.189	0.925	1.545	0.088	2.526	0.414	1.635	putative outer membrane lipoprotein
yaeE	STM0246	AAL19209	(286377..287030)	0.882	0.096	1.161	0.084	1.316	0.530	0.047	0.681	0.175	1.285	putative ABC superfamily (membrane) transport protein
abc	STM0247	AAL19210	(287023..288054)	0.958	0.074	1.526	0.346	1.593	0.802	0.179	0.948	0.316	1.181	putative ABC superfamily (atp_bind) transport system
yaeD	STM0248	AAL19211	288244..288810	7.012	0.637	3.706	0.678	0.529	4.948	0.383	3.431	0.479	0.693	putative dehydratase
ileV	STM0250						N/A					N/A		
alaV	STM0251						N/A					N/A		
aspU	STM0254						N/A					N/A		
yafB	STM0255	AAL19212	295069..295872	0.978	0.040	1.263	0.145	1.292	1.462	0.438	1.424	0.323	0.974	2,5-diketo-D-gluconate reductase B
yafC	STM0256	AAL19213	(295893..296807)	0.426	0.109	0.610	0.138	1.433	0.393	0.062	0.560	0.049	1.424	putative transcriptional regulator, LysR family
STM0257	STM0257	AAL19214	296912..298087	0.380	0.101	0.243	0.044	0.639	0.199	0.044	0.389	0.040	1.954	putative drug efflux protein (perhaps for chloramphenicol)
yafD	STM0258	AAL19215	298240..299019	2.511	0.142	1.246	0.166	0.496	0.688	0.063	0.704	0.016	1.025	putative cytoplasmic protein
yafE	STM0259	AAL19216	299097..299867	0.906	0.035	0.771	0.065	0.851	0.545	0.186	0.480	0.030	0.880	putative methyltransferase in menaquinone/biotin biosynthesis
dniR	STM0260	AAL19217	(299923..301290)	2.860	0.108	3.851	0.883	1.347	2.981	0.248	2.832	0.130	0.950	transcriptional regulator for nitrite reductase (cytochrome c552)
gloB	STM0261	AAL19218	(301362..302117)	0.689	0.037	0.950	0.062	1.379	0.430	0.032	0.699	0.058	1.625	hydroxyacylglutathione hydrolase
yafS	STM0262	AAL19219	302152..302874	0.698	0.022	0.640	0.006	0.917	0.379	0.089	0.369	0.037	0.973	putative SAM-dependent methyltransferase
rnhA	STM0263	AAL19220	(302871..303338)	0.826	0.040	0.558	0.029	0.675	0.457	0.134	0.517	0.074	1.131	RNase HI, degrades RNA of DNA-RNA hybrids
dnaQ	STM0264	AAL19221	303402..304133	0.936	0.090	1.026	0.165	1.096	0.626	0.063	0.728	0.110	1.162	DNA polymerase III, epsilon subunit, 3-5 exonucleolytic proofreading function
aspV	STM0265						N/A					N/A		
STM0266	STM0266	AAL19222	(304665..305720)	0.515	0.121	0.350	0.038	0.680	0.320	0.012	0.348	0.029	1.087	putative cytoplasmic protein
STM0267	STM0267	AAL19223	(305731..306726)	0.404	0.141	0.268	0.062	0.663	0.280	0.010	0.417	0.114	1.492	putative cytoplasmic protein

STM0268	STM0268	AAL19224	(306723..308606)					N/A					N/A	putative cytoplasmic protein
STM0269	STM0269	AAL19225	(308622..309116)	0.474	0.084	0.234	0.044	0.493	0.359	0.048	0.329	0.035	0.917	putative cytoplasmic protein
STM0270	STM0270	AAL19226	(309113..309937)	0.458	0.113	0.322	0.060	0.705	0.212	0.058	0.325	0.014	1.530	putative cytoplasmic protein
STM0271	STM0271	AAL19227	(309924..310826)	0.211	0.148	0.142	0.012	0.674	0.113	0.022	0.207	0.035	1.840	putative cytoplasmic protein
STM0272	STM0272	AAL19228	311194..313833					N/A					N/A	putative ATPase with chaperone activity; Homolog of Yersinia clpB
STM0273	STM0273	AAL19229	313933..314475	0.294	0.188	0.190	0.011	0.649	0.266	0.243	0.273	0.022	1.025	putative cytoplasmic protein
STM0274	STM0274	AAL19230	314499..316007	0.197	0.137	0.137	0.019	0.695	0.150	0.021	0.208	0.030	1.394	putative cytoplasmic protein
STM0274A	STM0274A	AAL19231	316070..316180					N/A					N/A	invasol SirA
STM0275	STM0275	AAL19232	316307..316639	0.280	0.095	0.211	0.045	0.754	0.497	0.118	0.551	0.062	1.108	putative cytoplasmic protein
STM0276	STM0276	AAL19233	316893..317378	0.134	0.098	0.103	0.007	0.772	0.421	0.024	1.308	0.069	3.111	putative cytoplasmic protein
STM0277	STM0277	AAL19234	317683..318168	0.226	0.104	0.231	0.029	1.020	0.653	0.465	0.635	0.100	0.973	putative cytoplasmic protein
STM0278	STM0278	AAL19235	318153..318536	0.290	0.132	0.178	0.012	0.611	0.871	0.221	0.744	0.033	0.854	putative periplasmic protein
STM0279	STM0279	AAL19236	318679..319164	0.228	0.113	0.138	0.011	0.607	0.710	0.043	1.027	0.069	1.448	putative cytoplasmic protein
STM0280	STM0280	AAL19237	319231..319767	0.207	0.125	0.197	0.020	0.954	0.303	0.024	0.795	0.091	2.622	putative outer membrane lipoprotein
STM0281	STM0281	AAL19238	319771..321114	0.222	0.142	0.100	0.026	0.452	0.316	0.048	0.669	0.090	2.115	putative cytoplasmic protein
STM0282	STM0282	AAL19239	321111..322415	0.264	0.150	0.125	0.014	0.471	0.472	0.090	0.702	0.054	1.487	putative outer membrane protein, OmpA family
STM0283	STM0283	AAL19240	322420..323193	0.205	0.102	0.108	0.027	0.530	0.422	0.132	0.356	0.037	0.843	putative inner membrane protein
STM0284	STM0284	AAL19241	323396..323827	1.180	0.536	0.456	0.058	0.387	1.240	0.366	0.647	0.047	0.521	putative shiga-like toxin A subunit
STM0285	STM0285	AAL19242	323861..327730					N/A					N/A	putative inner membrane protein
STM0286	STM0286	AAL19243	327730..328518	0.282	0.174	0.152	0.016	0.538	0.882	0.052	1.252	0.065	1.419	putative cytoplasmic protein
STM0287	STM0287	AAL19244	328515..328931	0.268	0.124	0.128	0.023	0.477	0.439	0.008	0.562	0.010	1.280	putative periplasmic protein
STM0288	STM0288	AAL19245	328955..329476	0.218	0.148	0.108	0.014	0.496	0.383	0.111	0.359	0.041	0.939	putative cytoplasmic protein
STM0289	STM0289	AAL19246	329873..332062	0.303	0.131	0.117	0.022	0.387	0.642	0.017	1.227	0.074	1.911	putative cytoplasmic protein
STM0290	STM0290	AAL19247	332086..332532	0.524	0.066	0.189	0.044	0.361	0.402	0.033	0.632	0.069	1.572	putative cytoplasmic protein
STM0291	STM0291	AAL19248	332551..336645					N/A					N/A	putative RHS-family protein
STM0292	STM0292	AAL19249	337095..337835	0.290	0.131	0.334	0.052	1.153	0.949	0.416	1.029	0.062	1.084	putative RHS-family protein
STM0293	STM0293	AAL19250	337829..338275	0.228	0.058	0.338	0.029	1.486	1.636	0.358	3.005	0.244	1.836	putative cytoplasmic protein
STM0294	STM0294	AAL19251	338838..339275	0.177	0.095	0.182	0.008	1.028	1.169	0.132	0.717	0.089	0.613	putative cytoplasmic protein
STM0295	STM0295	AAL19252	340044..340352	0.218	0.101	0.102	0.027	0.466	0.435	0.062	0.525	0.089	1.208	putative cytoplasmic protein
STM0296	STM0296	AAL19253	(340454..340702)	0.245	0.135	0.281	0.043	1.149	0.283	0.085	0.289	0.070	1.022	putative cytoplasmic protein
STM0297	STM0297	AAL19254	340755..340952	0.299	0.114	0.287	0.027	0.963	0.469	0.293	0.325	0.047	0.692	putative transposase
STM0298	STM0298	AAL19255	341178..341459	0.244	0.104	0.183	0.043	0.750	0.533	0.141	0.493	0.059	0.925	putative integrase core domain
safA	STM0299	AAL19256	342209..342721	0.188	0.089	0.091	0.016	0.483	6.987	0.864	4.635	0.355	0.663	putative outer membrane protein
safB	STM0300	AAL19257	342829..343542	0.223	0.115	0.120	0.015	0.536	1.044	0.108	1.145	0.079	1.097	putative fimbriae assembly chaparone
safC	STM0301	AAL19258	343566..346076	0.239	0.119	0.298	0.028	1.250	0.428	0.061	0.727	0.098	1.699	putative fimbriae usher
safD	STM0302	AAL19259	346098..346568	0.500	0.066	0.246	0.032	0.492	1.623	1.502	1.007	0.039	0.621	putative fimbriae subunit
ybeJ	STM0303	AAL19260	346974..347795	0.220	0.092	0.123	0.005	0.560	4.968	0.364	5.580	0.265	1.123	putative xylanase/chitin deacetylase

sinR	STM0304	AAL19261	348610..349557	0.605	0.051	0.596	0.078	0.984	6.216	0.806	5.785	0.370	0.931	transcriptional regulator
STM0305	STM0305	AAL19262	349674..349889	0.404	0.063	0.385	0.051	0.953	5.304	0.668	5.688	0.478	1.072	putative cytoplasmic protein
STM0306	STM0306	AAL19263	(349893..350612)	0.760	0.071	0.989	0.066	1.301	13.327	0.410	26.554	1.710	1.993	Homolog of sapA
STM0307	STM0307	AAL19264	(350943..351350)	0.678	0.068	0.488	0.092	0.720	4.595	0.512	2.866	0.499	0.624	homology to Shigella VirG protein
yafV	STM0308	AAL19265	(351721..352488)	2.769	0.371	0.864	0.159	0.312	1.621	0.100	1.409	0.277	0.869	putative amidohydrolase
yafH	STM0309	AAL19266	(352597..355041)	1.748	0.182	1.427	0.120	0.816	0.598	0.048	0.983	0.031	1.645	putative acyl-CoA dehydrogenase
ghmA	STM0310	AAL19267	355281..355859	3.658	0.340	3.590	0.583	0.981	2.133	0.572	1.775	0.274	0.832	phosphoheptose isomerase
yafJ	STM0311	AAL19268	356072..356839	1.338	0.082	1.218	0.149	0.910	1.241	0.387	1.174	0.121	0.946	putative glutamine amidotransferase
yafK	STM0312	AAL19269	(356810..357550)	1.400	0.202	0.869	0.226	0.621	1.436	0.121	0.893	0.064	0.622	putative periplasmic protein
dinP	STM0313	AAL19270	357800..358855	0.883	0.060	0.375	0.020	0.425	1.095	0.076	0.502	0.031	0.458	DNA polymerase IV, devoid of proofreading, damage-inducible protein P
STM0314	STM0314		0.382	0.115	0.335	0.067	0.878	2.103	0.544	1.232	0.068	0.586	pseudogene; frameshift relative to E. coli probable	
prfH	STM0315	AAL19271	360203..360817	0.391	0.098	0.635	0.133	1.624	1.149	0.068	1.048	0.194	0.912	putative peptide chain release factor
pepD	STM0316	AAL19272	(360973..362430)	1.798	0.222	9.322	0.747	5.183	1.163	0.129	2.724	0.088	2.342	aminoacyl-histidine dipeptidase (peptidase D)
gpt	STM0317	AAL19273	362679..363137	1.565	0.180	1.530	0.292	0.978	1.514	0.211	0.541	0.090	0.357	guanine-hypoxanthine phosphoribosyltransferase
yafA	STM0318	AAL19274	363226..364470	0.945	0.054	1.799	0.283	1.904	0.742	0.065	1.187	0.091	1.600	putative hydrolase of the alpha/beta superfamily
crl	STM0319	AAL19275	364528..364929	5.231	1.258	5.131	0.356	0.981	1.081	0.088	2.075	0.148	1.920	transcriptional regulator of cryptic csgA gene for curli surface fibers
phoE	STM0320	AAL19276	(364980..366032)	0.620	0.071	0.899	0.053	1.451	0.290	0.069	0.479	0.061	1.654	outer membrane pore protein e (e,ic,nmpab)
proB	STM0321	AAL19277	366315..367418	2.702	0.523	2.131	0.366	0.789	1.004	0.252	1.709	0.070	1.702	gamma-glutamate kinase
proA	STM0322	AAL19278	367430..368680	2.264	0.419	2.144	0.449	0.947	0.991	0.205	1.511	0.063	1.525	gamma-glutamylphosphate reductase
thrW	STM0323						N/A					N/A		
STM0324	STM0324	AAL19279	369158..369379	0.396	0.064	0.333	0.028	0.840	0.291	0.041	0.258	0.082	0.885	putative inner membrane protein
STM0325	STM0325	AAL19280	(369197..369997)	0.473	0.149	0.383	0.029	0.808	0.310	0.105	0.262	0.022	0.846	putative IS3 transposase
STM0326	STM0326	pseudogene; frameshift; putative HSP70 class			0.611	0.168	0.336	0.065	0.551	0.525	0.176	0.296	0.067	0.564
STM0327	STM0327	AAL19281	370739..371062	16.648	6.464	4.146	0.585	0.249	1.213	0.158	0.575	0.018	0.474	putative cytoplasmic protein
STM0328	STM0328	AAL19282	371403..372641	0.264	0.058	0.136	0.028	0.513	0.890	0.119	0.612	0.041	0.687	putative permease
STM0329	STM0329	AAL19283	372773..374194	0.276	0.114	0.227	0.035	0.824	1.264	0.190	1.067	0.068	0.844	putative 3-isopropylmalate isomerase (dehydratase), subunit with LeuD
STM0330	STM0330	AAL19284	374196..374822	0.293	0.173	0.194	0.044	0.662	0.606	0.024	0.566	0.040	0.934	putative 3-isopropylmalate isomerase (dehydratase), subunit with LeuC
STM0331	STM0331	AAL19285	374837..375715	0.230	0.097	0.195	0.057	0.851	0.436	0.026	0.608	0.052	1.395	putative fumarylacetoacetate (FAA) hydrolase
STM0332	STM0332	AAL19286	375715..376629	0.311	0.098	0.175	0.035	0.563	0.678	0.132	0.785	0.052	1.158	putative hydrolase or acyltransferase
STM0333	STM0333	AAL19287	376663..377628	0.411	0.109	0.203	0.023	0.495	0.370	0.030	0.353	0.014	0.953	putative transcriptional regulator, LysR family
STM0334	STM0334	AAL19288	(377573..377845)	0.361	0.072	0.115	0.012	0.319	0.617	0.121	0.313	0.029	0.507	putative cytoplasmic protein
STM0335	STM0335	AAL19289	378536..378934	0.231	0.068	0.103	0.015	0.443	1.169	0.110	0.426	0.066	0.364	putative outer membrane protein
stbE	STM0336	AAL19290	(378981..379739)	0.149	0.092	0.116	0.040	0.774	0.494	0.047	0.564	0.008	1.143	putative fimbriae; chaparone

stbD	STM0337	AAL19291	(379705..381030)	0.182	0.101	0.127	0.015	0.697	0.288	0.017	0.681	0.049	2.367	putative fimbriae; usher
stbC	STM0338	AAL19292	(381035..383596)	0.200	0.089	0.088	0.019	0.441	0.212	0.035	0.352	0.045	1.660	putative fimbriae; usher
stbB	STM0339	AAL19293	(383580..384341)	0.136	0.120	0.071	0.015	0.524	0.330	0.072	0.565	0.025	1.712	putative fimbriae; chaparone
stbA	STM0340	AAL19294	(384403..384939)	0.300	0.104	0.141	0.014	0.471	1.571	0.129	1.665	0.097	1.060	putative fimbriae; major subunit
STM0341	STM0341	AAL19295	385573..386337	0.305	0.054	0.227	0.043	0.743	12.684	1.481	3.130	0.096	0.247	putative inner membrane protein
STM0342	STM0342	AAL19296	386310..386609	0.353	0.067	0.164	0.036	0.464	8.499	0.105	3.331	0.422	0.392	putative periplasmic protein
STM0343	STM0343	AAL19297	387109..388683	0.192	0.077	0.116	0.017	0.603	1.603	0.062	0.718	0.078	0.448	putative Diguanylate cyclase/phosphodiesterase domain 1
STM0344	STM0344	AAL19298	388783..389526	0.619	0.052	0.285	0.006	0.460	3.663	0.097	1.455	0.087	0.397	putative response regulator
STM0345	STM0345	AAL19299	389499..389987	0.395	0.083	0.219	0.033	0.554	3.977	0.092	1.829	0.138	0.460	putative inner membrane protein
STM0346	STM0346	AAL19300	390388..390912	0.201	0.108	0.112	0.011	0.560	6.863	0.470	3.584	0.091	0.522	putative outer membrane protein; Homolog of ail and ompX
STM0347	STM0347	AAL19301	391056..391697	0.193	0.091	0.131	0.012	0.681	5.566	0.790	3.131	0.170	0.562	putative response regulator
STM0348	STM0348	AAL19302	391708..391932	0.430	0.098	0.274	0.057	0.638	6.498	0.498	4.000	0.216	0.616	putative inner membrane protein
STM0349	STM0349	AAL19303	391990..392349	0.315	0.127	0.183	0.055	0.580	6.629	0.348	3.836	0.262	0.579	putative outer membrane lipoprotein
STM0350	STM0350	AAL19304	(392419..393930)	0.302	0.156	0.123	0.030	0.409	0.578	0.047	0.436	0.038	0.753	homology to outer membrane efflux protein
STM0351	STM0351	AAL19305	(393893..397060)	0.201	0.140	0.137	0.002	0.684	0.117	0.008	0.230	0.029	1.971	putative cation efflux system protein
STM0352	STM0352	AAL19306	(397057..398283)	0.218	0.162	0.088	0.023	0.405	0.108	0.041	0.167	0.011	1.541	putative cation efflux pump
STM0353	STM0353	AAL19307	398560..400848					N/A					N/A	putative cation transport ATPase
STM0354	STM0354	AAL19308	400860..401324	0.805	0.058	0.800	0.068	0.993	0.346	0.093	0.452	0.038	1.308	putative transcriptional regulator
STM0355	STM0355	AAL19309	401402..401596	1.902	0.184	1.491	0.215	0.784	0.936	0.154	1.030	0.440	1.100	putative Copper chaperone
STM0356	STM0356	AAL19310	401889..403142	1.643	0.072	0.656	0.148	0.399	0.437	0.018	0.729	0.022	1.669	putative inner membrane protein
mod	STM0357	AAL19311	403331..405289	0.801	0.014	0.824	0.055	1.029	0.519	0.047	0.657	0.053	1.266	DNA methylase; restriction system
res	STM0358	AAL19312	405299..408271	0.550	0.058	0.748	0.056	1.359	0.562	0.067	0.726	0.039	1.291	DNA restriction (DNA helicase
STM0359	STM0359	AAL19313	408548..408649	0.723	0.173	0.658	0.138	0.910	6.756	1.068	2.244	0.141	0.332	putative cytoplasmic protein
STM0360	STM0360	AAL19314	408766..410169	0.335	0.114	0.154	0.029	0.460	3.764	0.947	3.115	0.201	0.827	cytochrome BD2 subunit I
STM0361	STM0361	AAL19315	410166..411176	0.634	0.028	0.285	0.044	0.449	3.028	0.635	3.313	0.181	1.094	cytochrome BD2 subunit II
STM0362	STM0362	AAL19316	411193..411417	0.441	0.097	0.254	0.027	0.575	1.824	0.032	0.960	0.073	0.526	putative cytoplasmic protein
STM0363	STM0363	AAL19317	411513..412517	0.698	0.025	0.305	0.047	0.437	0.339	0.016	0.706	0.110	2.082	putative transcription regulator, AraC family
foxA	STM0364	AAL19318	412663..414771	0.426	0.096	0.213	0.012	0.500	0.220	0.004	0.229	0.013	1.041	ferrioxamine receptor
yahN	STM0365	AAL19319	(414812..415444)	2.057	0.095	0.857	0.015	0.417	0.836	0.148	1.059	0.070	1.267	paral putative transport protein
yahO	STM0366	AAL19320	415676..415951	1.236	0.163	0.713	0.048	0.576	2.480	0.072	1.420	0.086	0.572	putative periplasmic protein
prpR	STM0367	AAL19321	(416087..417712)	2.794	0.310	1.874	0.205	0.670	0.385	0.059	0.581	0.028	1.510	regulator for prp operon (EBP family)
prpB	STM0368	AAL19322	417977..418864	0.553	0.059	0.784	0.124	1.419	2.382	0.251	3.423	0.150	1.437	putative carboxyphosphonoenolpyruvate mutase
prpC	STM0369	AAL19323	418987..420156	0.247	0.109	0.333	0.063	1.352	1.216	0.144	1.828	0.081	1.504	putative citrate synthase
prpD	STM0370	AAL19324	420196..421647	0.396	0.102	0.478	0.026	1.206	1.838	0.240	2.109	0.126	1.148	putative protein in propionate catabolism
prpE	STM0371	AAL19325	421688..423574	0.380	0.105	0.309	0.022	0.815	2.201	0.429	1.486	0.157	0.675	putative acetyl-CoA synthetase, propionate catabolism operon

hemB	STM0372	AAL19326	(423678..424652)	1.701	0.038	3.974	0.197	2.336	1.141	0.103	1.740	0.160	1.525	5-aminolevulinate dehydratase (porphobilinogen synthase)
yaiU	STM0373	AAL19327	425165..428101	0.256	0.085	0.346	0.034	1.352	1.651	0.003	1.477	0.046	0.895	flagellar protein; similar to 3rd module of ATP-binding onents of transporters
yaiV	STM0374	AAL19328	428187..428810	0.298	0.076	0.220	0.023	0.738	0.773	0.026	0.500	0.045	0.647	putative inner membrane protein
ampH	STM0375	AAL19329	(428855..429985)	2.419	0.359	3.460	0.449	1.430	21.881	2.345	39.554	5.148	1.808	penicillin- binding protein
sbmA	STM0376	AAL19330	430359..431579	0.597	0.064	0.686	0.049	1.149	0.591	0.064	0.617	0.059	1.044	putative ABC superfamily transporter
yaiW	STM0377	AAL19331	431594..432688	0.636	0.054	0.944	0.191	1.485	0.490	0.040	0.592	0.039	1.208	putative outer membrane lipoprotein
yaiY	STM0378	AAL19332	(432726..433034)	1.589	0.225	0.568	0.079	0.358	1.038	0.155	0.610	0.055	0.587	putative inner membrane protein
yaiZ	STM0379	AAL19333	433302..433517	10.395	1.246	1.382	0.111	0.133	1.398	0.032	0.801	0.090	0.573	putative inner membrane protein
ddlA	STM0380	AAL19334	(433543..434637)	6.499	0.205	1.697	0.370	0.261	2.161	0.259	1.299	0.067	0.601	D-alanine-D-alanine ligase A
STM0381	STM0381	AAL19335	434715..435428	0.696	0.070	0.227	0.020	0.326	0.423	0.042	0.417	0.041	0.984	putative inner membrane protein
STM0382	STM0382	AAL19336	435597..436808	0.343	0.122	0.155	0.020	0.452	0.412	0.041	0.325	0.022	0.788	putative permease
yaiB	STM0383	AAL19337	437099..437365	2.902	0.763	2.037	0.303	0.702	12.415	0.356	5.924	0.868	0.477	putative cytoplasmic protein
psiF	STM0384	AAL19338	437717..438037	0.848	0.095	0.427	0.033	0.503	2.003	0.102	1.323	0.140	0.661	induced by phosphate starvation
yaiC	STM0385	AAL19339	438129..439241	0.640	0.063	0.463	0.077	0.723	0.576	0.096	0.560	0.041	0.972	putative diguanylate cyclase/phosphodiesterase domain 1
proC	STM0386	AAL19340	(439256..440065)	2.520	0.368	3.281	0.565	1.302	1.524	0.161	2.428	0.147	1.593	pyrroline-5-carboxylate reductase
yaiI	STM0387	AAL19341	440205..440660	2.114	0.134	0.922	0.019	0.436	1.393	0.042	0.678	0.042	0.487	putative cytoplasmic protein
aroL	STM0388	AAL19342	440845..441390	1.750	0.043	1.355	0.198	0.775	1.197	0.103	1.030	0.123	0.861	shikimate kinase II
yaiA	STM0389	AAL19343	441417..441608	1.612	0.215	1.121	0.043	0.696	1.221	0.218	0.876	0.145	0.717	putative cytoplasmic protein
aroM	STM0390	AAL19344	441859..442536	0.886	0.007	0.728	0.055	0.822	0.907	0.095	1.074	0.035	1.184	protein of aro operon, regulated by aroR
yaiE	STM0391	AAL19345	442607..442891	2.823	0.589	1.104	0.095	0.391	1.463	0.123	0.866	0.041	0.592	putative cytoplasmic protein
rdgC	STM0392	AAL19346	(442929..443840)	3.109	0.252	1.102	0.052	0.355	1.524	0.118	1.009	0.095	0.662	putative exonuclease involved in removal of stalled replication fork
yajF	STM0393	AAL19347	443966..444874	1.001	0.016	1.070	0.157	1.069	0.692	0.000	1.009	0.072	1.458	putative sugar kinase/putative transcriptional regulator (NagC/XylR familiy)
araJ	STM0394	AAL19348	(444896..446068)	0.584	0.099	0.307	0.059	0.525	0.381	0.019	0.373	0.004	0.978	MFS family, arabinose polymer transporter
sbcC	STM0395	AAL19349	(446241..449381)					N/A					N/A	ATP-dependent dsDNA exonuclease
sbcD	STM0396	AAL19350	(449378..450580)	0.809	0.048	0.644	0.060	0.797	0.482	0.071	0.568	0.024	1.178	ATP-dependent dsDNA exonuclease
phoB	STM0397	AAL19351	450795..451484	1.358	0.081	0.762	0.159	0.562	2.934	0.414	3.406	0.227	1.161	response regulator in two-onent regulatory system with PhoR (or CreC), regulates pho regulon (OmpR family)
phoR	STM0398	AAL19352	451554..452849	0.688	0.037	0.573	0.043	0.832	1.609	0.037	1.649	0.114	1.025	sensory kinase in two-onent regulatory system with PhoB, regulates pho regulon
brnQ	STM0399	AAL19353	453258..454577	3.058	0.293	0.872	0.083	0.285	1.632	0.319	1.215	0.039	0.744	LIVCS family, branched chain amino acid transporter system II (LIV-II)
proY	STM0400	AAL19354	454652..456022	0.701	0.078	0.343	0.074	0.489	0.677	0.022	0.499	0.102	0.738	putative APC family, proline transporter
malZ	STM0401	AAL19355	456184..458001	0.744	0.067	0.599	0.113	0.804	0.570	0.020	0.420	0.032	0.737	maltodextrin glucosidase

STM0402	STM0402	AAL19356	(458073..458675)	14.614	0.889	19.262	0.807	1.318	10.613	1.354	18.880	1.682	1.779	putative thiol - alkyl hydroperoxide reductase
yajB	STM0403	AAL19357	(458885..459466)	1.693	0.084	2.292	0.506	1.354	1.196	0.036	1.321	0.265	1.104	putative cytoplasmic protein
queA	STM0404	AAL19358	459560..460624	1.448	0.090	1.009	0.073	0.697	1.627	0.067	0.780	0.037	0.480	S-adenosylmethionine-tRNA ribosyltransferase-isomerase
tgt	STM0405	AAL19359	460821..461948	4.082	0.086	2.981	0.307	0.730	3.909	0.153	1.579	0.081	0.404	tRNA-guanine transglycosylase
yajC	STM0406	AAL19360	461971..462303	10.789	0.115	14.437	1.793	1.338	8.700	0.816	7.246	0.277	0.833	preprotein translocase IISP family, membrane subunit
secD	STM0407	AAL19361	462331..464178	3.579	0.264	4.813	0.942	1.345	2.874	0.109	1.912	0.149	0.665	preprotein translocase, IISP family, part of the channel
secF	STM0408	AAL19362	464189..465160	2.096	0.036	2.819	0.200	1.345	1.576	0.096	1.074	0.041	0.682	preprotein translocase, IISP family, membrane subunit
STM0409	STM0409	AAL19363	465308..465673	0.688	0.042	0.535	0.028	0.778	0.645	0.163	0.473	0.028	0.734	hypothetical protein
STM0410	STM0410	AAL19364	465699..466391	0.422	0.063	0.304	0.033	0.721	0.300	0.113	0.260	0.023	0.867	putative regulatory protein
yajD	STM0411	AAL19365	466561..466908	2.059	0.168	1.154	0.101	0.560	0.686	0.022	0.537	0.071	0.782	putative cytoplasmic protein
STM0412	STM0412	AAL19366	(467156..467482)	3.015	0.772	2.165	0.194	0.718	1.380	0.140	1.151	0.163	0.834	putative inner membrane protein
tsx	STM0413	AAL19367	(467537..468400)	2.596	0.099	5.424	0.581	2.089	0.971	0.030	2.577	0.180	2.655	nucleoside channel; receptor of phage T6 and colicin K
yajI	STM0414	AAL19368	(468700..469239)	0.464	0.043	0.812	0.025	1.749	0.424	0.164	0.714	0.152	1.684	putative outer membrane lipoprotein
ybaD	STM0415	AAL19369	469391..469840					N/A					N/A	putative transcriptional regulator
ribD	STM0416	AAL19370	469844..470947	4.783	0.731	6.135	0.237	1.283	6.894	1.560	7.702	1.001	1.117	bifunctional pyrimidine deaminase/reductase in pathway of riboflavin synthesis
ribH	STM0417	AAL19371	471036..471506	9.459	0.925	7.517	1.543	0.795	10.333	2.057	8.385	0.775	0.811	riboflavin synthase, beta chain
nusB	STM0418	AAL19372	471527..471946	8.464	1.252	6.470	0.486	0.764	8.530	0.903	8.336	0.286	0.977	transcription termination; L factor
thiL	STM0419	AAL19373	472025..473002	1.453	0.069	1.486	0.158	1.023	2.186	0.341	2.340	0.199	1.071	thiamin-monophosphate kinase
pgpA	STM0420	AAL19374	472980..473495					N/A					N/A	phosphatidylglycerophosphatase A
yajO	STM0421	AAL19375	(473599..474573)	1.363	0.137	1.156	0.092	0.849	0.713	0.027	1.149	0.028	1.612	putative oxidoreductase / K + channel protein
dxs	STM0422	AAL19376	(474630..476492)	2.424	0.182	3.070	0.305	1.267	1.324	0.193	1.598	0.087	1.207	1-deoxyxylulose-5-phosphate synthase; flavoprotein
ispA	STM0423	AAL19377	(476516..477415)	3.252	0.339	3.643	0.131	1.120	1.477	0.088	2.121	0.117	1.436	geranyltranstransferase (farnesyldiphosphate synthase)
xseB	STM0424	AAL19378	(477416..477658)	4.628	0.648	2.666	0.426	0.576	1.635	0.104	1.501	0.057	0.918	exonuclease VII, small subunit
thiI	STM0425	AAL19379	477868..479316	1.312	0.034	0.928	0.183	0.708	0.978	0.024	0.626	0.027	0.640	sulfur transfer protein (from cys to ThiS and from IscS to U8-tRNA)
phnV	STM0426	AAL19380	(479360..480157)	0.432	0.095	0.165	0.029	0.380	0.207	0.016	0.216	0.014	1.043	2-aminoethylphosphonate transporter, memrane onent
phnU	STM0427	AAL19381	(480160..481020)	0.521	0.130	0.321	0.052	0.617	0.245	0.045	0.359	0.045	1.466	2-aminoethylphosphonate transporter, memrane onent

phnT	STM0428	AAL19382	(481023..482132)	0.273	0.115	0.245	0.029	0.896	0.158	0.037	0.339	0.079	2.146	2-aminoethylphosphonate transporter,ATPase onent
phnS	STM0429	AAL19383	(482138..483151)	0.242	0.098	0.169	0.052	0.699	0.115	0.013	0.292	0.051	2.540	2-aminoethylphosphonate transporter, periplasmic-binding onent
phnR	STM0430	AAL19384	(483349..484068)	0.500	0.173	0.421	0.029	0.843	0.352	0.062	0.346	0.032	0.981	2-aminoethylphosphonate transport, repressor
phnW	STM0431	AAL19385	484208..485311	0.252	0.147	0.112	0.011	0.442	0.164	0.042	0.285	0.017	1.743	2-aminoethylphosphonate transport
phnX	STM0432	AAL19386	485318..486130	0.318	0.128	0.210	0.036	0.659	0.170	0.013	0.266	0.045	1.564	2-aminoethylphosphonate transport
thiJ	STM0433	AAL19387	(486227..486817)	1.024	0.022	0.928	0.099	0.906	0.635	0.038	0.828	0.064	1.304	4-methyl-5(beta-hydroxyethyl)-thiazole synthesis
apbA	STM0434	AAL19388	(486780..487691)	0.871	0.054	0.964	0.050	1.107	0.707	0.142	0.839	0.143	1.188	ketopantoate reductase
yajQ	STM0435	AAL19389	487799..488308	1.134	0.109	2.940	0.568	2.592	0.623	0.181	1.067	0.023	1.713	putative cytoplasmic protein
yajR	STM0436	AAL19390	(488355..489704)	0.988	0.033	0.814	0.130	0.824	1.313	0.149	1.272	0.046	0.968	putative MFS family transporter
STM0436A	STM0436A	AAL19391	(489947..490108)					N/A					N/A	IS903 transposase
STM0437	STM0437	AAL19392	490256..491767	0.252	0.086	0.131	0.010	0.520	1.000	0.021	0.895	0.096	0.896	putative periplasmic protein
STM0438	STM0438	AAL19393	491989..493272	0.642	0.016	0.241	0.046	0.375	1.930	0.071	1.663	0.170	0.861	putative TPR repeat protein
cyoE	STM0439	AAL19394	(493354..494244)	30.652	5.862	2.570	0.185	0.084	14.628	2.468	15.141	1.400	1.035	protohaeme IX farnesyltransferase (haeme O biosynthesis)
cyoD	STM0440	AAL19395	(494256..494585)	33.136	3.071	5.522	0.742	0.167	18.888	3.302	22.223	0.473	1.177	cytochrome o ubiquinol oxidase subunit IV
cyoC	STM0441	AAL19396	(494585..495199)	36.743	4.447	10.988	0.577	0.299	24.591	0.609	23.168	1.747	0.942	cytochrome o ubiquinol oxidase subunit III
cyoB	STM0442	AAL19397	(495189..497180)	19.265	1.993	21.278	4.578	1.105	9.983	0.633	13.230	1.487	1.325	cytochrome o ubiquinol oxidase subunit I
cyoA	STM0443	AAL19398	(497191..498147)	12.922	0.341	26.536	3.447	2.054	5.859	0.489	15.841	1.371	2.704	cytochrome o ubiquinol oxidase subunit II
ampG	STM0444	AAL19399	(498600..500075)	1.516	0.165	1.711	0.329	1.129	1.051	0.070	1.016	0.125	0.966	MFS family, muropeptide transporter
yajG	STM0445	AAL19400	(500119..500751)	2.004	0.088	2.593	0.273	1.294	1.493	0.051	1.779	0.052	1.192	putative lipoprotein
bolA	STM0446	AAL19401	501001..501318	3.974	1.249	2.121	0.182	0.534	1.871	0.172	1.473	0.147	0.788	morphogene; putative regulator of murein genes (BolA family)
tig	STM0447	AAL19402	501665..502963	12.002	1.149	20.716	2.809	1.726	5.110	0.527	9.172	0.311	1.795	peptidyl-prolyl cis/trans isomerase, trigger factor; a molecular chaperone involved in cell division
clpP	STM0448	AAL19403	503210..503833	2.605	0.238	6.742	0.556	2.588	2.048	0.152	3.468	0.207	1.694	proteolytic subunit of clpA-clpP ATP-dependent serine protease, heat shock protein F21.5
clpX	STM0449	AAL19404	504085..505356	11.545	2.653	15.454	2.039	1.339	8.015	0.071	9.621	0.341	1.200	specificity onent of clpA-clpP ATP-dependent serine protease, chaperone
lon	STM0450	AAL19405	505542..507896	5.984	1.569	6.559	0.216	1.096	7.731	0.245	8.261	1.180	1.068	DNA-binding, ATP-dependent protease la; cleaves RcsA and SulA, heat shock k-protein (DNA binding activity)
hupB	STM0451	AAL19406	508105..508377	23.161	4.809	19.814	2.048	0.855	7.834	0.277	9.950	0.565	1.270	DNA-binding protein HU-beta, NS1 (HU-1)
cypD	STM0452	AAL19407	508668..510539	2.035	0.196	4.244	0.854	2.085	1.580	0.136	2.394	0.155	1.516	peptidyl prolyl isomerase
ybaV	STM0453	AAL19408	510688..511062	0.591	0.043	0.877	0.208	1.484	0.383	0.140	0.431	0.054	1.128	putative DNA uptake protein and related DNA-binding proteins
ybaW	STM0454	AAL19409	511166..511564	0.764	0.048	0.589	0.067	0.771	0.518	0.073	0.568	0.056	1.096	putative esterase
ybaX	STM0455	AAL19410	(511670..512365)	2.238	0.096	0.945	0.162	0.423	1.159	0.143	0.830	0.029	0.716	putative (aluminum) resistance protein

ybaE	STM0456	AAL19411	(512430..514130)	0.617	0.089	0.546	0.027	0.885	0.173	0.011	0.313	0.050	1.808	putative ABC transporter periplasmic binding protein
cof	STM0457	AAL19412	514231..515049	0.468	0.145	0.203	0.050	0.433	0.212	0.040	0.170	0.017	0.802	putative hydrolase
STM0458	STM0458	AAL19413	(515099..516154)	0.462	0.111	0.399	0.035	0.864	0.240	0.033	0.333	0.017	1.389	putative cysteine synthase/cystathionine beta-synthase
ybaO	STM0459	AAL19414	516267..516725	0.998	0.060	0.320	0.063	0.320	0.626	0.079	0.363	0.054	0.579	putative transcriptional regulator (AsnC familiy)
mdlA	STM0460	AAL19415	516766..518538	0.962	0.030	0.391	0.095	0.406	0.505	0.034	0.475	0.067	0.940	putative ABC superfamily (atp) transporter
mdlB	STM0461	AAL19416	518531..520312	1.113	0.087	0.441	0.026	0.396	0.581	0.117	0.436	0.033	0.751	putative ABC superfamily (atp&membrane) transporter
glnK	STM0462	AAL19417	520524..520862	0.379	0.069	0.246	0.066	0.648	0.194	0.044	0.396	0.121	2.040	regulatory protein, P-II 2, for nitrogen assimilation by glutamine synthetase, regulates GlnL (NRII) and GlnE (ATase)
amtB	STM0463	AAL19418	520894..522180	0.739	0.048	0.259	0.017	0.350	0.292	0.016	0.244	0.049	0.834	putative Amt family, ammonium transport protein
tesB	STM0464	AAL19419	(522280..523140)	0.697	0.044	0.925	0.170	1.327	0.745	0.033	0.693	0.107	0.931	acyl-CoA thioesterase II
ybaY	STM0465	AAL19420	523355..523924	5.842	1.129	1.884	0.121	0.323	14.026	2.985	11.020	0.351	0.786	glycoprotein/polysaccharide metabolism
ybaZ	STM0466	AAL19421	(523957..524346)	1.261	0.212	0.507	0.024	0.402	1.263	0.037	0.932	0.246	0.738	putative methyltransferase
ylaB	STM0468	AAL19422	(524577..526127)	0.628	0.059	0.332	0.061	0.529	0.345	0.026	0.344	0.036	0.995	putative diguanylate cyclase/phosphodiesterase domain 2
rpmE2	STM0469	AAL19423	526352..526612	0.935	0.065	0.759	0.058	0.812	0.497	0.147	0.497	0.046	1.001	putative 50S ribosomal protein L31 (second copy)
rpmJ2	STM0470	AAL19424	526618..526758	1.406	0.214	0.902	0.274	0.642	1.113	0.559	0.693	0.136	0.623	putative 50S ribosomal protein L36 (second copy)
ylaC	STM0471	AAL19425	(526814..527284)	1.777	0.096	1.769	0.273	0.995	1.216	0.052	1.749	0.117	1.439	putative inner membrane protein
maa	STM0472	AAL19426	(527401..527952)	0.827	0.016	0.827	0.100	1.000	3.444	0.116	2.035	0.126	0.591	maltose o-acetyltransferase
hha	STM0473	AAL19427	(528131..528349)	2.428	0.291	2.138	0.294	0.880	16.301	1.044	10.378	0.390	0.637	hemolysin expression modulating protein (involved in environmental regulation of virulence factors)
ybaJ	STM0474	AAL19428	(528377..528751)	1.536	0.155	1.303	0.092	0.849	11.830	0.643	5.582	0.261	0.472	putative cytoplasmic protein
acrB	STM0475	AAL19429	(529247..532396)	2.329	0.144	2.588	0.723	1.111	0.930	0.145	2.184	0.063	2.349	RND family, acridine efflux pump
acrA	STM0476	AAL19430	(532419..533612)	1.636	0.089	4.260	0.715	2.604	0.441	0.024	1.951	0.083	4.429	acridine efflux pump
acrR	STM0477	AAL19431	533754..534407	1.022	0.049	1.077	0.069	1.053	0.370	0.030	0.518	0.046	1.398	acrAB operon repressor (TetR/AcrR family)
aefA	STM0478	AAL19432	534526..537888	0.776	0.254	0.604	0.096	0.778	1.066	0.155	0.789	0.047	0.741	putative small-conductance mechanosensitive channel
STM0479	STM0479	AAL19433	(537930..538865)	0.824	0.063	0.756	0.037	0.917	0.424	0.014	0.379	0.042	0.894	putative transposase
ybaM	STM0480	AAL19434	(538935..539102)	0.631	0.073	0.492	0.083	0.780	0.356	0.032	0.479	0.043	1.344	putative inner membrane protein
priC	STM0481	AAL19435	(539116..539631)	1.216	0.055	0.709	0.130	0.583	0.603	0.049	0.727	0.021	1.205	primosomal replication protein N
ybaN	STM0482	AAL19436	539712..540089	1.430	0.164	0.358	0.023	0.250	0.838	0.030	0.688	0.060	0.820	putative phage gene 58
apt	STM0483	AAL19437	540242..540793	4.204	0.137	0.930	0.062	0.221	3.999	0.811	1.135	0.069	0.284	adenine phosphoribosyltransferase
dnaX	STM0484	AAL19438	540907..542835	4.424	0.909	2.305	0.399	0.521	3.624	0.981	1.372	0.218	0.379	DNA polymerase III, tau and gamma subunits; DNA elongation factor III

ybaB	STM0485	AAL19439	542881..543210	4.936	0.791	9.084	1.489	1.840	2.178	0.345	3.128	0.316	1.436	putative cytoplasmic protein
recR	STM0486	AAL19440	543210..543815	4.787	0.765	7.232	1.353	1.511	2.345	0.407	3.057	0.182	1.304	putative recombination protein, gap repair
htpG	STM0487	AAL19441	543902..545800	1.268	0.233	8.404	0.303	6.628	1.381	0.084	7.512	0.910	5.441	chaperone Hsp90, heat shock protein C 62.5
adk	STM0488	AAL19442	546041..546685	14.414	1.546	5.705	0.379	0.396	8.592	0.518	4.082	0.550	0.475	adenylate kinase
hemH	STM0489	AAL19443	546914..547876					N/A					N/A	ferrochelatase
aes	STM0490	AAL19444	(547873..548844)	0.654	0.053	0.489	0.106	0.747	0.302	0.076	0.278	0.017	0.919	acetyl esterase
gsk	STM0491	AAL19445	548997..550301	0.660	0.055	0.837	0.041	1.268	0.403	0.017	0.457	0.021	1.134	inosine-guanosine kinase
ybaL	STM0492	AAL19446	(550350..552026)	2.098	0.112	0.858	0.154	0.409	0.886	0.061	0.620	0.042	0.699	putative A2 family transport protein
fsr	STM0493	AAL19447	(552241..553461)	1.328	0.035	0.698	0.124	0.526	0.413	0.054	0.432	0.017	1.046	putative MFS family of transport protein
ushA	STM0494	AAL19448	553634..555286					N/A					N/A	UDP-sugar hydrolase 5'-nucleotidase
ybaK	STM0495	AAL19449	(555403..555882)	2.750	0.701	1.626	0.243	0.591	1.114	0.188	1.012	0.040	0.909	putative cytoplasmic protein
ybaP	STM0496	AAL19450	(556084..556878)	2.153	0.357	0.900	0.140	0.418	1.203	0.204	1.233	0.068	1.025	putative cytoplasmic protein
STM0497	STM0497	AAL19451	(556964..557791)	0.318	0.064	0.177	0.005	0.556	0.967	0.158	0.481	0.010	0.497	putative periplasmic protein
copA	STM0498	AAL19452	(557945..560446)	1.227	0.065	2.965	0.495	2.416	0.691	0.149	1.102	0.077	1.596	putative copper-transporting ATPase
cueR	STM0499	AAL19453	560556..560972	1.455	0.058	2.336	0.234	1.605	0.900	0.126	1.032	0.037	1.147	putative heavy metal transcriptional repressor (MerR family)
ybbJ	STM0500	AAL19454	(560973..561425)	2.759	0.296	2.335	0.197	0.846	2.376	0.677	3.224	0.161	1.357	putative Membrane protein implicated in regulation of membrane protease activity
ybbK	STM0501	AAL19455	(561422..562339)	2.438	0.270	1.943	0.286	0.797	2.106	0.253	2.479	0.101	1.177	putative inner membrane protein
ybbL	STM0502	AAL19456	562486..563163	0.509	0.080	0.494	0.041	0.971	0.499	0.036	0.567	0.025	1.135	putative ABC-type sugar/spermidine/putrescine transport system, ATPase onent
ybbM	STM0503	AAL19457	563150..563929	0.632	0.059	0.662	0.138	1.047	0.545	0.043	0.694	0.103	1.274	putative YbbM family transport protein, metal resistance protein
ybbN	STM0504	AAL19458	(564015..564869)	2.514	0.761	1.895	0.176	0.754	2.746	0.074	6.812	0.868	2.481	paral putative thioredoxin protein
ybbO	STM0505	AAL19459	(564929..565699)	1.112	0.031	1.197	0.085	1.076	0.715	0.035	0.815	0.067	1.140	putative oxidoreductase
tesA	STM0506	AAL19460	(565854..566468)	1.229	0.098	1.304	0.087	1.061	1.618	0.214	1.417	0.093	0.876	multifunctional acyl-CoA thioesterase I; also functions as protease I, lysophospholipaseL(I)
ybbA	STM0507	AAL19461	566439..567125	0.792	0.055	0.885	0.044	1.118	1.198	0.127	0.996	0.049	0.831	putative ABC superfamily (atp_bind) transporter
ybbP	STM0508	AAL19462	567122..569536	0.627	0.068			0.000	1.241	0.025			0.000	putative inner membrane protein
STM0509	STM0509	AAL19463	569722..570855	0.375	0.107	0.234	0.029	0.624	0.235	0.043	0.163	0.017	0.694	putative outer membrane protein
sfbA	STM0510	AAL19464	571112..571942	0.911	0.078			0.000	0.231	0.032			0.000	putative ABC-type transport system ATPase onent/cell division protein
sfbB	STM0511	AAL19465	571979..572995	0.752	0.034	0.243	0.036	0.323	0.204	0.003	0.303	0.016	1.482	putative ABC-type transport system ATPase onent/cell division protein
sfbC	STM0512	AAL19466	572988..573647	0.744	0.048	0.277	0.040	0.372	0.247	0.006	0.351	0.047	1.417	putative binding-protein-dependent transport systems inner membrane onent
ybbB	STM0513	AAL19467	(573686..574780)	0.685	0.102	1.073	0.154	1.566	0.353	0.013	0.675	0.040	1.912	putative ATPase
ybbS	STM0514	AAL19468	(574850..575776)	0.326	0.087	0.332	0.024	1.020	0.174	0.007	0.323	0.030	1.855	putative transcriptional regulator, LysR family

allA	STM0515	AAL19469	576003..576485	0.307	0.109	0.633	0.073	2.062	0.198	0.062	0.411	0.049	2.072	ureidoglycolate hydrolase
allR	STM0516	AAL19470	576564..577382	0.617	0.051	1.695	0.162	2.747	0.362	0.067	0.711	0.041	1.964	putative regulatory protein
gcl	STM0517	AAL19471	577467..579248	0.181	0.122	0.197	0.011	1.090	0.238	0.139	0.325	0.016	1.364	glyoxylate carboligase
gip	STM0518	AAL19472	579261..580037	0.293	0.131	0.178	0.062	0.608	0.413	0.036	0.542	0.022	1.312	glyoxylate -induced protein
glxR	STM0519	AAL19473	580138..581016	0.186	0.139	0.179	0.021	0.965	0.591	0.008	1.102	0.075	1.866	tartronic semialdehyde reductase
STM0520	STM0520	AAL19474	581082..582329	0.133	0.091	0.075	0.002	0.565	0.302	0.111	0.428	0.044	1.415	putative permease
ybbV	STM0521	AAL19475	582405..582659	0.177	0.082	0.124	0.026	0.701	0.412	0.163	0.458	0.021	1.111	putative cytoplasmic protein
allP	STM0522	AAL19476	582566..583879	0.167	0.111	0.075	0.005	0.446	0.662	0.037	0.788	0.027	1.191	putative NCS1 family, allantoin transport protein
allB	STM0523	AAL19477	583958..585319	0.211	0.135	0.176	0.034	0.833	2.724	0.074	5.080	0.239	1.865	allantoinase
ybbY	STM0524	AAL19478	585378..586676	0.155	0.114	0.071	0.008	0.460	0.496	0.031	0.594	0.071	1.198	putative transport protein
glxK	STM0525	AAL19479	586699..587847	0.265	0.154	0.165	0.020	0.621	0.783	0.074	0.879	0.054	1.123	glycerate kinase II
ylbA	STM0526	AAL19480	(587927..588712)	0.381	0.082	0.573	0.052	1.504	0.730	0.090	0.901	0.033	1.233	putative glyoxylate utilization
allC	STM0527	AAL19481	(588723..589958)	0.239	0.126	0.380	0.035	1.589	0.727	0.078	1.153	0.057	1.586	allantoate amidohydrolase
allD	STM0528	AAL19482	(589980..591029)	0.192	0.121	0.239	0.027	1.245	0.473	0.011	0.675	0.040	1.428	ureidoglycolate dehydrogenase
fdrA	STM0529	AAL19483	591360..593024	0.241	0.154	0.197	0.017	0.816	0.713	0.076	1.110	0.055	1.555	putative acyl-CoA synthetase, involved in protein transport
ylbE	STM0530	AAL19484	593034..594293	0.193	0.105	0.083	0.028	0.431	0.668	0.073	0.832	0.030	1.244	putative cytoplasmic protein
ylbF	STM0531	AAL19485	594305..595114	0.231	0.133	0.096	0.006	0.417	0.498	0.035	0.535	0.006	1.075	putative cytoplasmic protein
arcC	STM0532	AAL19486	595118..596011	0.570	0.041	0.274	0.042	0.481	0.456	0.045	0.594	0.060	1.301	putative carbamate kinase
purK	STM0533	AAL19487	(596052..597119)	1.264	0.190	1.245	0.128	0.985	0.824	0.080	1.577	0.085	1.914	phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO(2)-fixing subunit
purE	STM0534	AAL19488	(597116..597625)	0.996	0.173	1.012	0.100	1.017	0.854	0.147	0.966	0.018	1.131	phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit
lpxH	STM0535	AAL19489	(597743..598465)	3.365	0.282	1.404	0.220	0.417	1.925	0.271	1.096	0.049	0.569	UDP-2,3-diacylglucosamine hydrolase
ppiB	STM0536	AAL19490	(598468..598962)	18.135	5.187	8.034	1.169	0.443	6.585	1.241	6.149	0.463	0.934	peptidyl-prolyl cis-trans isomerase B (rotamase B)
cysS	STM0537	AAL19491	599135..600520	2.356	0.164	1.901	0.223	0.807	1.310	0.068	1.499	0.071	1.144	cysteine tRNA synthetase
STM0538	STM0538	AAL19492	(600564..601388)	0.432	0.056	0.492	0.080	1.140	0.469	0.395	0.333	0.011	0.711	putative outer membrane protein
STM0539	STM0539	AAL19493	(601385..601822)	0.965	0.050	0.971	0.254	1.006	0.878	0.977	0.613	0.088	0.698	putative inner membrane protein
ybcI	STM0540	AAL19494	(601815..602360)	0.318	0.160	0.264	0.015	0.830	0.334	0.160	0.307	0.012	0.919	putative membrane-bound metal-dependent hydrolases
ybcJ	STM0541	AAL19495	(602488..602700)	1.138	0.076	0.688	0.080	0.604	0.848	0.155	0.526	0.020	0.620	putative cytoplasmic protein
folD	STM0542	AAL19496	(602702..603568)	2.202	0.061	1.735	0.142	0.788	1.849	0.044	1.886	0.138	1.020	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase and 5,10-methylene-tetrahydrofolate cyclohydrolase
fimA	STM0543	AAL19497	604115..604672	0.894	0.104	2.411	0.191	2.697	48.904	1.817	4.567	0.140	0.093	major type 1 subunit fimbrin (pilin)
fimI	STM0544	AAL19498	604748..605281	0.629	0.105	0.420	0.063	0.667	15.672	0.452	0.878	0.130	0.056	fimbrial protein internal segment
fimC	STM0545	AAL19499	605325..606017	0.303	0.105	0.257	0.018	0.847	7.896	0.674	0.572	0.043	0.072	periplasmic chaperone, required for type 1 fimbriae

fimD	STM0546	AAL19500	606048..608660	0.216	0.106	0.140	0.047	0.650	3.707	0.300	0.390	0.020	0.105	outer membrane usher protein
fimH	STM0547	AAL19501	608675..609682					N/A					N/A	minor fimbrial subunit
fimF	STM0548	AAL19502	609692..610210	0.305	0.103	0.189	0.027	0.619	2.453	0.027	0.399	0.111	0.163	putative fimbrial protein
fimZ	STM0549	AAL19503	(610256..610888)	0.393	0.077	0.129	0.005	0.328	3.566	0.546	0.522	0.033	0.146	fimbrial protein Z, putative transcriptional regulator (LuxR/UhpA family)
fimY	STM0550	AAL19504	(611492..612214)	0.195	0.054	0.145	0.013	0.741	0.438	0.028	0.297	0.053	0.677	putative regulatory protein
STM0551	STM0551	AAL19505	(612233..612544)	0.311	0.057	0.140	0.029	0.451	1.079	0.074	0.453	0.033	0.420	putative Diguanylate cyclase/phosphodiesterase domain 0
fimW	STM0552	AAL19506	(612706..613302)	0.202	0.071	0.124	0.021	0.614	0.619	0.007	0.432	0.045	0.698	putative fimbrial protein
argU	STM0553						N/A					N/A		
STM0554	STM0554	AAL19507	(613593..613781)	0.362	0.106	0.174	0.039	0.479	0.398	0.095	0.286	0.009	0.719	homology to integrase protein of phage
STM0555	STM0555	pseudogene; frameshift relative to E. coli IS3			0.283	0.069	0.179	0.025	0.632	0.299	0.063	0.250	0.024	0.836
STM0556	STM0556	AAL19508	(614199..614417)	0.288	0.119	0.146	0.040	0.508	0.445	0.080	0.194	0.029	0.436	putative transposase
STM0557	STM0557	AAL19509	(614804..616456)					N/A					N/A	putative inner membrane protein
yfdH	STM0558	AAL19510	(616437..617363)	0.529	0.157	0.133	0.010	0.251	0.471	0.014	0.235	0.026	0.498	putative glycosyltransferase
STM0560	STM0560	pseudogene; in-frame stop following codon 56			0.281	0.130	0.139	0.047	0.496	0.400	0.156	0.259	0.014	0.647
STM0561	STM0561	AAL19512	(618590..618919)	0.508	0.096	0.181	0.019	0.356	1.396	0.100	0.662	0.070	0.474	Sensor protein
STM0562	STM0562	AAL19513	619028..619207	0.842	0.202	0.452	0.043	0.536	1.462	0.519	0.744	0.236	0.509	putative transport protein
STM0563	STM0563	AAL19514	(619258..620112)					N/A					N/A	putative transcriptional regulator (AraC/XylS family)
STM0564	STM0564	AAL19515	620328..621653	0.251	0.147	0.190	0.049	0.755	0.334	0.046	0.262	0.010	0.785	putative oxidoreductase
STM0565	STM0565	AAL19516	621810..622046	0.226	0.107	0.146	0.010	0.644	0.534	0.205	0.377	0.053	0.705	putative periplasmic protein
STM0566	STM0566	AAL19517	622059..622619	0.265	0.125	0.208	0.026	0.786	0.362	0.031	0.379	0.052	1.048	putative inner membrane protein
STM0567	STM0567	AAL19518	(622698..623873)	0.731	0.019	1.045	0.153	1.430	0.395	0.282	0.599	0.028	1.515	putative ATPase involved in DNA repair
pheP	STM0568	AAL19519	624199..625593	1.696	0.107	0.377	0.071	0.223	1.278	0.256	0.640	0.062	0.501	APC family, phenylalanene transporter
ybdG	STM0569	AAL19520	(625635..626882)	2.075	0.144	0.953	0.117	0.459	5.657	0.784	8.955	0.376	1.583	putative transport
apeE	STM0570	AAL19521	627193..629163	0.444	0.076	0.404	0.038	0.909	0.924	0.066	1.492	0.071	1.616	outer membrane N-acetyl phenylalanine beta-naphthyl ester-cleaving esterase
STM0571	STM0571	AAL19522	629330..632059	0.588	0.066	0.575	0.043	0.977	0.345	0.185	0.500	0.028	1.450	putative inner membrane protein
STM0572	STM0572	AAL19523	(632187..633173)	0.173	0.089	0.133	0.034	0.770	0.290	0.127	0.289	0.032	0.996	putative phosphosugar isomerases
STM0573	STM0573	AAL19524	(633240..634283)	0.201	0.096	0.154	0.017	0.766	0.231	0.186	0.272	0.015	1.179	putative inner membrane protein
STM0574	STM0574	AAL19525	(634316..635170)	0.161	0.099	0.129	0.052	0.799	0.112	0.041	0.159	0.021	1.423	putative transport protein, PTS system
STM0575	STM0575	AAL19526	(635173..635916)	0.205	0.140	0.135	0.035	0.659	0.129	0.052	0.228	0.015	1.769	putative inner membrane protein
STM0576	STM0576	AAL19527	(635931..636401)	0.219	0.143	0.192	0.017	0.879	0.174	0.098	0.219	0.019	1.259	putative transport protein, PTS system
STM0577	STM0577	AAL19528	(636379..636828)	0.274	0.098	0.288	0.042	1.053	0.146	0.037	0.214	0.023	1.467	putative transport protein, PTS system
nfnB	STM0578	AAL19529	(637028..637681)	2.025	0.096	2.621	0.606	1.294	1.054	0.174	1.039	0.102	0.985	dihydropteridine reductase/oxygen-insensitive NAD(P)H nitroreductase
ybdF	STM0579	AAL19530	(637778..638146)	0.753	0.055	0.751	0.114	0.998	0.397	0.048	0.420	0.029	1.058	putative cytoplasmic protein

STM0580	STM0580	AAL19531	(638146..638727)	1.301	0.153	0.914	0.132	0.702	0.651	0.026	0.814	0.040	1.252	putative regulatory protein
STM0581	STM0581	AAL19532	639016..639357	0.828	0.051	0.521	0.027	0.630	0.678	0.079	0.401	0.034	0.591	putative regulatory protein
ybdJ	STM0582	AAL19533	(639363..639611)	1.718	0.146	0.496	0.096	0.289	0.834	0.066	0.458	0.068	0.550	putative inner membrane protein
ybdK	STM0583	AAL19534	(639678..640796)	0.361	0.202	0.171	0.018	0.474	0.288	0.013	0.479	0.039	1.661	putative cytoplasmic protein
entD	STM0584	AAL19535	(640808..641512)	0.377	0.073	0.339	0.043	0.899	0.228	0.074	0.309	0.065	1.353	enterochelin synthetase, onent D (phoshpantetheinyltransferase)
fepA	STM0585	AAL19536	(641558..643813)	0.229	0.097	0.081	0.011	0.353	0.167	0.236	0.124	0.022	0.741	outer membrane porin, receptor for ferric enterobactin (enterochelin) and colicins B and D
fes	STM0586	AAL19537	644002..645216	0.421	0.142	0.478	0.056	1.137	0.297	0.316	0.441	0.150	1.487	enterochelin esterase
ybdZ	STM0587	AAL19538	645247..645465	0.547	0.187	0.285	0.024	0.521	0.381	0.232	0.325	0.048	0.852	putative cytoplasmic protein
entF	STM0588	AAL19539	645462..649346					N/A					N/A	enterobactin synthetase, onent F (nonribosomal peptide synthetase)
fepE	STM0589	AAL19540	649596..650732	0.392	0.081	0.361	0.046	0.920	0.712	0.009	0.540	0.032	0.758	ferric enterobactin (enterochelin) transporter
fepC	STM0590	AAL19541	(650785..651579)	0.829	0.030	0.292	0.048	0.353	0.272	0.040	0.372	0.016	1.367	ABC s+uperfamily (atp_bind), enterobactin transporter
fepG	STM0591	AAL19542	(651576..652565)	0.948	0.064	0.154	0.019	0.162	0.202	0.080	0.288	0.022	1.425	ABC superfamily (membrane), ferric enterobactin transporter
fepD	STM0592	AAL19543	(652565..653572)	1.005	0.055	0.148	0.029	0.147	0.165	0.038	0.247	0.013	1.500	ABC superfamily (membrane), ferric enterobactin (enterochelin) transporter
ybdA	STM0593	AAL19544	653683..654927	0.713	0.065	0.116	0.014	0.163	0.140	0.021	0.223	0.022	1.594	putative POT family transport protein
fepB	STM0594	AAL19545	(654990..655946)	0.536	0.030	0.170	0.016	0.316	0.157	0.021	0.289	0.028	1.839	ABC superfamily (peri_perm), ferric enterobactin (enterochelin) tranporter
entC	STM0595	AAL19546	656255..657430	0.339	0.061	0.142	0.020	0.418	0.209	0.399	0.201	0.076	0.962	isochorismate synthetase, enterochelin biosynthesis
entE	STM0596	AAL19547	657440..659050	0.252	0.078	0.115	0.014	0.458	0.129	0.075	0.205	0.006	1.588	2,3-dihydroxybenzoate-AMP ligase
entB	STM0597	AAL19548	659064..659921	0.354	0.083	0.159	0.020	0.451	0.175	0.040	0.240	0.019	1.370	2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochorismatase
entA	STM0598	AAL19549	659921..660676	0.503	0.036	0.232	0.026	0.461	0.180	0.029	0.282	0.025	1.571	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
ybdB	STM0599	AAL19550	660679..661092	0.786	0.073	0.951	0.215	1.209	0.261	0.073	0.597	0.031	2.286	putative protein PaaI, possibly involved in aromatic ounds catabolism
cstA	STM0600	AAL19551	661274..663379	5.982	1.604	6.411	0.897	1.072	1.266	0.114	3.207	0.202	2.533	carbon starvation protein
ybdD	STM0601	AAL19552	663443..663640	7.226	1.287	6.375	0.898	0.882	3.523	1.426	2.653	0.412	0.753	putative cytoplasmic protein
ybdH	STM0602	AAL19553	(663676..664764)	0.941	0.175	0.912	0.123	0.969	0.485	0.276	0.735	0.159	1.515	putative glycerol dehydrogenase
ybdL	STM0603	AAL19554	664891..666051	1.269	0.096	0.445	0.063	0.351	0.949	0.160	1.284	0.070	1.354	putative aminotransferase
ybdM	STM0604	AAL19555	(666052..666669)	0.513	0.044	0.425	0.008	0.829	2.774	0.308	5.138	0.253	1.853	putative transcriptional regulator
ybdN	STM0605	AAL19556	(666642..667877)	0.274	0.068	0.291	0.029	1.060	1.073	0.079	1.722	0.055	1.605	putative 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase

ybdO	STM0606	AAL19557	(668043..668945)	0.691	0.030	0.430	0.021	0.622	2.883	0.123	1.403	0.072	0.487	putative transcriptional regulator, LysR family
dsbG	STM0607	AAL19558	(669262..670008)	1.309	0.047	1.172	0.138	0.895	1.102	0.150	1.280	0.126	1.162	periplasmic disulfide isomerase, thiol-disulphide oxidase
ahpC	STM0608	AAL19559	670449..671012	16.484	1.232	13.717	2.408	0.832	12.565	0.970	13.288	0.282	1.058	alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides
ahpF	STM0609	AAL19560	671254..672819	1.647	0.099	1.388	0.156	0.843	2.247	0.058	3.058	0.220	1.361	alkyl hydroperoxide reductase, F52a subunit; detoxification of hydroperoxides
STM0610	STM0610	AAL19561	673151..673711	0.175	0.081	0.143	0.035	0.819	0.356	0.063	0.419	0.029	1.178	putative onent of anaerobic dehydrogenases
STM0611	STM0611	AAL19562	673704..675983	0.215	0.080	0.179	0.029	0.836	0.282	0.098	0.383	0.017	1.362	putative oxidoreductase protein
STM0612	STM0612	AAL19563	675980..676537	0.372	0.103	0.239	0.017	0.641	0.446	0.032	0.580	0.050	1.300	putative hydrogenase protein
STM0613	STM0613	AAL19564	676537..677304	1.376	0.145	0.745	0.055	0.541	1.155	0.174	1.047	0.044	0.907	putative hydrogenase protein
ybdQ	STM0614	AAL19565	(677372..677800)	13.683	1.862	6.420	0.234	0.469	7.134	0.329	6.158	0.480	0.863	putative Universal stress protein UspA and related nucleotide-binding protein
ybdR	STM0615	AAL19566	678023..679261	0.540	0.057	0.272	0.037	0.503	0.697	0.019	0.494	0.049	0.708	putative dehydrogenase
rnk	STM0616	AAL19567	(679344..679754)	4.369	0.543	2.466	0.467	0.565	3.409	0.110	1.553	0.117	0.455	regulator of nucleoside diphosphate kinase
rna	STM0617	AAL19568	(679989..680795)	1.365	0.034	2.156	0.203	1.579	3.637	0.215	5.672	0.718	1.560	RNase I, cleaves phosphodiester bond between any two nucleotides
citT	STM0618	AAL19569	(680905..682368)	0.493	0.063	0.273	0.018	0.554	0.594	0.072	0.487	0.011	0.819	DASS family, citrate:succinate transport (antiport) protein
citG	STM0619	AAL19570	(682406..683302)	0.294	0.088	0.168	0.011	0.572	0.325	0.015	0.413	0.073	1.270	putative modifier of citrate lyase protein
citX	STM0620	AAL19571	(683274..683825)	0.267	0.124	0.165	0.080	0.618	0.425	0.033	0.580	0.089	1.366	putative cytoplasmic protein
citF	STM0621	AAL19572	(683829..685358)	0.150	0.098	0.115	0.015	0.768	0.270	0.007	0.425	0.053	1.573	bifunctional citrate lyase alpha chain/citrate-A transferase
citE	STM0622	AAL19573	(685368..686276)	0.225	0.117	0.197	0.027	0.878	0.263	0.054	0.507	0.059	1.930	citrate lyase beta chain (acyl lyase subunit)
citD	STM0623	AAL19574	(686273..686569)	0.313	0.109	0.312	0.042	0.995	0.314	0.010	0.767	0.237	2.444	citrate lyase acyl carrier protein (gamma chain)
citC	STM0624	AAL19575	(686566..687642)	0.170	0.092	0.063	0.014	0.371	0.229	0.023	0.227	0.014	0.991	citrate lyase synthetase (citrate (pro-3S)-lyase ligase
dpiB	STM0625	AAL19576	688027..689688	0.265	0.088	0.195	0.015	0.736	1.830	0.325	0.852	0.031	0.466	sensory histidine kinase in two-onent regulatory system with DpiA, regulation of cit operon and plasmid inheritance genes
dpiA	STM0626	AAL19577	689657..690337	0.408	0.089	0.458	0.074	1.122	2.627	0.383	1.766	0.048	0.672	response regulator in two-onent regulatory system with DpiB, transcriptional regulation of cit operon (citrate fermentation) genes and of plasmid inheritance genes (OmpR family)
dcuC	STM0627	AAL19578	(690391..691776)	0.260	0.087	0.372	0.013	1.431	0.788	0.085	0.705	0.079	0.895	DcuC family, dicarboxylate transporter
pagP	STM0628	AAL19579	692155..692727	0.966	0.017	0.791	0.058	0.819	10.819	0.465	3.762	0.380	0.348	PhoPQ-activated gene
cspE	STM0629	AAL19580	692915..693124	36.260	9.084	18.999	3.305	0.524	18.549	0.848	7.169	0.579	0.386	RNA chaperone, negative regulator of cspA transcription
crcB	STM0630	AAL19581	(693182..693565)	1.846	0.262	1.057	0.153	0.573	1.595	0.195	0.763	0.129	0.479	high-copy crc-csp restores normal chromosome condensation in presence of camphor or mukB mutations
ybeM	STM0631	AAL19582	693656..694444	0.735	0.022	0.420	0.070	0.571	0.702	0.040	0.491	0.055	0.699	putative hydrolase

ybeC	STM0632	AAL19583	694573..694776	1.165	0.208	1.298	0.152	1.114	1.569	0.112	1.164	0.126	0.742	putative Sec-independent protein secretion pathway onent
lipA	STM0633	AAL19584	(694862..695827)	3.953	0.091	5.135	0.423	1.299	2.057	0.204	1.814	0.144	0.882	lipoate synthase, an iron-sulfur enzyme
ybeF	STM0634	AAL19585	(696033..696986)	0.359	0.067	0.404	0.102	1.124	1.361	0.163	1.581	0.094	1.162	putative transcriptional regulator, LysR family
lipB	STM0635	AAL19586	(697288..697863)	1.788	0.198	0.866	0.067	0.485	1.140	0.030	0.849	0.114	0.745	putative ligase in lipoate biosynthesis
ybeD	STM0636	AAL19587	(698029..698292)	3.112	0.862	1.705	0.226	0.548	4.447	0.239	1.820	0.080	0.409	putative cytoplasmic protein
dacA	STM0637	AAL19588	(698401..699612)	4.285	0.355	1.927	0.308	0.450	4.285	0.345	2.205	0.190	0.515	D-alanyl-D-alanine carboxypeptidase, penicillin-binding protein 5
rlpA	STM0638	AAL19589	(699752..700897)					N/A					N/A	a minor lipoprotein
mrdB	STM0639	AAL19590	(700908..702020)	0.661	0.042	0.599	0.072	0.906	0.770	0.095	0.601	0.053	0.781	rod shape-determining membrane protein; cell elongation in e phase
mrdA	STM0640	AAL19591	(702023..703924)	0.407	0.076	0.653	0.058	1.607	0.386	0.018	0.498	0.050	1.291	cell elongation specific transpeptidase of penicillin-binding protein 2 (peptidoglycan synthetase)
ybeA	STM0641	AAL19592	(703955..704422)	0.787	0.092	1.788	0.114	2.270	0.771	0.116	0.974	0.070	1.263	putative cytoplasmic protein
ybeB	STM0642	AAL19593	(704426..704743)	1.012	0.086	1.773	0.136	1.752	1.008	0.058	1.181	0.108	1.172	putative ACR, homolog of plant Iojap protein
cobC	STM0643	AAL19594	(705072..705680)	0.535	0.054	0.897	0.164	1.677	0.355	0.048	0.976	0.171	2.750	alpha ribazole-5'-P phosphatase in cobalamin synthesis
cobD	STM0644	AAL19595	705777..706871	0.686	0.096	1.026	0.095	1.495	0.622	1.415	0.579	0.284	0.932	putative aminotransferase in cobalamin synthesis
nadD	STM0645	AAL19596	(706846..707487)	0.523	0.081	1.113	0.207	2.128	0.346	0.045	0.517	0.030	1.496	putative Nicotinic acid mononucleotide adenylyltransferase
holA	STM0646	AAL19597	(707489..708520)	1.324	0.098	2.363	0.425	1.785	0.968	0.087	1.202	0.021	1.242	DNA polymerase III, delta subunit
rlpB	STM0647	AAL19598	(708520..709110)	2.612	0.360	3.863	0.516	1.479	1.994	0.149	2.787	0.250	1.398	a minor lipoprotein
leuS	STM0648	AAL19599	(709125..711707)	1.686	0.079	5.526	0.242	3.278	1.367	0.037	1.751	0.177	1.281	leucine tRNA synthetase
STM0649	STM0649	AAL19600	711944..712285	0.315	0.117	0.338	0.102	1.073	0.232	0.111			0.000	putative hydrolase N-terminus
STM0650	STM0650	AAL19601	712302..713474	0.232	0.111	0.161	0.025	0.692	0.247	0.026	0.231	0.019	0.936	putative hydrolase C-terminus
STM0651	STM0651	AAL19602	713524..714477	0.747	0.052	0.180	0.038	0.241	1.413	0.212	0.464	0.057	0.329	putative permease
STM0652	STM0652	AAL19603	714545..716473	0.582	0.059	1.152	0.084	1.981	0.512	0.051	0.672	0.090	1.313	putative sigma-54 dependent transcriptional regulator
ybeL	STM0653	AAL19604	716566..717039	3.693	0.490	2.423	0.105	0.656	1.250	0.192	1.091	0.022	0.873	putative cytoplasmic protein
ybeQ	STM0654	AAL19605	(717078..718073)	0.709	0.070	0.337	0.017	0.476	0.587	0.075	0.790	0.026	1.346	putative TPR repeat protein
ybeR	STM0655	AAL19606	718198..718905	0.164	0.126	0.116	0.025	0.709	0.655	0.054	1.089	0.033	1.664	putative cytoplasmic protein
ybeS	STM0656	AAL19607	718902..720335	0.264	0.134	0.166	0.014	0.628	0.778	0.018	0.956	0.081	1.228	putative molecular chaperone, DnaJ family
ybeU	STM0657	AAL19608	720347..721042	0.324	0.108	0.150	0.021	0.461	0.774	0.024	0.671	0.031	0.867	putative cytoplasmic protein
ybeV	STM0658	AAL19609	721039..722511	0.330	0.121	0.174	0.009	0.526	0.577	0.086	0.728	0.029	1.263	putative molecular chaperone, DnaJ family
hscC	STM0659	AAL19610	(722533..724212)	0.337	0.092	0.475	0.059	1.410	0.233	0.018	0.283	0.019	1.213	putative heatshock protein, homolog of hsp70 in Hsc66 subfamily
STM0660	STM0660	AAL19611	(724288..725526)	0.957	0.057	0.944	0.048	0.986	0.477	0.095	0.870	0.070	1.823	putative cytoplasmic protein

ybeK	STM0661	AAL19612	(725558..726493)	0.938	0.083	1.815	0.137	1.935	0.353	0.002	1.145	0.056	3.245	putative purine nucleoside hydrolase
gltL	STM0662	AAL19613	(726610..727335)	5.396	2.116	3.298	0.250	0.611	0.828	0.038	0.847	0.003	1.023	ABC superfamily (atp_bind), glutamate/aspartate transporter
gltK	STM0663	AAL19614	(727335..728009)	3.006	0.828	3.128	0.253	1.041	0.420	0.041	0.786	0.040	1.871	ABC superfamily (membrane), glutamate/aspartate transporter
gltJ	STM0664	AAL19615	(728009..728749)	2.303	0.750	5.007	0.920	2.174	0.290	0.013	0.918	0.027	3.164	ABC superfamily (membrane), glutamate/aspartate transporter
gltI	STM0665	AAL19616	(728909..729835)	15.088	4.046	21.028	3.340	1.394	1.307	0.142	2.914	0.170	2.229	ABC superfamily (bind_prot), glutamate/aspartate transporter
lnt	STM0666	AAL19617	(730172..731710)	1.221	0.152	1.141	0.186	0.935	1.305	0.124	1.091	0.079	0.836	apolipoprotein N-acyltransferase, copper homeostasis protein, inner membrane
ybeX	STM0667	AAL19618	(731730..732608)	2.074	0.219	2.479	0.338	1.195	2.044	0.025	3.329	0.331	1.628	putative CBS domain-containing protein
ybeY	STM0668	AAL19619	(732766..733239)	2.569	0.642	2.120	0.452	0.825	4.339	0.714	5.576	0.158	1.285	putative metal-dependent hydrolase
phoL	STM0669	AAL19620	(733236..734321)	3.330	0.857	2.640	0.204	0.793	5.311	0.968	6.623	0.426	1.247	putative phosphate starvation-inducible protein, ATP-binding
miaB	STM0670	AAL19621	(734487..735911)	3.420	0.166	2.382	0.499	0.697	3.626	0.554	3.954	0.370	1.091	methylthiolation of isopentenylated A37 derivatives in rRNA
ubiF	STM0671	AAL19622	736055..737230	1.458	0.146	1.351	0.154	0.927	0.700	0.063	0.936	0.072	1.337	putative monooxygenase
STM0672	STM0672	AAL19623	(737297..737872)	1.088	0.078	0.767	0.060	0.705	0.704	0.153	0.656	0.084	0.932	putative inner membrane protein
glnX	STM0673						N/A					N/A		
glnV	STM0674						N/A					N/A		
metU	STM0675						N/A					N/A		
glnW	STM0676						N/A					N/A		
glnU	STM0677						N/A					N/A		
leuW	STM0678						N/A					N/A		
metT	STM0679						N/A					N/A		
asnB	STM0680	AAL19624	(738939..740603)	0.702	0.117	1.897	0.211	2.704	0.717	0.136	1.733	0.045	2.418	asparagine synthetase B
nagD	STM0681	AAL19625	(740893..741645)	1.578	0.071	1.722	0.132	1.091	0.793	0.027	0.906	0.034	1.143	putative phosphatase in N-acetylglucosamine metabolism
nagC	STM0682	AAL19626	(741692..742912)	0.862	0.040	2.428	0.392	2.816	0.415	0.053	0.943	0.087	2.271	transcriptional repressor of nag (N-acetylglucosamine) operon (NagC/XylR family)
nagA	STM0683	AAL19627	(742917..744071)	1.315	0.075	3.449	0.429	2.622	0.556	0.065	1.050	0.090	1.888	N-acetylglucosamine-6-phosphate deacetylase
nagB	STM0684	AAL19628	(744131..744931)	4.002	0.273	7.396	0.475	1.848	1.157	0.145	2.651	0.164	2.292	glucosamine-6-phosphate deaminase
nagE	STM0685	AAL19629	745258..747210	4.261	0.529	6.362	0.395	1.493	1.259	0.133	1.731	0.136	1.375	Sugar Specific PTS family, n-acetylglucosamine-specific enzyme IIABC
glnS	STM0686	AAL19630	747421..749088	1.544	0.087	5.690	0.888	3.684	0.886	0.084	1.719	0.109	1.939	glutamine tRNA synthetase
ybfM	STM0687	AAL19631	749534..750940	2.076	0.162	1.701	0.112	0.819	0.170	0.060	0.312	0.038	1.831	putative outer membrane protein
ybfN	STM0688	AAL19632	750990..751322	4.155	1.156	3.126	0.204	0.753	0.402	0.048	0.974	0.046	2.423	putative lipoprotein

citA	STM0689	AAL19633	(751371..752675)	0.861	0.042	0.351	0.078	0.408	0.318	0.057	0.364	0.031	1.145	citrate-proton symporter
citB	STM0690	AAL19634	(752726..753865)	0.378	0.085	0.254	0.034	0.672	0.199	0.027	0.338	0.014	1.699	citrate utilization protein b
STM0691	STM0691	AAL19635	(753852..755255)	0.725	0.039	0.452	0.053	0.623	0.346	0.044	0.517	0.068	1.493	putative periplasmic protein
STM0692	STM0692	AAL19636	(755353..756279)	1.005	0.085	1.328	0.044	1.320	0.505	0.025	0.669	0.034	1.325	putative transcriptional regulator, LysR family
fur	STM0693	AAL19637	(756394..756846)	16.227	2.929	6.300	0.713	0.388	5.792	0.548	3.391	0.156	0.585	transcriptional repressor of iron-responsive genes (Fur family) (ferric uptake regulator)
fldA	STM0694	AAL19638	(757128..757658)	11.938	1.667	5.262	0.862	0.441	7.304	0.686	6.112	0.315	0.837	flavodoxin 1
ybfE	STM0695	AAL19639	(757809..758102)	1.803	0.240	1.362	0.199	0.755	1.198	0.043	0.932	0.175	0.778	LexA regulated, putative SOS response
ybfF	STM0696	AAL19640	(758236..759006)	4.371	0.720	1.601	0.047	0.366	2.073	0.495	1.942	0.135	0.937	putative enzyme
seqA	STM0697	AAL19641	759191..759733	5.670	0.666	3.953	0.640	0.697	2.675	0.424	2.224	0.153	0.831	negative modulator of initiation of replication, inhibits open lex formation, mutation in gene alters cell membrane
pgm	STM0698	AAL19642	759758..761398	7.954	0.768	10.681	0.458	1.343	4.169	0.249	4.531	0.528	1.087	phosphoglucomutase
STM0699	STM0699	AAL19643	(761513..761998)	0.431	0.048	4.733	0.381	10.992	0.296	0.014	0.306	0.014	1.035	putative cytoplasmic protein
potE	STM0700	AAL19644	(762063..763382)	0.372	0.109			0.000	0.294	0.043			0.000	APC family, putrescine/ornithine antiporter
speF	STM0701	AAL19645	(763379..765577)	0.249	0.113	14.578	1.352	58.660	0.283	0.064	0.291	0.043	1.028	ornithine decarboxylase isozyme, inducible
kdpE	STM0702	AAL19646	(766339..767016)	0.729	0.077	1.118	0.188	1.535	0.972	0.129	1.440	0.054	1.482	response regulator in two-onent regulatory system with KdpD, regulates kdp operon encoding a high-affinity K translocating ATPase (OmpR family)
kdpD	STM0703	AAL19647	(767013..769697)	0.412	0.081	0.484	0.011	1.174	0.554	0.309	0.752	0.055	1.356	sensory kinase in two-onent regulatory system wtih KdpE, regulates kdp operon (high-affinity potassium transport system)
kdpC	STM0704	AAL19648	(769694..770278)	0.426	0.120	0.282	0.030	0.661	0.430	0.105	0.645	0.046	1.500	P-type ATPase, high-affinity potassium transport system, C chain
kdpB	STM0705	AAL19649	(770287..772335)	0.404	0.145	0.220	0.045	0.545	0.342	0.020	0.630	0.056	1.843	P-type ATPase, high-affinity potassium transport system, B chain
kdpA	STM0706	AAL19650	(772356..774035)	0.277	0.145	0.135	0.025	0.485	0.408	0.076	0.679	0.032	1.665	P-type ATPase, high-affinity potassium transport system, A chain
STM0707	STM0707	AAL19651	(774035..774124)					N/A	2.317				0.000	putative outer membrane protein
ybfA	STM0708	AAL19652	774461..774667	0.557	0.113	0.758	0.195	1.359	0.788	0.031	0.753	0.196	0.955	putative periplasmic protein
phrB	STM0709	AAL19653	774778..776199	0.819	0.038	0.300	0.014	0.367	0.992	0.103	0.684	0.080	0.689	deoxyribodipyrimidine photolyase (photoreactivation)
ybgH	STM0710	AAL19654	(776238..777719)	0.440	0.061	0.237	0.039	0.538	0.274	0.003	0.288	0.031	1.050	putative POT family transport protein
ybgI	STM0711	AAL19655	778048..778791	5.452	1.402	2.510	0.448	0.460	2.597	0.773	4.869	0.088	1.875	putative cytoplasmic protein
ybgJ	STM0712	AAL19656	778807..779463	4.363	1.144	3.031	0.243	0.695	2.735	0.981	4.488	0.061	1.641	putative carboxylase
ybgK	STM0713	AAL19657	779457..780389	3.184	0.982	1.856	0.170	0.583	2.129	0.572	2.873	0.018	1.350	putative carboxylase
ybgL	STM0714	AAL19658	780379..781113	1.973	0.353	1.285	0.142	0.651	1.578	0.246	2.078	0.092	1.317	putative lactam utilization protein
STM0715	STM0715	AAL19659	781437..781568	0.490	0.174	0.539	0.210	1.099	1.269	0.461	0.953	0.134	0.751	putative cytoplasmic protein
STM0716	STM0716	AAL19660	781628..782194	0.433	0.068	0.341	0.053	0.788	0.413	0.013	0.625	0.025	1.514	putative phage integrase
STM0717	STM0717	AAL19661	782654..782989	0.172	0.075	0.134	0.006	0.781	0.159	0.103	0.145	0.009	0.913	putative inner membrane protein
STM0718	STM0718	AAL19662	782991..783731	0.314	0.088	0.169	0.035	0.539	0.169	0.011	0.248	0.019	1.469	putative cytoplasmic protein

STM0719	STM0719	AAL19663	784017..785168	0.226	0.078	0.141	0.012	0.623	0.304	0.076	0.281	0.015	0.923	putative UDP-galactopyranose mutase
STM0720	STM0720	AAL19664	785165..786061	0.202	0.096	0.097	0.015	0.482	0.280	0.013	0.170	0.007	0.609	putative glycosyl transferase
STM0721	STM0721	AAL19665	786074..787207	0.261	0.091	0.121	0.022	0.465	0.421	0.067	0.214	0.027	0.508	putative glycosyl transferase
STM0722	STM0722	AAL19666	787336..788106	0.255	0.107	0.113	0.035	0.442	0.514	0.042	0.352	0.016	0.684	putative ABC transporter permease protein
STM0723	STM0723	AAL19667	788110..788820	0.200	0.090	0.127	0.025	0.632	0.479	0.043	0.340	0.076	0.711	putative ABC-type polysaccharide/polyol phosphate transport system, ATPase onent
STM0724	STM0724	AAL19668	788914..790692			5.089		N/A					N/A	putative glycosyltransferase, cell wall biogenesis
STM0725	STM0725	AAL19669	790885..791718	0.213	0.060	0.102	0.016	0.480	0.915	0.009	0.517	0.012	0.565	putative glycosyltransferase, cell wall biogenesis
STM0726	STM0726	AAL19670	791776..793671	0.203	0.068	0.135	0.018	0.667	0.705	0.013	0.489	0.032	0.693	putative glycosyl transferase
STM0727	STM0727	AAL19671	793739..793876	0.812	0.245	0.405	0.077	0.499	1.076	0.246	0.877	0.067	0.815	putative cytoplasmic protein
nei	STM0728	AAL19672	793925..794716	1.358	0.121	0.979	0.073	0.721	1.229	0.155	1.288	0.173	1.048	endonuclease VIII removing oxidized pyrimidines may also remove oxidized purines in absence of MutY and Fpg
abrB	STM0729	AAL19673	(794771..795817)	0.973	0.028	1.486	0.116	1.528	0.347	0.048	0.626	0.044	1.804	putative transport protein
gltA	STM0730	AAL19674	(795954..797237)	12.355	1.760	30.895	1.703	2.501	2.466	0.172	6.574	0.626	2.666	citrate synthase
STM0731	STM0731	AAL19675	797197..797583	21.957	3.168	36.938	5.589	1.682	3.335	0.158	7.481	0.310	2.243	putative inner membrane protein
sdhC	STM0732	AAL19676	797992..798381	10.084	0.711	32.955	4.087	3.268	3.940	0.157	5.571	0.765	1.414	succinate dehydrogenase, cytochrome b556
sdhD	STM0733	AAL19677	798375..798722	18.690	3.494	38.102	4.286	2.039	9.424	1.213	11.314	0.553	1.201	succinate dehydrogenase, hydrophobic subunit
sdhA	STM0734	AAL19678	798722..800488	17.160	3.661	57.242	5.407	3.336	8.744	1.501	14.776	0.415	1.690	succinate dehydrogenase, flavoprotein subunit
sdhB	STM0735	AAL19679	800502..801221	29.030	9.161	37.398	1.353	1.288	12.572	0.799	15.893	1.390	1.264	succinate dehydrogenase, Fe-S protein
sucA	STM0736	AAL19680	801745..804546					N/A					N/A	2-oxoglutarate dehydrogenase (decarboxylase onent)
sucB	STM0737	AAL19681	804561..805769	8.920	2.077	9.647	0.972	1.082	4.036	0.476	5.223	0.513	1.294	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 onent)
sucC	STM0738	AAL19682	805911..807077	7.940	0.705	8.249	1.581	1.039	3.784	0.304	4.425	0.285	1.169	succinyl-CoA synthetase, beta subunit
sucD	STM0739	AAL19683	807077..807946	4.952	0.796	5.652	0.686	1.142	1.911	0.090	2.904	0.164	1.520	succinyl-CoA synthetase, alpha subunit
cydA	STM0740	AAL19684	809529..811097	1.472	0.066	48.283	9.824	32.803	2.349	0.207	2.520	0.192	1.073	cytochrome d terminal oxidase, polypeptide subunit I
cydB	STM0741	AAL19685	811113..812252	2.005	0.099	45.421	2.216	22.655	2.481	0.450	3.319	0.243	1.338	cytochrome d terminal oxidase polypeptide subunit II
ybgT	STM0742	AAL19686	812267..812380	1.421	0.097	28.247	2.579	19.874	1.973	0.722	2.445	0.382	1.239	putative outer membrane lipoprotein
ybgE	STM0743	AAL19687	812517..812798	1.218	0.075	6.766	1.009	5.556	1.181	0.094	1.056	0.072	0.894	putative inner membrane lipoprotein
ybgC	STM0744	AAL19688	813027..813431	2.709	0.476	1.657	0.175	0.612	2.452	0.179	0.904	0.129	0.369	putative esterase
tolQ	STM0745	AAL19689	813428..814120	2.543	0.062	2.165	0.210	0.851	2.633	0.299	1.587	0.104	0.603	tol protein, membrane-spanning inner membrane proteins, required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm
tolR	STM0746	AAL19690	814124..814552	1.564	0.083	1.877	0.094	1.201	1.625	0.022	1.564	0.046	0.963	tol protein, role in outer membrane integrity, uptake of group A colicins (TonB independent), and translocation of phage DNA to cytoplasm
tolA	STM0747	AAL19691	814617..815840	2.258	0.376	2.801	0.158	1.240	2.356	0.345	1.963	0.183	0.833	tol protein, membrane spanning protein

tolB	STM0748	AAL19692	815964..817256	9.172	0.371	6.947	0.553	0.757	8.562	0.979	8.367	0.641	0.977	tol protein required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm, may be part of multiprotein peptidoglycan recycling lex (Two domains)
pal	STM0749	AAL19693	817291..817815	22.515	2.335	26.376	3.969	1.171	15.494	0.207	25.889	1.932	1.671	tol protein required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA to cytoplasm
ybgF	STM0750	AAL19694	817825..818613	10.172	1.119	6.317	0.678	0.621	6.752	0.129	6.824	0.481	1.011	putative periplasmic protein
lysT	STM0751						N/A					N/A		
valT	STM0752						N/A					N/A		
lysW	STM0753						N/A					N/A		
lysY	STM0754						N/A					N/A		
lysZ	STM0755						N/A					N/A		
nadA	STM0756	AAL19695	820233..821276	0.468	0.094	0.328	0.014	0.701	0.343	0.037	0.292	0.026	0.852	quinolinate synthetase, A protein
pnuC	STM0757	AAL19696	821301..822020	0.702	0.049	0.311	0.067	0.443	0.696	0.052			0.000	NMN family, nucleoside/purine/pyrimidine transporter
ybgR	STM0758	AAL19697	(822017..822955)	0.684	0.042	0.358	0.045	0.523	0.762	0.032	0.462	0.029	0.606	putative CDF family transport protein
ybgS	STM0759	AAL19698	(823066..823452)	0.830	0.038	0.524	0.094	0.632	3.075	0.409	1.180	0.037	0.384	putative homeobox protein
aroG	STM0760	AAL19699	823772..824824	4.329	0.796	1.902	0.233	0.439	2.145	0.234	2.467	0.151	1.150	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, phenylalanine repressible)
STM0761	STM0761	AAL19700	(824918..825463)	0.474	0.039	0.459	0.055	0.968	1.173	0.174	0.902	0.042	0.769	fumarate hydratase Class I anaerobic
STM0762	STM0762	AAL19701	(825478..826323)	0.475	0.106	0.375	0.021	0.790	2.559	0.137	1.003	0.038	0.392	fumarate hydratase, alpha subunit
STM0763	STM0763	AAL19702	826492..827343	0.955	0.108	0.372	0.068	0.389	2.874	0.579	1.138	0.075	0.396	transcriptional regulator, lysR family
STM0764	STM0764	AAL19703	(827344..828327)	0.882	0.261	0.152	0.037	0.172	1.237	0.134	0.526	0.026	0.425	transcriptional regulator, lysR family
STM0765	STM0765	AAL19704	828571..829818	0.162	0.093	0.109	0.026	0.677	0.519	0.107	0.292	0.009	0.563	putative cation transporter
dcoC	STM0766	AAL19705	829868..830113					N/A					N/A	Oxalacetate decarboxylase: gamma chain
dcoA	STM0767; pseudogene; frameshift relative to				0.282	0.190	0.142	0.012	0.505	0.525	0.046	0.669	0.033	1.275
dcoB	STM0768	AAL19706	831919..833220					N/A					N/A	Oxalacetate decarboxylase: beta chain
STM0769	STM0769	AAL19707	833339..834037	0.440	0.097	0.228	0.020	0.517	0.477	0.045	0.469	0.019	0.983	putative cytoplasmic protein
STM0770	STM0770	AAL19708	834417..835496	0.245	0.090	0.181	0.041	0.739	0.150	0.004	0.196	0.016	1.309	putative ABC transport protein
STM0771	STM0771	AAL19709	835496..836272	0.567	0.029	0.597	0.104	1.053	0.351	0.046	0.516	0.081	1.473	putative ABC-type cobalamin/Fe3+-siderophores transport system, ATPase onent
gpmA	STM0772	AAL19710	(836363..837115)	12.345	3.048	8.541	1.461	0.692	5.562	0.385	8.472	0.508	1.523	phosphoglyceromutase 1
galM	STM0773	AAL19711	(837339..838379)	2.880	0.504	5.317	0.787	1.846	1.780	0.296	3.429	0.148	1.927	galactose-1-epimerase (mutarotase)
galK	STM0774	AAL19712	(838373..839521)					N/A					N/A	galactokinase
galT	STM0775	AAL19713	(839524..840570)	1.391	0.031	3.702	0.674	2.661	1.227	0.022	2.627	0.121	2.140	galactose-1-phosphate uridylyltransferase
galE	STM0776	AAL19714	(840581..841597)	0.646	0.038	1.665	0.237	2.577	0.697	0.028	1.496	0.074	2.147	UDP-galactose 4-epimerase
STM0777	STM0777	AAL19715	(841820..842728)	0.308	0.093	0.227	0.043	0.737	0.440	0.061	0.486	0.029	1.103	putative inner membrane protein
modF	STM0778	AAL19716	(842899..844374)	3.120	0.434	1.173	0.155	0.376	1.117	0.237	0.939	0.055	0.840	putative ABC superfamily (atp_bind), molybdenum transporter

modE	STM0779	AAL19717	(844442..845230)	3.208	0.406	1.738	0.227	0.542	1.599	0.352	1.693	0.160	1.059	transcriptional repressor of modABCD operon (molybdate uptake)
STM0780	STM0780	AAL19718	845359..845508	2.180	0.467	0.806	0.114	0.370	1.482	0.141	0.438	0.094	0.296	putative outer membrane or exported
modA	STM0781	AAL19719	845675..846448	3.508	1.014	5.318	0.876	1.516	0.573	0.065	0.955	0.054	1.666	ABC superfamily (peri_perm), molybdate transporter
modB	STM0782	AAL19720	846448..847137	2.350	0.379	2.638	0.115	1.123	0.625	0.080	0.682	0.028	1.091	ABC superfamily (membrane), molybdate transporter
modC	STM0783	AAL19721	847140..848198	1.081	0.145	2.646	0.409	2.448	0.249	0.031	0.498	0.031	2.000	ABC superfamily (atp_bind), molybdate transporter
ybhA	STM0784	AAL19722	(848199..849017)	2.376	0.406	0.947	0.070	0.398	1.331	0.314	0.890	0.054	0.669	putative hydrolase of the HAD superfamily
ybhE	STM0785	AAL19723	849181..850176	3.709	0.876	1.249	0.124	0.337	2.001	0.510	2.359	0.193	1.179	putative 3-carboxymuconate cyclase
ybhC	STM0786	AAL19724	(850320..851603)	3.395	0.228	3.108	0.505	0.915	1.361	0.187	1.773	0.061	1.303	putative pectinesterase
hutI	STM0787	AAL19725	851841..853064	6.391	1.826	4.668	0.722	0.730	1.323	0.272	2.314	0.151	1.750	Imidazolonepropionase
hutG	STM0788	AAL19726	853061..854002	6.410	2.009	3.695	0.246	0.576	1.638	0.037	2.414	0.079	1.474	formimionoglutamate hydrolase
hutC	STM0789	AAL19727	854047..854772	4.108	1.519	1.911	0.142	0.465	0.963	0.235	1.577	0.126	1.638	histidine utilization repressor
hutU	STM0790; pseudogene; frameshift relative to				4.615	2.721	4.327	0.662	0.937	1.692	0.571	2.337	0.206	1.382
hutH	STM0791	AAL19728	856655..858175	2.924	1.684	1.733	0.067	0.593	1.391	0.145	1.476	0.096	1.061	histidine ammonia lyase
ybhB	STM0792	AAL19729	(858260..858736)	2.522	0.649	1.518	0.161	0.602	4.336	0.721	4.241	0.632	0.978	putative Phospholipid-binding protein
bioA	STM0793	AAL19730	(858794..860083)	0.374	0.088	0.148	0.006	0.394	0.227	0.075	0.275	0.036	1.212	7,8-diaminopelargonic acid synthetase
bioB	STM0794	AAL19731	860170..861210	0.238	0.104	0.137	0.042	0.573	0.137	0.043	0.214	0.043	1.558	biotin synthetase
bioF	STM0795	AAL19732	861207..862364	0.301	0.091	0.119	0.037	0.396	0.166	0.058	0.205	0.034	1.232	7-keto-8-aminopelargonic acid synthetase
bioC	STM0796	AAL19733	862348..863103	0.310	0.085	0.118	0.016	0.380	0.125	0.006	0.242	0.030	1.935	biotin biosynthesis; reaction prior to pimeloyl CoA
bioD	STM0797	AAL19734	863096..863782	0.307	0.089	0.157	0.019	0.510	0.140	0.049	0.243	0.048	1.737	dethiobiotin synthetase
uvrB	STM0798	AAL19735	864433..866454	0.552	0.049	0.660	0.080	1.195	0.820	0.035	0.950	0.026	1.158	UvrB with UvrAC is a DNA excision repair enzyme
STM0799	STM0799	AAL19736	866763..866936	0.565	0.099	0.377	0.124	0.668	1.349	0.514	0.940	0.137	0.696	putative cytoplasmic protein
slrP	STM0800	AAL19737	866944..869241	0.329	0.065	0.630	0.122	1.914	1.620	0.151	2.513	0.398	1.551	leucine-rich repeat protein
ybhK	STM0801	AAL19738	(869333..870241)	0.496	0.075	0.659	0.042	1.329	0.528	0.067	0.641	0.063	1.214	putative cytoplasmic protein
moaA	STM0802	AAL19739	870638..871627	1.833	0.262	1.857	0.144	1.013	1.077	0.205	0.841	0.050	0.781	molybdopterin biosynthesis, protein A
moaB	STM0803	AAL19740	871649..872161					N/A					N/A	molybdopterin biosynthesis, protein B
moaC	STM0804	AAL19741	872164..872649	2.507	0.512	4.465	0.379	1.781	1.588	0.394	2.046	0.123	1.289	molybdopterin biosynthesis, protein C
moaD	STM0805	AAL19742	872636..872887	2.936	0.483	3.665	0.210	1.248	1.724	0.343	1.813	0.204	1.052	molybdopterin biosynthesis protein
moaE	STM0806	AAL19743	872889..873341	2.949	0.463	2.902	0.290	0.984	1.879	0.279	1.502	0.099	0.800	molybdopterin converting factor, subunit 2
ybhL	STM0807	AAL19744	873389..874093	7.476	0.709	2.515	0.412	0.336	3.822	0.516	2.202	0.149	0.576	putative permease
ybhM	STM0808	AAL19745	874240..874947	0.366	0.031	0.212	0.032	0.579	1.541	0.332	1.573	0.102	1.021	putative integral membrane protein
STM0809	STM0809	AAL19746	874971..875579	0.192	0.074	0.114	0.014	0.596	2.171	0.239	2.775	0.230	1.278	putative inner membrane protein
STM0810	STM0810	AAL19747	875587..876147	0.180	0.074	0.124	0.026	0.692	1.588	0.311	2.064	0.086	1.299	putative inner membrane protein

ybhN	STM0811	AAL19748	(876150..877112)	0.343	0.118	0.211	0.025	0.617	0.637	0.072	0.759	0.049	1.192	putative negative regulator
ybhO	STM0812	AAL19749	(877112..878353)	0.225	0.115	0.146	0.019	0.647	0.370	0.026	0.614	0.036	1.660	cardiolipin (CL) synthase
ybhP	STM0813	AAL19750	(878350..879108)	0.558	0.037	0.403	0.066	0.723	0.476	0.028	0.690	0.030	1.450	putative cytoplasmic protein
ybhQ	STM0814	AAL19751	879241..879651	13.389	2.104	5.766	0.331	0.431	2.623	0.644	2.230	0.137	0.850	putative inner membrane protein
ybhR	STM0815	AAL19752	(879613..880719)	0.826	0.067	0.792	0.032	0.959	0.435	0.039	0.780	0.083	1.792	putative ABC superfamily (membrane) transport protein
ybhS	STM0816	AAL19753	(880835..881965)	0.451	0.033	0.338	0.013	0.751	0.442	0.041	0.643	0.048	1.454	putative ABC superfamily (membrane) transport protein
ybhF	STM0817	AAL19754	(881958..883694)	0.467	0.075	0.646	0.107	1.384	0.500	0.136	0.851	0.015	1.703	putative ABC-type multidrug transport system, ATPase onent
STM0818	STM0818	AAL19755	(883687..884682)	0.792	0.047	0.944	0.084	1.192	0.482	0.027	1.367	0.039	2.833	membrane permeases, predicted cation efflux pump
ybiH	STM0819	AAL19756	(884682..885356)	0.729	0.021	0.460	0.021	0.631	0.440	0.070	1.108	0.094	2.519	putative transcriptional repressor (TetR/AcrR family)
rhlE	STM0820	AAL19757	885586..886950	1.010	0.037	0.251	0.024	0.249	1.372	0.159	0.459	0.056	0.335	putative ATP-dependent RNA helicase
dinG	STM0821	AAL19758	887158..889302	1.058	0.064	0.462	0.093	0.436	0.680	0.076	0.481	0.020	0.707	LexA regulated (SOS) repair enzyme
ybiB	STM0822	AAL19759	889332..890306	1.764	0.141	0.710	0.058	0.402	1.092	0.162	0.891	0.036	0.816	putative transferase
ybiJ	STM0823	AAL19760	(890462..890722)	0.642	0.041	0.401	0.051	0.625	2.192	0.191	0.871	0.068	0.398	putative periplasmic protein
ybiI	STM0825	AAL19761	(891007..891273)	0.613	0.048	0.293	0.068	0.478	0.512	0.112	0.418	0.040	0.815	putative DnaK suppressor protein
ybiN	STM0826	AAL19762	891478..892404	0.682	0.050	0.396	0.040	0.581	0.593	0.031	0.436	0.050	0.736	putative SAM-dependent methyltransferase
ybiO	STM0827	AAL19763	(892401..894623)	0.491	0.062	0.385	0.032	0.783	0.372	0.078	0.442	0.019	1.189	paral putative transport protein
glnQ	STM0828	AAL19764	(894742..895464)	2.259	0.565	5.693	0.958	2.520	0.455	0.100	0.826	0.018	1.814	ABC superfamily (atp_bind), glutamine high-affinity transporter
glnP	STM0829	AAL19765	(895461..896120)	2.697	0.473	5.301	0.811	1.965	0.500	0.009	0.730	0.185	1.460	ABC superfamily (membrane), glutamine high-affinity transporter
glnH	STM0830	AAL19766	(896264..897010)	7.650	1.076	13.623	1.295	1.781	1.086	0.126	2.032	0.036	1.871	ABC superfamily (bind_prot), glutamine high-affinity transporter
dps	STM0831	AAL19767	(897487..897990)	6.765	1.427	9.878	0.988	1.460	37.834	0.766	26.469	0.854	0.700	stress response DNA-binding protein; starvation induced resistance to H2O2
ybiF	STM0832	AAL19768	(898293..899180)	1.946	0.136			0.000	1.140	0.173			0.000	putative permease
ompX	STM0833	AAL19769	899534..900049	37.301	4.879	7.036	0.367	0.189	28.598	2.981	27.205	2.634	0.951	outer membrane protease, receptor for phage OX2
ybiP	STM0834	AAL19770	(900112..901692)	0.807	0.071	0.428	0.056	0.530	0.735	0.068	0.561	0.096	0.763	putative Integral membrane protein
STM0835	STM0835	AAL19771	902271..902744	2.145	0.286	0.937	0.041	0.437	1.077	0.197	0.735	0.039	0.682	putative Mn-dependent transcriptional regulator.
ybiR	STM0836	AAL19772	902741..903853	0.797	0.032	0.431	0.077	0.541	0.501	0.034	0.396	0.035	0.791	putative Di- and tricarboxylate transporters
ybiS	STM0837	AAL19773	(903897..904817)	0.697	0.040			0.000	0.853	0.081			0.000	putative periplasmic protein
ybiT	STM0838	AAL19774	905036..906628	1.876	0.062	0.850	0.067	0.453	1.523	0.025	0.974	0.137	0.640	putative ATPase onent of ABC transporter with duplicated ATPase domain

STM0839	STM0839	AAL19775	907237..907980	0.231	0.082	0.133	0.011	0.575	0.669	0.032	0.445	0.038	0.666	putative inner membrane protein
ybiV(2)	STM0840	AAL19776	(908009..908728)	0.604	0.043	0.341	0.078	0.565	0.584	0.006	0.567	0.035	0.971	putative hydrolase of the HAD superfamily
ybiU	STM0841	AAL19777	(908933..910198)	0.410	0.041	0.409	0.036	0.998	0.281	0.039	0.392	0.012	1.393	putative cytoplasmic protein
ybiV(1)	STM0842	AAL19778	910460..911269	1.920	0.129	0.806	0.163	0.420	1.265	0.051	0.715	0.040	0.565	putative hydrolase of the HAD superfamily
pflF	STM0843	AAL19779	(911347..913779)	0.282	0.083	0.254	0.016	0.898	0.135	0.004	0.231	0.050	1.704	putative pyruvate formate lyase
pflE	STM0844	AAL19780	(913785..914684)	0.305	0.097	0.278	0.027	0.913	0.205	0.017	0.263	0.022	1.281	putative pyruvate formate lyase activating enzyme
moeB	STM0845	AAL19781	(914962..915711)	1.500	0.113	1.163	0.250	0.776	0.888	0.039	0.915	0.080	1.030	molybdopterin biosynthesis
moeA	STM0846	AAL19782	(915711..916952)	1.258	0.117	1.379	0.184	1.096	0.945	0.108	1.086	0.255	1.149	molybdopterin biosynthesis protein
ybiK	STM0847	AAL19783	917149..918090	3.892	1.145	2.058	0.257	0.529	1.214	0.200	2.133	0.315	1.757	putative asparaginase
yliA	STM0848	AAL19784	918101..919972	3.231	0.718	0.901	0.147	0.279	0.958	0.264	1.023	0.029	1.068	putative ATPase onents of ABC-type transport system, contain duplicated ATPase domain
yliB	STM0849	AAL19785	920005..921543	1.149	0.194	1.252	0.036	1.089	0.548	0.020	0.791	0.039	1.444	putative ABC transporter periplasmic binding protein
yliC	STM0850	AAL19786	921604..922524	0.981	0.067	0.443	0.085	0.452	0.531	0.068	0.465	0.022	0.875	putative ABC transporter periplasmic binding protein
yliD	STM0851	AAL19787	922527..923438	1.122	0.139	0.386	0.014	0.344	0.609	0.132	0.456	0.035	0.748	putative ABC transporter inner membrane onent
yliG	STM0852	AAL19788	(923529..924854)	0.467	0.075	0.746	0.119	1.598	0.464	0.010	0.611	0.008	1.316	putative Fe-S oxidoreductases family 1
yliH	STM0853	AAL19789	925085..925468	0.697	0.097	0.551	0.029	0.791	0.712	0.219	0.735	0.160	1.031	putative cytoplasmic protein
STM0854	STM0854	AAL19790	926181..926696	0.247	0.100	0.161	0.034	0.651	5.357	0.914	1.150	0.082	0.215	putative cytoplasmic protein
STM0855	STM0855	AAL19791	926614..927468	0.256	0.093			0.000	7.880	0.582	2.627		0.333	putative electron transfer flavoprotein beta subunit
STM0856	STM0856	AAL19792	927479..928426	0.200	0.079	0.138	0.041	0.691	6.092	0.066	2.389	0.265	0.392	putative electron transfer flavoprotein alpha subunit
STM0857	STM0857	AAL19793	928720..929883	0.187	0.077	0.111	0.013	0.596	4.185	0.094	2.493	0.080	0.596	putative acyl-CoA dehydrogenase
STM0858	STM0858	AAL19794	930332..932017	0.175	0.091	0.103	0.013	0.588	2.209	0.050	1.934	0.322	0.875	putative dehydrogenase (flavoproteins)
STM0859	STM0859	AAL19795	(932023..932913)	0.263	0.098			0.000	3.902	0.190			0.000	putative transcriptional regulator, LysR family
STM0860	STM0860	AAL19796	(933178..933603)	0.529	0.013	0.258	0.038	0.487	2.514	0.451	1.380	0.230	0.549	putative inner membrane protein
yliI	STM0861	AAL19797	933950..934630	0.409	0.076	0.454	0.078	1.109	0.468	0.035	0.610	0.053	1.304	putative dehydrogenase
yliJ	STM0862	AAL19798	(934627..935253)	2.038	0.207	2.242	0.254	1.100	2.180	0.162	2.697	0.216	1.237	putative glutathione S-transferase
dacC	STM0863	AAL19799	935497..936699	0.791	0.018	1.432	0.166	1.810	2.091	0.025	3.468	0.058	1.658	D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6a
deoR	STM0864	AAL19800	(936744..937502)					N/A					N/A	transcriptional repressor for deoxyribose operon (DeoR family)
ybjG	STM0865	AAL19801	(937574..938182)	2.676	0.317	1.072	0.128	0.401	10.067	1.642	3.186	0.191	0.317	putative permease
mdfA	STM0866	AAL19802	938495..939727	0.822	0.074	0.434	0.059	0.528	0.922	0.086	0.351	0.024	0.381	multidrug translocase
STM0867	STM0867	AAL19803	(939781..940596)	1.360	0.067	0.579	0.051	0.426	0.561	0.037	0.754	0.040	1.345	putative hydrolase
STM0868	STM0868	AAL19804	(940593..941804)	0.742	0.078	0.251	0.034	0.339	0.332	0.020	0.249	0.023	0.750	putative transport protein/putative regulatorn

STM0869	STM0869	AAL19805	941972..942592	0.725	0.057	0.250	0.018	0.345	0.411	0.019	0.308	0.019	0.750	paral putative regulator (TetR/Acr family)
STM0870	STM0870	AAL19806	(942709..944394)	0.672	0.046	0.329	0.087	0.490	1.312	0.276	0.627	0.082	0.478	putative transport protein
ybjM	STM0871	AAL19807	944665..945042	0.774	0.029	0.472	0.037	0.610	0.659	0.069	0.462	0.022	0.701	putative inner membrane protein
grxA	STM0872	AAL19808	(945074..945337)	5.312	1.703	3.021		0.569	2.312	0.170			0.000	glutaredoxin1 redox coenzyme for glutathione-dependent ribonucleotide reductase
ybjC	STM0873	AAL19809	945507..945797	1.356	0.112	0.746	0.087	0.550	1.237	0.049	0.737	0.048	0.596	putative inner membrane protein
mdaA	STM0874	AAL19810	945781..946503	1.153	0.059	0.936	0.040	0.812	1.189	0.204	1.205	0.042	1.013	oxygen-insensitive NADPH nitroreductase
rimK	STM0875	AAL19811	946561..947463	2.271	0.111	0.733	0.100	0.323	1.608	0.169	0.654	0.090	0.407	ribosomal protein S6 modification protein
ybjN	STM0876	AAL19812	947560..948036	1.845	0.098	0.675	0.064	0.366	1.178	0.043	0.667	0.045	0.566	putative cytoplasmic protein
potF	STM0877	AAL19813	948385..949497	0.483	0.065	0.248	0.034	0.514	0.474	0.007	0.465	0.017	0.982	ABC superfamily (peri_perm), putrescine transporter
potG	STM0878	AAL19814	949585..950718	0.546	0.067	0.198	0.014	0.363	0.575	0.032	0.387	0.018	0.673	ABC superfamily (atp_bind), putrescine transporter
potH	STM0879	AAL19815	950728..951681	0.404	0.062	0.182	0.033	0.451	0.354	0.019	0.405	0.056	1.144	ABC superfamily (membrane), putrescine transporter
potI	STM0880	AAL19816	951678..952523	0.677	0.040	0.319	0.049	0.470	0.416	0.087	0.453	0.095	1.089	ABC superfamily (membrane), putrescine transporter
ybjO	STM0881	AAL19817	952597..953070	1.203	0.025	0.374	0.065	0.311	0.864	0.146	0.487	0.019	0.564	putative inner membrane protein
ybjF	STM0882	AAL19818	953113..954243	0.725	0.058	0.325	0.037	0.448	0.767	0.022	0.443	0.050	0.578	putative tRNA (uracil-5-)-methyltransferase
STM0884	STM0884	AAL19819	954526..955869	0.231	0.091	0.091	0.007	0.394	0.401	0.008	0.293	0.014	0.730	putative inner membrane protein; homology to SgaT from Vibrio
STM0885	STM0885	AAL19820	955899..956219	0.216	0.089	0.173	0.024	0.801	0.650	0.041	0.713	0.096	1.096	putative inner membrane protein; homology to SgaT from Vibrio
STM0886	STM0886	AAL19821	956229..957716					N/A					N/A	putative sulfatase
artJ	STM0887	AAL19822	(957935..958666)					N/A					N/A	ABC superfamily (bind_prot), arginine 3rd transport system
artM	STM0888	AAL19823	(958903..959571)	0.882	0.060	1.352	0.166	1.533	0.628	0.026	0.673	0.010	1.071	ABC superfamily (membrane), arginine 3rd transport system
artQ	STM0889	AAL19824	(959571..960287)	0.671	0.022	1.620	0.170	2.416	0.470	0.014	0.555	0.030	1.181	ABC superfamily (membrane), arginine 3rd transport system
artI	STM0890	AAL19825	(960294..961025)	0.800	0.059	5.163	0.749	6.455	0.440	0.029	1.085	0.056	2.462	ABC superfamily (bind_prot), arginine transport system
artP	STM0891	AAL19826	(961043..961771)	1.867	0.136	1.912	0.214	1.024	1.073	0.063	0.998	0.115	0.930	ABC superfamily (atp&memb), arginine transport system
ybjP	STM0892	AAL19827	(962001..962516)	2.507	0.524	3.917	0.604	1.562	2.150	0.503	2.699	0.084	1.255	putative lipoprotein
STM0893	STM0893	AAL19828	(962612..963937)	1.746	0.302	1.841	0.191	1.055	1.653	0.091	1.682	0.050	1.018	Fels-1 prophage; putative integrase
STM0894	STM0894	AAL19829	(963965..964207)	0.386	0.049	0.309	0.046	0.800	0.683	0.127	0.742	0.041	1.086	Fels-1 prophage; putative excisionase
STM0895	STM0895	AAL19830	(964573..964881)	0.391	0.080	0.408	0.062	1.044	0.453	0.098	0.826	0.037	1.824	Fels-1 prophage

STM0896	STM0896	AAL19831	(965341..965733)	0.307	0.112	0.195	0.033	0.636	0.636	0.015	1.634	0.193	2.569	Fels-1 prophage
STM0897	STM0897	AAL19832	(966309..966725)	0.333	0.108			0.000	1.543	0.074			0.000	Fels-1 prophage
STM0898	STM0898	AAL19833	(967911..968606)	1.289	0.061	0.899	0.067	0.697	1.130	0.135	0.858	0.073	0.760	Fels-1 prophage; predicted transcriptional regulator
STM0898A	STM0898A	AAL19834	968719..968973					N/A					N/A	Fels-1 prophage; putative protein
STM0899	STM0899	AAL19835	969473..969841	0.432	0.061	0.620	0.150	1.434	0.536	0.030	0.804	0.077	1.500	Fels-1 prophage
STM0900	STM0900	AAL19836	969999..971582	0.283	0.068	0.231	0.037	0.817	0.379	0.117	0.577	0.058	1.523	Fels-1 prophage; putative DNA or RNA helicases of superfamily II
STM0901	STM0901	AAL19837	971579..972547	0.166	0.103	0.141	0.003	0.851	0.214	0.007	0.435	0.049	2.030	Fels-1 prophage; putative phage DNA primase
STM0902	STM0902	AAL19838	972547..973407	0.211	0.085	0.208	0.028	0.989	0.259	0.009	0.454	0.004	1.753	Fels-1 prophage
STM0903	STM0903	AAL19839	973404..974219	0.456	0.105	0.531	0.038	1.163	0.706	0.017	0.826	0.044	1.171	Fels-1 prophage; putative chaparone
STM0904	STM0904	AAL19840	(974374..974766)	0.421	0.039	0.247	0.044	0.587	3.534	0.991	1.898	0.085	0.537	Fels-1 prophage
STM0905	STM0905	AAL19841	975824..976222	0.898	0.049	0.431	0.046	0.480	5.546	0.229	1.682	0.074	0.303	Fels-1 prophage
STM0906	STM0906	AAL19842	976812..977156	0.288	0.052	0.301	0.032	1.045	0.952	0.031	1.163	0.046	1.221	Fels-1 prophage
STM0907	STM0907	AAL19843	977159..977773	0.472	0.104	0.267	0.020	0.565	0.708	0.027	1.046	0.063	1.477	Fels-1 prophage; putative chitinase
STM0908	STM0908	AAL19844	977770..978255	0.249	0.100	0.174	0.008	0.698	0.455	0.071	0.641	0.015	1.407	Fels-1 prophage
STM0909	STM0909	AAL19845	979090..979581	0.206	0.097	0.134	0.032	0.654	0.358	0.026	0.481	0.022	1.341	Fels-1 prophage
STM0910	STM0910	AAL19846	979568..981676	0.269	0.119	0.139	0.038	0.518	0.690	0.004	0.665	0.053	0.964	Fels-1 prophage
STM0911	STM0911	AAL19847	981876..983411	0.264	0.104	0.163	0.026	0.618	1.088	0.153	1.395	0.183	1.281	Fels-1 prophage
STM0912	STM0912	AAL19848	983263..985449	0.265	0.084	0.230	0.032	0.865	1.211	0.275	1.897	0.049	1.567	Fels-1 prophage; protease subunits of ATP-dependent proteases, ClpP family
STM0913	STM0913	AAL19849	(985463..986134)					N/A					N/A	Fels-1 prophage
STM0914	STM0914	AAL19850	986133..986717	0.300	0.122	0.217	0.026	0.723	0.873	0.071	1.497	0.089	1.714	Fels-1 prophage; putative phage tail onent
STM0915	STM0915	AAL19851	986714..987115	0.221	0.097	0.198	0.042	0.895	0.511	0.081	1.057	0.037	2.070	Fels-1 prophage
STM0916	STM0916	AAL19852	987126..987869	0.262	0.092	0.241	0.063	0.921	0.994	0.154	1.394	0.051	1.402	Fels-1 prophage; putative major tail protein
STM0917	STM0917	AAL19853	988336..988653	0.338	0.104	0.243	0.027	0.718	1.082	0.206	1.392	0.101	1.286	Fels-1 prophage; putative minor tail protein
STM0918	STM0918	AAL19854	988625..991786	0.416	0.148	0.465	0.014	1.120	0.600	0.071	0.914	0.040	1.523	Fels-1 prophage; putative minor tail protein
STM0919	STM0919	AAL19855	991786..992115	0.956	0.078	0.624	0.073	0.653	1.376	0.217	1.125	0.133	0.817	Fels-1 prophage; putative minor tail protein
STM0920	STM0920	AAL19856	992242..992760	16.554	2.575	6.472	1.148	0.391	21.703	2.549	9.179	0.693	0.423	Fels-1 prophage; ail and ompX Homolog
STM0921	STM0921	AAL19857	992892..993587	1.163	0.137	1.074	0.181	0.924	1.858	0.268	2.289	0.144	1.232	Fels-1 prophage; putative minor tail protein
STM0922	STM0922	AAL19858	993599..994333	0.475	0.093	0.553	0.036	1.163	0.973	0.147	1.431	0.039	1.471	Fels-1 prophage; putative tail assembly protein
STM0923	STM0923	AAL19859	994231..994908	0.396	0.080	0.357	0.041	0.902	0.770	0.092	1.020	0.057	1.324	Fels-1 prophage; putative tail assembly protein
STM0924	STM0924	AAL19860	(994962..995486)	0.479	0.229	0.493	0.059	1.029	0.723	0.009	1.494	0.168	2.067	Fels-1 prophage; putative Cu/Zn superoxide dismutase
STM0925	STM0925	AAL19861	995580..999026	0.486	0.276	0.306	0.024	0.631	0.530	0.156	0.632	0.072	1.192	Fels-1 prophage; putative host specificity protein
STM0926	STM0926	AAL19862	999070..1001442	0.290	0.117	0.146	0.009	0.502	0.368	0.039	0.493	0.023	1.340	Fels-1 prophage; putative minor tail protein
STM0927	STM0927	AAL19863	1001442..1002017	0.220	0.079	0.164	0.037	0.742	0.904	0.084	0.570	0.038	0.631	Fels-1 prophage; putative tail assembly protein
nanH	STM0928	AAL19864	(1002088..1003326)	1.755	0.154	1.276	0.214	0.727	12.510	1.217	4.899	0.249	0.392	sialidase (neuraminidase)

STM0929	STM0929	AAL19865	(1003900..1004271)	1.725	0.223	0.625	0.181	0.362	6.939	0.462	3.424	0.122	0.493	putative inner membrane protein
orfB	STM0930	AAL19866	1005367..1005690	12.887	3.705	3.753	0.479	0.291	10.318	1.566	7.576	0.672	0.734	putative cytoplasmic protein
ybjR	STM0931	AAL19867	1005687..1006517	6.941	1.571	3.421	0.441	0.493	5.689	0.775	4.924	0.331	0.866	putative aminidase
STM0932	STM0932	AAL19868	(1006514..1007527)	1.121	0.173	0.931	0.040	0.830	0.899	0.155	0.860	0.065	0.956	putative nucleoside-diphosphate-sugar epimerase
ybjT	STM0933	AAL19869	(1007623..1009056)	1.646	0.260	1.138	0.044	0.691	0.679	0.056	0.802	0.051	1.181	putative nucleoside-diphosphate-sugar epimerase
ltaA	STM0934	AAL19870	(1009067..1010068)	4.332	1.005	2.038	0.337	0.470	1.547	0.409	2.285	0.179	1.477	L-allo-threonine aldolase
poxB	STM0935	AAL19871	(1010107..1011825)	0.436	0.031	0.454	0.039	1.042	0.638	0.068	1.269	0.027	1.988	pyruvate dehydrogenase/oxidase FAD and thiamine PPi cofactors, cytoplasmic in absence of cofactors
hcr	STM0936	AAL19872	(1011983..1012954)	0.426	0.027	2.141	0.161	5.028	0.211	0.016	0.356	0.042	1.691	NADH oxidoreductase for h gene product
h	STM0937	AAL19873	(1012963..1014615)	0.359	0.103	2.181	0.286	6.069	0.174	0.001	0.233	0.047	1.341	hybrid cluster protein; similar to prismane-protein homolog
ybjE	STM0938	AAL19874	(1014759..1015658)	2.490	0.326	0.895	0.179	0.360	1.270	0.313	0.794	0.055	0.625	putative inner membrane protein
ybjD	STM0939	AAL19875	1015860..1017518	0.653	0.098	0.945	0.184	1.445	0.772	0.027	0.738	0.008	0.956	homology with RecF protein
ybjX	STM0940	AAL19876	(1017515..1018483)	10.507	0.201	3.173	0.171	0.302	19.320	2.365	5.180	0.614	0.268	Homolog of virK
ybjY	STM0941	AAL19877	1018611..1019729	0.812	0.041	1.151	0.119	1.418	2.892	0.126	4.036	0.193	1.396	paral putative membrane protein
ybjZ	STM0942	AAL19878	1019726..1021672	1.054	0.043	1.272	0.065	1.206	2.516	0.171	3.537	0.268	1.406	putative ABC superfamily (atp&memb) transport protein
cspD	STM0943	AAL19879	(1021802..1022023)	13.285	3.598	11.571	0.923	0.871	2.768	0.093	3.817	0.341	1.379	similar to CspA but not cold shock induced
yljA	STM0944	AAL19880	1022347..1022667	7.095	2.069	6.806	1.177	0.959	3.162	0.199	4.145	0.096	1.311	putative cytoplasmic protein
clpA	STM0945	AAL19881	1022698..1024974	6.352	1.952	12.724	0.825	2.003	3.041	0.048	6.134	0.389	2.017	ATP-binding subunit of serine protease
tnpA_1	STM0946	AAL19882	1025166..1025624	0.844	0.081	1.040	0.127	1.232	1.020	0.061	0.600	0.068	0.588	IS200 transposase
STM0947	STM0947	AAL19883	(1026087..1026770)	0.226	0.067	0.229	0.051	1.010	0.130	0.008	0.249	0.059	1.914	putative integrase protein
STM0948	STM0948	AAL19884	(1026941..1027342)	0.215	0.067	0.254	0.050	1.185	0.167	0.029	0.321	0.023	1.926	putative cytoplasmic protein
serW	STM0949						N/A					N/A		
STM0950	STM0950	AAL19885	(1027679..1028356)	0.263	0.047	0.553	0.049	2.105	0.303	0.059	0.787	0.119	2.593	Homolog of slsA in STM
STM0951	STM0951	AAL19886	(1028376..1029236)	0.204	0.099			0.000	0.191	0.080			0.000	putative cytoplasmic protein
STM0952	STM0952	AAL19887	1029345..1030256	0.525	0.091	0.481	0.078	0.917	0.442	0.040	0.445	0.043	1.006	putative transcriptional regulator, lysR family
infA	STM0953	AAL19888	(1030347..1030565)	10.886	1.859	1.906	0.156	0.175	11.067	2.302	1.708	0.160	0.154	protein chain initiation factor IF-1
STM0954	STM0954	AAL19889	(1030493..1030876)	3.994	0.518	1.163	0.143	0.291	5.927	0.477	1.413	0.149	0.238	putative inner membrane protein
aat	STM0955	AAL19890	(1030877..1031581)	1.200	0.086	0.474	0.083	0.395	0.966	0.173	0.674	0.121	0.698	leucyl, phenylalanyl-tRNA-protein transferase
cydC	STM0956	AAL19891	(1031626..1033347)	1.732	0.054	0.801	0.136	0.462	1.360	0.376	1.020	0.083	0.750	ABC superfamily (atp&memb), cytochrome-related transporter
cydD	STM0957	AAL19892	(1033348..1035114)	1.294	0.121	1.017	0.207	0.786	1.339	0.099	1.230	0.056	0.919	ABC superfamily (atp&memb), cytochrome-related transporter, Zn sensitive
trxB	STM0958	AAL19893	(1035228..1036196)	8.395	0.811	7.900	0.711	0.941	9.628	1.601	11.343	0.360	1.178	thioredoxin reductase

lrp	STM0959	AAL19894	1036742..1037236	12.185	1.561	7.501	0.864	0.616	5.348	0.402	6.379	0.271	1.193	regulator for lrp regulon and high-affinity branched-chain amino acid transport system; mediator of of leucine response (AsnC family)
ftsK	STM0960	AAL19895	1037371..1041426					N/A					N/A	cell division protein, required for cell division and chromosome partitioning
lolA	STM0961	AAL19896	1041566..1042180	5.234	1.709	4.715	0.848	0.901	4.120	0.645	3.021	0.217	0.733	periplasmic protein effects translocation of lipoproteins from inner membrane to outer membrane
ycaJ	STM0962	AAL19897	1042190..1043533	2.512	0.638	2.497	0.164	0.994	1.821	0.215	1.797	0.152	0.986	paral putative polynucleotide enzyme
serS	STM0963	AAL19898	1043792..1045084	2.647	0.618	7.078	0.546	2.674	1.536	0.029	2.687	0.311	1.749	serine tRNA synthetase ; also charges selenocystein tRNA with serine
dmsA	STM0964	AAL19899	1045321..1047765	0.173	0.084	4.913	0.722	28.442	0.144	0.068	0.195	0.061	1.352	anaerobic dimethyl sulfoxide reductase, subunit A
dmsB	STM0965	AAL19900	1047776..1048393	0.205	0.104	4.158	0.747	20.244	0.117	0.010	0.188	0.024	1.611	anaerobic dimethyl sulfoxide reductase, subunit B
dmsC	STM0966	AAL19901	1048395..1049258	1.110	1.279	3.396	0.369	3.058	1.079	0.733	0.887	0.449	0.822	anaerobic dimethyl sulfoxide reductase, subunit C
ycaD	STM0968	AAL19902	1049608..1050756	0.180	0.112	0.332	0.014	1.850	0.554	0.033	0.293	0.008	0.529	putative MFS family transport protein
ycaM	STM0969	AAL19903	1050974..1052395	0.595	0.111	0.286	0.028	0.481	3.267	0.679	0.542	0.039	0.166	putative APC family, amino-acid transporter
pflA	STM0970	AAL19904	(1052688..1053512)	1.782	0.072	1.356	0.060	0.761	1.955	0.024	1.325	0.090	0.678	pyruvate formate lyase activating enzyme 1
STM0971	STM0971	AAL19905	(1053604..1053930)	0.429	0.099	0.533	0.029	1.242	0.934	0.106	0.597	0.057	0.639	putative cytoplasmic protein
STM0972	STM0972	AAL19906	1054061..1055020	0.377	0.036	1.501	0.321	3.981	9.787	0.981	7.341	0.370	0.750	homologous to secreted protein sopD
pflB	STM0973	AAL19907	(1055096..1057378)	1.579	0.057	37.967	1.835	24.045	3.843	0.014	8.841	1.008	2.301	pyruvate formate lyase I, induced anaerobically
focA	STM0974	AAL19908	(1057438..1058295)	0.850	0.027	2.160	0.191	2.540	3.635	0.586	2.530	0.236	0.696	putative FNT family, formate transporter (formate channel 1)
ycaO	STM0975	AAL19909	(1058700..1060460)	0.890	0.141	0.516	0.040	0.580	1.240	0.031	0.564	0.115	0.455	putative cytoplasmic protein
ycaP	STM0976	AAL19910	1060597..1061289	0.557	0.045	0.527	0.043	0.947	0.483	0.004	0.598	0.146	1.239	putative inner membrane protein
serC	STM0977	AAL19911	1061475..1062563	5.251	0.682			0.000	4.156	0.115			0.000	3-phosphoserine aminotransferase / phosphohydroxythreonine transaminase
aroA	STM0978	AAL19912	1062634..1063917	1.164	0.760	1.533	0.289	1.318	1.632	0.056	1.898	0.102	1.164	3-enolpyruvylshikimate-5-phosphate synthetase
ycaL	STM0979	AAL19913	1064060..1064821	0.781	0.048	0.796	0.171	1.019	0.465	0.029	0.472	0.080	1.015	putative Zn-dependent protease with chaperone function
cmk	STM0980	AAL19914	1064994..1065677	2.371	0.114	3.512	0.566	1.481	1.789	0.351	1.664	0.208	0.930	cytidine monophosphate (CMP) kinase
rpsA	STM0981	AAL19915	1065791..1067464	29.756	1.502	47.445	2.280	1.594	10.815	2.251	12.855	1.727	1.189	30S ribosomal subunit protein S1
himD	STM0982	AAL19916	1067620..1067904	4.899	0.654	7.680	0.968	1.568	4.500	0.092			0.000	integration host factor (IHF), beta subunit; site-specific recombination
ycaI	STM0983	AAL19917	1068134..1070398	0.476	0.096			0.000	0.287	0.087			0.000	putative recombination protein
msbA	STM0984	AAL19918	1070435..1072183	0.978	0.072	1.086	0.099	1.110	1.112	0.047	0.893	0.078	0.803	ABC superfamily (atp&membrane) transport protein; multicopy repressor of htrB
lpxK	STM0985	AAL19919	1072180..1073157	1.639	0.161	1.078	0.077	0.658	1.321	0.119	0.926	0.052	0.701	tetraacyldisaccharide 4' kinase (lipid A 4'kinase)

ycaQ	STM0986	AAL19920	1073201..1074433	0.850	0.038	0.570	0.038	0.670	0.656	0.128	0.394	0.037	0.601	putative cytoplasmic protein
ycaR	STM0987	AAL19921	1074485..1074667	1.430	0.067	2.407	0.718	1.683	0.890	0.186	0.751	0.084	0.843	putative inner membrane protein
kdsB	STM0988	AAL19922	1074664..1075410	1.461	0.082	3.638	0.178	2.490	0.611	0.246	0.898	0.059	1.470	CTP:CMP-3-deoxy-D-manno-octulosonate transferase
STM0989	STM0989	AAL19923	1075621..1076514	0.680	0.040			0.000	0.337	0.032			0.000	mukF protein (killing factor KicB)
ycbC	STM0990	AAL19924	(1076494..1077270)	0.620	0.036	0.424	0.038	0.684	0.373	0.022	0.416	0.016	1.115	putative KicA protein
smtA	STM0991	AAL19925	1077406..1078209	3.377	0.561	2.850	0.200	0.844	1.062	0.255	0.892	0.072	0.840	S-adenosylmethionine-dependent methyltransferase
mukF	STM0992	AAL19926	1078202..1079524	2.682	0.188	2.762	0.512	1.030	1.258	0.169	0.994	0.126	0.790	mukF protein (killing factor KICB)
mukE	STM0993	AAL19927	1079505..1080209	3.027	0.358	3.215	0.207	1.062	2.235	0.243	1.904	0.149	0.852	putative chromosome partitioning
mukB	STM0994	AAL19928	1080209..1084675			5.186		N/A	1.630	5.689	0.826		0.507	kinesin-line cell division protein involved in sister chromosome partitioning
ycbB	STM0995	AAL19929	1085020..1086861	2.985	0.539	3.921	0.790	1.313	1.609	0.211	2.009	0.136	1.248	putative periplasmic protein
ycbK	STM0996	AAL19930	1087121..1087669	15.952	3.103	13.064	1.567	0.819	7.403	1.377	5.946	0.547	0.803	putative outer membrane protein
ycbL	STM0997	AAL19931	1087697..1088344	10.531	2.213	8.948	1.510	0.850	5.429	0.580	3.966	0.306	0.730	putative Metallo-beta-lactamase
aspC	STM0998	AAL19932	(1088406..1089596)	6.983	0.773	7.391	0.558	1.058	3.177	0.069	4.694	0.285	1.478	aspartate aminotransferase
ompF	STM0999	AAL19933	(1089781..1090872)					N/A					N/A	outer membrane protein 1a (ia;b;f), porin
asnS	STM1000	AAL19934	(1091479..1092879)	4.343	0.330	5.276	0.575	1.215	3.524	0.331	5.043	0.342	1.431	asparagine tRNA synthetase
STM1001	STM1001	AAL19935	(1093080..1093541)	1.069	0.018	0.814	0.156	0.762	3.319	0.537	3.044	0.398	0.917	putative leucine response regulator
STM1002	STM1002	AAL19936	1093858..1095072	0.220	0.071	0.181	0.009	0.823	0.639	0.054	0.545	0.099	0.853	putatiave diaminopropionate ammonia lyase
STM1003	STM1003	AAL19937	1095317..1096753	0.224	0.084	0.128	0.015	0.572	0.634	0.083	0.554	0.072	0.874	putative transcriptional regulator, Lrp family
pncB	STM1004	AAL19938	(1096831..1098033)	1.520	0.045	0.937	0.109	0.616	1.721	0.179	1.201	0.068	0.698	nicotinate phosphoribosyltransferase
STM1005	STM1005	AAL19939	(1098228..1099520)	1.805	0.182	1.026	0.038	0.568	0.767	0.080	0.554	0.066	0.721	Gifsy-2 prophage; integrase
STM1006	STM1006	AAL19940	(1099565..1099813)	0.641	0.052	0.392	0.059	0.611	0.351	0.100	0.409	0.110	1.165	Gifsy-2 prophage; excisionase
STM1007	STM1007	AAL19941	(1099854..1100093)	0.226	0.083	0.248	0.028	1.099	0.239	0.115	0.442	0.024	1.851	Gifsy-2 prophage
STM1008	STM1008	AAL19942	(1100136..1101293)	0.212	0.072	0.179	0.021	0.843	0.129	0.021	0.364	0.045	2.822	Gifsy-2 prophage
STM1009	STM1009	AAL19943	(1101256..1104141)	0.147	0.102	0.134	0.020	0.910	0.111	0.017	0.281	0.014	2.528	Gifsy-2 prophage; exodeoxyribonuclease
STM1010	STM1010	AAL19944	(1104268..1104567)					N/A					N/A	Gifsy-2 prophage
STM1011	STM1011	AAL19945	(1104740..1105000)	0.331	0.048	0.249	0.013	0.751	0.474	0.001	0.371	0.046	0.784	Gifsy-2 prophage
STM1012	STM1012	AAL19946	(1105050..1105460)	1.929	0.366	0.542	0.109	0.281	0.647	0.047	0.443	0.022	0.684	Gifsy-2 prophage; probable regulatory protein
STM1013	STM1013	AAL19947	1105785..1106159	0.331	0.070	0.173	0.023	0.525	0.339	0.021	0.442	0.045	1.304	Gifsy-2 prophage; probable regulatory protein
STM1014	STM1014	AAL19948	1106244..1107227	0.312	0.094	0.130	0.041	0.416	0.232	0.008	0.291	0.021	1.259	Gifsy-2 prophage; probable regulatory protein
STM1015	STM1015	AAL19949	1107230..1107979	0.195	0.106	0.120	0.015	0.616	0.176	0.024	0.239	0.032	1.362	Gifsy-2 prophage; ATPase involved in DNA replication initiation
STM1016	STM1016	AAL19950	1107990..1108337	0.345	0.105	0.167	0.023	0.483	0.266	0.016	0.285	0.010	1.069	Gifsy-2 prophage
STM1017	STM1017	AAL19951	1108334..1108645	0.563	0.051	0.343	0.014	0.608	0.452	0.109	0.384	0.014	0.849	Gifsy-2 prophage
STM1018	STM1018	AAL19952	1108723..1109013	3.586	0.788	1.968	0.154	0.549	1.626	0.088	0.786	0.008	0.483	Gifsy-2 prophage
STM1019	STM1019	AAL19953	1109305..1109538	1.100	0.110	0.454	0.043	0.413	1.465	0.158	0.768	0.140	0.525	Gifsy-2 prophage

STM1020	STM1020	AAL19954	1109954..1110556	0.352	0.116	0.224	0.013	0.637	0.358	0.044	0.348	0.041	0.972	Gifsy-2 prophage
STM1021	STM1021	AAL19955	1110765..1111376	0.275	0.104	0.173	0.046	0.628	0.196	0.052	0.305	0.034	1.558	Gifsy-2 prophage
STM1022	STM1022	AAL19956	1111509..1112306	0.217	0.088	0.140	0.012	0.644	0.176	0.043	0.191	0.043	1.087	Gifsy-2 prophage; putative molecular chaperone, DnaJ family
STM1023	STM1023	AAL19957	1112373..1112690	0.919	0.111	0.347	0.071	0.377	0.908	0.046	0.313	0.041	0.345	Gifsy-2 prophage
STM1024	STM1024	AAL19958	1112864..1112989	0.970	0.161	0.552	0.116	0.569	2.374	0.889	0.701	0.168	0.295	Gifsy-2 prophage
STM1025	STM1025	AAL19959	(1113125..1113574)	0.714	0.091	0.549	0.139	0.769	3.536	1.309	1.233	0.045	0.349	Gifsy-2 prophage
STM1026	STM1026	AAL19960	(1113935..1114447)	0.266	0.081	0.395	0.027	1.483	0.370	0.038	0.555	0.038	1.499	Gifsy-2 prophage
STM1027	STM1027	AAL19961	1114978..1115226	0.245	0.130	0.138	0.055	0.563	0.282	0.019	0.247	0.017	0.876	Gifsy-2 prophage
STM1028	STM1028	AAL19962	1115210..1115662	0.239	0.113	0.134	0.009	0.562	0.219	0.030	0.267	0.023	1.216	Gifsy-2 prophage; lysozyme
STM1029	STM1029	AAL19963	1115680..1116159	0.246	0.115			0.000	0.240	0.006			0.000	Gifsy-2 prophage
STM1030	STM1030	AAL19964	1116367..1116900	0.202	0.109	0.140	0.010	0.691	0.168	0.069	0.258	0.049	1.534	Gifsy-2 prophage
STM1031	STM1031	AAL19965	1116857..1118995	0.216	0.084	0.130	0.025	0.601	0.146	0.052	0.199	0.020	1.363	Gifsy-2 prophage
STM1032	STM1032	AAL19966	1119429..1120742	0.255	0.075			0.000	0.263	0.060			0.000	Gifsy-2 prophage
STM1033	STM1033	AAL19967	1120666..1122747	0.201	0.092	0.246	0.023	1.221	0.183	0.016	0.364	0.041	1.992	Gifsy-2 prophage; resembles Clp protease
STM1034	STM1034	AAL19968	1122838..1123161	0.315	0.110	0.456	0.151	1.448	0.263	0.213	0.362	0.049	1.379	Gifsy-2 prophage; putative RecA/RadA recombinase
STM1035	STM1035	AAL19969	1123154..1123453	0.183	0.111	0.151	0.010	0.828	0.165	0.073	0.210	0.029	1.273	Gifsy-2 prophage; ATP-binding sugar transporter-like protein
STM1036	STM1036	AAL19970	1123434..1124000	0.188	0.095			0.000	0.164	0.071			0.000	Gifsy-2 prophage; probable minor tail protein
STM1037	STM1037	AAL19971	1123997..1124398	0.176	0.082	0.148	0.011	0.838	0.199	0.084	0.191	0.020	0.961	Gifsy-2 prophage; probable minor tail protein
STM1038	STM1038	AAL19972	1124410..1125159	0.230	0.114	0.197	0.035	0.857	0.146	0.035	0.230	0.007	1.570	Gifsy-2 prophage; probable major tail protein
STM1039	STM1039	AAL19973	1125205..1125603	0.178	0.091	0.168	0.046	0.944	0.180	0.112	0.257	0.052	1.431	Gifsy-2 prophage; probable minor tail protein
STM1040	STM1040	AAL19974	1125600..1125929	0.234	0.106	0.184	0.038	0.784	0.256	0.117	0.320	0.007	1.249	Gifsy-2 prophage; probable minor tail protein
STM1041	STM1041	AAL19975	1126009..1128996	0.197	0.095	0.178	0.031	0.901	0.139	0.025	0.265	0.023	1.903	Gifsy-2 prophage; probable minor tail protein
STM1042	STM1042	AAL19976	1128993..1129325	0.292	0.110	0.209	0.007	0.715	0.370	0.046	0.439	0.027	1.188	Gifsy-2 prophage; probable minor tail protein
STM1043	STM1043	AAL19977	1129424..1129921	0.334	0.018	0.305	0.024	0.912	0.815	0.093	0.754	0.135	0.924	Gifsy-2 prophage; attachment and invasion protein homolog
STM1045	STM1045	AAL19979	1130676..1131371	0.412	0.088	0.449	0.057	1.089	1.027	0.581	0.773	0.160	0.753	Gifsy-2 prophage; probable minor tail protein
STM1046	STM1046	AAL19980	1131381..1132118	0.295	0.055	0.265	0.036	0.899	0.353	0.223	0.353	0.035	1.001	Gifsy-2 prophage; probable tail assembly protein
STM1047	STM1047	AAL19981	1132016..1132720	0.391	0.068	0.323	0.038	0.827	0.230	0.081	0.407	0.025	1.768	Gifsy-2 prophage; probable tail assembly protein
STM1048	STM1048	AAL19982	1132792..1135239	0.201	0.079	0.120	0.013	0.598	0.141	0.043	0.195	0.023	1.381	Gifsy-2 prophage; host specificity protein J, phage lambda
STM1049	STM1049	AAL19983	1136476..1138914					N/A					N/A	Gifsy-2 prophage; probable tail fiber protein
STM1050	STM1050	AAL19984	1138914..1139495	0.222	0.095	0.136	0.009	0.614	0.646	0.247	0.460	0.040	0.712	Gifsy-2 prophage; tail fiber assembly like-protein
sseI	STM1051	AAL19985	1139971..1140939					N/A					N/A	Gifsy-2 prophage; putative type III secreted protein
STM1052	pseudogene; in-frame stop following codon 112				0.365	0.074	0.199	0.018	0.545	1.764	0.160	1.784	0.122	1.011

STM1053	STM1053	AAL19986	(1141587..1142213)	0.214	0.085	0.104	0.029	0.487	0.595	0.072	0.526	0.067	0.884	Gifsy-2 prophage
STM1054	STM1054	AAL19987	(1142282..1142581)	0.563	0.047	0.363	0.055	0.645	2.138	0.204	1.017	0.094	0.476	Gifsy-2 prophage
STM1055	STM1055	AAL19988	(1142566..1143252)	1.309	0.123	0.551	0.212	0.421	5.272	0.432	2.156	0.062	0.409	Gifsy-2 prophage
STM1056	STM1056	AAL19989	(1143523..1143714)	0.747	0.138	0.457	0.049	0.611	2.453	0.245	0.827	0.071	0.337	Gifsy-2 prophage; Homolog of msgA
pepN	STM1057	AAL19990	1144141..1146753	3.309	0.479	2.411	0.436	0.729	3.140	0.413	3.205	0.187	1.021	aminopeptidase N
pyrD	STM1058	AAL19991	1146961..1147971	0.820	0.142	0.585	0.059	0.714	0.736	0.015	0.538	0.066	0.730	dihydro-orotate oxidase
ycbW	STM1059	AAL19992	1148137..1148679	2.137	0.117	1.730	0.038	0.809	8.861	0.666	6.710	0.411	0.757	putative cytoplasmic protein
STM1060	STM1060	AAL19993	(1148676..1149785)	0.515	0.046	0.492	0.093	0.956	0.925	0.140	0.816	0.075	0.882	putative iron-sulfur protein
ycbY	STM1061	AAL19994	1149884..1151992	0.973	0.021	0.913	0.142	0.938	1.173	0.161	0.778	0.108	0.664	putative N6-adenine-specific DNA methylase
uup	STM1062	AAL19995	1152005..1153912	0.797	0.037	1.263	0.197	1.585	0.640	0.017	0.705	0.043	1.102	putative ATPase onent of ABC transporters with duplicated ATPase domain
pqiA	STM1063	AAL19996	1153927..1155180	1.607	0.097	0.716	0.032	0.445	1.122	0.132	0.592	0.018	0.528	paraquat-inducible protein A
pqiB	STM1064	AAL19997	1155185..1156825	0.709	0.009	0.893	0.174	1.260	0.607	0.037	0.690	0.031	1.136	paraquat-inducible protein B
ymbA	STM1065	AAL19998	1156822..1157385	0.660	0.033	1.056	0.027	1.601	0.450	0.042	0.639	0.035	1.420	putative outer membrane protein
rmf	STM1066	AAL19999	1157641..1157808	1.681	0.257	1.512	0.233	0.899	1.887	0.071	1.224	0.155	0.649	ribosome modulation factor (involved in dimerization of 70S ribosomes)
fabA	STM1067	AAL20000	(1157908..1158426)	9.748	2.202	4.563	0.824	0.468	5.893	0.371	1.798	0.090	0.305	beta-hydroxydecanoyl thioester dehydrase (trans-2-decenoyl-A isomerase)
lonH	STM1068	AAL20001	(1158495..1160255)	1.596	0.186	1.693	0.092	1.061	0.855	0.030	0.759	0.073	0.888	putative protease
ycbG	STM1069	AAL20002	1160441..1160893	3.814	0.830	3.072	0.440	0.805	1.310	0.149	1.789	0.379	1.366	putative cytoplasmic protein
ompA	STM1070	AAL20003	(1160965..1162017)	13.939	1.553	52.264	9.328	3.750	8.525	0.118	36.507	2.148	4.282	putative hydrogenase, membrane onent
sulA	STM1071	AAL20004	(1162374..1162883)	1.262	0.143	2.179	0.244	1.727	2.251	0.167	1.952	0.281	0.867	suppressor of lon; inhibitor of cell division and FtsZ ring formation upon DNA damage/inhibition, HslVU and Lon involved in its turnover
yccR	STM1072	AAL20005	1163100..1163705	0.497	0.037	0.794	0.120	1.596	0.390	0.210	0.477	0.045	1.223	putative DNA transformation protein
yccS	STM1073	AAL20006	(1163692..1165845)	0.416	0.058	0.653	0.133	1.568	0.357	0.105	0.453	0.007	1.269	putative efflux (PET) family transporter
yccF	STM1074	AAL20007	(1165864..1166310)	0.470	0.072	0.748	0.077	1.592	0.298	0.013	0.453	0.021	1.518	putative inner membrane protein
helD	STM1075	AAL20008	1166434..1168488	0.770	0.063	1.068	0.142	1.388	0.425	0.021	0.785	0.076	1.846	DNA helicase IV
mgsA	STM1076	AAL20009	(1168524..1168982)	4.646	1.115	2.750	0.216	0.592	0.689	0.105	0.715	0.061	1.037	methylglyoxal synthase
yccT	STM1077	AAL20010	(1169077..1169739)	0.389	0.064	0.329	0.069	0.844	0.201	0.094	0.200	0.014	0.994	putative periplasmic protein
STM1078	STM1078	AAL20011	1169910..1170326	0.992	0.091	1.151	0.045	1.160	0.628	0.075	0.900	0.065	1.432	putative cytoplasmic protein
yccV	STM1079	AAL20012	(1170371..1170688)	1.211	0.340	1.311	0.087	1.083	1.165	0.061	2.308	0.119	1.981	putative inner membrane protein
yccW	STM1080	AAL20013	(1170746..1171957)	0.501	0.061	0.740	0.035	1.476	0.376	0.012	0.496	0.022	1.321	putative SAM-dependent methyltransferase
STM1081	STM1081	AAL20014	1172172..1172720	0.510	0.020	0.345	0.071	0.676	0.324	0.060	0.401	0.065	1.238	putative outer membrane protein
STM1082	STM1082	AAL20015	1172746..1173525	1.224	0.017	0.552	0.072	0.451	0.902	0.139	0.717	0.023	0.795	bacterial regulatory protein, AraC family
yccX	STM1083	AAL20016	1173574..1173855	1.074	0.057	0.684	0.092	0.637	1.030	0.026	0.922	0.102	0.895	putative phosphohydrolase
yccK	STM1084	AAL20017	(1173852..1174181)	2.293	0.317	1.711	0.244	0.746	2.589	0.099	1.780	0.140	0.687	putative sulfite reductase, gamma subunit
yccA	STM1085	AAL20018	(1174268..1174927)	8.433	0.468	4.940	0.468	0.586	22.060	5.405	13.479	0.745	0.611	putative TEGT family carrier/transport protein
serT	STM1086						N/A					N/A		

pipA	STM1087	AAL20019	(1175548..1176228)	0.465	0.019	0.279	0.042	0.601	0.922	0.245	0.716	0.062	0.777	Pathogenicity island encoded protein: SPI3
pipB	STM1088	AAL20020	(1176450..1177325)	0.242	0.063	0.258	0.040	1.066	3.345	0.474	2.975	0.281	0.889	Pathogenicity island encoded protein: SPI3
STM1089	STM1089	AAL20021	1177543..1177863	0.643	0.071	0.973	0.048	1.513	3.696	0.398	5.049	0.731	1.366	putative inner membrane protein
pipC	STM1090	AAL20022	(1177873..1178214)	2.804	0.608	3.851	0.290	1.374	26.602	2.689	47.361	4.388	1.780	Pathogenicity island encoded protein: homologous to ipgE of Shigella
sopB	STM1091	AAL20023	(1178231..1179916)	4.742	1.533	9.969	2.482	2.102	5.791	0.345	14.620	1.812	2.525	Salmonella outer protein: homologous to ipgD of Shigella
orfX	STM1092	AAL20024	1180248..1180418	0.369	0.064	1.966	0.162	5.325	0.788	0.330	1.270	0.372	1.611	putative cytoplasmic protein
STM1093	STM1093	AAL20025	(1180419..1180529)	1.195	0.143	1.478	0.534	1.237	1.774	3.305	1.107	0.347	0.624	putative cytoplasmic protein
pipD	STM1094	AAL20026	(1180638..1182107)	0.322	0.083	0.580	0.094	1.799	0.907	0.030	1.967	0.190	2.169	Pathogenicity island encoded protein: SPI3
copS	STM1095	AAL20027	(1182280..1183644)	0.291	0.070	0.227	0.023	0.782	0.290	0.037	0.363	0.012	1.253	Copper resistance; histidine kinase
copR	STM1096	AAL20028	(1183637..1184383)	0.586	0.056	0.304	0.025	0.518	0.990	0.361	0.499	0.096	0.504	Copper resistance; transcriptional regulatory protein
STM1097	STM1097	AAL20029	1184453..1184863	0.404	0.038	0.458	0.039	1.135	0.365	0.039	0.405	0.067	1.110	putative periplasmic or exported protein
hpaC	STM1098	AAL20030	(1185196..1185708)	0.318	0.056	0.261	0.048	0.819	0.213	0.021	0.386	0.057	1.814	4-hydroxyphenylacetate catabolism
hpaB	STM1099	AAL20031	(1185726..1187288)	0.169	0.070	0.169	0.021	0.997	0.104	0.043	0.208	0.011	1.994	4-hydroxyphenylacetate catabolism
hpaR	STM1100	AAL20032	(1187506..1187946)	0.331	0.048	0.497	0.014	1.503	0.165	0.045	0.221	0.033	1.336	4-hydroxyphenylacetate catabolism
hpaG	STM1101	AAL20033	1188221..1189510	0.380	0.018	0.433	0.043	1.139	0.137	0.018	0.382	0.053	2.790	4-hydroxyphenylacetate catabolism
hpaE	STM1102	AAL20034	1189507..1190973					N/A					N/A	4-hydroxyphenylacetate catabolism
hpaD	STM1103	AAL20035	1190975..1191826	0.411	0.035	0.439	0.058	1.068	0.236	0.054	0.457	0.045	1.942	4-hydroxyphenylacetate catabolism
hpaF	STM1104	AAL20036	1191836..1192216	0.401	0.074	0.324	0.025	0.810	0.543	0.614	0.494	0.126	0.910	4-hydroxyphenylacetate catabolism
hpaH	STM1105	AAL20037	1192359..1193162	0.313	0.063	0.339	0.012	1.083	0.193	0.050	0.468	0.041	2.423	4-hydroxyphenylacetate catabolism
hpaI	STM1106	AAL20038	1193173..1193964	0.218	0.063	0.200	0.015	0.916	0.133	0.043	0.390	0.067	2.920	4-hydroxyphenylacetate catabolism
hpaX	STM1107	AAL20039	1194036..1195412	0.205	0.087	0.183	0.048	0.890	0.128	0.018	0.255	0.037	1.983	4-hydroxyphenylacetate catabolism
hpaA	STM1108	AAL20040	1195422..1196318	0.207	0.093	0.194	0.030	0.935	0.164	0.019	0.355	0.069	2.161	4-hydroxyphenylacetate catabolism
STM1109	STM1109	AAL20041	1196332..1197270	0.266	0.051	0.200	0.013	0.752	0.316	0.022	0.309	0.035	0.977	putative periplasmic protein
STM1110	STM1110	AAL20042	(1197678..1198040)	0.186	0.038	0.261	0.105	1.405	5.210	0.923	1.170	0.143	0.225	putative cytoplasmic protein
yccD	STM1111	AAL20043	(1198694..1198999)	1.725	0.359	2.652	0.237	1.538	1.848	0.508	1.823	0.150	0.986	putative cytoplasmic protein
cbpA	STM1112	AAL20044	(1198999..1199919)	1.677	0.066	2.331	0.262	1.389	1.197	0.211	1.482	0.142	1.238	curved DNA-binding protein
scsA	STM1113	AAL20045	1200154..1200516	2.952	0.613	0.955	0.272	0.324	3.396	1.106	1.024	0.138	0.302	Suppression of copper sensitivity: putative copper binding protein
scsB	STM1114	AAL20046	1200565..1202451	0.372	0.074	0.177	0.015	0.476	0.393	0.065	0.267	0.011	0.679	Suppression of copper sensitivity: lipoprotein modification in lgt mutants of E. coli
scsC	STM1115	AAL20047	1202448..1203071	0.358	0.075	0.286	0.042	0.797	0.371	0.053	0.308	0.096	0.830	Suppression of copper sensitivity: lipoprotein modification in lgt mutants of E. coli
scsD	STM1116	AAL20048	1203061..1203567	0.630	0.115	0.489	0.086	0.775	0.668	0.132	0.837	0.276	1.252	Suppression of copper sensitivity: lipoprotein modification in lgt mutants of E. coli
agp	STM1117	AAL20049	1203700..1204941	1.213	0.261	5.041	0.922	4.157	0.422	0.021	1.274	0.068	3.020	glucose-1-phosphatase

yccJ	STM1118	AAL20050	(1204975..1205202)	1.532	0.213	3.360	0.277	2.193	1.871	0.246	1.971	0.398	1.054	putative cytoplasmic protein
wraB	STM1119	AAL20051	(1205223..1205819)	2.269	0.322	6.506	1.273	2.867	3.770	1.267	4.759	0.203	1.262	trp-repressor binding protein
ycdF	STM1120; pseudogene; in-frame stops following				1.996	0.486	1.405	0.077	0.704	2.152	0.426	1.182	0.698	0.549
ymdF	STM1121	AAL20052	1206204..1206371	1.145	0.454	0.838	0.148	0.732	1.109	0.459	0.957	0.230	0.863	putative cytoplasmic protein
ycdC	STM1122	AAL20053	1206508..1207146	1.392	0.472	0.984	0.067	0.707	0.847	0.059	0.781	0.073	0.922	putative transcriptional repressor (TetR/AcrR family)
STM1123	STM1123	AAL20054	(1207143..1207538)	4.307	2.154	4.166	0.862	0.967	1.929	0.193	3.052	0.344	1.582	putative periplasmic protein
putA	STM1124	AAL20055	(1208415..1211558)	10.301	3.641	26.617	2.153	2.584	2.321	0.279	7.113	0.837	3.065	bifunctional in plasma membrane proline dehydrogenase and pyrroline-5-carboxylate dehydrogenase OR in cytoplasm a transcriptional repressor
putP	STM1125	AAL20056	1211980..1213488	29.327	7.749	11.200	0.846	0.382	2.582	0.725	2.180	0.209	0.844	SSS family, major sodium/proline symporter
phoH	STM1126	AAL20057	1214315..1215169	2.240	0.812	3.627	0.650	1.619	1.078	0.082	2.834	0.236	2.630	PhoB-dependent, ATP-binding pho regulon onent
STM1127	STM1127	AAL20058	(1215275..1216156)	1.801	0.170	1.403	0.150	0.779	1.541	0.101	1.502	0.197	0.975	putative transcriptional regulator
STM1128	STM1128	AAL20059	(1216441..1217937)	20.201	4.803	6.167	4.642	0.305	1.056	0.081	0.949		0.899	putative sodium/glucose cotransporter
STM1129	STM1129	AAL20060	(1218274..1218954)	50.027	5.813	11.130	0.596	0.222	0.385	0.038	1.143	0.161	2.970	putative inner membrane protein
STM1130	STM1130	AAL20061	1219460..1220620	16.377	2.202	12.826	3.220	0.783	0.447	0.077	1.730	0.072	3.870	putative inner membrane protein
STM1131	STM1131	AAL20062	1220666..1221358	11.482	4.281	6.312	0.694	0.550	0.646	0.047	1.270	0.045	1.966	putative outer membrane protein
STM1132	STM1132	AAL20063	1221641..1222921	2.640	1.462	2.508	0.139	0.950	0.507	0.068	0.795	0.045	1.568	putative sugar transport protein
STM1133	STM1133	AAL20064	1222932..1224038	1.997	0.553	2.229	0.233	1.116	0.995	0.007	1.755	0.060	1.764	putative dehydrogenases and related proteins
serX	STM1134						N/A					N/A		
ycdW	STM1135	AAL20065	1225066..1226004	2.141	0.280	1.469	0.068	0.686	1.215	0.108	1.276	0.055	1.050	paral putative oxidoreductase
ycdX	STM1136	AAL20066	1226088..1226825	2.777	0.298	1.317	0.235	0.474	1.637	0.242	1.502	0.133	0.918	putative Histidinol phosphatase and related hydrolases of the PHP family
ycdY	STM1137	AAL20067	1226849..1227403	2.543	0.061	1.040	0.164	0.409	1.610	0.036	0.781	0.122	0.485	paral putative oxidoreductase onent
ycdZ	STM1138	AAL20068	1227456..1227986	2.120	0.174	0.551	0.046	0.260	1.458	0.128	0.541	0.074	0.371	putative inner membrane protein
csgG	STM1139	AAL20069	(1228025..1228858)	0.272	0.071	0.199	0.030	0.730	0.234	0.014	0.371	0.046	1.586	putative transcriptional regulator in curly assembly/transport, 2nd curli operon
csgF	STM1140	AAL20070	(1228885..1229301)	0.192	0.050	0.181	0.089	0.945	0.182	0.033	0.336	0.036	1.850	curli production assembly/transport onent, 2nd curli operon
csgE	STM1141	AAL20071	(1229328..1229723)	0.199	0.072	0.171	0.042	0.860	0.277	0.125	0.433	0.052	1.562	curli production assembly/transport onent, 2nd curli operon
csgD	STM1142	AAL20072	(1229728..1230378)	0.187	0.067	0.158	0.080	0.848	0.381	0.017	0.517	0.032	1.359	putative transcriptional regulator (LuxR/UhpA family)
csgB	STM1143	AAL20073	1231133..1231588	0.232	0.075	0.260	0.060	1.119	0.522	0.122	0.717	0.084	1.373	minor curlin subunit precursor, nucleator for assembly of adhesive surface organelles
csgA	STM1144	AAL20074	1231630..1232085	0.420	0.211	0.403	0.056	0.960	1.002	0.103	1.407	0.116	1.404	curlin major subunit, coiled surface structures; cryptic
csgC	STM1145	AAL20075	1232147..1232473	0.386	0.085	0.883	0.062	2.287	0.348	0.090	0.384	0.019	1.103	putative curli production protein

ymdA	STM1146	AAL20076	1232604..1232924	0.948	0.094	2.988	0.777	3.151	0.447	0.041	0.465	0.068	1.040	putative periplasmic protein
STM1147	STM1147	AAL20077	1233013..1233552	2.708	0.448	4.309	0.158	1.591	1.948	0.570	1.453	0.084	0.746	putative ACR related to the C-terminal domain of histone macroH2A1
ymdC	STM1148	AAL20078	1233491..1234975	1.401	0.195	1.597	0.255	1.140	1.496	0.456	1.501	0.096	1.003	putative phospholipase
mdoC	STM1149	AAL20079	(1234992..1236146)	0.678	0.153	0.444	0.088	0.655	0.974	0.243	0.400	0.049	0.411	membrane protein required for succinyl substitution of glucan backbone of OPG (osmoregulated periplasmic glucan)
mdoG	STM1150	AAL20080	1236418..1237953	1.500	0.227	5.063	0.325	3.375	1.204	0.075	1.853	0.179	1.539	periplasmic glucans biosynthesis protein
mdoH	STM1151	AAL20081	1237946..1240489	1.503	0.156	2.353	0.459	1.565	2.000	0.054	1.243	0.049	0.622	membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO)/synthesis of OPGs (osmoregulated periplasmic glucans)
yceK	STM1152	AAL20082	1240563..1240790	0.842	0.170	0.709	0.085	0.842	1.217	0.466	0.915	0.032	0.752	putative outer membrane lipoprotein
msyB	STM1153	AAL20083	(1240791..1241165)	0.554	0.059	0.683	0.062	1.234	0.590	0.046	0.945	0.015	1.603	acidic protein suppresses mutants lacking function of protein export
yceE	STM1154	AAL20084	(1241247..1242461)	0.377	0.079	0.310	0.043	0.821	0.334	0.010	0.309	0.031	0.926	putative MFS family transport protein
htrB	STM1155	AAL20085	(1242616..1243536)	0.514	0.047	0.681	0.115	1.324	0.522	0.103	0.399	0.021	0.765	lauroyl/myristoyl acyltransferase involved in lipid A biosynthesis
yceA	STM1156	AAL20086	1243756..1244808	1.212	0.091	0.326	0.033	0.269	1.764	0.175	0.804	0.049	0.456	putative enzyme related to sulfurtransferases
yceI	STM1157	AAL20087	(1244860..1245435)	0.763	0.129	0.343	0.033	0.450	0.829	0.755	0.627	0.057	0.757	putative secreted protein
STM1158	STM1158	AAL20088	(1245432..1246004)	0.346	0.034	0.165	0.018	0.478	0.354	0.010	0.398	0.028	1.124	putative inner membrane protein
yceO	STM1159	AAL20089	(1246267..1246380)	0.813	0.089	1.461	0.262	1.797	0.569	0.031	1.098	0.092	1.930	putative inner membrane protein
solA	STM1160	AAL20090	(1246421..1247539)	0.694	0.028	1.193	0.047	1.720	0.593	0.057	1.074	0.140	1.811	putative sarcosine oxidase
yceP	STM1161	AAL20091	(1247652..1247906)	2.606	1.001	2.026	0.401	0.777	2.730	0.158	2.448	0.109	0.897	putative cytoplasmic protein
dinI	STM1162	AAL20092	(1248196..1248441)	1.349	0.223	0.739	0.034	0.548	1.435	0.122	1.140	0.104	0.795	DNA damage-inducible protein I, inhibits UmuD processing
pyrC	STM1163	AAL20093	(1248515..1249561)	1.239	0.080	1.614	0.228	1.303	0.683	0.050	1.531	0.213	2.242	dihydro-orotase
yceB	STM1164	AAL20094	(1249666..1250226)	2.495	0.385	1.478	0.102	0.592	1.257	0.144	1.029	0.049	0.819	putative outer membrane lipoprotein
grxB	STM1165	AAL20095	(1250351..1250998)	3.895	0.507	4.808	0.362	1.234	2.583	0.115	2.611	0.097	1.011	glutaredoxin 2
yceL	STM1166	AAL20096	(1251062..1252270)	0.733	0.023			0.000	0.577	0.045			0.000	putative MFS superfamily transport protein
rimJ	STM1167	AAL20097	1252507..1253091	1.842	0.214	3.408	0.420	1.850	0.545	0.237	0.800	0.157	1.467	acetylation of N-terminal alanine of 30S ribosomal subunit protein S5
yceH	STM1168	AAL20098	1253127..1253774	3.097	0.976	4.783	1.108	1.544	0.903	0.150	1.270	0.139	1.408	putative cytoplasmic protein
mviM	STM1169	AAL20099	1253776..1254699	2.273	0.426	2.261	0.207	0.995	0.716	0.073	0.966	0.026	1.348	putative virulence factor
mviN	STM1170	AAL20100	1254964..1256538	0.995	0.035	0.777	0.113	0.782	0.846	0.014	0.455	0.029	0.538	putative virulence factor
flgN	STM1171	AAL20101	(1256619..1257041)	5.903	1.846	9.533	0.991	1.615	0.306	0.061	0.551	0.072	1.800	flagellar biosynthesis: belived to be export chaperone for FlgK and FlgL
flgM	STM1172	AAL20102	(1257046..1257339)	5.701	1.297	12.775	1.274	2.241	0.238	0.031	0.429	0.040	1.802	anti-FliA (anti-sigma) factor; also known as RflB protein
flgA	STM1173	AAL20103	(1257431..1258090)	2.101	0.202	11.190	1.449	5.327	0.278	0.226	0.419	0.190	1.504	flagellar biosynthesis; assembly of basal-body periplasmic P ring

flgB	STM1174	AAL20104	1258247..1258663	4.009	0.354	14.352	1.954	3.580	0.399	0.956	0.580	0.050	1.455	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgC	STM1175	AAL20105	1258667..1259071	3.951	0.416	25.654	3.508	6.492	0.116	0.048	0.228	0.120	1.961	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgD	STM1176	AAL20106	1259083..1259781	3.941	0.536	30.569	1.326	7.757	0.146	0.095	0.221	0.022	1.509	flagellar biosynthesis, initiation of hook assembly
flgE	STM1177	AAL20107	1259808..1261019	4.189	0.548	49.796	2.494	11.888	0.129	0.017	0.248	0.022	1.920	flagellar biosynthesis, hook protein
flgF	STM1178	AAL20108	1261040..1261795	3.936	0.559	32.494	5.506	8.255	0.180	0.030	0.334	0.124	1.858	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgG	STM1179	AAL20109	1261809..1262591	3.112	0.336	29.543	7.531	9.494	0.195	0.037	0.245	0.053	1.253	flagellar biosynthesis, cell-distal portion of basal-body rod
flgH	STM1180	AAL20110	1262646..1263344	2.333	0.310	11.670	0.585	5.003	0.099	0.017	0.194	0.034	1.967	flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	STM1181	AAL20111	1263356..1264453	1.792	0.131	8.778	1.186	4.899	0.089	0.016	0.187	0.019	2.110	putative flagella basal body protein
flgJ	STM1182	AAL20112	1264453..1265403	1.314	0.055	7.747	1.677	5.893	0.210	0.066	0.213	0.021	1.015	flagellar biosynthesis
flgK	STM1183	AAL20113	1265468..1267129	1.286	0.151	15.040	1.814	11.692	0.098	0.051	0.213	0.037	2.174	flagellar biosynthesis, hook-filament junction protein 1
flgL	STM1184	AAL20114	1267144..1268097	2.647	0.546	23.051	3.300	8.707	0.135	0.041	0.286	0.018	2.121	flagellar biosynthesis; hook-filament junction protein
rne	STM1185	AAL20115	(1268354..1271557)	3.065	0.489	8.740	0.385	2.852	1.486	0.010	2.842	0.190	1.913	RNase E
STM1186	STM1186	pseudogene; in-frame stop following codon 97; no				6.484	1.015	4.182	0.769	0.645	2.692	0.118	1.796	0.152 0.667
rluC	STM1187	AAL20116	1272131..1273090	1.088	0.049	0.919	0.097	0.844	0.796	0.041	0.566	0.030	0.712	23S rRNA pseudouridylate synthase
STM1188	STM1188	AAL20117	1273246..1273989	0.635	0.032	0.477	0.061	0.751	0.606	0.148	0.348	0.029	0.575	putative inner membrane lipoprotein
yceF	STM1189	AAL20118	(1274491..1275075)	2.462	0.332	1.380	0.289	0.560	2.297	1.812	1.113	0.066	0.484	putative inhibitor of septum formation
yceD	STM1190	AAL20119	1275273..1275794	64.854	5.454	20.546	2.144	0.317	40.828	0.629	15.710	0.912	0.385	putative metal-binding
rpmF	STM1191	AAL20120	1275846..1276019	54.792	14.107	27.212	3.636	0.497	27.479	1.038	15.723	1.525	0.572	50S ribosomal subunit protein L32
plsX	STM1192	AAL20121	1276153..1277232	3.701	0.464	3.007	0.406	0.813	4.809	0.158	2.277	0.111	0.474	putative fatty acid/phospholipid synthesis protein
fabH	STM1193	AAL20122	1277312..1278265	5.653	0.254	6.471	0.681	1.145	5.129	0.498	3.908	0.143	0.762	3-oxoacyl-[acyl-carrier-protein] synthase III; acetylCoA A transacylase
fabD	STM1194	AAL20123	1278281..1279210	6.016	0.082	9.734	0.869	1.618	6.581	0.356	10.711	0.610	1.628	malonyl-CoA-[acyl-carrier-protein] transacylase
fabG	STM1195	AAL20124	1279223..1279957	22.428	0.617	20.193	3.084	0.900	10.944	0.312	11.710	0.825	1.070	3-oxoacyl-[acyl-carrier-protein] reductase
aP	STM1196	AAL20125	1280113..1280349	24.896	0.659	19.811	2.205	0.796	8.747	1.017	6.714	0.409	0.768	acyl carrier protein
fabF	STM1197	AAL20126	1280435..1281676	23.883	1.649	14.572	0.698	0.610	7.686	0.477	4.416	0.645	0.575	3-oxoacyl-[acyl-carrier-protein] synthase II
pabC	STM1198	AAL20127	1281800..1282609	1.363	0.035	0.697	0.093	0.511	0.873	0.087	0.697	0.081	0.798	4-amino-4-deoxychorismate lyase
yceG	STM1199	AAL20128	1282612..1283634	0.578	0.038	0.561	0.110	0.971	0.498	0.120	0.458	0.027	0.920	putative periplasmic solute-binding protein
tmk	STM1200	AAL20129	1283624..1284265	3.117	0.519	1.809	0.391	0.580	2.224	0.349	1.450	0.117	0.652	thymidylate kinase
holB	STM1201	AAL20130	1284262..1285266	2.939	0.302	1.615	0.143	0.550	1.982	0.421	1.839	0.131	0.928	DNA polymerase III, delta prime subunit
ycfH	STM1202	AAL20131	1285277..1286074	2.672	0.355	1.054	0.036	0.395	2.220	0.629	1.308	0.228	0.589	putative metal-dependent hydrolase

ptsG	STM1203	AAL20132	1286369..1287802	2.487	0.089	3.154	0.384	1.268	3.164	0.298	7.528	0.505	2.379	Sugar Specific PTS family, glucose-specific IIBConent
fhuE	STM1204	AAL20133	(1287887..1290061)	0.331	0.087	0.292	0.052	0.882	0.232	0.002	0.264	0.012	1.135	outer membrane receptor for Fe(III)-coprogen, Fe(III)-ferrioxamine B and Fe(III)-rhodotrulic acid uptake
ycfF	STM1205	AAL20134	1290403..1290762	4.736	0.592	3.533	0.668	0.746	5.907	4.823	3.184	0.504	0.539	putative protein kinase C inhibitor
ycfL	STM1206	AAL20135	1290765..1291139	3.630	0.358	3.505	0.602	0.966	4.826	5.750	2.596	0.362	0.538	putative outer membrane lipoprotein
ycfM	STM1207	AAL20136	1291153..1291791	2.557	0.343	2.764	0.270	1.081	2.050	0.112	2.722	0.183	1.328	putative outer membrane lipoprotein
ycfN	STM1208	AAL20137	1291772..1292596	2.795	0.577	1.634	0.299	0.585	1.447	0.265	1.639	0.146	1.133	putative cytoplasmic protein
nagZ	STM1209	AAL20138	1292607..1293632	4.440	0.547	2.036	0.194	0.459	2.599	0.429	1.842	0.070	0.709	putative glycosyl hydrolase
ycfP	STM1210	AAL20139	1293657..1294199	7.723	1.733	7.693	1.008	0.996	4.578	1.122	2.912	0.669	0.636	putative esterase
ndh	STM1211	AAL20140	1294454..1295758	0.729	0.028	0.839	0.147	1.151	0.931	0.049	0.566	0.021	0.608	respiratory NADH dehydrogenase 2; cupric reductase
ycfJ	STM1212	AAL20141	1295937..1296476	0.308	0.052	0.999	0.150	3.242	0.443	0.514	0.692	0.067	1.563	putative outer membrane lipoprotein
ycfQ	STM1213	AAL20142	(1296551..1297186)	0.450	0.043	1.955	0.171	4.347	0.334	0.013	0.802	0.045	2.400	putative transcriptional repressor (TetR/AcrR family)
ycfR	STM1214	AAL20143	1297428..1297685	0.396	0.062	0.383	0.032	0.968	1.803	0.059	1.105	0.111	0.613	putative outer membrane protein
ycfS	STM1215	AAL20144	(1297782..1298747)	0.616	0.068	0.376	0.061	0.611	2.407	0.270	0.758	0.074	0.315	putative periplasmic protein
mfd	STM1216	AAL20145	(1298895..1302341)	0.935	0.082	1.044	0.136	1.117	0.625	0.006	0.930	0.054	1.489	transcription-repair coupling factor
ycfU	STM1217	AAL20146	1302568..1303878	2.234	0.079	1.018	0.118	0.456	1.891	0.277	1.080	0.039	0.571	ABC transporter, integral membrane protein
ycfV	STM1218	AAL20147	1303871..1304572	3.720	0.460	1.425	0.239	0.383	3.024	0.088	1.424	0.051	0.471	ABC transporter, ATP-binding protein
ycfW	STM1219	AAL20148	1304572..1305816	2.369	0.214	1.273	0.058	0.537	1.642	0.193	1.002	0.047	0.611	ABC transporter, integral membrane protein
ycfX	STM1220	AAL20149	1305845..1306756	2.699	0.313	1.862	0.190	0.690	2.077	0.326	1.621	0.130	0.780	putative regulator (NagC/XylR family)
cobB	STM1221	AAL20150	1306775..1307596	3.740	0.653	3.386	0.200	0.905	2.692	0.400	4.670	0.312	1.735	putative nicotinate-nucleotide dimethylbenzimidazolephosphoribosltransferase, homolog of virulence factor
potD	STM1222	AAL20151	(1307678..1308724)	1.262	0.086	3.259	0.490	2.582	2.995	0.165	7.922	0.745	2.645	ABC superfamily (peri_perm), spermidine/putrescine transporter
potC	STM1223	AAL20152	(1308749..1309528)	0.853	0.037	1.008	0.061	1.182	4.072	0.581	4.196	0.559	1.030	ABC superfamily (membrane), spermidine/putrescine transporter
sifA	STM1224	AAL20153	(1309844..1310854)	0.319	0.075	0.229	0.051	0.716	2.997	0.346	4.879	0.262	1.628	lysosomal glycoprotein (lgp)-containing structures; replication in macrophages
potB	STM1225	AAL20154	(1311183..1312046)	0.576	0.119	0.353	0.054	0.614	1.368	0.256	0.524	0.028	0.383	ABC superfamily (membrane), spermidine/putrescine transporter
potA	STM1226	AAL20155	(1312030..1313166)	0.574	0.062	0.756	0.112	1.316	0.950	0.036	0.795	0.060	0.837	ABC superfamily (atp_bind), spermidine/putrescine transporter
pepT	STM1227	AAL20156	1313417..1314646	0.671	0.057	2.345	0.280	3.496	0.676	0.140	0.700	0.108	1.035	putative peptidase T(aminotripeptidase)
STM1228	STM1228	AAL20157	1314650..1315984	0.405	0.037	0.794	0.156	1.962	0.331	0.032	0.407	0.051	1.230	putative periplasmic protein
ycfD	STM1229	AAL20158	(1316024..1317145)	4.787	0.664	1.885	0.195	0.394	3.833	0.925	2.321	0.098	0.606	putative cytoplasmic protein

phoQ	STM1230	AAL20159	(1317226..1318689)	1.898	0.081	3.707	0.436	1.953	5.834	0.123	5.293	0.249	0.907	sensory kinase protein in two-onent regulatory system with PhoP, ligand is Mg+
phoP	STM1231	AAL20160	(1318689..1319363)	2.808	0.108	10.586	1.047	3.770	7.424	0.167	11.778	0.714	1.587	response regulator in two-onent regulatory system with PhoQ, transcribes genes expressed under low Mg+ concentration (OmpR family)
purB	STM1232	AAL20161	(1319487..1320857)	0.714	0.128	1.816	0.395	2.543	0.662	0.046	0.942	0.051	1.424	adenylosuccinate lyase
ycfC	STM1233	AAL20162	(1320861..1321508)	1.293	0.116	1.799	0.443	1.391	2.696	2.076	1.573	0.248	0.583	membrane associated protein of unknown function
trmU	STM1234	AAL20163	(1321589..1322740)	1.358	0.055	2.156	0.199	1.587	1.311	0.037	0.935	0.097	0.713	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
ymfB	STM1235	AAL20164	(1322749..1323210)	0.522	0.049	0.843	0.116	1.615	0.609	0.522	0.589	0.073	0.968	putative MutT-like protein
STM1236	STM1236	AAL20165	(1323222..1323551)	0.443	0.037	0.911	0.073	2.057	0.487	0.402	0.598	0.078	1.228	putative periplasmic protein
ymfC	STM1237	AAL20166	(1323548..1324213)	1.306	0.119			0.000	0.607	0.107			0.000	putative ribosomal large subunit pseudouridine synthase
icdA	STM1238	AAL20167	1324385..1325635	18.775	3.904	22.034	1.152	1.174	7.043	0.592	11.779	0.855	1.672	isocitrate dehydrogenase in e14 prophage, specific for NADP+
STM1239	STM1239	AAL20168	1326083..1327207	1.185	0.159	0.970	0.087	0.819	9.806	0.636	2.460	0.444	0.251	putative cytoplasmic protein
envF	STM1240	AAL20169	(1328189..1328977)	0.194	0.056	0.197	0.037	1.012	0.902	0.120	0.898	0.021	0.995	putative envelope lipoprotein
msgA	STM1241	AAL20170	(1329466..1329705)	0.446	0.066	0.610	0.097	1.367	2.149	0.136	2.238	0.080	1.041	Macrophage survival gene; reduced mouse virulence
envE	STM1242	AAL20171	(1329896..1330417)	0.461	0.071	0.352	0.082	0.764	9.385	1.556	9.057	0.722	0.965	putative envelope protein
STM1243	STM1243	AAL20172	(1330832..1331044)	0.279	0.055	0.270	0.084	0.968	2.873	0.027	1.900	0.485	0.661	homology with cold shock proteins
pagD	STM1244	AAL20173	(1331176..1331439)	0.371	0.022	0.914	0.104	2.461	13.188	1.335	5.350	0.542	0.406	PhoP regulated
STM1245	STM1245	pseudogene; in-frame stop following codon 4			0.708	0.364	0.663	0.223	0.935	7.018	0.119	3.388	0.904	0.483
pagC	STM1246	AAL20174	1332251..1332808	0.915	0.055	0.648	0.032	0.709	99.076	4.892	47.673	7.863	0.481	PhoP regulated: reduced macrophage survival
STM1247	STM1247						N/A					N/A		
STM1248	STM1248	pseudogene; frameshift		1.862	0.219	1.667	0.288	0.896	2.453	0.333	1.164	0.149	0.475	
STM1249	STM1249	AAL20175	(1334045..1334389)	1.835	0.430	1.919	0.343	1.046	9.145	0.792	6.105	0.692	0.668	putative periplasmic protein
STM1250	STM1250	AAL20176	1335092..1335364	0.716	0.133	0.783	0.056	1.093	2.894	0.042	1.548	0.358	0.535	putative cytoplasmic protein
agsA	STM1251	AAL20177	1335516..1335983	0.953	0.160	1.229	0.192	1.289	3.393	0.054	7.218	0.425	2.127	Molecular chaperone (small heat shock protein) Tomoyasu, T (2003) J. Bact. 185: 6331-9
STM1252	STM1252	AAL20178	1336322..1337365	0.553	0.025	0.401	0.065	0.725	1.779	0.423	1.489	0.083	0.837	putative cytoplasmic protein
STM1253	STM1253	AAL20179	(1337448..1337978)	3.539	0.824	1.529	0.303	0.432	20.577	2.041	5.284	0.266	0.257	putative inner membrane protein
STM1254	STM1254	AAL20180	(1338127..1338441)	8.485	2.795	6.223	1.135	0.733	51.246	5.620	9.350	1.011	0.182	putative outer membrane lipoprotein
STM1255	STM1255	AAL20181	1339123..1340757	0.885	0.094	2.940	0.149	3.323	0.671	0.097	0.627	0.051	0.935	putative ABC transporter periplasmic binding protein
STM1256	STM1256	AAL20182	1340757..1341731	0.556	0.078	0.808	0.071	1.452	0.370	0.061	0.321	0.022	0.867	putative ABC transporter
STM1257	STM1257	AAL20183	1341721..1342533	0.572	0.036	0.612	0.120	1.071	0.302	0.016	0.284	0.048	0.940	putative ABC transporter

STM1258	STM1258	AAL20184	1342527..1343324	0.418	0.031	0.798	0.069	1.907	0.299	0.077	0.321	0.020	1.072	putative ATPase onent of ABC-type transport system, contain duplicated ATPase domain
STM1259	STM1259	AAL20185	1343318..1343908	0.391	0.080	0.680	0.165	1.740	0.371	0.112	0.403	0.165	1.086	putative ATPase onent of ABC-type transport system, contain duplicated ATPase domain
STM1260	STM1260	AAL20186	(1343990..1345123)	0.509	0.035	0.271	0.079	0.531	0.746	0.020	0.757	0.032	1.015	putative inner membrane protein
STM1261	STM1261	AAL20187	1345317..1345643	2.271	4.590	0.452	0.085	0.199	1.281	0.176	0.916	0.065	0.715	putative cytoplasmic protein
STM1262	STM1262						N/A					N/A		
STM1263	STM1263	AAL20188	1345840..1346487					N/A					N/A	putative periplasmic protein
aadA	STM1264	AAL20189	1346596..1347384	0.491	0.002	0.174	0.037	0.354	1.020	0.294	0.460	0.019	0.451	Aminoglycoside adenyltransferase
STM1265	STM1265	AAL20190	1347529..1348122	0.517	0.040	0.206	0.056	0.399	2.377	0.099	0.763	0.018	0.321	putative response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain
STM1266	STM1266	AAL20191	1348191..1349039					N/A					N/A	putative transcriptional regulator
STM1267	STM1267	AAL20192	(1349294..1349542)	2.354	0.347	0.630	0.116	0.268	10.898	0.345	5.878	0.312	0.539	putative cytoplasmic protein
STM1268	STM1268	AAL20193	(1349621..1349770)	1.152	0.269	0.671	0.125	0.582	4.241	1.402	2.530	0.291	0.597	putative cytoplasmic protein
STM1269	STM1269	AAL20194	1349853..1350398	0.843	0.076	0.494	0.087	0.586	12.009	0.437	11.950	0.474	0.995	putative chorismate mutase
yeaS	STM1270	AAL20195	1350595..1351233	4.819	0.039	1.034	0.083	0.215	7.040	1.548	3.299	0.192	0.469	paral putative transport protein
yeaR	STM1271	AAL20196	1351406..1351768	0.500	0.038	0.452	0.057	0.904	0.525	0.064	0.713	0.037	1.359	putative cytoplasmic protein
yoaG	STM1272	AAL20197	1351771..1351953	0.398	0.058	0.362	0.053	0.909	0.570	0.162	0.595	0.103	1.043	putative cytoplasmic protein
STM1273	STM1273	AAL20198	1352183..1352824	0.438	0.063	0.148	0.021	0.339	0.403	0.079	0.256	0.019	0.636	putative nitric oxide reductase
yeaQ	STM1274	AAL20199	1353139..1353387	1.043	0.241	0.544	0.075	0.522	2.202	0.028	1.301	0.072	0.591	putative inner membrane protein
yaoF	STM1275	AAL20200	1353820..1354071	1.102	0.136	0.931	0.095	0.845	2.849	0.066	2.906	0.178	1.020	putative hemolysin
STM1276	STM1276	AAL20201	1354140..1354451	1.356	0.090	1.062	0.136	0.783	2.017	0.202	2.435	0.161	1.207	putative periplasmic protein
yeaO	STM1277	AAL20202	(1354437..1354784)	1.048	0.119	1.264	0.169	1.206	0.975	0.206	1.061	0.031	1.088	putative cytoplasmic protein
yeaN	STM1278	AAL20203	(1354903..1356087)	1.283	0.112	0.317	0.061	0.247	0.762	0.188	0.539	0.151	0.708	putative MFS family transport protein (amino acid/amine transport)
yeaM	STM1279	AAL20204	1356188..1356982	0.538	0.079	0.360	0.012	0.670	0.516	0.120	0.411	0.031	0.797	putative regulator (AraC/XylS family)
yeaL	STM1280	AAL20205	(1357003..1357407)	1.356	0.079	0.480	0.043	0.354	1.657	0.236	0.661	0.146	0.399	putative inner membrane protein
STM1281	STM1281	AAL20206	1357613..1357720	1.551	0.636	1.184	0.191	0.763	4.173	5.417	2.263	0.305	0.542	putative inner membrane protein
yeaK	STM1282	AAL20207	(1357717..1358235)	0.846	0.059	0.844	0.146	0.997	3.403	2.040	2.442	0.290	0.718	putative cytoplasmic protein
yeaJ	STM1283	AAL20208	(1358285..1359778)	0.425	0.070	0.349	0.026	0.820	2.562	0.076	1.181	0.096	0.461	putative Methyl-accepting chemotaxis protein; Diguanylate cyclase/phosphodiesterase domain 1
yeaH	STM1284	AAL20209	(1360419..1361705)	0.813	0.062	1.083	0.085	1.332	4.189	0.088	2.629	0.110	0.628	putative cytoplasmic protein
yeaG	STM1285	AAL20210	(1361828..1363762)	0.568	0.040	0.580	0.084	1.021	0.730	0.009	1.401	0.194	1.918	putative Ser protein kinase
mipA	STM1286	AAL20211	1364189..1364935	17.241	3.590	13.317	2.104	0.772	11.915	2.101	13.679	0.731	1.148	scaffolding protein for murein-synthesizing holoenzyme
STM1287	STM1287	AAL20212	1365225..1366421	0.429	0.090	0.439	0.093	1.022	0.338	0.077	0.402	0.094	1.189	arylsulfatase regulator
STM1288	STM1288	AAL20213	1366518..1367375	1.847	0.420	1.113	0.122	0.603	0.794	0.073	0.729	0.035	0.918	putative aldehyde reductase
yeaD	STM1289	AAL20214	(1367474..1368358)	1.485	0.144	3.045	0.477	2.050	1.835	0.053	2.124	0.216	1.158	putative enzymes related to aldose 1-epimerase

gapA	STM1290	AAL20215	(1368693..1369688)	38.801	5.650	43.045	7.074	1.109	30.071	2.808	37.124	2.294	1.235	glyceraldehyde-3-phosphate dehydrogenase A
yeaA	STM1291	AAL20216	1370000..1370443	9.922	1.191	8.838	0.426	0.891	3.422	0.594	4.753	0.202	1.389	putative domain frequently associated with peptide methionine sulfoxide reductase
yeaC	STM1292	AAL20217	1370485..1370763					N/A					N/A	putative cytoplasmic protein
pncA	STM1293	AAL20218	(1371115..1371771)	2.030	0.265	1.819	0.159	0.896	1.363	0.057	1.385	0.019	1.016	nicotinamidase/ pyrazinamidase
ansA	STM1294	AAL20219	(1371798..1372814)	1.114	0.188			0.000	0.919	0.097			0.000	cytoplasmic L-asparaginase I
sppA	STM1295	AAL20220	(1372910..1374766)	2.134	0.246	1.299	0.261	0.609	1.352	0.076	1.107	0.068	0.819	protease IV, a signal peptide peptidase
ydjA	STM1296	AAL20221	1374940..1375491	3.788	0.481	1.960	0.336	0.517	1.426	0.177	1.358	0.063	0.953	putative oxidoreductase
selD	STM1297	AAL20222	1375609..1376652	3.079	0.457	3.286	0.484	1.067	1.500	0.226	1.615	0.106	1.077	selenophosphate synthase
topB	STM1298	AAL20223	1376657..1378606	2.823	0.613	2.597	0.452	0.920	1.295	0.127	1.268	0.069	0.979	DNA topoisomerase III
gdhA	STM1299	AAL20224	(1378636..1379979)	2.193	0.511	1.163	0.171	0.530	0.899	0.025	0.709	0.054	0.788	glutamate dehydrogenase, NADP-specific
STM1300	STM1300	AAL20225	1380218..1380493	1.074	0.079	4.332	0.365	4.032	0.339	0.189	0.385	0.038	1.136	putative periplasmic protein
STM1301	STM1301	AAL20226	(1380453..1380869)	1.124	0.173	2.792	0.386	2.483	0.408	0.179	0.584	0.006	1.434	putative mutator MutT protein
xthA	STM1302	AAL20227	(1380942..1381748)	1.171	0.139	1.906	0.060	1.627	0.456	0.064	0.869	0.041	1.907	exonuclease III, may repair singlet oxygen induced lesions
astC	STM1303	AAL20228	1382194..1383420	5.585	2.848	0.956	0.041	0.171	0.997	0.036	0.869	0.052	0.872	succinylornithine transaminase, also has acetylornitine transaminase activity
astA	STM1304	AAL20229	1383411..1384445	2.809	1.662	0.475	0.068	0.169	0.732	0.110	0.502	0.048	0.685	arginine succinyltransferase
astD	STM1305	AAL20230	1384442..1385920	1.613	0.998	0.321	0.032	0.199	0.833	0.135	0.555	0.013	0.667	succinylglutamic semialdehyde dehydrogenase
astB	STM1306	AAL20231	1385917..1387260	0.872	0.548	0.179	0.034	0.205	0.591	0.091	0.391	0.018	0.662	succinylarginine dihydrolase
astE	STM1307	AAL20232	1387253..1388221	0.573	0.105	0.173	0.015	0.302	0.822	0.141	0.528	0.017	0.642	succinylglutamate desuccinylase
spy	STM1308	AAL20233	1388557..1389042	0.967	0.159	0.627	0.028	0.648	21.492	0.516	12.134	1.037	0.565	periplasmic protein related to spheroblast formation
STM1309	STM1309	AAL20234	(1389117..1390025)	0.481	0.037	0.399	0.079	0.831	1.539	0.067	0.840	0.034	0.546	putative nuclease subunit of the excinuclease lex
nadE	STM1310	AAL20235	(1390119..1390946)	1.030	0.112	2.223	0.244	2.159	0.594	0.073	1.499	0.112	2.522	NAD synthetase, prefers NH3 over glutamine
osmE	STM1311	AAL20236	1391165..1391506	2.339	0.498	2.413	0.532	1.032	2.456	0.147	2.351	0.366	0.957	transcriptional activator of ntrL gene
celA	STM1312	AAL20237	1391807..1392127					N/A					N/A	PTS family, sugar specific enzyme IIB for cellobiose, arbutin, and salicin
celB	STM1313	AAL20238	1392210..1393568	1.016	0.087	0.549	0.059	0.541	0.555	0.056	0.757	0.084	1.364	PTS family, sugar specific enzyme II for cellobiose, arbutin, and salicin
celC	STM1314	AAL20239	1393619..1393966	0.843	0.042	0.899	0.045	1.067	0.701	0.098	1.534	0.057	2.190	PTS family, sugar specific enzyme III for cellobiose, arbutin, and salicin
celD	STM1315	AAL20240	1393977..1394819	0.549	0.028	0.594	0.129	1.081	0.635	0.097	1.186	0.032	1.866	transcriptional repressor of cel operon (AraC/XylS family)
celF	STM1316	AAL20241	1394944..1396299	0.345	0.017	0.503	0.085	1.456	1.307	0.042	1.856	0.128	1.420	phospho-beta-glucosidase (cellobiose-6-phosphate hydrolase)
celG	STM1317	AAL20242	1396312..1397070	0.612	0.047	0.473	0.033	0.773	3.142	0.346	2.580	0.088	0.821	putative glucosidase

katE	STM1318	AAL20243	(1397114..1399366)	0.485	0.045	0.974	0.067	2.006	0.740	0.136	1.399	0.028	1.889	catalase; hydroperoxidase HPII(III), RpoS dependent
cedA	STM1319	AAL20244	1399731..1399973	0.607	0.040	0.390	0.037	0.642	1.098	0.066	0.944	0.226	0.860	cell division modulator, affects inhibition after overreplication of chromosome in dnaAcos mutants
ydjN	STM1320	AAL20245	(1400075..1401466)	0.846	0.065	0.400	0.051	0.472	6.669	1.228	2.526	0.131	0.379	part of a kinase, putative domain shared with transporter
ydjM	STM1321	AAL20246	(1401603..1402202)	0.469	0.058	0.269	0.052	0.574	0.798	0.088	0.525	0.041	0.657	LexA regulated gene, putative SOS response
yniC	STM1322	AAL20247	(1402340..1403008)	2.529	0.147	1.238	0.128	0.489	5.055	0.854	4.930	0.203	0.975	putative enzyme
yniB	STM1323	AAL20248	1403157..1403693	2.103	0.192	0.673	0.050	0.320	1.571	0.312	0.948	0.058	0.604	putative regulator
STM1324	STM1324	AAL20249	(1403736..1404596)	2.462	0.076	2.493	0.502	1.012	1.331	0.062	1.582	0.037	1.188	putative cytoplasmic protein
ydiZ	STM1325	AAL20250	(1404703..1404993)	0.819	0.110	1.125	0.060	1.373	0.870	0.049	0.973	0.073	1.118	putative cytoplasmic protein
pfkB	STM1326	AAL20251	(1405090..1406022)	0.776	0.112			0.000	1.435	0.057			0.000	6-phosphofructokinase II
ydiY	STM1327	AAL20252	1406311..1407069	0.321	0.077	0.470	0.051	1.461	1.183	0.076	0.664	0.115	0.561	putative salt-induced outer membrane protein
STM1328	STM1328	AAL20253	(1407118..1408077)	0.639	0.067	3.319	0.466	5.196	4.801	0.555	5.797	0.373	1.207	putative outer membrane protein
STM1329	STM1329	AAL20254	1408220..1408534					N/A					N/A	putative inner membrane protein
STM1330	STM1330	AAL20255	1408531..1409385	0.319	0.064	0.544	0.084	1.705	1.657	0.200	2.785	0.200	1.681	putative DNA/RNA non-specific endonuclease
STM1331	STM1331	AAL20256	1409558..1409764	1.104	0.096	1.125	0.093	1.019	2.304	0.045	0.995	0.140	0.432	putative inner membrane protein
rfc	STM1332	AAL20257	(1410087..1411310)	2.091	0.125	0.686	0.091	0.328	1.779	0.216	0.867	0.124	0.487	O-antigen polymerase
thrS	STM1333	AAL20258	1412202..1414130	4.417	0.479	13.285	0.667	3.007	2.118	0.083	3.561	0.252	1.682	threonine tRNA synthetase
infC	STM1334	AAL20259	1414242..1414676	63.800	8.236	58.418	2.855	0.916	30.431	1.863	22.761	1.325	0.748	protein chain initiation factor IF-3
rpmI	STM1335	AAL20260	1414772..1414969	80.091	10.151	52.184	8.072	0.652	41.299	2.669	31.807	1.551	0.770	50S ribosomal subunit protein L35
rplT	STM1336	AAL20261	1415020..1415376	22.809	4.729	30.229	3.143	1.325	13.558	2.678	14.426	0.438	1.064	50S ribosomal subunit protein L20
pheS	STM1337	AAL20262	1415678..1416661	1.452	0.032	4.342	0.997	2.990	1.514	0.104	2.951	0.316	1.949	phenylalanine tRNA synthetase, alpha-subunit
pheT	STM1338	AAL20263	1416677..1419064	3.126	0.149	4.535	0.468	1.451	3.764	0.155	5.080	0.091	1.350	phenylalanine tRNA synthetase, beta-subunit
himA	STM1339	AAL20264	1419069..1419368	16.686	4.010	9.172	0.909	0.550	13.556	0.866	13.228	0.426	0.976	integration host factor (IHF), alpha subunit
btuC	STM1340	AAL20265	1419571..1420551	1.768	0.041	0.850	0.121	0.481	1.035	0.056	0.736	0.026	0.711	ABC superfamily (membrane), vitamin B12 transport protein
btuE	STM1341	AAL20266	1420643..1421194	0.775	0.055	1.178	0.023	1.521	0.542	0.062	0.841	0.033	1.551	ABC superfamily (binding protein), vitamin B12 transport protein
btuD	STM1342	AAL20267	1421194..1421943	0.510	0.034	0.776	0.035	1.522	0.407	0.014	0.638	0.074	1.568	ABC superfamily (binding protein), vitamin B12 transport protein
nlpC	STM1343	AAL20268	1422020..1422484	0.747	0.076	0.609	0.051	0.815	1.440	0.177	2.096	0.208	1.456	lipoprotein
ydiV	STM1344	AAL20269	1422798..1423511	0.459	0.044	0.414	0.050	0.901	2.974	0.171	1.570	0.125	0.528	putative Diguanylate cyclase/phosphodiesterase domain 1
ydiU	STM1345	AAL20270	1423573..1425015	3.073	0.228	0.419	0.064	0.136	2.020	0.163	0.806	0.038	0.399	putative cytoplasmic protein
ydiE	STM1346	AAL20271	(1425050..1425241)	0.916	0.142	0.221	0.041	0.241	0.653	0.227	0.394	0.058	0.603	putative cytoplasmic protein
aroH	STM1347	AAL20272	(1425398..1426444)	0.596	0.053	0.898	0.092	1.505	0.526	0.137	0.719	0.038	1.367	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase), tryptophan repressible

ydiA	STM1348	AAL20273	(1426600..1427433)	0.927	0.047	1.119	0.091	1.207	0.773	0.071	0.888	0.083	1.148	putative inner membrane protein
pps	STM1349	AAL20274	1427770..1430148	11.340	1.336	11.892	0.406	1.049	10.447	0.698	15.303	1.218	1.465	phosphoenolpyruvate synthase
ydiD	STM1350	AAL20275	(1430189..1431829)	0.542	0.022	0.391	0.038	0.722	0.430	0.031	0.439	0.040	1.020	Homolog of a plant pathogenicity factor
ydiT	STM1351	AAL20276	(1431919..1432212)	0.242	0.082	0.174	0.015	0.720	0.483	0.345	0.280	0.026	0.579	putative ferredoxin
ydiS	STM1352	AAL20277	(1432209..1433495)	0.191	0.097	0.111	0.017	0.584	0.226	0.023	0.197	0.009	0.871	flavoprotein
ydiR	STM1353	AAL20278	(1433552..1434487)	0.232	0.077	0.190	0.019	0.822	0.440	0.023	0.493	0.047	1.121	putative electron transfer flavoprotein
ydiQ	STM1354	AAL20279	(1434509..1435273)	0.431	0.047	0.136	0.016	0.315	0.251	0.024	0.272	0.014	1.085	putative electron transfer flavoprotein
ydiP	STM1355	AAL20280	1435737..1436627	0.141	0.059	0.124	0.030	0.876	0.494	0.131	0.585	0.036	1.184	putative transcription regulator, AraC family
ydiO	STM1356	AAL20281	(1436703..1437854)	0.295	0.081	0.314	0.019	1.064	0.625	0.070	1.412	0.031	2.259	putative acyl-CoA dehydrogenase
ydiF	STM1357	AAL20282	(1437868..1439421)	0.125	0.081	0.115	0.031	0.923	0.404	0.030	0.810	0.050	2.005	putative acetyl-CoA:acetoacetyl-CoA transferase beta subunit
aroD	STM1358	AAL20283	(1439617..1440375)	0.397	0.051	0.542	0.035	1.363	0.448	0.058	1.052	0.078	2.352	3-dehydroquinate dehydratase
ydiB	STM1359	AAL20284	(1440420..1441286)	0.148	0.063	0.142	0.002	0.966	0.256	0.038	0.534	0.020	2.085	putative shikimate 5-dehydrogenase
ydiN	STM1360	AAL20285	(1441353..1442588)	0.120	0.076	0.078	0.005	0.650	0.215	0.015	0.252	0.016	1.175	putative MFS family transport protein
ydiM	STM1361	AAL20286	(1442952..1444163)	0.168	0.075	0.146	0.015	0.868	0.452	0.043	0.321	0.013	0.711	putative MFS family transport protein
ydiL	STM1362	AAL20287	(1444304..1444663)	0.289	0.100	0.162	0.029	0.559	0.435	0.071	0.396	0.096	0.912	putative cytoplasmic protein
ydiK	STM1364	AAL20288	(1445121..1446239)	1.335	0.045			0.000	1.191	0.245			0.000	putative permease
ydiJ	STM1365	AAL20289	1446504..1449560					N/A					N/A	paral putative oxidase
STM1366	STM1366	AAL20290	1449557..1449967	1.063	0.074	1.141	0.050	1.073	0.990	0.159	0.708	0.043	0.715	putative protein PaaI, possibly involved in aromatic ounds catabolism
ydiH	STM1367	AAL20291	1450027..1450254	1.202	0.197	0.714	0.088	0.594	1.070	0.138	0.670	0.148	0.627	putative cytoplasmic protein
STM1368	STM1368	AAL20292	(1450542..1451888)	0.387	0.109	0.331	0.074	0.855	0.306	0.012	0.289	0.024	0.945	putative Na+-dicarboxylate symporter
sufA	STM1369	AAL20293	1452315..1452683	0.188	0.038	0.175	0.034	0.929	0.149	0.048	0.292	0.086	1.953	putative HesB-like domain
sufB	STM1370	AAL20294	1452692..1454179	0.245	0.057	0.207	0.013	0.844	0.238	0.128	0.310	0.045	1.298	putative ABC transporter
sufC	STM1371	AAL20295	1454196..1454942	0.297	0.084	0.512	0.629	1.722	0.272	0.070	0.486	0.040	1.786	putative ABC superfamily (atp_bind) transport protein
sufD	STM1372	AAL20296	1454917..1456188	0.527	0.023	0.393	0.056	0.745	0.479	0.034	0.843	0.047	1.759	required for stability of iron-sulfur onent of FhuF
sufS	STM1373	AAL20297	1456185..1457405	0.364	0.044	0.267	0.039	0.732	0.305	0.009	0.484	0.022	1.587	selenocysteine lyase
ynhA	STM1374	AAL20298	1457418..1457834	0.458	0.037	0.412	0.023	0.899	0.358	0.034	0.416	0.040	1.161	putative SufE protein probably involved in Fe-S center assembly
ynhG	STM1375	AAL20299	1457989..1458990	1.746	0.360	1.885	0.353	1.080	1.293	0.145	1.440	0.092	1.114	putative LysM domain
lppB	STM1376	AAL20300	(1459057..1459296)	6.727	1.258	9.072	0.962	1.349	4.591	1.559	5.532	0.164	1.205	putative methyl-accepting chemotaxis protein
lpp	STM1377	AAL20301	(1459379..1459615)	77.943	20.047	87.453	12.318	1.122	43.996	6.284	30.440	4.610	0.692	murein lipoprotein, links outer and inner membranes
pykF	STM1378	AAL20302	(1459926..1461338)	1.274	0.120	4.144	0.489	3.254	1.870	0.028	3.176	0.193	1.698	pyruvate kinase I (formerly F), fructose stimulated
orf48	STM1379	AAL20303	(1461740..1463083)	0.289	0.074	0.377	0.022	1.307	0.895	0.101	1.756	0.193	1.962	putative amino acid permease
orf32	STM1380	AAL20304	(1463105..1463998)	0.463	0.026	0.434	0.098	0.937	0.955	0.116	1.903	0.105	1.994	putative hydrolase or acyltransferase

orf245	STM1381	AAL20305	(1464057..1464794)	0.203	0.072	0.453	0.039	2.228	1.885	0.202	2.892	0.124	1.534	putative cytoplasmic protein
orf408	STM1382	AAL20306	(1464806..1466032)	0.130	0.078	0.246	0.033	1.894	0.341	0.041	0.612	0.041	1.794	putative regulatory protein, deoR family
ttrA	STM1383	AAL20307	(1466355..1469417)	0.183	0.067	0.206	0.036	1.124	0.124	0.001	0.229	0.007	1.851	Tetrathionate reductase lex, subunit A
ttrC	STM1384	AAL20308	(1469410..1470432)	0.251	0.076	0.148	0.048	0.591	0.169	0.022	0.249	0.039	1.471	Tetrathionate reductase lex, subunit C
ttrB	STM1385	AAL20309	(1470433..1471185)					N/A					N/A	Tetrathionate reductase lex, subunit B
ttrS	STM1386	AAL20310	1471349..1473127	4.137	0.432	2.804	0.497	0.678	0.679	0.052	0.726	0.031	1.069	Tetrathionate reductase lex: sensory transduction histidine kinase
ttrR	STM1387	AAL20311	1473102..1473722	1.266	0.128	1.354	0.233	1.069	0.287	0.018	0.453	0.049	1.579	Tetrathionate reductase lex: response regulator
orf70	STM1388	AAL20312	1473820..1474032	3.278	0.811	1.419	0.163	0.433	1.052	0.100	0.891	0.066	0.847	putative cytoplasmic protein
orf319	STM1389	AAL20313	(1474128..1475087)	1.854	0.344	1.081	0.110	0.583	0.631	0.022	0.918	0.098	1.454	putative inner membrane protein
orf242	STM1390	AAL20314	(1475260..1475988)	0.529	0.054	0.396	0.013	0.749	2.589	0.133	3.427	0.097	1.324	putative regulatory proteins, merR family
ssrB	STM1391	AAL20315	(1476167..1476805)	0.378	0.048	0.295	0.027	0.779	18.756	1.405	18.416	1.477	0.982	Secretion system regulator: transcriptonal activator, homologous with degU/uvrY/bvgA
ssrA	STM1392	AAL20316	(1476836..1479598)	0.221	0.048	0.174	0.025	0.789	2.184	0.090	1.731	0.101	0.792	Secretion system regulator:Sensor onent
ssaB	STM1393	AAL20317	1479999..1480400	0.226	0.062	0.190	0.079	0.841	2.038	0.074	1.506	0.141	0.739	Secretion system apparatus
ssaC	STM1394	AAL20318	1480402..1481895	0.187	0.051	0.158	0.015	0.845	4.356	0.118	3.894	0.389	0.894	Secretion system apparatus
ssaD	STM1395	AAL20319	1481876..1483087					N/A					N/A	Secretion system apparatus
ssaE	STM1396	AAL20320	1483095..1483337	0.380	0.082	0.365	0.027	0.960	4.599	0.380	4.117	0.320	0.895	Secretion system effector
sscA	STM1399	AAL20323	1484521..1484994	0.279	0.057	0.203	0.043	0.727	7.167	0.169	9.267	0.506	1.293	Secretion system chaparone
sseC	STM1400	AAL20324	1484997..1486451	0.220	0.091	0.216	0.052	0.984	5.337	0.499	8.977	0.322	1.682	Secretion system effector
sseD	STM1401	AAL20325	1486467..1487054	0.177	0.078	0.190	0.072	1.073	3.552	0.041	5.087	0.668	1.432	Secretion system effector
sseE	STM1402	AAL20326	1487057..1487473	0.164	0.071	0.202	0.026	1.230	2.950	0.151	9.483	1.255	3.214	Secretion system effector
sscB	STM1403	AAL20327	1487525..1487959	0.149	0.054	0.213	0.054	1.428	2.378	0.054	6.045	0.238	2.542	Secretion system chaparone
sseF	STM1404	AAL20328	1487975..1488757	0.205	0.093	0.142	0.014	0.694	0.929	0.034	1.824	0.296	1.963	Secretion system effector
sseG	STM1405	AAL20329	1488754..1489443	0.174	0.072	0.138	0.016	0.793	1.036	0.102	1.957	0.265	1.889	Secretion system effector
ssaG	STM1406	AAL20330	1489537..1489752	0.298	0.162	0.243	0.082	0.815	6.186	0.047	8.588	0.334	1.388	Secretion system apparatus
ssaH	STM1407	AAL20331	1489793..1490020	0.437	0.056	0.291	0.013	0.668	16.500	0.331	12.663	1.252	0.767	Secretion system apparatus
ssaI	STM1408	AAL20332	1490032..1490280	0.300	0.060	0.203	0.035	0.677	11.598	1.817	12.372	0.704	1.067	Secretion system apparatus
ssaJ	STM1409	AAL20333	1490277..1491026	0.245	0.074	0.152	0.035	0.620	8.553	0.625	6.503	0.474	0.760	Secretion system apparatus: homology with the yscJ/mxiJ/prgK family of lipoproteins
STM1410	STM1410	AAL20334	1491044..1491592	0.150	0.058	0.080	0.022	0.536	4.511	0.187	4.765	0.367	1.056	putative cytoplasmic protein
ssaK	STM1411	AAL20335	1491589..1492263	0.145	0.058	0.123	0.030	0.848	4.390	0.326	4.909	0.690	1.118	Secretion system apparatus
ssaL	STM1412	AAL20336	1492229..1493245	0.209	0.098	0.143	0.039	0.686	4.748	0.094	9.967	0.698	2.099	Secretion system apparatus
ssaM	STM1413	AAL20337	1493303..1493671	0.703	0.191	0.425	0.116	0.604	10.047	1.005	9.628	0.769	0.958	Secretion system apparatus
ssaV	STM1414	AAL20338	1493656..1495701	0.166	0.105	0.254	0.013	1.534	5.633	1.153	4.220	0.200	0.749	Secretion system apparatus: homology with the LcrD family of proteins
ssaN	STM1415	AAL20339	1495691..1496992	0.207	0.075	0.239	0.013	1.156	5.023	0.390	6.014	0.401	1.197	Secretion system apparatus: homology with the YscN family of proteins

ssaO	STM1416	AAL20340	1496995..1497372	0.205	0.081	0.301	0.111	1.471	2.464	0.380	5.234	0.372	2.124	Secretion system apparatus
ssaP	STM1417	AAL20341	1497353..1497727	0.250	0.028	0.167	0.028	0.666	1.280	0.028	2.750	0.239	2.148	Secretion system apparatus
ssaQ	STM1418	AAL20342	1497708..1498676					N/A					N/A	Secretion system apparatus
ssaR	STM1419	AAL20343	1498744..1499391	0.182	0.072	0.105	0.017	0.575	10.483	0.646	6.169	0.580	0.588	Secretion system apparatus: homology with YscR of the secretion system of Yersinia
ssaS	STM1420	AAL20344	1499388..1499654	0.571	0.155	0.307	0.050	0.537	11.302	0.130	4.926	0.641	0.436	Secretion system apparatus: homology with YscS of the secretion system of Yersinia
ssaT	STM1421	AAL20345	1499655..1500434	0.171	0.078	0.072	0.011	0.419	7.671	2.290	2.495	0.327	0.325	Secretion system apparatus: homology with YscT of the secretion system of Yersinia
ssaU	STM1422	AAL20346	1500431..1501489	0.222	0.057	0.116	0.021	0.520	3.664	0.461	1.802	0.052	0.492	Secretion system apparatus: homology with YscU of the secretion system of Yersinia
valW	STM1423						N/A					N/A		
valV	STM1424						N/A					N/A		
ydhE	STM1425	AAL20347	(1501962..1503335)					N/A					N/A	putative MATE family transport protein
ribE	STM1426	AAL20348	1503552..1504193	2.411	0.223	1.796	0.293	0.745	4.310	0.352	3.322	0.095	0.771	riboflavin synthase, alpha chain
cfa	STM1427	AAL20349	(1504235..1505383)	0.900	0.022	1.979	0.189	2.198	1.000	0.018	2.505	0.155	2.505	cyclopropane fatty acyl phospholipid synthase
ydhC	STM1428	AAL20350	(1505673..1506878)	0.576	0.081	0.464	0.097	0.805	0.481	0.031	0.653	0.041	1.358	putative MFS family transport protein
ydhB	STM1429	AAL20351	1506991..1507923	0.505	0.084	0.470	0.039	0.931	0.307	0.025	0.367	0.055	1.198	putative transcriptional regulator, LysR family
purR	STM1430	AAL20352	(1507920..1508945)	1.438	0.130	1.469	0.307	1.021	0.901	0.007	0.775	0.173	0.861	transcriptional repressor for pur regulon, glyA, glnB, prsA, speA (GalR/LacI family)
sodB	STM1431	AAL20353	(1509413..1509994)	20.699	3.762	20.217	1.716	0.977	19.255	1.921	23.944	3.415	1.244	superoxide dismutase, iron
ydhO	STM1432	AAL20354	(1510121..1510975)	1.387	0.091	1.890	0.226	1.363	1.329	0.067	1.966	0.070	1.479	putative cell wall-associated hydrolase
ydhD	STM1433	AAL20355	1511277..1511624	7.336	1.564	3.555	0.160	0.485	4.370	0.510	1.975	0.107	0.452	putative glutaredoxin protein
rnt	STM1434	AAL20356	(1511702..1512349)	3.108	0.273	1.394	0.063	0.449	2.188	0.048	1.119	0.075	0.511	RNase T, degrades tRNA, has exonuclease and ssDNAse activity
gloA	STM1435	AAL20357	(1512450..1512857)	2.759	0.114	2.120	0.410	0.768	0.959	0.043	0.937	0.064	0.977	glyoxalase I, nickel isomerase
nemA	STM1436	AAL20358	(1512926..1514023)	1.182	0.056	1.704	0.313	1.441	0.559	0.077	1.042	0.040	1.863	N-ethylmaleimide reductase
ydhM	STM1437	AAL20359	(1514082..1514681)	0.712	0.051			0.000	0.373	0.016			0.000	putative transcriptional repressor (TetR/AcrR family)
ydhL	STM1438	AAL20360	1514784..1515023	0.942	0.155	0.307	0.031	0.326	0.432	0.054	0.239	0.045	0.553	putative oxidoreductase
ydhF	STM1439	AAL20361	1515074..1515970	4.645	0.353	1.388	0.367	0.299	1.116	0.098	0.596	0.098	0.534	putative aldo/keto reductase
sodC	STM1440	AAL20362	1516050..1516571	1.836	0.337	0.877	0.108	0.478	0.953	0.235	1.625	0.140	1.704	copper/zinc superoxide dismutase
STM1441	STM1441	AAL20363	(1516547..1518586)	0.508	0.060	0.393	0.076	0.774	0.411	0.078	0.405	0.064	0.986	putative inner membrane protein
ydhJ	STM1442	AAL20364	(1518586..1519482)	0.707	0.032	0.431	0.053	0.610	0.600	0.002	0.552	0.087	0.919	putative multidrug resistance efflux pump
ydhI	STM1443	AAL20365	(1519449..1519685)	0.972	0.025	0.440	0.093	0.453	1.001	0.098	0.533	0.052	0.533	putative inner membrane protein
slyA	STM1444	AAL20366	1519880..1520320	4.441	0.789	3.761	0.161	0.847	9.179	0.947	6.153	0.349	0.670	transcriptional regulator for hemolysin (MarR family)
slyB	STM1445	AAL20367	(1520368..1520835)	5.562	0.805	12.795	1.666	2.300	5.394	0.309	8.204	0.756	1.521	putative outer membrane lipoprotein

ydhH	STM1446	AAL20368	1521107..1522228	0.800	0.033	0.847	0.044	1.058	0.712	0.130	1.278	0.104	1.795	putative cytoplasmic protein
ydhA	STM1447	AAL20369	1522316..1522645	1.123	0.153	0.730	0.168	0.651	0.691	0.038	0.483	0.051	0.700	putative outer membrane lipoprotein
pdxH	STM1448	AAL20370	1522704..1523360	3.174	0.087	1.369	0.197	0.431	1.794	0.257	1.927	0.134	1.074	pyridoxine 5'-phosphate oxidase
tyrS	STM1449	AAL20371	1523487..1524761	11.194	0.467	5.272	0.169	0.471	5.961	0.634	3.347	0.269	0.562	tyrosine tRNA synthetase
pdxY	STM1450	AAL20372	1524821..1525681	5.818	0.327	2.948	0.543	0.507	3.516	0.623	2.330	0.244	0.663	pyridoxal kinase 2/pyridoxine kinase
gst	STM1451	AAL20373	(1525740..1526345)	1.678	0.128	4.322	0.295	2.576	2.553	0.039	3.887	0.474	1.522	glutathionine S-transferase
ydgR	STM1452	AAL20374	(1526450..1527955)	14.321	0.560	3.037	0.287	0.212	2.899	0.410	2.827	0.071	0.975	putative POT family, peptide transport protein
nth	STM1453	AAL20375	(1528557..1529192)	0.706	0.117			0.000	0.486	0.010			0.000	endonuclease III; DNA glycosylase/apyrimidinic (AP) lyase
ydgQ	STM1454	AAL20376	(1529192..1529884)	1.021	0.152	0.709	0.106	0.694	1.143	0.220	1.050	0.069	0.919	putative NADH-quinone reductase, membrane protein
ydgP	STM1455	AAL20377	(1529887..1530507)	0.701	0.110	0.959	0.133	1.369	0.798	0.041	0.903	0.034	1.131	putative Na+-transporting NADH:ubiquinone oxidoreductase gamma subunit
ydgO	STM1456	AAL20378	(1530511..1531569)	0.725	0.162	0.684	0.034	0.943	0.798	0.139	0.677	0.040	0.848	putative oxidoreductase
STM1457	STM1457	AAL20379	(1531570..1533777)					N/A					N/A	putative respiratory-chain NADH dehydrogenase
ydgM	STM1458	AAL20380	(1533770..1534348)	0.984	0.055	0.684	0.119	0.695	1.198	0.143	0.742	0.077	0.619	putative alternative beta subunit of Na+-transporting NADH:ubiquinone oxidoreductase
STM1459	STM1459	AAL20381	(1534348..1534929)	1.261	0.073	0.487	0.111	0.386	1.666	0.264	0.718	0.033	0.431	putative oxidoreductase, inner membrane protein
ydgK	STM1460	AAL20382	(1535006..1535446)	1.342	0.055	1.250	0.284	0.932	1.984	0.233	1.376	0.119	0.693	putative inner membrane protein
ydgT	STM1461	AAL20383	(1535535..1535750)	2.871	0.086	2.109	0.171	0.734	5.957	1.074	3.023	0.313	0.507	putative cytoplasmic protein
ydgJ	STM1462	AAL20384	1536306..1537421	1.502	0.087	1.646	0.357	1.095	1.287	0.146	1.688	0.189	1.311	putative oxidoreductase
add	STM1463	AAL20385	(1537496..1538497)	2.231	0.271	2.445	0.199	1.096	2.872	0.176	1.839	0.107	0.640	adenosine deaminase
malY	STM1464; pseudogene; in-frame stop following codon					0.641	0.067			0.000	0.719	0.042		0.000
malX	STM1465; pseudogene; frameshift				0.918	0.077	0.527	0.047	0.574	0.965	0.022	0.392	0.047	0.406
ydgA	STM1466	AAL20386	(1539201..1540709)	1.999	0.136	2.572	0.253	1.286	2.934	0.057	3.000	0.080	1.023	putative periplasmic protein
manA	STM1467	AAL20387	(1540812..1541987)	2.030	0.197	2.824	0.222	1.391	1.140	0.080	1.998	0.147	1.754	mannose-6-phosphate isomerase
fumA	STM1468	AAL20388	1542187..1543929	10.350	1.022	13.817	1.283	1.335	2.166	0.016	2.496	0.154	1.153	fumarase A (fumarate hydratase class I), aerobic isozyme
fumC	STM1469	AAL20389	1544000..1545403	6.497	2.445	8.439	1.246	1.299	1.213	0.109	2.069	0.065	1.706	fumarase C (fumarate hydratase Class II)
tus	STM1470	AAL20390	(1545400..1546329)	1.333	0.460	1.363	0.248	1.023	0.374	0.033	0.514	0.055	1.377	replication termination protein
rstB	STM1471	AAL20391	(1546405..1547706)	0.324	0.033	0.231	0.029	0.713	0.200	0.025	0.311	0.034	1.553	sensory histidine kinase in two-onent regulatory system with RstA
STM1472	STM1472	AAL20392	(1547817..1549523)	0.243	0.089	0.151	0.014	0.623	0.255	0.105	0.300	0.037	1.177	putative periplasmic protein
ompN	STM1473	AAL20393	(1549676..1550809)	1.143	0.162	1.454	0.269	1.272	7.529	1.484	5.070	0.309	0.673	outer membrane protein N, non-specific porin
STM1474	STM1474	pseudogene; frameshift		0.758	0.141	0.673	0.178	0.888	2.146	0.354	1.176	0.344	0.548	
rstA	STM1475	AAL20394	(1551289..1552020)	2.013	0.221	1.340	0.243	0.666	7.862	0.250	4.438	0.196	0.564	response regulator in two-onent regulatory system with RstB (OmpR family)

ydgC	STM1476	AAL20395	1552147..1552482	0.946	0.105	0.307	0.032	0.324	0.720	0.089	0.467	0.035	0.648	putative inner membrane protein
ydgI	STM1477	AAL20396	(1552544..1553926)	0.592	0.056	0.223	0.035	0.376	0.710	0.080	0.245	0.021	0.345	putative amino acid transporter
ydgH	STM1478	AAL20397	(1554224..1555168)	14.911	2.507	5.789	0.674	0.388	6.054	0.835	3.822	0.442	0.631	putative periplasmic protein
pntA	STM1479	AAL20398	1555695..1557224	1.417	0.112	3.968	0.254	2.799	1.125	0.062	1.829	0.168	1.626	pyridine nucleotide transhydrogenase (proton pump), alpha subunit
pntB	STM1480	AAL20399	1557235..1558623	2.544	0.190	5.599	0.264	2.201	1.555	0.147	3.051	0.217	1.962	pyridine nucleotide transhydrogenase (proton pump), beta subunit
STM1481	STM1481	AAL20400	(1558798..1559832)	0.466	0.055	0.490	0.039	1.051	1.684	0.259	0.746	0.038	0.443	putative membrane transport protein
ydgF	STM1482	AAL20401	1560250..1560612	1.607	0.027	2.318	0.260	1.442	6.310	1.468	2.372	0.074	0.376	putative membrane transporter of cations and cationic drugs
ydgE	STM1483	AAL20402	1560599..1560928	1.187	0.125	1.846	0.287	1.556	3.887	0.792	2.128	0.087	0.548	putative membrane transporter of cations and cationic drugs
STM1484	STM1484	AAL20403	(1560968..1561789)	0.691	0.033	1.003	0.060	1.450	2.071	0.238	1.154	0.053	0.557	putative protease
STM1485	STM1485	AAL20404	(1562058..1562342)	0.596	0.069	0.292	0.043	0.490	23.133	4.893	2.366	0.157	0.102	acid shock protein
ynfM	STM1486	AAL20405	(1562701..1563954)	0.256	0.044	0.132	0.007	0.517	0.295	0.014	0.232	0.032	0.787	putative MFS familty transport protein
ynfL	STM1487	AAL20406	1564074..1564973	0.473	0.049	0.283	0.035	0.599	0.323	0.040	0.438	0.034	1.356	putative transcriptional regulator, LysR family
mlc	STM1488	AAL20407	1565101..1566321	0.780	0.048	1.024	0.030	1.313	0.466	0.012	0.978	0.067	2.100	transcriptional repressor of ptsG and ptsHI, global repressor of carbohydrate metabolism (pts operon) (NagC/XylR family)
ynfK	STM1489	AAL20408	1566447..1567142	0.582	0.040	0.680	0.074	1.168	0.410	0.009	0.407	0.017	0.991	putative dethiobiotin synthase
STM1490	STM1490	AAL20409	(1567098..1568387)	0.491	0.031	0.243	0.041	0.496	0.317	0.045	0.277	0.024	0.874	putative chloride channel protein
STM1491	STM1491	AAL20410	(1568523..1569671)	0.831	0.236	0.380	0.050	0.457	1.238	0.106	0.995	0.083	0.803	ABC-type proline/glycine betaine transport systems, ATPase onent
STM1492	STM1492	AAL20411	(1569671..1570318)	0.588	0.077	0.345	0.061	0.586	0.628	0.095	0.707	0.033	1.126	putative binding-protein-dependent transport system, inner membrane onent
STM1493	STM1493	AAL20412	(1570328..1571230)	0.333	0.025	0.217	0.018	0.652	0.312	0.031	0.540	0.052	1.730	putative periplasmic onent, ABC transport system
STM1494	STM1494	AAL20413	(1571259..1571969)	0.560	0.042	0.241	0.037	0.430	0.534	0.023	0.531	0.033	0.994	ABC-type transport systems, permease onents
ynfI	STM1495	AAL20414	(1572274..1572888)	2.704	0.126	1.129	0.272	0.418	1.148	0.278	0.955	0.074	0.832	putative onent of anaerobic dehydrogenases
STM1496	STM1496	AAL20415	(1572931..1573788)					N/A					N/A	putative dimethylsulfoxide reductase
STM1497	STM1497	AAL20416	(1573790..1574407)					N/A					N/A	putative dimethyl sulphoxide reductase
STM1498	STM1498	AAL20417	(1574418..1576853)	0.160	0.107	1.130	0.118	7.075	0.191	0.089	0.147	0.020	0.767	putative dimethyl sulphoxide reductase
STM1499	STM1499	AAL20418	(1576952..1579393)	0.247	0.072	1.033	0.134	4.178	0.152	0.026	0.192	0.009	1.262	putative dimethyl sulphoxide reductase, chain A1
ynfD	STM1500	AAL20419	(1579547..1579855)	0.846	0.050	1.753	0.154	2.073	0.610	0.128	0.830	0.023	1.361	putative outer membrane protein
ynfC	STM1501	AAL20420	1579950..1580669	1.131	0.049	0.969	0.135	0.857	0.553	0.097	0.642	0.055	1.162	putative inner membrane lipoprotein
speG	STM1502	AAL20421	(1580710..1581270)	6.940	0.666	5.377	0.920	0.775	2.583	0.246	2.544	0.127	0.985	spermidine N1-acetyltransferase
ynfB	STM1503	AAL20422	(1581306..1581647)	4.678	0.259	4.065	0.470	0.869	2.572	0.049	2.278	0.101	0.886	putative periplasmic protein
ynfA	STM1504	AAL20423	1581800..1582126	1.103	0.066	0.437	0.063	0.396	0.505	0.177	0.318	0.052	0.631	putative inner membrane lipoprotein

rspA	STM1505	AAL20424	1582248..1583462	0.491	0.055	0.331	0.028	0.674	0.162	0.011	0.296	0.027	1.827	putative dehydratase, starvation sensing protein
rspB	STM1506	AAL20425	1583473..1584492	0.342	0.068	0.297	0.041	0.868	0.153	0.012	0.245	0.026	1.606	putative dehydrogenase
ydfJ	STM1507	AAL20426	1584546..1585523	0.254	0.079	0.267	0.027	1.048	0.213	0.021	0.275	0.007	1.290	putative transport protein
ydfI	STM1508	AAL20427	1586069..1587535	0.380	0.053	0.642	0.129	1.689	0.644	0.048	0.974	0.050	1.513	putative mannitol dehydrogenase
ydfZ	STM1509	AAL20428	(1587602..1587805)	0.485	0.037	4.552	0.326	9.392	0.406	0.097	0.530	0.054	1.304	putative cytoplasmic protein
ydfH	STM1510	AAL20429	(1587986..1588672)	0.854	0.039	1.170	0.131	1.370	0.876	0.008	1.077	0.076	1.229	putative regulatory protein, gntR family
ydfG	STM1511	AAL20430	(1588802..1589548)	3.097	0.147	3.514	0.657	1.135	1.615	0.161	1.782	0.164	1.104	putative oxidoreductase
d	STM1512	AAL20431	1589687..1591729	0.540	0.041	0.838	0.089	1.553	0.608	0.032	0.821	0.042	1.351	dipeptidyl carboxypeptidase II
STM1513	STM1513	AAL20432	1592074..1592256	0.351	0.085	0.443	0.023	1.264	32.214	5.794	4.125	0.531	0.128	putative cytoplasmic protein
ydeJ	STM1514	AAL20433	(1592376..1592903)	0.263	0.070	0.201	0.029	0.766	2.729	0.227	0.955	0.059	0.350	putative etence-damaged protein
ydeI	STM1515	AAL20434	1593330..1593722	0.532	0.035	0.213	0.036	0.401	8.551	0.863	2.503	0.270	0.293	putative periplasmic protein
ydeE	STM1516	AAL20435	(1594414..1595601)	0.415	0.019	0.170	0.016	0.410	0.275	0.004	0.242	0.020	0.881	putative MFS family transport protein
ydeD	STM1517	AAL20436	1595829..1596731	0.559	0.047	0.331	0.101	0.591	0.276	0.061	0.199	0.012	0.720	putative permease, integral membrane protein
marB	STM1518	AAL20437	(1596850..1597065)	0.778	0.055	0.541	0.124	0.696	0.548	0.230	0.393	0.107	0.717	multiple antibiotic resistance protein
marA	STM1519	AAL20438	(1597094..1597528)	0.370	0.070	0.740	0.021	2.001	0.252	0.025	0.348	0.050	1.383	transcriptional activator of defense systems (AraC/XylS family), multiple antibiotic resistance protein
marR	STM1520	AAL20439	(1597497..1597931)	0.217	0.068	0.341	0.022	1.570	0.181	0.027	0.320	0.055	1.765	transcriptional repressor of marRAB operon, multiple antibiotic resistance protein
marC	STM1521	AAL20440	1598190..1598855	0.774	0.082	0.421	0.089	0.544	1.366	0.236	1.119	0.045	0.819	putative MarC Transporter, multiple antibiotic resistance protein
ydeA	STM1522	AAL20441	(1598902..1600092)	0.213	0.074	0.187	0.034	0.874	0.304	0.025	0.335	0.024	1.102	MFS family, L-arabinose/isopropyl-beta-D-thiogalactopyranoside export protein, contributes to control of arabinose regulon
yneJ	STM1523	AAL20442	(1600208..1601080)	0.401	0.039	0.217	0.030	0.540	0.196	0.007	0.325	0.027	1.659	putative transcriptional regulator, LysR family
yneI	STM1524	AAL20443	1601183..1602571	0.401	0.033	0.381	0.009	0.950	0.312	0.013	0.327	0.009	1.047	putative succinate-semialdehyde dehydrogenase
yneH	STM1525	AAL20444	1602644..1603570	0.808	0.114	0.474	0.087	0.587	0.722	0.054	0.420	0.110	0.581	putative glutaminase
yneG	STM1526	AAL20445	1603570..1603929	0.510	0.029	0.279	0.015	0.546	0.516	0.070	0.434	0.081	0.841	putative cytoplasmic protein
STM1527	STM1527	AAL20446	1604153..1605100	0.352	0.039	0.127	0.027	0.360	0.858	0.118	0.496	0.071	0.578	putative inner membrane protein
STM1528	STM1528	AAL20447	(1605156..1605698)	0.157	0.078	0.124	0.023	0.790	1.072	0.059	2.324	0.124	2.168	putative outer membrane protein
STM1529	STM1529	AAL20448	1605547..1605873	0.240	0.067	0.212	0.017	0.882	1.385	0.027	1.898	0.189	1.371	putative inner membrane protein
STM1530	STM1530	AAL20449	1606415..1607533	0.220	0.095	0.221	0.017	1.002	0.186	0.021	0.206	0.018	1.106	putative outer membrane protein
STM1531	STM1531	AAL20450	(1607674..1608015)	0.224	0.066	0.279	0.028	1.243	0.346	0.039	0.827	0.067	2.388	putative hydrogenase
STM1532	STM1532	AAL20451	(1608028..1608915)	0.251	0.086	0.358	0.087	1.427	0.416	0.041	0.967	0.078	2.323	putative dehydrogenase protein
STM1533	STM1533	AAL20452	(1608903..1609964)	0.332	0.060	0.486	0.073	1.464	0.478	0.061	1.919	0.115	4.011	putative hydrogenase
STM1534	STM1534	AAL20453	(1609982..1610392)	0.439	0.064	0.599	0.042	1.364	0.611	0.011	2.646	0.279	4.333	putative hydrogenase
STM1535	STM1535	AAL20454	(1610389..1610688)	0.327	0.081	0.765	0.009	2.339	0.638	0.093	2.949	0.178	4.625	putative hydrogenase protein
STM1536	STM1536	AAL20455	(1610688..1611296)	0.419	0.039	0.827	0.063	1.974	0.799	0.141	3.146	0.061	3.937	putative hydrogenase maturation protease

STM1537	STM1537	AAL20456	(1611302..1612045)	0.368	0.077	0.586	0.018	1.592	0.598	0.122	2.135	0.181	3.570	putative Ni/Fe-hydrogenase 1 b-type cytochrome subunit
STM1538	STM1538	AAL20457	(1611996..1613798)	0.300	0.086	1.029	0.030	3.433	0.467	0.104	1.734	0.109	3.715	putative hydrogenase-1 large subunit
STM1539	STM1539	AAL20458	(1613801..1614904)	0.216	0.092	0.766	0.132	3.550	0.394	0.014	1.931	0.207	4.899	putative hydrogenase-1 small subunit
STM1540	STM1540	AAL20459	1615333..1616424	0.338	0.046	0.464	0.069	1.371	3.080	0.660	18.775	0.759	6.097	putative hydrolase
STM1541	STM1541	AAL20460	1616470..1617261	0.814	0.027	0.736	0.066	0.904	0.717	0.014	1.119	0.202	1.562	putative regulatory protein, gntR family
STM1542	STM1542	AAL20461	(1617320..1618345)	0.187	0.047	0.290	0.043	1.550	0.722	0.208	1.563	0.177	2.166	putative zinc-binding dehydrogenase
STM1543	STM1543	AAL20462	(1618320..1619606)	0.251	0.061	0.226	0.037	0.901	0.941	0.144	1.109	0.036	1.179	putative transport protein
pqaA	STM1544	AAL20463	(1619783..1621339)	0.147	0.052	0.149	0.025	1.008	1.092	0.076	1.522	0.176	1.394	PhoPQ-regulated protein
STM1545	STM1545	AAL20464	(1621409..1622650)	0.131	0.072	0.092	0.022	0.701	0.234	0.057	0.290	0.067	1.244	putative multidrug efflux protein
STM1546	STM1546	AAL20465	(1622640..1624148)	0.249	0.058	0.213	0.011	0.857	0.384	0.183	0.401	0.049	1.046	putative monooxygenase
STM1547	STM1547	AAL20466	1624193..1624681	0.569	0.035	0.365	0.037	0.641	1.140	0.336	0.974	0.036	0.855	putative marR-family transcriptional regulator
STM1548	STM1548	AAL20467	1624913..1625953	0.420	0.066	0.306	0.049	0.729	20.778	0.501	17.370	1.187	0.836	putative S-adenosylmethionine:tRNA-ribosyltransferase-isomerase
STM1549	STM1549	AAL20468	(1626005..1626394)	0.954	0.028	0.650	0.054	0.682	3.481	0.050	3.292	0.353	0.946	putative translation initiation inhibitor
STM1550	STM1550	AAL20469	(1626565..1626849)	0.631	0.120	0.474	0.031	0.750	0.870	0.116	0.840	0.074	0.966	putative cytoplasmic protein
STM1551	STM1551	AAL20470	(1626839..1627087)	0.604	0.053			0.000	0.737	0.154			0.000	putative cytoplasmic protein
STM1552	STM1552	AAL20471	1627919..1628827	0.270	0.094	0.199	0.050	0.739	0.760	0.053	0.670	0.024	0.882	putative cytoplasmic protein
STM1553	STM1553	pseudogene; frameshift		0.186	0.072	0.128	0.024	0.687	0.293	0.108	0.251	0.029	0.855	
STM1554	STM1554	AAL20472	(1630405..1631871)	1.288	0.119	0.349	0.043	0.271	1.000	0.010	0.702	0.090	0.702	putative coiled-coil protein
STM1555	STM1555	AAL20473	1632130..1633137	0.533	0.072	0.319	0.037	0.598	1.440	0.200	0.813	0.023	0.565	putative transcriptional regulator
STM1556	STM1556	AAL20474	1633281..1634732	0.200	0.073			0.000	0.287	0.011			0.000	putative Na+/H+ antiporter
STM1557	STM1557	AAL20475	1634745..1635947	0.372	0.067	0.285	0.039	0.766	0.589	0.043	0.313	0.022	0.531	putative aminotransferase
STM1558	STM1558	AAL20476	(1636060..1638135)	0.332	0.063	0.314	0.045	0.946	0.527	0.058	0.654	0.095	1.241	putative glycosyl hydrolase
STM1559	STM1559	AAL20477	(1638192..1640720)	0.132	0.056	0.134	0.026	1.019	0.182	0.021	0.478	0.040	2.625	putative glycosyl hydrolase
STM1560	STM1560	AAL20478	(1640717..1642501)	0.155	0.058	0.150	0.014	0.970	0.189	0.015	0.629	0.038	3.321	putative alpha amylase
STM1561	STM1561	AAL20479	(1642630..1643415)	0.198	0.063	0.184	0.011	0.927	0.325	0.079	0.485	0.042	1.491	putative outer membrane or secreted lipoprotein
STM1562	STM1562	AAL20480	(1643558..1643887)	0.222	0.043			0.000	1.065	0.169			0.000	putative periplasmic transport protein
osmC	STM1563	AAL20481	(1644237..1644668)	0.909	0.183	0.384	0.015	0.423	4.450	0.496	2.524	0.193	0.567	putative resistance protein, osmotically inducible
yddX	STM1564	AAL20482	1645181..1645396	0.717	0.099	0.878	0.086	1.225	13.108	1.058	8.469	0.925	0.646	putative cytoplasmic protein
rpsV	STM1565	AAL20483	1645491..1645634	3.471	0.952	2.882	0.511	0.830	13.304	0.804	8.195	0.261	0.616	30S ribosomal subunit protein S22
sfcA	STM1566	AAL20484	1645811..1647508	1.756	0.223	2.775	0.310	1.580	2.417	0.049	2.683	0.371	1.110	NAD-linked malate dehydrogenase
adhP	STM1567	AAL20485	1647794..1648804	2.082	0.048	1.547	0.164	0.743	1.301	0.049	1.416	0.030	1.088	alcohol dehydrogenase, propanol preferring
fdnI	STM1568	AAL20486	(1648895..1649551)	0.462	0.082	6.156	0.582	13.323	0.493	0.024	0.660	0.026	1.341	formate dehydrogenase-N, cytochrome B556(Fdn) gamma subunit, nitrate-inducible
fdnH	STM1569	AAL20487	(1649544..1650428)	0.640	0.075	11.053	1.730	17.266	0.330	0.039	1.016	0.048	3.076	formate dehydrogenase-N, Fe-S beta subunit, nitrate-inducible
fdnG	STM1570	AAL20488	(1650442..1653489)	0.903	0.202	10.470	0.821	11.594	0.572	0.154	1.590	0.303	2.780	putative molybdopterin oxidoreductases

yddG	STM1571	AAL20489	1653824..1654648	0.758	0.038	1.126	0.105	1.485	0.463	0.041	0.446	0.030	0.964	putative permease
nmpC	STM1572	AAL20490	1655173..1656261	68.408	6.571	161.029	12.070	2.354	10.661	1.736	15.761	1.073	1.478	new outer membrane protein; predicted bacterial porin
STM1573	STM1573	AAL20491	1656405..1656785	2.229	0.288	3.474	0.809	1.559	1.051	0.036	1.095	0.136	1.042	putative cytoplasmic protein
smvA	STM1574	AAL20492	(1656810..1658297)	0.905	0.105	0.679	0.148	0.751	1.213	0.270	0.608	0.025	0.501	Methyl viologen resistance
STM1575	STM1575	AAL20493	1658415..1658993	1.020	0.119	0.524	0.149	0.514	0.821	0.162	0.541	0.023	0.659	putative transcriptional regulator, TetR family
narU	STM1576	AAL20494	1659208..1660596					N/A					N/A	MFS superfamily, nitrate extrusion protein
narZ	STM1577	AAL20495	1660688..1664428	0.209	0.111	0.444	0.018	2.123	0.617	0.692	0.771	0.177	1.250	nitrate reductase 2, alpha subunit
narY	STM1578	AAL20496	1664425..1665969					N/A					N/A	nitrate reductase 2, beta subunit
narW	STM1579	AAL20497	1665969..1666664	0.241	0.078	0.305	0.051	1.268	0.423	0.036	0.886	0.101	2.098	nitrate reductase 2, delta subunit, assembly function
narV	STM1580	AAL20498	1666661..1667341	0.405	0.055	0.236	0.018	0.583	0.639	0.160	0.774	0.047	1.212	nitrate reductase 2, gamma subunit
yddE	STM1581	AAL20499	1667447..1668340	1.030	0.051	0.694	0.022	0.674	0.921	0.033	0.661	0.115	0.718	putative phenazine biosynthesis protein
nhoA	STM1582	AAL20500	(1668376..1669221)	1.265	0.027	0.460	0.065	0.364	2.043	0.135	1.414	0.107	0.692	putative arylamine N-acetyltransferase
STM1583	STM1583	AAL20501	(1669505..1670137)	0.855	0.097	1.054	0.090	1.233	8.251	0.176	10.533	0.935	1.276	putative cytoplasmic protein
ansP	STM1584	AAL20502	1670649..1672142	1.430	0.125	0.259	0.057	0.181	0.657	0.108	0.333	0.039	0.506	APC family, L-asparagine transport protein
STM1585	STM1585	AAL20503	(1672219..1672440)	0.490	0.036	0.233	0.046	0.477	0.417	0.120	0.322	0.045	0.772	putative outer membrane lipoprotein
STM1586	STM1586	AAL20504	(1672585..1673646)	2.004	0.226	0.303	0.021	0.151	0.481	0.005	0.481	0.006	1.000	putative periplasmic protein
yncD	STM1587	AAL20505	1673910..1676030	0.347	0.052	0.262	0.067	0.756	0.458	0.115	0.577	0.036	1.261	paral putative outer membrane receptor
yncC	STM1588	AAL20506	(1676097..1676762)	0.307	0.085	0.220	0.037	0.717	6.214	1.199	4.954	0.306	0.797	putative regulatory protein, gntR family
yncB	STM1589	AAL20507	(1677096..1678166)	0.491	0.034	0.740	0.154	1.507	0.898	0.026	1.294	0.103	1.441	putative NADP-dependent oxidoreductase
yncA	STM1590	AAL20508	1678345..1678860	5.026	1.441	1.250	0.148	0.249	1.110	0.267	1.208	0.159	1.089	putative acyltransferase
ydcZ	STM1591	AAL20509	1678860..1679309	3.461	0.732	0.951	0.114	0.275	0.812	0.164	0.690	0.117	0.850	putative inner membrane protein
ydcY	STM1592	AAL20510	(1679314..1679547)	1.488	0.189	1.172	0.181	0.788	0.651	0.005	0.705	0.017	1.083	putative cytoplasmic protein
srfA	STM1593	AAL20511	1679771..1681090	0.826	0.087	7.113	0.877	8.609	0.124	0.046	0.220	0.031	1.776	ssrAB activated gene
srfB	STM1594	AAL20512	1681095..1684076	1.321	0.025	7.542	0.440	5.708	0.344	0.092	0.447	0.034	1.297	ssrAB activated gene
srfC	STM1595	AAL20513	1684073..1686217	0.837	0.050	6.391	0.207	7.635	0.284	0.123	0.355	0.038	1.251	ssrAB activated gene: predicted coiled-coil structure
ydcX	STM1596	AAL20514	(1686262..1686525)	1.009	0.043	1.779	0.244	1.762	0.628	0.023	0.658	0.051	1.048	putative inner membrane protein
ydcW	STM1597	AAL20515	(1686834..1688279)	1.038	0.168	0.603	0.105	0.581	3.938	0.834	4.871	0.280	1.237	putative aldehyde dehydrogenase
ydcR	STM1598	AAL20516	(1688394..1689818)	0.745	0.056	1.052	0.169	1.412	3.850	0.024	9.425	0.369	2.448	putative regulatory protein, gntR family
pdgL	STM1599	AAL20517	(1689954..1690724)	0.331	0.068	0.978	0.209	2.954	2.682	0.111	11.128	1.485	4.149	Periplasmic dipeptidase for D-ala-D-ala digestion in peptidoglycan
STM1600	STM1600	AAL20518	(1690983..1691213)	0.484	0.060	0.269	0.056	0.557	10.755	2.065	2.151	0.724	0.200	putative inner membrane protein
ugtL	STM1601	AAL20519	(1691246..1691644)	0.380	0.038	0.192	0.046	0.505	15.476	2.921	4.508	0.331	0.291	putative membrane protein: homology with chitinase from Schizosaccharomyces
sifB	STM1602	AAL20520	1692181..1693131	0.242	0.066	0.123	0.020	0.509	18.295	2.475	6.516	0.346	0.356	Salmonella translocated effector: translocated by SPI-2

yncJ	STM1603	AAL20521	1693405..1693635	0.411	0.047	0.216	0.071	0.526	10.022	1.420	5.443	0.152	0.543	putative periplasmic protein
yd	STM1604	AAL20522	(1693636..1695600)	0.394	0.081	0.421	0.055	1.068	1.079	0.063	0.551	0.088	0.511	putative collagenase
ydcN	STM1605	AAL20523	(1695679..1696215)	0.515	0.023	0.542	0.100	1.052	0.277	0.076	0.388	0.028	1.401	putative oxidoreductase/putative repressor
STM1606	STM1606	AAL20524	1696306..1697484	0.696	0.078	0.502	0.023	0.722	0.366	0.022	0.608	0.029	1.663	putative benzoate membrane transport protein
STM1607	STM1607	AAL20525	(1697538..1698206)	1.318	0.017	1.844	0.205	1.399	0.890	0.032	0.964	0.044	1.083	putative outer membrane lipoprotein
tehB	STM1608	AAL20526	(1698362..1698958)	2.057	0.244	2.449	0.407	1.190	1.364	0.162	1.191	0.027	0.873	paral putative methyltransferase; tellurite resistance
tehA	STM1609	AAL20527	(1698945..1699958)	0.562	0.053	0.485	0.056	0.862	0.413	0.057	0.409	0.008	0.989	TDT family, K+-tellurite ethidium and proflavin transport protein
ydcK	STM1610	AAL20528	1700065..1701045	0.314	0.051	0.255	0.065	0.812	0.191	0.003	0.307	0.028	1.609	putative nucleoside-diphosphate-sugar pyrophosphorylases involved in lipopolysaccharide biosynthesis
rimL	STM1611	AAL20529	(1701042..1701581)	0.449	0.064	0.483	0.049	1.075	0.350	0.030	0.443	0.060	1.266	acetyl transferase, modifies N-terminal serine of 50S ribosomal subunit protein L7/L12
STM1612	STM1612	AAL20530	1701798..1702916	0.351	0.080	0.349	0.042	0.997	0.231	0.024	0.317	0.037	1.373	putative cellulase protein
STM1613	STM1613	AAL20531	1702913..1703194	0.410	0.060	0.313	0.050	0.764	0.254	0.095	0.480	0.068	1.886	putative PTS system, enzymeIIB onent
STM1614	STM1614	AAL20532	1703205..1704518	0.297	0.082	0.232	0.027	0.784	0.215	0.011	0.359	0.014	1.669	putative PTS system enzyme IIC onent
STM1615	STM1615	AAL20533	1704532..1705338	0.482	0.063	0.243	0.010	0.504	0.351	0.032	0.713	0.033	2.028	putative nucleoside triphosphatase
STM1616	STM1616	AAL20534	1705470..1705907	0.443	0.042	0.444	0.046	1.002	0.309	0.020	0.871	0.081	2.821	putative Sugar Specific PTS Enzyme II
STM1617	STM1617	AAL20535	1705919..1706551	0.262	0.091	0.414	0.067	1.581	0.207	0.009	0.575	0.050	2.780	putative ribulose-phosphate 3-epimerase
STM1618	STM1618	AAL20536	1706567..1707358	0.332	0.094	0.317	0.030	0.955	0.259	0.065	0.469	0.022	1.813	putative transcriptional repressor of sgc operon (DeoR family)
STM1619	STM1619	AAL20537	1707358..1707795	0.390	0.039	0.285	0.043	0.732	0.323	0.052	0.470	0.024	1.453	cryptic aminoglycoside resistance gene
STM1620	STM1620	AAL20538	(1707842..1709044)	0.171	0.059	0.111	0.027	0.649	0.212	0.030	0.246	0.012	1.158	putative oxidase
STM1621	STM1621	AAL20539	(1709056..1709631)	0.265	0.082	0.178	0.032	0.672	0.316	0.033	0.267	0.014	0.845	putative periplasmic protein
ydcG	STM1622	AAL20540	(1709827..1711482)	1.970	0.330	1.209	0.156	0.613	2.296	0.156	1.165	0.079	0.507	paral putative periplasmic glucans biosynthesis protein
STM1623	STM1623	AAL20541	(1711702..1713210)	3.178	0.718	0.703	0.105	0.221	1.538	0.444	1.187	0.045	0.772	putative carboxylesterase
STM1624	STM1624	AAL20542	(1713259..1714602)	2.303	0.384	0.550	0.128	0.239	1.098	0.027	0.711	0.060	0.647	putative cytoplasmic protein
ydcI	STM1625	AAL20543	1714895..1715818	7.281	0.749	7.293	1.160	1.002	1.218	0.104	3.085	0.084	2.532	putative transcriptional regulators, LysR family
trg	STM1626	AAL20544	(1715879..1717504)	1.349	0.115	5.879	0.542	4.358	0.201	0.044	0.243	0.014	1.210	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
STM1627	STM1627	AAL20545	(1717673..1718791)	1.610	0.131	1.052	0.048	0.653	1.633	0.181	1.109	0.098	0.679	alcohol dehydrogenase class III
STM1628	STM1628	AAL20546	(1718823..1719098)	1.167	0.112	0.621	0.051	0.532	1.479	0.121	0.945	0.080	0.639	putative cytoplasmic protein
STM1629	STM1629	AAL20547	1719621..1720022	0.224	0.047	0.189	0.044	0.842	8.725	0.862	4.863	0.252	0.557	putative dipicolinate reductase
STM1630	STM1630	AAL20548	(1720151..1720867)	0.141	0.052	0.125	0.032	0.886	6.863	2.332	1.594	0.105	0.232	putative inner membrane protein
sseJ	STM1631	AAL20549	1721293..1722519	0.139	0.047	0.114	0.040	0.818	0.691	0.011	0.869	0.041	1.258	Salmonella translocated effector: regulated by SPI-2
STM1632	STM1632	AAL20550	(1722640..1722984)	0.180	0.030	0.110	0.020	0.610	1.205	0.087	0.530	0.049	0.440	putative inner membrane protein

STM1633	STM1633	AAL20551	1723891..1724652	0.295	0.068	0.180	0.035	0.609	32.637	1.163	14.202	1.022	0.435	putative periplasmic binding protein
STM1634	STM1634	AAL20552	1724659..1725306	0.171	0.070	0.102	0.017	0.593	8.138	0.696	3.050	0.376	0.375	putative amino acid ABC transporter permease onent
STM1635	STM1635	AAL20553	1725331..1726062	0.144	0.071	0.099	0.016	0.686	1.854	0.038	2.076	0.182	1.119	putative ABC-type polar amino acid transport system, ATPase onent
STM1636	STM1636	AAL20554	1726059..1726739	0.167	0.071	0.117	0.015	0.699	3.761	1.215	2.137	0.382	0.568	putative ABC-type transport system probable membrane spanning protein
STM1637	STM1637	AAL20555	1726876..1728426	0.162	0.068	0.138	0.038	0.854	1.092	0.159	1.156	0.078	1.059	putative inner membrane protein
STM1638	STM1638	AAL20556	1729115..1729552	1.072	0.061	1.360	0.202	1.269	1.031	0.058	1.329	0.046	1.289	putative SAM-dependent methyltransferases
cybB	STM1639	AAL20557	(1729823..1730353)	1.784	0.086	0.701	0.146	0.393	1.380	0.270	0.871	0.110	0.631	cytochrome b(561)
ydcF	STM1640	AAL20558	(1730470..1731270)	1.199	0.072	1.155	0.068	0.964	0.851	0.218	1.236	0.149	1.452	putative inner membrane protein
hrpA	STM1641	AAL20559	(1731334..1735236)	0.704	0.042	0.868	0.081	1.234	0.422	0.023	0.463	0.025	1.097	helicase, ATP-dependent
aD	STM1642	AAL20560	1735437..1736042	0.972	0.021	0.636	0.048	0.654	0.840	0.073	0.767	0.073	0.912	acyl carrier protein phosphodiesterase
STM1643	STM1643	AAL20561	(1736039..1736488)	0.993	0.035	0.329	0.059	0.332	2.066	0.346	1.310	0.242	0.634	putative inner membrane protein
ydbL	STM1644	AAL20562	(1736631..1736954)	0.696	0.050	0.427	0.146	0.613	1.320	0.282	0.970	0.163	0.735	putative periplasmic protein
ynbE	STM1645	AAL20563	(1736962..1737153)	0.571	0.233	0.411	0.097	0.720	0.830	0.075	0.992	0.144	1.195	putative outer membrane lipoprotein
ydbH	STM1646	AAL20564	(1737153..1739789)	0.362	0.045	0.241	0.034	0.666	0.580	0.058	0.512	0.052	0.883	putative periplasmic protein
ldhA	STM1647	AAL20565	1740029..1741018	0.546	0.022	1.272	0.216	2.332	0.831	0.127	1.579	0.060	1.900	fermentative D-lactate dehydrogenase, NAD-dependent
hslJ	STM1648	AAL20566	1741129..1741539	1.740	0.025	1.098	0.084	0.631	1.311	0.199	1.375	0.111	1.049	heat shock protein hslJ
STM1649	STM1649	AAL20567	(1741583..1741738)	6.205	0.709	2.605	0.375	0.420	4.880	1.139	4.158	0.684	0.852	putative cytoplasmic protein
STM1650	STM1650	AAL20568	1741765..1742064	1.560	0.262	0.900	0.099	0.577	1.067	0.114	1.209	0.117	1.133	putative reverse transcriptase
nifJ	STM1651	AAL20569	1742125..1745649	0.642	0.028	0.519	0.043	0.809	1.278	0.057	1.127	0.168	0.882	putative pyruvate-flavodoxin oxidoreductase
ynaF	STM1652	AAL20570	1746131..1746565	5.601	1.965	8.999	1.740	1.607	1.589	0.105	1.724	0.199	1.085	putative universal stress protein
STM1653	STM1653	AAL20571	(1746615..1746953)	0.921	0.064	1.509	0.256	1.638	2.398	0.379	1.441	0.114	0.601	putative membrane transporter of cations
ydaO	STM1654	AAL20572	1747309..1748244					N/A					N/A	putative ATPase
dbpA	STM1655	AAL20573	(1748288..1749661)	0.630	0.038	0.300	0.071	0.475	1.283	0.265	0.817	0.069	0.637	ATP-dependent RNA helicase, stimulated by 23S rRNA
STM1656	STM1656	AAL20574	(1750148..1751131)	0.419	0.037	0.417	0.033	0.994	0.364	0.026	0.400	0.010	1.099	putative Zn transport protein
STM1657	STM1657	AAL20575	(1751277..1752431)	0.282	0.035	0.512	0.069	1.814	0.337	0.013	0.719	0.025	2.134	putative methyl-accepting chemotaxis protein
ydaL	STM1658	AAL20576	(1752842..1753405)	0.531	0.032	0.794	0.099	1.496	0.416	0.026	0.957	0.093	2.299	putative Smr domain
ogt	STM1659	AAL20577	1753663..1754178	1.563	0.095	1.494	0.198	0.956	1.155	0.123	1.674	0.064	1.450	O-6-alkylguanine-DNA/cysteine-protein methyltransferase
fnr	STM1660	AAL20578	1754332..1755126	9.651	1.713	12.468	2.462	1.292	3.063	0.374	3.847	0.472	1.256	transcriptional regulation of aerobic, anaerobic respiration, osmotic balance (CRP family)
ydaA	STM1661	AAL20579	1755277..1756224	3.918	0.246	9.113	0.683	2.326	1.999	0.115	2.676	0.294	1.339	putative universal stress protein
ynaJ	STM1662	AAL20580	(1756279..1756533)	4.848	1.167	2.225	0.486	0.459	4.286	0.759	1.468	0.135	0.343	putative inner membrane protein
ynaI	STM1663	AAL20581	1756772..1757803	0.458	0.031	0.435	0.045	0.950	0.874	0.052	0.722	0.038	0.826	putative integral membrane protein

STM1664	STM1664	AAL20582	(1757889..1758491)	0.634	0.062	0.690	0.047	1.089	0.459	0.031	0.572	0.054	1.246	putative transcriptional regulator
STM1665	STM1665	AAL20583	1758535..1759221	0.618	0.039	0.623	0.123	1.007	0.504	0.024	0.466	0.044	0.925	putative cytoplasmic protein
STM1666	STM1666	pseudogene; in-frame stop following codon 24			0.331	0.032	0.327	0.056	0.989	1.384	0.055	0.435	0.049	0.314
STM1667	STM1667	AAL20584	(1759693..1760250)	0.261	0.081	0.211	0.022	0.810	10.089	1.674	1.990	0.121	0.197	putative thiol peroxidase
STM1668	STM1668	AAL20585	(1760349..1761179)	0.263	0.077	0.149	0.026	0.565	3.581	0.131	0.832	0.025	0.232	putative outer membrane or exported
STM1669	STM1669	AAL20586	(1761200..1763182)	0.181	0.085	0.103	0.029	0.568	2.766	0.080	0.578	0.012	0.209	homology to invasin C of Yersinia; intimin
STM1670	STM1670	AAL20587	(1763257..1764102)	0.171	0.078	0.100	0.029	0.581	10.085	1.653	0.604	0.010	0.060	putative serine/threonine protein kinase
STM1671	STM1671	AAL20588	1764396..1765253	0.144	0.055	0.105	0.013	0.733	1.310	0.091	0.398	0.050	0.303	putative bacterial regulatory helix-turn-helix proteins, araC family
STM1672	STM1672	AAL20589	1765644..1766753	0.395	0.073	0.926	0.061	2.341	5.560	0.276	4.944	0.437	0.889	putative cytoplasmic protein
STM1673	STM1673	AAL20590	(1766967..1767221)	0.451	0.095	0.304	0.078	0.674	1.079	0.109			0.000	putative outer membrane lipoprotein
STM1674	STM1674	AAL20591	(1767332..1767922)	0.363	0.041	0.338	0.018	0.931	0.395	0.032	0.433	0.042	1.096	putative bacterial regulatory helix-turn-helix proteins, araC family
STM1675	STM1675	AAL20592	1768000..1768713	1.324	0.089	0.651	0.045	0.491	0.582	0.085	0.732	0.024	1.257	putative short-chain alcohol dehydrogenase
STM1676	STM1676	AAL20593	(1768804..1769673)	0.725	0.034	0.386	0.052	0.532	3.850	0.676	3.353	0.173	0.871	putative aldo/keto reductase family
STM1677	STM1677	AAL20594	(1769947..1770852)	0.416	0.120	0.268	0.038	0.643	0.307	0.010	0.369	0.029	1.200	putative transcriptional regulator, LysR family
STM1678	STM1678	AAL20595	1770971..1771900	0.398	0.063	0.450	0.094	1.130	0.377	0.081	0.326	0.056	0.865	putative 2'-hydroxyisoflavone reductase
mppA	STM1679	AAL20596	(1771997..1773610)	0.856	0.042	1.957	0.252	2.287	0.833	0.011	1.136	0.128	1.365	periplasmic murein tripeptide transport protein, also negative regulator of mulitple antibiotic resistance
ycjI	STM1680	AAL20597	1773800..1774528	1.032	0.043	1.020	0.084	0.989	2.495	0.293	2.430	0.038	0.974	putative carboxypeptidase
ycjG	STM1681	AAL20598	(1774503..1775468)	1.712	0.181	1.657	0.148	0.968	2.197	0.256	2.137	0.156	0.973	putative chloromuconate cycloisomerase (muconate cycloisomerase)
tpx	STM1682	AAL20599	1775584..1776090	28.682	4.597	10.787	1.731	0.376	18.035	0.137	11.370	0.348	0.630	thiol peroxidase
tyrR	STM1683	AAL20600	(1776180..1777721)					N/A					N/A	transcriptional regulator of aromatic amino acid biosynthesis genes (aroF, aroG, tyrA) and aromatic amino acid transport, has intrinsic ATPase and phosphatase activity (EBP family)
ycjF	STM1684	AAL20601	(1777869..1778930)	0.582	0.018	0.715	0.185	1.228	0.891	0.172	1.196	0.114	1.342	putative inner membrane protein
ycjX	STM1685	AAL20602	(1778927..1780330)	0.731	0.023			0.000	1.515	0.205			0.000	putative ATPase
pspE	STM1686	AAL20603	(1780473..1780787)	0.689	0.057	1.359	0.361	1.973	0.694	0.039	0.707	0.073	1.020	phage shock protein
pspD	STM1687	AAL20604	(1780863..1781081)	0.474	0.066	0.846	0.191	1.786	0.775	0.196	0.978	0.092	1.262	phage shock protein
pspC	STM1688	AAL20605	(1781104..1781463)	0.782	0.064	1.006	0.054	1.286	1.494	0.176	1.903	0.101	1.273	phage shock protein; regulatory gene, activates expression of psp operon with PspB
pspB	STM1689	AAL20606	(1781463..1781687)	0.954	0.041	1.097	0.078	1.150	1.679	0.065	2.112	0.189	1.258	phage shock protein; regulatory gene, activates expression of psp operon with PspC
pspA	STM1690	AAL20607	(1781747..1782415)	1.353	0.137	1.969	0.229	1.456	2.987	0.154	4.010	0.173	1.342	phage shock protein; negative regulatory gene for the psp opreon
pspF	STM1691	AAL20608	1782586..1783566	0.364	0.072	0.480	0.086	1.319	0.261	0.044	0.400	0.044	1.533	transcription activator
sapA	STM1692	AAL20609	1783678..1785327	0.459	0.010	0.685	0.042	1.492	0.332	0.017	0.491	0.122	1.476	ABC superfamily (periplasm), peptide transport protein

sapB	STM1693	AAL20610	1785324..1786289	0.732	0.027	0.344	0.022	0.470	0.600	0.070	0.488	0.038	0.814	ABC superfamily (membrane), peptide transport protein
sapC	STM1694	AAL20611	1786276..1787166	1.387	0.032	0.553	0.104	0.399	1.038	0.228	0.703	0.045	0.677	ABC superfamily (membrane), peptide transport protein
sapD	STM1695	AAL20612	1787166..1788158	1.693	0.102	0.827	0.131	0.488	1.035	0.048	0.643	0.078	0.622	ABC superfamily (atp-binding), peptide transport protein
sapF	STM1696	AAL20613	1788160..1788966	0.986	0.023	0.843	0.084	0.855	0.647	0.052	0.611	0.068	0.944	ABC superfamily (atp-binding), peptide transport protein
STM1697	STM1697	AAL20614	(1789095..1789691)	6.044	0.961	0.616	0.125	0.102	3.887	0.954	1.047	0.077	0.269	putative Diguanylate cyclase/phosphodiesterase domain 2
STM1698	STM1698	AAL20615	(1790157..1791530)	0.445	0.025	0.200	0.019	0.449	0.985	0.023	0.436	0.031	0.443	putative inner membrane protein
STM1698A	STM1698A	AAL20616	1791565..1791744					N/A					N/A	putative e6 protein
ycjE	STM1699	AAL20617	1791719..1792018	1.512	0.287	0.622	0.034	0.411	1.245	0.067	0.845	0.119	0.679	putative cytoplasmic protein
fabI	STM1700	AAL20618	1792136..1792924	16.533	1.428	3.860	0.499	0.233	13.179	0.079	5.996	0.330	0.455	enoyl-[acyl-carrier-protein] reductase (NADH)
yciW	STM1701	AAL20619	1793124..1794104	0.636	0.063	0.328	0.038	0.515	0.815	0.018	0.447	0.033	0.548	putative cytoplasmic protein
rnb	STM1702	AAL20620	1794346..1796280					N/A					N/A	RNase II, mRNA degradation
yciR	STM1703	AAL20621	1796542..1798524	0.279	0.068	0.332	0.048	1.191	0.232	0.048	0.350	0.037	1.506	putative PAS/PAC domain; diguanylate cyclase/phosphodiesterase domain 1; Diguanylate cyclase/phosphodiesterase domain 2
yciT	STM1704	AAL20622	1798912..1799664	1.168	0.103	1.003	0.138	0.858	0.826	0.013	1.012	0.116	1.225	putative regulatory protein, deoR family
osmB	STM1705	AAL20623	1799923..1800141	0.705	0.115	0.604	0.069	0.856	3.864	0.385	3.021	0.428	0.782	osmotically inducible lipoprotein
yciH	STM1706	AAL20624	(1800261..1800587)	0.927	0.062	0.734	0.060	0.792	1.124	0.168	0.766	0.127	0.681	putative translation initiation factor SUI1
pyrF	STM1707	AAL20625	(1800587..1801324)	1.668	0.138	1.030	0.057	0.617	1.740	0.258	1.382	0.397	0.794	orotidine-5'-phosphate decarboxylase
yciM	STM1708	AAL20626	(1801515..1802684)	3.110	0.459	0.979	0.202	0.315	2.464	0.337	1.361	0.081	0.552	putative N-acetylglucosaminyl transferase
yciS	STM1709	AAL20627	(1802691..1802999)	7.440	0.875	0.983	0.206	0.132	5.874	1.277	1.979	0.108	0.337	putative inner membrane protein
pgpB	STM1710	AAL20628	(1803149..1803913)	0.847	0.048	0.524	0.040	0.619	0.844	0.074	0.794	0.064	0.942	phosphatidylglycerophosphate phosphatase B
ribA	STM1711	AAL20629	1804109..1804699	3.017	0.040	1.149	0.217	0.381	1.819	0.163	1.238	0.088	0.681	GTP cyclohydrolase II
acnA	STM1712	AAL20630	(1804755..1807430)	2.027	0.542	1.637	0.287	0.807	1.575	0.177	2.446	0.198	1.553	aconitate hydratase 1
cysB	STM1713	AAL20631	(1808407..1809381)	1.782	0.047	1.517	0.058	0.852	1.339	0.079	1.112	0.039	0.831	transcriptional regulator for cysteine regulon (LysR familiy)
topA	STM1714	AAL20632	(1809792..1812389)	2.878	0.268	1.929	0.201	0.670	2.067	0.260	1.737	0.067	0.840	DNA topoisomerase type I, omega protein
yciN	STM1715	AAL20633	1812792..1813043	1.730	0.235	1.157	0.158	0.669	0.933	0.088	0.757	0.025	0.811	putative cytoplasmic protein
sohB	STM1716	AAL20634	(1813085..1814131)	1.337	0.094	1.226	0.154	0.917	1.111	0.045	1.230	0.068	1.107	putative peptidase
yciK	STM1717	AAL20635	1814369..1815130	2.548	0.337	3.824	0.641	1.501	0.989	0.167	1.905	0.280	1.926	putative oxoacyl-(acyl carrier protein) reductase
btuR	STM1718	AAL20636	1815127..1815717	2.410	0.421	3.866	0.586	1.604	1.022	0.028	1.294	0.204	1.266	cob(I)alamin and cobinamide adenolsyltransferase
yciL	STM1719	AAL20637	(1815804..1816679)	3.371	0.106	1.947	0.283	0.577	2.338	0.274	0.978	0.059	0.418	putative ribosomal large subunit pseudouridine synthase
yciO	STM1720	AAL20638	(1816780..1817400)	1.436	0.086	1.508	0.195	1.049	0.968	0.023	0.872	0.067	0.901	putative translation factor

trpH	STM1721	AAL20639	(1817408..1818289)	1.301	0.126	1.116	0.093	0.858	0.915	0.123	0.908	0.168	0.992	trpR controlled transcriptional unit in the 5' upstream region of the trp operon
trpL	STM1722	AAL20640	1818411..1818455	2.628	0.772			0.000	6.131				0.000	trp operon leader peptide
trpE	STM1723	AAL20641	1818550..1820112	0.182	0.070	0.189	0.038	1.038	0.098	0.031	0.332	0.142	3.388	anthranilate synthase, onent I
trpD	STM1724	AAL20642	1820112..1821707	0.495	0.186	0.414	0.089	0.836	0.359	0.144	0.617	0.267	1.717	anthranilate synthase, onent II, bifunctional: glutamine amidotransferase and phosphoribosylanthranilate transferase
trpC	STM1725	AAL20643	1821711..1823069	1.012	0.151	0.548	0.077	0.541	0.687	0.082	0.666	0.118	0.969	bifunctional: N-(5-phosphoribosyl)anthranilate isomerase; indole-3-glycerolphosphate synthetase
trpB	STM1726	AAL20644	1823079..1824272	0.680	0.046	0.670	0.104	0.985	0.663	0.057	0.699	0.109	1.054	tryptophan synthase, beta protein
trpA	STM1727	AAL20645	1824272..1825078	0.742	0.035	0.688	0.076	0.927	1.050	0.076	0.793	0.082	0.756	tryptophan synthase, alpha protein
yciG	STM1728	AAL20646	1825558..1825740	0.285	0.069	0.398	0.128	1.398	28.499	0.867	13.094	0.976	0.459	putative cytoplasmic protein
yciF	STM1729	AAL20647	1825830..1826333	0.156	0.072	0.303	0.035	1.940	22.369	3.761	14.910	1.380	0.667	putative cytoplasmic protein
yciE	STM1730	AAL20648	1826407..1826913	0.294	0.122	0.448	0.148	1.524	20.936	4.094	22.462	0.808	1.073	putative cytoplasmic protein
STM1731	STM1731	AAL20649	1826933..1827811	0.262	0.082	2.099	0.199	8.012	13.756	2.212	15.771	1.704	1.146	putative catalase
ompW	STM1732	AAL20650	(1827893..1828531)	0.483	0.083	31.967		66.193	0.926	0.212	1.044	0.047	1.127	outer membrane protein W; colicin S4 receptor; putative transporter
STM1733	STM1733	AAL20651	1828869..1829273	1.016	0.104	2.382	0.301	2.345	0.788	0.055	1.762	0.162	2.235	putative ferredoxin
yciC	STM1734	AAL20652	1829299..1830042	1.866	0.074	1.555	0.204	0.834	3.306	0.016	2.087	0.152	0.631	putative inner membrane protein
yciB	STM1735	AAL20653	1830099..1830638	2.146	0.191	1.272	0.072	0.593	6.178	0.778	2.721	0.315	0.440	putative intracellular septation protein
yciA	STM1736	AAL20654	1830799..1831200	2.542	0.314	1.154	0.062	0.454	1.683	0.080	0.908	0.037	0.539	putative Acyl-CoA hydrolase
tonB	STM1737	AAL20655	(1831260..1831988)	0.429	0.032	0.444	0.040	1.036	0.288	0.056	0.506	0.028	1.759	energy transducer; uptake of iron, cyanocobalimin; sensitivity to phages, colicins
yciI	STM1738	AAL20656	1832212..1832508	3.369	1.138	2.002	0.389	0.594	0.691	0.027	0.590	0.049	0.853	putative cytoplasmic protein
cls	STM1739	AAL20657	1832868..1834328	0.839	0.037	0.586	0.069	0.698	0.516	0.035	0.490	0.032	0.951	cardiolipin synthase
yciU	STM1740	AAL20658	1834362..1834691	1.730	0.132			0.000	1.644	0.055			0.000	putative cytoplasmic protein
STM1741	STM1741	AAL20659	(1834739..1835575)	3.091	0.260	1.052	0.173	0.340	2.861	0.465	1.515	0.047	0.530	putative voltage-gated potassium channel
oppF	STM1742	AAL20660	(1835623..1836627)	9.059	1.709	3.548	0.271	0.392	8.937	1.747	4.373	0.378	0.489	ABC superfamily (atp-binding), oligopeptide transport protein
oppD	STM1743	AAL20661	(1836624..1837631)	5.473	0.936	5.968	1.124	1.090	5.883	0.448	3.934	0.368	0.669	ABC superfamily (atp-binding), oligopeptide transport protein
oppC	STM1744	AAL20662	(1837643..1838551)	3.188	0.663	3.338	0.142	1.047	3.513	0.526	2.896	0.350	0.824	ABC superfamily (membrane), oligopeptide transport protein
oppB	STM1745	AAL20663	(1838566..1839486)	6.675	1.128	4.210	0.196	0.631	8.499	0.800	4.701	0.521	0.553	ABC superfamily (membrane), oligopeptide transport protein
oppA	STM1746	AAL20664	(1839608..1841356)	6.650	1.233	9.262	1.144	1.393	7.004	0.602	7.667	0.387	1.095	ABC superfamily (periplasm), oligopeptide transport protein with chaperone properties
STM1747	STM1747	AAL20665	1841307..1841621	2.326	0.474	4.216	0.452	1.812	1.688	0.108	2.064	0.400	1.223	putative inner membrane protein

ychE	STM1748	AAL20666	(1842004..1842651)	0.884	0.068	0.447	0.072	0.506	1.351	0.345	0.369	0.033	0.273	putative integral membrane proteins of the MarC family
adhE	STM1749	AAL20667	1843128..1845806	0.499	0.022	3.023	0.612	6.053	0.651	0.068	1.691	0.154	2.599	iron-dependent alcohol dehydrogenase of the multifunctional alcohol dehydrogenase AdhE
tdk	STM1750	AAL20668	(1846003..1846620)	3.254	0.207	1.403	0.119	0.431	3.839	0.425	2.728	0.083	0.711	thymidine kinase
hns	STM1751	AAL20669	1847283..1847696	21.505	3.770	23.476	1.942	1.092	1.004	0.191	0.792	0.072	0.788	DNA-binding protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator
galU	STM1752	AAL20670	(1847828..1848736)	0.525	0.565	3.728	0.391	7.100	2.802		3.004	0.141	1.072	glucose-1-phosphate uridylyltransferase
hnr	STM1753	AAL20671	(1848939..1849952)	0.941	0.047	1.253	0.290	1.331	0.856	0.139	1.006	0.121	1.176	Response regulator in protein turnover: mouse virulence
ychK	STM1754	AAL20672	(1850043..1850948)	2.726	0.096	1.609	0.164	0.590	1.647	0.033	1.729	0.214	1.050	putative phosphoesterase
ychJ	STM1755	AAL20673	1851059..1851517	1.326	0.047	1.330	0.118	1.003	0.848	0.064	1.042	0.036	1.229	putative cytoplasmic protein
purU	STM1756	AAL20674	1851568..1852410	1.635	0.136	2.379	0.373	1.455	1.030	0.096	1.715	0.073	1.666	formyltetrahydrofolate hydrolase
tyrT	STM1757						N/A					N/A		
tyrV	STM1759						N/A					N/A		
STM1760	STM1760	AAL20675	(1853726..1855255)	0.329	0.043	0.461	0.099	1.400	0.227	0.018	0.288	0.015	1.266	putative TPR repeat protein
narI	STM1761	AAL20676	(1855497..1856174)	0.282	0.056	4.729	0.586	16.741	0.188	0.017	0.700	0.049	3.731	nitrate reductase 1, cytochrome b(NR), gamma subunit
narJ	STM1762	AAL20677	(1856174..1856884)	0.254	0.111	7.624	0.965	30.043	0.124	0.002	0.598	0.041	4.835	nitrate reductase 1, delta subunit, chaperone required for molybdenum cofactor assembly in nitrate reductase 1
narH	STM1763	AAL20678	(1856881..1858416)	0.151	0.082	5.684	0.430	37.717	0.167	0.115	0.669	0.027	4.004	nitrate reductase 1, FeS (beta) subunit
narG	STM1764	AAL20679	(1858413..1862156)					N/A					N/A	nitrate reductase 1, alpha subunit
narK	STM1765	AAL20680	(1862544..1863941)	0.176	0.098	1.006		5.718	0.177	0.016	0.451		2.549	MFS superfamily, nitrite extrusion protein
narX	STM1766	AAL20681	1864282..1866078	0.887	0.043	0.444	0.043	0.501	0.728	0.048	0.960	0.037	1.318	sensory histidine kinase in two onent regulatory system with NarL, senses nitrate/nitrite, regulates anaerobic respiration and fermentation
narL	STM1767	AAL20682	1866071..1866721	0.714	0.031	0.883	0.168	1.236	0.702	0.029	1.489	0.088	2.120	response regulator in two-onent regulatory system with NarX (or NarQ), regulates anaerobic respiration and fermentation (LuxR/UhpA familiy)
ychP	STM1768	AAL20683	(1866722..1868146)	0.529	0.053			0.000	1.080	0.103			0.000	putative invasin
ychN	STM1769	AAL20684	1868323..1868676	1.865	0.332	1.259	0.209	0.675	1.423	0.085	1.106	0.026	0.778	putative ACR involved in intracellular sulfur reduction
chaB	STM1770	AAL20685	(1868756..1868986)	0.784	0.086	0.668	0.121	0.852	1.282	0.002	0.766	0.132	0.597	cation transport regulator
chaA	STM1771	AAL20686	1869253..1870353	2.523	0.120	0.790	0.082	0.313	7.322	0.736	1.764	0.127	0.241	CaCA family, sodium-calcium/proton antiporter
kdsA	STM1772	AAL20687	(1870407..1871261)	11.664	0.163	5.118	0.499	0.439	4.958	1.881	4.185	0.346	0.844	3-deoxy-D-manno-octulosonic acid 8-P synthetase
ychA	STM1773	AAL20688	(1871299..1872108)	3.876	0.099	1.463	0.163	0.378	2.637	0.252	1.417	0.068	0.537	putative transcriptional regulator
sirC	STM1774	AAL20689	(1872112..1872501)	1.457	0.090	0.644	0.048	0.442	1.006	0.125	0.587	0.082	0.583	Regulation of invasion genes
hemK	STM1775	AAL20690	(1872498..1873331)	1.028	0.028	0.837	0.100	0.815	0.761	0.050	0.539	0.038	0.708	putative protoporphyrinogen oxidase
prfA	STM1776	AAL20691	(1873331..1874413)	1.845	0.231	2.212	0.204	1.199	1.384	0.058	1.427	0.183	1.031	peptide chain release factor RF-1

hemA	STM1777	AAL20692	(1874454..1875710)	2.593	0.239	1.873	0.186	0.723	1.423	0.274	1.671	0.147	1.175	glutamyl tRNA reductase
lolB	STM1778	AAL20693	1876024..1876647	0.830	0.030	1.767	0.316	2.130	0.722	0.031	1.288	0.161	1.784	outer membrane lipoprotein
ipk	STM1779	AAL20694	1876644..1877495	4.326	0.378	4.456	0.494	1.030	1.878	0.239	2.083	0.226	1.109	isopentenyl monophosphate kinase
prsA	STM1780	AAL20695	1877761..1878708	15.066	0.380	20.531	1.449	1.363	6.547	0.254	7.135	0.400	1.090	phosphoribosylpyrophosphate synthetase
ychM	STM1781	AAL20696	1878857..1880518	1.205	0.110	1.224	0.117	1.016	0.796	0.065	0.626	0.034	0.787	putative SulP family transport protein
ychH	STM1782	AAL20697	(1880563..1880841)	4.998	0.161	3.861	0.185	0.773	0.473	0.033	0.458		0.968	putative inner membrane protein
pth	STM1783	AAL20698	1881093..1881701	0.908	0.032	1.296	0.127	1.428	0.394	0.018	0.595	0.069	1.510	peptidyl-tRNA hydrolase
ychF	STM1784	AAL20699	1881818..1882909	2.119	0.145	2.763	0.111	1.304	1.710	0.075	1.619	0.080	0.947	putative GTP-binding protein
STM1785	STM1785	AAL20700	(1883068..1884333)	0.465	0.041	0.306	0.049	0.658	1.159	0.066	0.588	0.079	0.507	putative cytoplasmic protein
STM1786	STM1786	AAL20701	1884828..1885946	0.187	0.083	0.168	0.033	0.901	0.098	0.028	0.244	0.017	2.490	hydrogenase-1 small subunit
STM1787	STM1787	AAL20702	1885943..1887736	0.178	0.079	0.163	0.015	0.912	0.076	0.006	0.208	0.018	2.756	hydrogenase-1 large subunit
STM1788	STM1788	AAL20703	1887755..1888486	0.161	0.101	0.167	0.035	1.033	0.084	0.021	0.175	0.024	2.101	putative Ni/Fe-hydrogenase 1 b-type cytochrome subunit
STM1789	STM1789	AAL20704	1888483..1889079	0.192	0.086	0.121	0.010	0.628	0.114	0.030	0.177	0.008	1.553	putative hydrogenase maturation protease
STM1790	STM1790	AAL20705	1889069..1889473	0.230	0.084	0.191	0.041	0.834	0.133	0.050	0.219	0.032	1.641	putative thiol-disulfide isomerase and thioredoxins
STM1791	STM1791	AAL20706	1889470..1890318	0.209	0.099	0.201	0.039	0.961	0.111	0.037	0.202	0.013	1.828	putative hydrogenase-1 protein
STM1792	STM1792	AAL20707	1890393..1891937	0.265	0.110	0.586	0.100	2.217	0.159	0.034	0.223	0.011	1.403	putative cytochrome oxidase, subunit I
STM1793	STM1793	AAL20708	1891949..1893085	0.443	0.050	0.635	0.085	1.431	0.197	0.014	0.249	0.016	1.267	putative cytochrome oxidase, subunit II
STM1794	STM1794	AAL20709	1893098..1893187	2.014	0.680	1.390	0.048	0.690	0.898	0.362	0.999	0.727	1.113	putative periplasmic protein
STM1795	STM1795	AAL20710	1893531..1894856			15.337	2.501	N/A	3.427	0.280	2.984	0.152	0.871	putative Homolog of glutamic dehyrogenase
treA	STM1796	AAL20711	1895070..1896782	1.445	0.362	1.630	0.238	1.128	1.062	0.065	2.497	0.134	2.350	trehalase, periplasmic
ymgE	STM1797	AAL20712	(1896845..1897099)	0.790	0.111	0.437	0.046	0.553	1.514	0.018	0.892	0.051	0.589	putative transglycosylase-associated protein
ycgR	STM1798	AAL20713	1897268..1898002	0.641	0.025	1.489	0.173	2.325	0.194	0.018	0.697	0.032	3.589	putative inner membrane protein
emtA	STM1799	AAL20714	(1898016..1898627)	0.742	0.075	0.840	0.108	1.132	0.545	0.059	0.468	0.039	0.859	membrane-bound lytic murein transglycosylase E
ycgQ	STM1800	AAL20715	1898798..1899712	1.370	0.055	0.783	0.035	0.572	0.768	0.117	0.999	0.062	1.300	putative homologs of microcin C7 resistance protein MccF
ycgO	STM1801	AAL20716	1899809..1901542	2.895	0.452	0.658	0.080	0.227	1.216	0.333	0.777	0.051	0.639	putative A1 family, Na:H transport protein
dadX	STM1802	AAL20717	(1901605..1902675)	11.473	5.345	3.105	0.408	0.271	2.067	0.309	2.364	0.058	1.144	alanine racemase 2, catabolic
dadA	STM1803	AAL20718	(1902689..1903987)			8.243	1.258	N/A	3.995	1.320	6.159	0.460	1.542	D-amino acid dehydrogenase subunit
ycgB	STM1804	AAL20719	1904310..1905842	0.664	0.081	0.714	0.106	1.074	0.461	0.031	0.968	0.027	2.099	putative cytoplasmic protein
fadR	STM1805	AAL20720	(1905889..1906608)	1.851	0.087	1.953	0.334	1.055	0.807	0.105	0.903	0.024	1.120	negative regulator for fad regulon and positive activator of fabA (GntR family)
nhaB	STM1806	AAL20721	1906828..1908372	1.525	0.062	1.689	0.107	1.107	0.855	0.010	0.946	0.058	1.106	NhaB family of transport protein, Na+/H+ antiporter, regulator of intracellular pH
dsbB	STM1807	AAL20722	1908514..1909044			0.859	0.141	N/A	1.866		0.936	0.027	0.502	putative disulfide oxidoreductase, reoxidizes DsbA protein

STM1808	STM1808	AAL20723	1909153..1909494	0.738	0.051	1.119	0.202	1.516	0.515	0.032	0.760	0.028	1.476	putative cytoplasmic protein
STM1809	STM1809	AAL20724	(1909566..1909739)	1.243	0.156	2.059	0.221	1.657	0.744	0.082	0.836	0.070	1.124	putative cytoplasmic protein
STM1810	STM1810	AAL20725	(1909931..1910068)	0.541	0.207	0.426	0.058	0.787	0.751	0.169	0.560	0.359	0.746	putative cytoplasmic protein
ycgN	STM1811	AAL20726	(1910420..1910881)	1.290	0.078	0.832	0.065	0.645	1.319	0.287	0.910	0.062	0.689	putative cytoplasmic protein
ycgM	STM1812	AAL20727	(1910959..1911618)	1.366	0.189	1.451	0.255	1.063	1.562	0.088	1.866	0.090	1.195	putative Fumarylacetoacetate (FAA) hydrolase family
ycgL	STM1813	AAL20728	(1911668..1912000)	1.450	0.202	2.100	0.285	1.449	1.320	0.167	1.809	0.053	1.370	putative cytoplasmic protein
minC	STM1814	AAL20729	1912087..1912794	5.711	0.823	5.833	0.739	1.021	4.906	0.003	4.884	0.712	0.996	cell division inhibitor; activated MinC inhibits FtsZ ring formation
minD	STM1815	AAL20730	1912818..1913630	10.722	1.364	15.693	2.607	1.464	6.642	0.185	11.656	0.232	1.755	cell division inhibitor, a membrane ATPase, activates MinC, directs division apparatus to middle of cell by oscillating from one half to other
minE	STM1816	AAL20731	1913634..1913900	5.217	1.059	6.120	0.914	1.173	3.637	0.440	4.065	0.258	1.118	cell division topological specificity factor, reverses MinC inhibition of FtsZ ring formation
rnd	STM1817	AAL20732	(1914022..1915149)	2.283	0.125	0.998	0.070	0.437	1.965	0.274	1.004	0.043	0.511	RNase D, processes tRNA precursor
fadD	STM1818	AAL20733	(1915222..1916907)	1.473	0.212	2.923	0.303	1.984	0.483	0.021	0.800	0.049	1.657	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)
slp	STM1819	AAL20734	(1917112..1917693)	1.074	0.071	1.324	0.124	1.233	0.765	0.063	0.554	0.065	0.724	putative outer membrane protein
yeaZ	STM1820	AAL20735	(1917765..1918460)	1.602	0.044	2.026	0.365	1.265	0.991	0.107	0.703	0.068	0.710	putative molecular chaperone
yoaA	STM1821	AAL20736	(1918518..1920428)	1.155	0.128	0.714	0.135	0.618	0.823	0.149	0.659	0.058	0.801	putative DNA helicase
yoaB	STM1822	AAL20737	1920559..1920903	5.799	1.169	1.484	0.173	0.256	1.933	0.073	0.812	0.076	0.420	putative translation initiation inhibitor
yoaH	STM1823	AAL20738	(1920909..1921088)	2.375	0.304	0.818	0.112	0.344	1.200	0.013	0.579	0.087	0.482	putative cytoplasmic protein
pabB	STM1824	AAL20739	1921169..1922533	1.365	0.140	1.057	0.176	0.774	1.063	0.287	1.434	0.122	1.349	p-aminobenzoate synthetase, onent I
yeaB	STM1825	AAL20740	1922537..1923115	0.885	0.074	1.355	0.120	1.532	0.672	0.080	1.432	0.044	2.132	putative NTP pyrophosphohydrolase
sdaA	STM1826	AAL20741	1923379..1924743	3.927	0.327	3.826	0.475	0.974	3.384	0.067	1.974	0.260	0.583	L-serine deaminase I/L-threonine deaminase I
STM1827		AAL20742	1924779..1926482	0.440	0.037	0.246	0.044	0.559	0.336	0.021	0.316	0.013	0.940	putative diguanylate cyclase/phosphodiesterase
yoaE	STM1828	AAL20743	(1926504..1928060)	0.888	0.034	0.820	0.049	0.924	1.374	0.194	1.818	0.082	1.324	putative inner membrane protein
STM1829		AAL20744	(1928048..1928383)	0.922	0.088	1.166	0.142	1.265	1.570	0.225	1.655	0.061	1.054	putative cytoplasmic protein
manX	STM1830	AAL20745	1928533..1929501	3.895	0.522	14.804	2.283	3.800	4.953	0.311	6.547	0.332	1.322	Sugar Specific PTS family, mannose-specific enzyme IIAB
manY	STM1831	AAL20746	1929554..1930354	3.159	0.309	20.686	3.305	6.548	4.146	0.101	5.859	0.213	1.413	Sugar Specific PTS family, mannose-specific enzyme IIC
manZ	STM1832	AAL20747	1930358..1931218	2.982	0.512	10.556	1.598	3.540	5.300	0.499	3.313	0.151	0.625	Sugar Specific PTS family, mannose-specific enzyme IID
STM1833	STM1833	AAL20748	1931276..1931746	0.552	0.035	1.377	0.073	2.494	1.101	0.146	1.030	0.063	0.936	putative inner membrane protein
yebN	STM1834	AAL20749	1932090..1932710	0.689	0.051	0.506	0.022	0.734	1.647	0.326	0.563	0.027	0.342	putative YebN family transport protein
rrmA	STM1835	AAL20750	(1932707..1933516)	1.111	0.082	0.408	0.040	0.367	1.237	0.155	0.602	0.042	0.487	23S rRNA m1G745 methyltransferase
STM1836	STM1836	AAL20751	(1933582..1935327)	0.715	0.031	0.507	0.099	0.709	0.864	0.018	0.801	0.050	0.927	putative penicillin-binding protein-3

cspC	STM1837	AAL20752	(1935547..1935756)	121.067	21.344	28.310	4.307	0.234	72.530	3.307	21.663	2.423	0.299	cold shock protein, multicopy suppresses mukB mutants, putative regulator
yobF	STM1838	AAL20753	(1935769..1935912)	148.009	11.258	24.519	2.953	0.166	88.950	11.155	29.495	1.900	0.332	putative cytoplasmic protein
STM1839	STM1839	AAL20754	(1936561..1936848)	3.643	0.243	1.618	0.137	0.444	21.189	4.984	11.308	1.080	0.534	putative periplasmic or exported protein
yobG	STM1840	AAL20755	(1936919..1937062)	3.014	0.515	1.207	0.216	0.400	22.525	3.243	9.485		0.421	putative inner membrane protein
STM1841	STM1841	AAL20756	1937220..1937459	0.988	0.142	1.601	0.180	1.620	5.107	0.861	4.789	0.990	0.938	putative outer membrane or exported
kdgR	STM1842	AAL20757	(1937671..1938462)	3.755	0.269	3.975	0.738	1.059	2.276	0.071	3.001	0.212	1.319	putative transcriptional repressor (IclR family)
STM1843	STM1843	AAL20758	1938638..1940011	0.583	0.067	0.318	0.040	0.545	1.200	0.199	0.653	0.043	0.545	putative transport protein
htpX	STM1844	AAL20759	(1940059..1940940)	3.622	0.386	3.239	0.378	0.894	6.423	0.837	5.208	0.291	0.811	heat shock protein, integral membrane protein
prc	STM1845	AAL20760	(1941134..1943182)	1.621	0.024	2.433	0.428	1.501	1.627	0.191	1.340	0.070	0.824	carboxy-terminal protease for penicillin-binding protein 3
proQ	STM1846	AAL20761	(1943202..1943888)	12.372	1.875			0.000	7.631	0.485			0.000	activator of proP
yebR	STM1847	AAL20762	(1943986..1944570)	5.922	0.988	2.264	0.192	0.382	3.471	1.025	3.656	0.111	1.053	putative GAF domain-containing protein
yebS	STM1848	AAL20763	1944612..1945895	0.957	0.062	0.377	0.063	0.394	1.762	0.237	0.997	0.050	0.566	putative inner membrane protein
STM1849	STM1849	AAL20764	1945858..1948497	0.544	0.034	0.415	0.044	0.763	1.100	0.109	1.057	0.019	0.961	putative inner membrane protein
yebU	STM1850	AAL20765	1948575..1950014	0.354	0.077	0.322	0.059	0.909	0.454	0.032	0.483	0.030	1.066	paral putative rRNA methyltransferase
STM1851	STM1851	AAL20766	1950129..1950368	0.548	0.067	0.255	0.053	0.465	1.652	0.125	1.183	0.136	0.716	putative cytoplasmic protein
yebW	STM1852	AAL20767	1950479..1950670	0.560	0.059	0.274	0.021	0.489	1.197	0.190	0.811	0.083	0.678	putative inner membrane lipoprotein
prpA	STM1853	AAL20768	(1950689..1951339)	0.273	0.043	0.107	0.034	0.393	4.584	0.342	2.372	0.097	0.518	serine/threonine protein phosphatase
STM1854	STM1854	AAL20769	(1951563..1951727)	0.545	0.163	0.201	0.036	0.369	27.077	3.729	7.090	0.239	0.262	putative inner membrane protein
sopE2	STM1855	AAL20770	(1952012..1952734)	0.553	0.099	0.348	0.022	0.630	6.183	0.839	2.253	0.220	0.364	TypeIII-secreted protein effector: invasion-associated protein
STM1856	STM1856	AAL20771	1953418..1953813	0.281	0.044	0.201	0.050	0.717	0.771	0.047	0.504	0.068	0.654	putative cytoplasmic protein
STM1857	STM1857	AAL20772	(1955007..1955426)	0.614	0.035	1.039	0.098	1.693	0.530	0.071	1.021	0.042	1.926	putative acetyltransferase
STM1858	STM1858	AAL20773	1955796..1956065	0.267	0.079	0.250	0.009	0.936	0.482	0.226	0.629	0.107	1.305	putative cytoplasmic protein
STM1859	STM1859	AAL20774	1956231..1956371	0.409	0.100	0.390	0.111	0.952	1.296	0.440	1.196	0.052	0.923	putative cytoplasmic protein
STM1860	STM1860	AAL20775	(1956854..1957711)	0.149	0.068	0.111	0.014	0.743	0.126	0.015	0.225	0.022	1.786	putative transposase
STM1861	STM1861	AAL20776	1957835..1958203					N/A					N/A	putative cytoplasmic protein
pagO	STM1862	AAL20777	1959507..1960421	0.292	0.079	0.171	0.026	0.586	18.721	2.551	6.768	0.988	0.362	PhoPQ-activated gene; predicted integral membrane protein
STM1863	STM1863	AAL20778	1960554..1960712	0.355	0.080	0.433	0.140	1.219	24.940	4.184	13.014	1.361	0.522	putative inner membrane protein
STM1864	STM1864	AAL20779	1960722..1961336	0.164	0.065	0.095	0.011	0.579	23.045	4.196	18.012	1.087	0.782	putative inner membrane protein
STM1865	STM1865	AAL20780	(1961663..1961788)	0.329	0.153	0.421	0.118	1.279	2.092	0.118	1.675	0.243	0.801	putative cytoplasmic protein
STM1866	pseudogene; in-frame stop following codon 23				0.618	0.061	0.483	0.054	0.781	7.959	0.955	4.118	0.209	0.517
pagK	STM1867	AAL20781	1963179..1963379	0.512	0.149	0.290	0.043	0.567	14.464	1.875	6.121	0.394	0.423	PhoPQ-activated gene
mig-3	STM1868	AAL20782	(1963476..1964357)	0.237	0.074	0.147	0.044	0.620	1.168	0.035	0.592	0.073	0.507	Homology to phage-tail assembly proteins
STM1868A	STM1868A	AAL20783	1965083..1965250					N/A					N/A	lytic enzyme
STM1869	STM1869	AAL20784	(1965507..1966040)	0.152	0.101	0.124	0.014	0.814	0.158	0.023	0.337	0.048	2.132	Homology to phage-tail assembly proteins

STM1869A	STM1869A	AAL20785	(1966094..1966381)					N/A					N/A	hypothetical protein
STM1870	STM1870	AAL20786	1966514..1967008	0.169	0.097	0.122	0.030	0.720	0.127	0.012	0.154	0.038	1.215	Homology to recE (exoVIII) in E. coli
STM1871	STM1871	AAL20787	1967026..1967922	0.208	0.041	0.187	0.016	0.899	0.118	0.026	0.221	0.018	1.872	putative phage integrase protein
STM1872	STM1872	AAL20788	(1968119..1968238)	2.673	0.921	0.866	0.137	0.324	4.378	1.544	1.238	0.713	0.283	putative cytoplasmic protein
STM1873	STM1873	AAL20789	(1968296..1968649)	0.767	0.088	0.930	0.117	1.213	0.530	0.032	0.820	0.107	1.548	putative periplasmic or exported protein
STM1874	STM1874	AAL20790	(1968666..1969541)	1.489	0.043	1.863	0.314	1.252	0.772	0.082	0.938	0.026	1.214	putative inner membrane protein
yobA	STM1875	AAL20791	(1969542..1969916)	1.507	0.043	1.969	0.172	1.307	0.743	0.086	1.120	0.056	1.508	putative homolog of Cu resistance protein CopC
holE	STM1876	AAL20792	1970054..1970284	0.893	0.076	0.691	0.116	0.774	0.799	0.307	0.444	0.073	0.556	DNA polymerase III, theta subunit
STM1877	STM1877	AAL20793	1970392..1971048	1.016	0.111	0.541	0.072	0.533	1.043	0.055	0.918	0.074	0.880	putative amidohydrolase
exoX	STM1878	AAL20794	1971072..1971770	1.858	0.153	1.420	0.089	0.764	1.268	0.055	1.351	0.115	1.065	DNA exonuclease X, degrades ss and ds DNA with 3'-5' polarity
ptrB	STM1879	AAL20795	(1971805..1973856)	0.798	0.010	0.636	0.101	0.796	1.024	0.082	0.924	0.010	0.902	protease II
yebE	STM1880	AAL20796	(1974069..1974728)	1.629	0.308	0.933	0.148	0.573	6.120	0.678	1.686	0.109	0.276	putative inner membrane protein
yebF	STM1881	AAL20797	(1974822..1975175)	0.936	0.062	0.465	0.081	0.497	2.413	0.065	1.559	0.254	0.646	putative periplasmic protein
yebG	STM1882	AAL20798	(1975243..1975533)	0.829	0.028	0.694	0.033	0.837	1.578	0.068	0.819	0.068	0.519	DNA damage-inducible gene in SOS regulon, dependent on cyclic AMP and H-NS
purT	STM1883	AAL20799	1975664..1976842	0.414	0.108	0.442	0.018	1.068	0.291	0.021	0.417	0.031	1.434	phosphoribosylglycinamide formyltransferase 2
eda	STM1884	AAL20800	(1976942..1977583)	2.885	0.366	3.149	0.339	1.092	1.872	0.424	3.310	0.236	1.768	multifunctional:2-keto-3-deoxygluconate 6-phosphate aldolase; 2-keto-4-hydroxyglutarate aldolase; oxaloacetate decarboxylase
edd	STM1885	AAL20801	(1977621..1979432)	0.631	0.238	0.234	0.037	0.371	0.531	0.330	0.569	0.096	1.071	6-phosphogluconate dehydratase
zwf	STM1886	AAL20802	(1979667..1981142)	0.851	0.094	2.961	0.286	3.481	0.500	0.035	1.310	0.100	2.622	glucose-6-phosphate dehydrogenase
yebK	STM1887	AAL20803	1981484..1982353	0.528	0.032	1.770	0.298	3.354	0.237	0.020	0.635	0.044	2.681	putative transcriptional regulator
pykA	STM1888	AAL20804	1982477..1983919	1.615	0.180	11.604	1.160	7.183	1.068	0.033	3.647	0.278	3.414	pyruvate kinase II, glucose stimulated
msbB	STM1889	AAL20805	(1983992..1984963)	1.571	0.050	1.183	0.213	0.753	1.646	0.159	0.986	0.085	0.599	myristoyl transferase in lipid A biosynthesis, suppressor of htrB (lpxL)
yebA	STM1890	AAL20806	(1985080..1986399)	1.148	0.082	3.316	0.211	2.888	1.096	0.014	1.290	0.122	1.176	putative Peptidase
znuA	STM1891	AAL20807	(1986415..1987416)	1.320	0.149	2.576	0.517	1.952	0.589	0.046	0.725	0.056	1.230	ABC superfamily (bind_prot) high affinity Zn transport protein
znuC	STM1892	AAL20808	1987387..1988193	0.849	0.039	0.795	0.057	0.937	0.343	0.016	0.523	0.033	1.527	ABC superfamily (atp_bind) high affinity Zn transport protein
zunB	STM1893	AAL20809	1988190..1988975	0.648	0.020	0.528	0.073	0.815	0.411	0.005	0.468	0.058	1.140	ABC superfamily (atp_bind) high affinity Zn transport protein
ruvB	STM1894	AAL20810	(1989054..1990064)	3.015	0.731	1.375	0.283	0.456	3.764	0.858	2.494	0.216	0.663	Holliday junction helicase, subunit B
ruvA	STM1895	AAL20811	(1990073..1990684)	1.221	0.188	1.025	0.179	0.840	1.799	0.171	1.508	0.181	0.838	Holliday junction helicase subunit A
STM1896	STM1896	AAL20812	1991104..1992000	0.216	0.100	0.166	0.006	0.769	0.378	0.049	0.296	0.020	0.783	putative cytoplasmic protein
yebB	STM1897	AAL20813	1992627..1993226	0.443	0.052	0.589	0.037	1.328	0.717	0.052	0.661	0.046	0.921	putative periplasmic protein
ruvC	STM1898	AAL20814	(1993228..1993749)	2.335	0.259	2.674	0.166	1.145	1.366	0.167	1.587	0.070	1.162	Holliday junction nuclease
yebC	STM1899	AAL20815	(1993786..1994526)	4.648	0.244	5.400	0.249	1.162	2.972	0.287	3.825	0.186	1.287	putative cytoplasmic protein

ntpA	STM1900	AAL20816	(1994556..1995008)	3.687	0.169	3.540	0.567	0.960	3.012	0.506	2.947	0.226	0.978	dATP pyrophosphohydrolase
aspS	STM1901	AAL20817	(1995111..1996883)	3.083	0.107	6.457	0.253	2.094	3.141	0.119	4.985	0.614	1.587	aspartate tRNA synthetase
yecD	STM1902	AAL20818	1997208..1997774	1.056	0.081	0.872	0.170	0.825	1.012	0.084	1.069	0.093	1.056	putative isochorismatase
yecE	STM1903	AAL20819	1997771..1998589	0.811	0.023	0.800	0.078	0.986	0.776	0.098	1.146	0.112	1.478	putative cytoplasmic protein
yecN	STM1904	AAL20820	1998642..1999037	3.716	0.381	1.255	0.137	0.338	2.569	0.482	1.661	0.202	0.646	putative inner membrane protein
yecO	STM1905	AAL20821	1999078..1999821	1.825	0.127	1.375	0.174	0.754	2.064	0.138	1.447	0.041	0.701	putative SAM-dependent methyltransferases
ye	STM1906	AAL20822	1999818..2000789	1.399	0.086	1.264	0.196	0.903	1.553	0.326	1.137	0.050	0.732	putative enzyme
cutC	STM1907	AAL20823	(2001025..2001771)	3.050	0.989	1.046	0.098	0.343	1.538	0.145	0.818	0.053	0.531	copper homeostasis protein
yecM	STM1908	AAL20824	(2001791..2002360)	1.510	0.286	0.517	0.076	0.342	0.853	0.100	0.638	0.023	0.748	putative cytoplasmic protein
argS	STM1909	AAL20825	2002597..2004330	1.406	0.062	2.063	0.206	1.468	1.847	0.059	1.784	0.121	0.966	arginine tRNA synthetase
STM1910	STM1910	AAL20826	2004519..2006390	0.269	0.061	0.182	0.018	0.678	0.265	0.012	0.239	0.037	0.901	putative penicillin-binding protein
STM1911	STM1911	AAL20827	(2006444..2007583)	0.430	0.040	0.558	0.077	1.299	0.157	0.021	0.329	0.051	2.091	putative cytoplasmic protein
flhE	STM1912	AAL20828	(2007820..2008212)					N/A					N/A	flagellar protein
flhA	STM1913	AAL20829	(2008212..2010290)	1.266	0.190	2.000	0.116	1.579	0.315	0.155	0.226	0.054	0.716	flagellar biosynthesis; possible export of flagellar proteins
flhB	STM1914	AAL20830	(2010283..2011434)					N/A					N/A	putative part of export apparatus for flagellar proteins
cheZ	STM1915	AAL20831	(2011628..2012272)	12.254	3.685	20.206	0.829	1.649	0.307	0.030	0.534	0.042	1.741	chemotactic response; CheY protein phophatase
cheY	STM1916	AAL20832	(2012283..2012672)	21.926	3.224	25.511	4.645	1.163	0.423	0.066	0.604	0.073	1.429	chemotaxis regulator, transmits chemoreceptor signals to flagelllar motor onents
cheB	STM1917	AAL20833	(2012690..2013739)	9.533	2.230	9.773	0.869	1.025	0.206	0.047	0.309	0.030	1.497	methyl esterase, response regulator for chemotaxis (cheA sensor)
cheR	STM1918	AAL20834	(2013736..2014602)	5.107	1.225	6.237	0.308	1.221	0.118	0.023	0.227	0.043	1.917	glutamate methyltransferase, response regulator for chemotaxis
cheM	STM1919	AAL20835	(2014756..2016417)					N/A					N/A	methyl accepting chemotaxis protein II, aspartate sensor-receptor
cheW	STM1920	AAL20836	(2016654..2017157)	5.436	1.359	21.256	1.554	3.910	0.177	0.033	0.335	0.070	1.897	purine-binding chemotaxis protein; regulation
cheA	STM1921	AAL20837	(2017178..2019193)	3.528	0.634	14.059	1.773	3.985	0.126	0.042	0.221	0.010	1.755	sensory histitine protein kinase, transduces signal between chemo- signal receptors and CheB and CheY
motB	STM1922	AAL20838	(2019198..2020127)	2.103	0.273	8.767	1.385	4.168	0.175	0.061	0.216	0.063	1.232	enables flagellar motor rotation, linking torque machinery to cell wall
motA	STM1923	AAL20839	(2020124..2021011)	4.258	0.758	5.533	0.348	1.299	0.164	0.049	0.216	0.024	1.314	proton conductor onent of motor, torque generator
flhC	STM1924	AAL20840	(2021136..2021720)	3.396	0.446	5.036	1.153	1.483	0.533	0.044	0.926	0.062	1.740	regulator of flagellar biosynthesis, acts on class 2 operons
flhD	STM1925	AAL20841	(2021717..2022067)	3.817	0.138	6.347	0.232	1.663	0.490	0.025	1.123	0.066	2.292	regulator of flagellar biosynthesis, acts on class 2 operons

STM1926	STM1926	AAL20842	2022741..2022857	0.660	0.305	0.948	0.159	1.437	1.400	0.658	1.025	0.914	0.732	putative cytoplasmic protein
yecG	STM1927	AAL20843	2022854..2023282	1.340	0.149	0.852	0.135	0.636	0.932	0.318	0.646	0.133	0.693	putative universal stress protein
otsA	STM1928	AAL20844	(2023300..2024721)	0.438	0.035	0.599	0.087	1.369	0.884	0.024	1.622	0.092	1.834	trehalose-6-phosphate synthase
otsB	STM1929	AAL20845	(2024696..2025499)	0.325	0.081	0.360	0.099	1.109	0.767	0.121	0.882	0.065	1.150	trehalose-6-phosphate phophatase, biosynthetic
STM1930	STM1930	pseudogene; frameshift		0.956	0.120	0.792	0.235	0.828	0.767	0.024	0.630	0.194	0.821	
araH	STM1931	AAL20846	(2026132..2026689)	0.403	0.057	0.348	0.033	0.863	0.430	0.170	0.460	0.034	1.070	putative intracellular protease/amidase
ftnB	STM1932	AAL20847	2027240..2027743	0.914	0.100	0.601	0.029	0.657	4.227	0.041	2.351	0.132	0.556	ferritin-like protein
STM1933	STM1933	AAL20848	(2027922..2028560)	0.467	0.068	0.578		1.239	0.585	0.060	0.495		0.847	putative ribose 5-phosphate isomerase
STM1934	STM1934	AAL20849	2028816..2029151	1.481	0.186	2.278	0.242	1.538	0.925	0.045	0.636	0.125	0.688	putative outer membrane lipoprotein
ftn	STM1935	AAL20850	2029391..2029888	6.770	0.519	7.553	0.183	1.116	21.307	1.781	7.100	1.060	0.333	cytoplasmic ferritin
yecH	STM1936	AAL20851	(2029934..2030173)	0.981	0.033	1.463	0.147	1.491	2.692	0.146	1.358	0.109	0.504	putative cytoplasmic protein
tyrP	STM1937	AAL20852	2030400..2031611	1.017	0.064	0.686	0.091	0.674	0.794	0.034	0.467	0.070	0.588	HAAAP family, tyrosine-specific transport protein
yecA	STM1938	AAL20853	(2031686..2032351)	6.002	1.327	3.829	0.783	0.638	2.269	0.169	1.246	0.088	0.549	putative metal-binding protein related to the C-terminal domain of SecA
STM1939	STM1939	AAL20854	(2032589..2032915)	0.894	0.085	0.873	0.136	0.976	2.985	0.168	2.262	0.140	0.758	putative glucose-6-phosphate dehydrogenase
STM1940	STM1940	AAL20855	(2033128..2034567)	0.356	0.052	0.450	0.021	1.262	2.070	0.118	3.180	0.300	1.536	putative cell wall-associated hydrolase
STM1941	STM1941	AAL20856	(2034780..2035112)	0.730	0.044	0.397	0.076	0.544	4.661	1.034	3.399	0.153	0.729	putative inner membrane protein
leuZ	STM1942						N/A					N/A		
cysT	STM1943						N/A					N/A		
glyW	STM1944						N/A					N/A		
pgsA	STM1945	AAL20857	(2035813..2036361)	5.268	0.410	1.368	0.262	0.260	1.904	0.447	1.470	0.028	0.772	phosphatidylglycerophosphate synthetase (CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase)
uvrC	STM1946	AAL20858	(2036418..2038250)	1.091	0.039	1.448	0.118	1.327	1.387	0.036	0.974	0.086	0.702	UvrC with UvrAB is a DNA excision repair enzyme
uvrY	STM1947	AAL20859	(2038247..2038903)	4.583	0.465	3.579	0.067	0.781	6.467	0.769	3.460	0.215	0.535	putative response regulator (LuxR/UhpA familiy)
STM1948	STM1948	AAL20860	2039215..2039370	0.930	0.099	0.544	0.047	0.585	1.274	0.344	0.651	0.064	0.511	putative inner membrane protein
yecF	STM1949	AAL20861	2039367..2039591	2.809	0.419	1.230	0.346	0.438	2.978	0.140	1.199	0.163	0.403	putative cytoplasmic protein
sdiA	STM1950	AAL20862	(2039658..2040380)	3.497	0.340	1.128	0.200	0.323	0.538	0.016	1.001	0.145	1.860	transcriptional regulator of ftsQAZ gene cluster (LuxR/UhpA family)
yecC	STM1951	AAL20863	(2040612..2041364)	0.717	0.008	1.130	0.122	1.576	0.544	0.033	0.641	0.023	1.178	putative ABC-type polar amino acid transport system, ATPase onent
yecS	STM1952	AAL20864	(2041361..2042029)	0.866	0.041	1.399	0.104	1.616	0.902	0.084	0.852	0.019	0.944	putative ABC-type amino acid transporter, permease onent
yedO	STM1953	AAL20865	(2042050..2043036)	0.955	0.051	1.402	0.226	1.468	0.890	0.107	0.939	0.193	1.055	putative 1-cyclopropane-carboxylate deaminase
fliY	STM1954	AAL20866	(2043190..2043990)	1.210	0.208	8.970	0.379	7.415	0.948	0.122	1.115	0.051	1.177	putative periplasmic binding transport protein
fliZ	STM1955	AAL20867	(2044137..2044688)	2.613	0.483	33.925	5.861	12.982	0.270	0.053	0.416	0.121	1.540	putative regulator of FliA
fliA	STM1956	AAL20868	(2044747..2045466)	6.002	0.276	45.442	4.147	7.571	0.243	0.120	0.329	0.047	1.356	sigma F (sigma 28) factor of RNA polymerase, transcription of late flagellar genes (class 3a and 3b operons)

tnpA_2	STM1957	AAL20869	(2045735..2046193)					N/A					N/A	transposase for IS200
fliB	STM1958	AAL20870	(2046374..2047579)	1.179	0.034	5.829	0.614	4.946	0.196	0.004	0.312	0.024	1.591	N-methylation of lysine residues in flagellin
fliC	STM1959	AAL20871	(2047658..2049145)	12.541	0.573	72.576	7.100	5.787	0.202	0.009	0.513	0.049	2.543	flagellar biosynthesis; flagellin, filament structural protein
fliD	STM1960	AAL20872	2049402..2050805	2.193	0.285	31.808	3.030	14.506	0.250	0.141	0.614	0.236	2.460	flagellar biosynthesis; filament capping protein; enables filament assembly
fliS	STM1961	AAL20873	2050820..2051227	3.520	0.311	19.838	2.355	5.636	0.170	0.066	0.247	0.120	1.454	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)
fliT	STM1962	AAL20874	2051227..2051595	3.652	0.732	12.192	1.241	3.338	0.361	0.442	0.453	0.242	1.253	flagellar biosynthesis; possible export chaperone for FliD
amyA	STM1963	AAL20875	2051667..2053151	0.358	0.029	0.829	0.137	2.318	0.327	0.078	0.455	0.200	1.391	cytoplasmic alpha-amylase
yedD	STM1964	AAL20876	(2053191..2053616)	1.358	0.223	1.501	0.281	1.105	1.911	0.881	1.786	0.327	0.935	putative outer membrane lipoprotein
yedE	STM1965	AAL20877	2053742..2055007	0.372	0.098	0.501	0.021	1.347	0.332	0.063	0.432	0.095	1.301	paral putative membrane onent of transport system
yedF	STM1966	AAL20878	2055004..2055237	0.278	0.070	0.584	0.107	2.096	0.514	0.057	0.566	0.115	1.100	putative transcriptional regulator
STM1967	STM1967	AAL20879	2055502..2055888	0.491	0.069	1.553	0.300	3.164	1.626	0.042	1.312	0.054	0.807	putative 50S ribosomal protein
fliE	STM1968	AAL20880	(2056008..2056322)	1.439	0.098	5.600	1.100	3.892	0.279	0.042	0.658	0.347	2.355	putative Flagellar hook-basal body protein
fliF	STM1969	AAL20881	2056539..2058221	2.973	0.263	7.965	0.322	2.680	0.211	0.026	0.490	0.288	2.319	flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein
fliG	STM1970	AAL20882	2058214..2059209	6.950	0.113	14.288	2.855	2.056	0.214	0.021	0.274	0.053	1.278	flagellar biosynthesis, onent of motor switching and energizing
fliH	STM1971	AAL20883	2059202..2059909	7.357	0.938	11.279	1.797	1.533	0.183	0.012	0.267	0.041	1.457	flagellar biosynthesis; possible export of flagellar proteins
fliI	STM1972	AAL20884	2059909..2061279	4.005	0.395	6.084	0.574	1.519	0.153	0.039	0.301	0.063	1.973	flagellum-specific ATP synthase
fliJ	STM1973	AAL20885	2061301..2061744	0.944	0.048	6.972	0.600	7.384	0.103	0.026	0.243	0.048	2.364	flagellar fliJ protein
fliK	STM1974	AAL20886	2061741..2062958	1.182	0.031	12.982	1.585	10.981	0.128	0.017	0.343	0.145	2.672	flagellar hook-length control protein
fliL	STM1975	AAL20887	2063063..2063530	3.135	0.681	17.026	2.300	5.432	0.191	0.036	0.251	0.022	1.317	flagellar biosynthesis
fliM	STM1976	AAL20888	2063535..2064539	2.384	0.221	10.933	0.474	4.586	0.182	0.058	0.240	0.020	1.319	flagellar biosynthesis, onent of motor switch and energizing
fliN	STM1977	AAL20889	2064536..2064949	5.842	0.874	12.022	0.741	2.058	0.776	0.124	0.785	0.044	1.012	flagellar biosynthesis, onent of motor switch and energizing
fliO	STM1978	AAL20890	2064949..2065326	4.707	0.362	9.349	1.981	1.986	1.037	0.841	1.134	0.159	1.094	flagellar biosynthesis
fliP	STM1979	AAL20891	2065326..2066063	2.096	0.086	3.569	0.265	1.702	0.436	0.082	0.502	0.130	1.150	flagellar biosynthesis
fliQ	STM1980	AAL20892	2066073..2066342	1.277	0.070	1.586	0.233	1.242	0.714	0.205	0.754	0.334	1.056	flagellar biosynthesis
fliR	STM1981	AAL20893	2066351..2067145	0.690	0.023	0.565	0.059	0.819	0.918	0.060	1.102	0.018	1.200	putative flagellar biosynthetic protein
rcsA	STM1982	AAL20894	2067427..2068050	0.472	0.030	0.326	0.031	0.692	6.747	0.688	1.801	0.026	0.267	positive transcriptional regulator of capsular/exo-polysaccharide synthesis (LuxR/UhpA family)
yodD	STM1984	AAL20895	2068412..2068639	0.434	0.043	0.308	0.060	0.710	0.844	0.060	0.823	0.192	0.975	putative cytoplasmic protein

yedP	STM1986	AAL20896	2068949..2069764	0.358	0.048	0.202	0.044	0.565	0.575	0.022	0.566	0.004	0.983	putative hydrolase of the HAD superfamily
STM1987	STM1987	AAL20897	(2069743..2071455)	0.814	0.045	0.305	0.035	0.374	0.839	0.086	0.504	0.031	0.601	putative inner membrane protein
STM1988	STM1988	AAL20898	(2071620..2071865)	1.668	0.262	0.508	0.082	0.305	2.072	0.166	0.645	0.125	0.311	putative cytoplasmic protein
yedI	STM1989	AAL20899	(2071882..2072793)	1.172	0.034	0.421	0.077	0.359	0.864	0.085	0.470	0.014	0.544	putative inner membrane protein
yedA	STM1990	AAL20900	2072969..2073889	0.860	0.030	0.238	0.043	0.277	0.469	0.094	0.318	0.031	0.678	putative permease
vsr	STM1991	AAL20901	(2073878..2074348)	0.771	0.087	0.495	0.054	0.642	0.502	0.075	0.440	0.019	0.877	DNA mismatch endonuclease, patch repair protein
dcm	STM1992	AAL20902	(2074329..2075759)	0.740	0.039	0.921	0.066	1.245	0.409	0.010	0.583	0.049	1.425	DNA cytosine methylase
yedJ	STM1993	AAL20903	(2075833..2076528)	0.709	0.036	0.508	0.096	0.716	0.480	0.020	0.537	0.103	1.119	putative hydrolase
STM1994	STM1994	AAL20904	(2076620..2076919)	0.466	0.094	0.302	0.171	0.648	0.377	0.029			0.000	putative inner membrane protein
ompS	STM1995	AAL20905	2077569..2078765					N/A					N/A	putative porin
cspB	STM1996	AAL20906	(2079225..2079437)	6.241	0.693	1.177	0.005	0.189	5.493	0.795	1.209	0.016	0.220	putative cold-shock protein
umuC	STM1997	AAL20907	(2079892..2081160)	0.424	0.078	0.372	0.069	0.877	0.492	0.108	0.456	0.158	0.927	error-prone repair: onent of DNA polymerase V with UmuD'
umuD	STM1998	AAL20908	(2081163..2081582)	0.446	0.071	0.316	0.033	0.709	0.561	0.090	0.424	0.023	0.756	error-prone repair: SOS-response transcriptional repressors (LexA homologs, RecA-mediated autopeptidases)
STM1999	STM1999	AAL20909	(2081709..2081870)	0.422	0.037	0.262	0.037	0.621	0.563	0.169	0.453	0.079	0.805	putative cytoplasmic protein
serU	STM2000						N/A					N/A		
yeeI	STM2001	AAL20910	2082351..2083148	6.253	0.541	3.000	0.352	0.480	1.627	0.022	1.629	0.027	1.001	putative inner membrane protein
STM2003	STM2003	pseudogene; frameshift		0.510	0.040	0.324	0.051	0.636	0.354	0.169	0.377	0.024	1.068	
asnT	STM2004						N/A					N/A		
STM2005	STM2005	AAL20911	2084458..2084931	0.455	0.077	0.286	0.069	0.628	0.366	0.056	0.344	0.057	0.938	putative endoprotease
STM2006	STM2006	AAL20912	2085406..2086104	0.239	0.103	0.110	0.042	0.459	0.160	0.013	0.185	0.018	1.156	putative branched chain amino acid transport protein
STM2007	STM2007	AAL20913	2086921..2088615	0.138	0.050	0.127	0.007	0.917	0.129	0.026	0.173	0.027	1.338	putative TPR repeat protein
STM2008	STM2008	AAL20914	2088672..2090402					N/A					N/A	putative periplasmic protein
amn	STM2009	AAL20915	(2091307..2092761)	0.570	0.060	1.235	0.327	2.166	0.602	0.506	1.007	0.177	1.672	AMP nucleosidase
STM2010	STM2010	AAL20916	2092807..2092968	0.528	0.163	0.619	0.067	1.173	0.662	0.550	0.515	0.116	0.778	putative cytoplasmic protein
STM2011	STM2011	AAL20917	(2092957..2093283)					N/A					N/A	putative cytoplasmic protein
asnW	STM2012						N/A					N/A		
yeeO	STM2013	AAL20918	(2094377..2095834)	0.434	0.052	0.178	0.018	0.410	0.299	0.013	0.241	0.020	0.808	putative MATE family transport protein
asnU	STM2014						N/A					N/A		
erfK	STM2015	AAL20919	(2096296..2097225)	0.404	0.045	0.723	0.066	1.790	0.708	0.151	0.688	0.053	0.971	putative periplasmic protein
cobT	STM2016	AAL20920	(2097303..2098373)	1.014	0.074	2.461	0.712	2.427	3.412	0.478	1.958	0.178	0.574	nicotinate-nucleotide dimethylbenzimidazole-P phophoribosyl transferase
cobS	STM2017	AAL20921	(2098400..2099143)	0.625	0.108	1.401	0.190	2.240	2.278	0.473	1.409	0.066	0.618	cobalamin 5'-phosphate synthase
cobU	STM2018	AAL20922	(2099140..2099685)	0.430	0.078	1.269	0.212	2.949	1.594	0.397	0.920	0.119	0.577	bifunctional: cobinamide kinase; cobinamide phosphate guanylyltransferase

cbiP	STM2019	AAL20923	(2099682..2101202)	0.671	0.068	1.920	0.340	2.860	1.991	0.264	1.171	0.051	0.588	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiO	STM2020	AAL20924	(2101199..2102014)	0.400	0.047	1.404	0.046	3.508	2.011	0.182	1.135	0.184	0.565	synthesis of vitamin B12 adenosyl cobalamide precursor
cboQ	STM2021	AAL20925	(2102023..2102700)	0.407	0.049	1.661	0.122	4.077	3.148	0.928	1.835	0.063	0.583	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiN	STM2022	AAL20926	(2102687..2102968)	0.438	0.140	1.987	0.186	4.538	4.810	0.313	2.405	0.287	0.500	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiM	STM2023	AAL20927	(2102970..2103707)	0.549	0.115	2.150	0.316	3.913	5.235	1.612	2.285	0.242	0.437	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiL	STM2024	AAL20928	(2103704..2104417)	0.405	0.068	3.201	0.331	7.908	4.035	0.637	2.844	0.403	0.705	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiK	STM2025	AAL20929	(2104414..2105208)	0.289	0.061	3.682	0.382	12.748	2.908	0.464	2.827	0.166	0.972	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiJ	STM2026	AAL20930	(2105211..2106002)	0.387	0.138	2.733	0.704	7.069	3.050	0.054	1.502	0.152	0.493	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiH	STM2027	AAL20931	(2105999..2106724)	0.320	0.089	3.986	0.191	12.461	4.064	0.981	3.365	0.474	0.828	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiG	STM2028	AAL20932	(2106724..2107779)	0.338	0.063	3.569	0.609	10.563	4.907	0.980	2.936	0.241	0.598	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiF	STM2029	AAL20933	(2107760..2108533)	0.402	0.042	4.446	0.334	11.063	5.457	0.326	3.175	0.201	0.582	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiT	STM2030	AAL20934	(2108517..2109095)	0.484	0.028	2.710	0.536	5.598	3.287	0.690	2.086	0.279	0.635	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiE	STM2031	AAL20935	(2109085..2109690)	0.531	0.032	2.411	0.209	4.539	4.650	1.028	2.581	0.235	0.555	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiD	STM2032	AAL20936	(2109684..2110823)	0.589	0.079	3.387	0.690	5.748	3.974	1.132	2.745	0.181	0.691	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiC	STM2033	AAL20937	(2110823..2111455)	0.566	0.098	2.263	0.049	4.001	4.746	0.206	2.324	0.425	0.490	synthesis of vitamin B12 adenosyl cobalamide precursor
cibB	STM2034	AAL20938	(2111466..2112425)	0.787	0.067	1.294	0.322	1.644	2.771	0.918	1.680	0.141	0.606	synthesis of vitamin B12 adenosyl cobalamide precursor
cbiA	STM2035	AAL20939	(2112422..2113801)	0.492	0.033			0.000	2.215	0.168			0.000	synthesis of vitamin B12 adenosyl cobalamide precursor
pocR	STM2036	AAL20940	(2114399..2115310)	2.095	0.718	3.823	0.348	1.825	5.474	17.665	2.336	0.123	0.427	Propanediol utilization: transcriptional regulation, AraC family
pduF	STM2037	AAL20941	(2115527..2116321)	0.384	0.077	0.208	0.024	0.543	1.128	0.106	0.472	0.023	0.418	Propanediol utilization: propanediol diffusion facilitator

pduA	STM2038	AAL20942	2116846..2117130	0.296	0.113	0.333	0.036	1.125	0.215	0.046	0.264	0.025	1.229	Propanediol utilization: polyhedral bodies
pudB	STM2039	AAL20943	2117238..2117939	0.290	0.104	0.517	0.193	1.785	0.219	0.032	0.396	0.157	1.809	Propanediol utilization: polyhedral bodies
pduC	STM2040	AAL20944	2117958..2119622	0.247	0.099	0.510	0.028	2.061	0.211	0.034	0.377	0.038	1.787	Propanediol utilization: dehydratase, large subunit
pduD	STM2041	AAL20945	2119633..2120307	0.190	0.093	0.336	0.024	1.769	0.122	0.061	0.259	0.058	2.120	Propanediol utilization: dehydratase, medium subunit
pduE	STM2042	AAL20946	2120322..2120843	0.170	0.120	0.317	0.021	1.861	0.123	0.066	0.224	0.035	1.826	Propanediol utilization: dehydratase, small subunit
pduG	STM2043	AAL20947	2120853..2122685	0.226	0.096	0.332	0.076	1.468	0.174	0.166	0.277	0.032	1.599	Propanediol utilization: diol dehydratase reactivation
pduH	STM2044	AAL20948	2122675..2123025	0.225	0.087	0.339	0.013	1.505	0.286	0.067	0.391	0.189	1.367	Propanediol utilization: diol dehydratase reactivation
pduJ	STM2045	AAL20949	2123044..2123319	0.263	0.083	0.292	0.053	1.107	0.224	0.036	0.322	0.060	1.437	Propanediol utilization: polyhedral bodies
pduK	STM2046	AAL20950	2123323..2123805	0.176	0.078	0.227	0.031	1.288	0.124	0.025	0.240	0.044	1.939	Propanediol utilization: polyhedral bodies
pduL	STM2047	AAL20951	2123805..2124437	0.246	0.088	0.273	0.051	1.113	0.152	0.021	0.321	0.147	2.107	Propanediol utilization
pduM	STM2048	AAL20952	2124434..2124925	0.313	0.170	0.452	0.126	1.442	0.245	0.019	0.440	0.171	1.798	Propanediol utilization
pduN	STM2049	AAL20953	2124929..2125204	0.271	0.138	0.337	0.086	1.242	0.255	0.243	0.439	0.084	1.724	Propanediol utilization: polyhedral bodies
pduO	STM2050	AAL20954	2125214..2126224	0.289	0.109	0.246	0.041	0.851	0.194	0.049	0.295	0.128	1.521	Propanediol utilization: B12 related
pduP	STM2051	AAL20955	2126221..2127615	0.254	0.123	0.217	0.031	0.854	0.166	0.014	0.244	0.036	1.471	Propanediol utilization: CoA-dependent propionaldehyde dehydrogenase
pduQ	STM2052	AAL20956	2127627..2128739	0.210	0.138	0.265	0.030	1.262	0.160	0.081	0.246	0.020	1.538	Propanediol utilization: propanol dehydrogenase
pduS	STM2053	AAL20957	2128736..2130091	0.305	0.121	0.239	0.058	0.783	0.194	0.076	0.270	0.021	1.390	Propanediol utilization: polyhedral bodies
pduT	STM2054	AAL20958	2130094..2130648	0.263	0.142	0.242	0.045	0.920	0.178	0.017	0.259	0.143	1.454	Propanediol utilization: polyhedral bodies
pduU	STM2055	AAL20959	2130648..2130998	0.333	0.085	0.196	0.047	0.589	0.278	0.055	0.213	0.049	0.767	Propanediol utilization: polyhedral bodies
pduV	STM2056	AAL20960	2131003..2131455	0.196	0.107	0.154	0.016	0.789	0.126	0.059	0.223	0.020	1.773	Propanediol utilization
pduW	STM2057	AAL20961	2131440..2132654	0.265	0.087	0.180	0.049	0.680	0.184	0.070	0.236	0.034	1.280	Propanediol utilization: propionate kinase
pduX	STM2058	AAL20962	2132712..2133614	0.931	0.085	0.440	0.039	0.473	0.601	0.129	0.519	0.107	0.864	Propanediol utilization
yeeX	STM2059	AAL20963	(2133648..2133983)	5.716	1.397	2.761	0.466	0.483	4.362	0.327	2.994	0.122	0.686	putative cytoplasmic protein
yeeA	STM2060	AAL20964	(2134228..2135286)	0.749	0.046	0.936	0.114	1.249	0.905	0.049	0.700	0.044	0.774	putative inner membrane protein
sbmC	STM2061	AAL20965	(2135405..2135872)	3.664	0.464	2.254	0.166	0.615	4.732	0.458	2.109	0.123	0.446	DNA gyrase inhibitor
dacD	STM2062	AAL20966	(2136025..2137197)	0.543	0.075	0.635	0.092	1.169	0.711	0.138	0.643	0.042	0.904	DD-carboxypeptidase, penicillin-binding protein 6b
phsC	STM2063	AAL20967	(2137321..2138085)	0.751	0.103	2.261	0.543	3.012	0.406	0.057	0.458	0.029	1.129	Hydrogen sulfide production: membrane anchoring protein
phsB	STM2064	AAL20968	(2138082..2138660)	0.497	0.060	3.156	0.328	6.355	0.197	0.012	0.401	0.025	2.030	Hydrogen sulfide production: iron- sulfur subunit; electron transfer
phsA	STM2065	AAL20969	(2138675..2140951)	0.363	0.062	3.962	0.616	10.900	0.137	0.011	0.336	0.034	2.455	Hydrogen sulfide production: membrane anchoring protein

sopA	STM2066	AAL20970	2141570..2143918					N/A					N/A	Secreted effector protein of Salmonella dublin
sbcB	STM2067	AAL20971	2144261..2145691	0.963	0.052	1.168	0.198	1.212	1.108	0.171	1.446	0.069	1.305	exonuclease I, 3' --> 5' specific; deoxyribophosphodiesterase
yeeF	STM2068	AAL20972	(2145827..2147191)	1.305	0.244	0.526	0.083	0.403	3.260	0.325	0.730	0.110	0.224	putative APC family, amino acid transport protein
yeeY	STM2069	AAL20973	(2147471..2148385)					N/A					N/A	putative transcriptional regulator, LysR family
yeeZ	STM2070	AAL20974	(2148431..2149255)	2.478	0.226	1.180	0.191	0.476	2.461	0.313	1.928	0.114	0.783	putative dehydratase
hisG	STM2071	AAL20975	2149615..2150514	0.497	0.061	0.580	0.091	1.166	0.304	0.027	0.440	0.014	1.445	ATP phosphoribosyltransferase
hisD	STM2072	AAL20976	2150617..2151921	0.566	0.072	1.089	0.111	1.925	0.368	0.068	0.661	0.025	1.795	histidinal dehydrogenase (also histidinol dehydrogenase activity)
hisC	STM2073	AAL20977	2151918..2152997	0.453	0.066	1.075	0.071	2.375	0.297	0.035	0.663	0.035	2.232	histidinol phosphate aminotransferase
hisB	STM2074	AAL20978	2152994..2154061	0.508	0.030	1.627	0.089	3.202	0.366	0.037	0.603	0.041	1.647	bifunctional: imidazoleglycerol-phosphate dehydratase; histidinol-phosphatase
hisH	STM2075	AAL20979	2154058..2154651	0.586	0.068	1.340	0.208	2.286	0.376	0.044	0.683	0.069	1.817	glutamine amidotransferase, subunit with HisF
hisA	STM2076	AAL20980	2154651..2155388					N/A					N/A	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase
hisF	STM2077	AAL20981	2155370..2156146	1.354	0.140	1.490	0.211	1.101	1.094	0.227	1.293	0.128	1.182	imidazole glycerol phosphate synthase, subunit with HisH
hisI	STM2078	AAL20982	2156140..2156751	1.114	0.132	1.416	0.251	1.271	1.138	0.048	1.313	0.136	1.154	bifunctional: phosphoribosyl-AMP cyclohydrolase; phosphoribosyl-ATP pyrophosphatase
wzzB	STM2079	AAL20983	(2156832..2157815)	1.477	0.167	2.281	0.323	1.545	3.638	0.273	3.852	0.162	1.059	regulator of length of O-antigen onent of lipopolysaccharide chains
udg	STM2080	AAL20984	(2157958..2159124)	1.656	0.114	1.079	0.118	0.651	24.481	0.924	10.062	0.341	0.411	UDP-glucose/GDP-mannose dehydrogenase
gnd	STM2081	AAL20985	(2159361..2160767)	3.863	0.495	8.925	1.541	2.310	4.560	0.284	4.777	0.298	1.047	gluconate-6-phosphate dehydrogenase, decarboxylating
rfbP	STM2082	AAL20986	(2160931..2162361)	2.790	0.150	1.462	0.106	0.524	5.477	0.856	2.775	0.243	0.507	LPS side chain defect: bifunctional enzyme: undecaprenol-phosphate galactosephosphotransferase, and O-antigen transfer
rfbK	STM2083	AAL20987	(2162433..2163866)	2.535	0.090	1.509	0.170	0.595	4.350	0.392	3.023	0.277	0.695	LPS side chain defect: phosphomannomutase
rfbM	STM2084	AAL20988	(2163853..2165292)	2.619	0.248	1.772	0.293	0.677	3.633	0.222	2.383	0.338	0.656	LPS side chain defect: mannose-1-phosphate guanylyltransferase
rfbN	STM2085	AAL20989	(2165293..2166237)	6.634	0.233	1.634	0.306	0.246	9.462	2.004	3.342	0.093	0.353	LPS side chain defect: rhamnosyl transferase
rfbU	STM2086	AAL20990	(2166238..2167299)	6.203	0.397	1.171	0.095	0.189	9.055	2.226	3.038	0.129	0.336	LPS side chain defect: mannosyl transferase
rfbV	STM2087	AAL20991	(2167619..2168620)	10.886	0.761	1.756	0.136	0.161	16.619	3.371	4.715	0.641	0.284	LPS side chain defect: abequosyltransferase
rfbX	STM2088	AAL20992	(2168625..2169917)	4.196	0.489	0.968	0.138	0.231	7.172	1.686	2.922	0.127	0.407	LPS side chain defect: putative O-antigen transferase
rfbJ	STM2089	AAL20993	(2169999..2170898)	2.493	0.095	2.333	0.153	0.936	5.270	0.228	4.307	0.235	0.817	LPS side chain defect: CDP-abequose synthase
rfbH	STM2090	AAL20994	(2170926..2172239)	3.719	0.244	8.749	0.513	2.353	3.363	0.094	8.106	0.765	2.410	LPS side chain defect: CDP-6deoxy-D-xylo-4-hexulose-3-dehydrase

rfbG	STM2091	AAL20995	(2172266..2173345)	3.509	0.216	5.025	0.620	1.432	3.289	0.047	3.504	0.464	1.065	LPS side chain defect: CDP glucose 4,6-dehydratase
rfbF	STM2092	AAL20996	(2173350..2174123)	7.018	0.321	6.678	1.006	0.951	7.055	1.254	5.501	0.324	0.780	LPS side chain defect: glucose-1-phosphate cytidylyltransferase
rfbI	STM2093	AAL20997	(2174120..2175112)	4.404	0.192	4.105	0.770	0.932	4.163	0.251	1.832	0.266	0.440	LPS side chain defect: CDP-6-deoxy-delta3,4-glucoseen reductase
rfbC	STM2094	AAL20998	(2175118..2175669)	2.300	0.027	2.829	0.310	1.230	2.736	0.088	1.951	0.081	0.713	dTDP-4,deoxyrhamnose 3,5 epimerase
rfbA	STM2095	AAL20999	(2175670..2176548)	0.947	0.048	2.091	0.332	2.207	1.025	0.072	0.962	0.067	0.939	dTDP-glucose pyrophosphorylase
rfbD	STM2096	AAL21000	(2176596..2177495)	1.126	0.077	3.250	0.207	2.887	1.425	0.031	1.375	0.155	0.965	TDP-rhamnose synthetase
rfbB	STM2097	AAL21001	(2177495..2178580)	2.573	0.258	2.439	0.371	0.948	3.165	0.134	1.600	0.071	0.505	dTDP-glucose 4,6 dehydratase
galF	STM2098	AAL21002	(2178957..2179850)	7.844	0.690	3.289	0.144	0.419	13.349	0.179	5.555	0.509	0.416	putative glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase), non-catalytic subunit
wcaM	STM2099	AAL21003	(2180028..2181431)	0.351	0.110	0.288	0.014	0.818	1.509	0.120	0.807	0.145	0.535	putative colanic acid biosynthesis protein
wcaL	STM2100	AAL21004	(2181442..2182662)	0.282	0.138	0.217	0.045	0.769	2.868	0.454	1.845	0.171	0.643	putative glycosyl transferase in colanic acid gene cluster
wcaK	STM2101	AAL21005	(2182659..2183939)	0.244	0.124	0.148	0.070	0.607	2.765	0.261	1.618	0.302	0.585	putative galactokinase in colanic acid gene cluster
wzxC	STM2102	AAL21006	(2183961..2185439)	0.196	0.126	0.074	0.007	0.379	1.182	0.080	0.453	0.048	0.383	putative export protein in colanic acid gene cluster
wcaJ	STM2103	AAL21007	(2185572..2186966)	0.227	0.083	0.158	0.013	0.696	2.742	0.294	1.315		0.480	putative UDP-glucose lipid carrier transferase/glucose-1-phosphate transferase in colanic acid gene cluster
sG	STM2104	AAL21008	(2187020..2188390)	1.147	0.367	2.181	0.309	1.901	8.290	5.247	2.654	1.034	0.320	phosphomannomutase in colanic acid gene cluster
manC	STM2105	AAL21009	(2188501..2189943)	0.502	0.175	0.972	0.125	1.935	10.805	0.091	4.599	0.849	0.426	mannose-1-phosphate in colanic acid gene cluster
wcaI	STM2106	AAL21010	(2189940..2191163)	0.317	0.092	0.187	0.064	0.591	17.420	4.835	6.237	1.076	0.358	putative glycosyl transferase in colanic acid biosynthesis
wcaH	STM2107	AAL21011	(2191160..2191663)	0.413	0.089	0.346	0.169	0.838	15.621	3.635	5.114	0.446	0.327	GDP-mannose mannosyl hydrolase in colanic acid biosynthesis
wcaG	STM2108	AAL21012	(2191635..2192600)	0.273	0.111	0.143	0.034	0.524	22.177	6.867	10.836	1.526	0.489	bifunctional GDP fucose synthetase in colanic acid biosyntheis
gmd	STM2109	AAL21013	(2192603..2193724)	0.175	0.104	0.089	0.007	0.508	20.911	4.142	11.160	0.469	0.534	GDP-D-mannose dehydratase in colanic acid gene cluster
wcaF	STM2110	AAL21014	(2193748..2194302)	0.191	0.088	0.156	0.010	0.816	8.081	0.372	3.107	0.586	0.385	putative acyltransferase in colanic acid biosynthesis
wcaE	STM2111	AAL21015	(2194318..2195064)					N/A					N/A	putative transferase in colanic acid biosynthesis
wcaD	STM2112	AAL21016	(2195077..2196291)	0.180	0.094	0.091	0.015	0.506	4.893	0.438	0.931	0.045	0.190	putative colanic acid polymerase

wcaC	STM2113	AAL21017	(2196266..2197483)	0.362	0.130	0.180	0.021	0.498	4.091	0.827	1.607	0.143	0.393	putative glycosyl transferase in colanic acid biosynthesis
wcaB	STM2114	AAL21018	(2197480..2197968)	0.274	0.122	0.242	0.028	0.883	4.211	1.161	1.163	0.101	0.276	putative acyl transferase in colanic acid biosynthesis
wcaA	STM2115	AAL21019	(2197971..2198813)	0.245	0.098	0.168	0.043	0.684	4.199	0.808	1.230	0.048	0.293	putative glycosyl transferase in colanic acid biosynthesis
wzc	STM2116	AAL21020	(2198900..2201059)	0.142	0.100	0.115	0.011	0.810	2.097	0.355	0.844	0.052	0.402	putative tyrosine-protein kinase in colanic acid export
wzb	STM2117	AAL21021	(2201056..2201505)	0.272	0.114	0.212	0.054	0.781	2.620	0.511	1.362	0.174	0.520	putative protein-tyrosine-phosphatase in colanic acid export
wza	STM2118	AAL21022	(2201511..2202650)	0.156	0.105	0.104	0.011	0.663	1.516	0.085	0.734	0.017	0.484	putative polysaccharide export protein, outer membrane
yegH	STM2119	AAL21023	2203325..2204905	0.552	0.091	0.524	0.022	0.950	0.900	0.018	0.813	0.049	0.903	putative inner membrane protein
asmA	STM2120	AAL21024	(2204991..2206847)	2.129	0.309	1.445	0.126	0.679	1.386	0.340	1.155	0.077	0.833	suppressor of ompF assembly mutants
dcd	STM2121	AAL21025	(2206886..2207467)	3.605	0.600	2.272	0.373	0.630	2.610	0.634	2.107	0.216	0.808	dUTPase
udk	STM2122	AAL21026	(2207558..2208199)	1.602	0.170	1.257	0.055	0.785	1.702	0.010	0.910	0.069	0.535	uridine/cytidine kinase
yegE	STM2123	AAL21027	2208530..2211520					N/A					N/A	putative PAS/PAC domain; Diguanylate cyclase/phosphodiesterase domain 1, Diguanylate cyclase/phosphodiesterase domain 2,
alkA	STM2124	AAL21028	(2211488..2212357)	0.555	0.041	0.209	0.034	0.376	0.488	0.057	0.439	0.059	0.899	3-methyl-adenine DNA glycosylase II, inducible
yegD	STM2125	AAL21029	2212491..2213843	0.613	0.017	0.232	0.042	0.379	0.943	0.120	0.397	0.032	0.421	putative heat shock protein (Hsp70/DnaK)
STM2126	STM2126	AAL21030	2214284..2215525					N/A					N/A	putative HlyD family secretion protein
yegN	STM2127	AAL21031	2215525..2218647	0.331	0.111	0.273	0.045	0.824	0.259	0.095	0.408	0.030	1.573	paral putative outer membrane receptor
yegO	STM2128	AAL21032	2218648..2221728	0.347	0.103	0.178	0.031	0.513	0.209	0.101	0.216	0.030	1.031	putative resistance protein (efflux transporter), outer membrane
yegB	STM2129	AAL21033	2221725..2223137	0.651	0.066	0.177	0.014	0.271	0.644	0.075	0.409	0.018	0.634	putative MFS family transport protein
baeS	STM2130	AAL21034	2223137..2224540	0.573	0.030	0.391	0.071	0.683	0.750	0.042	0.748	0.254	0.997	sensory kinase in two-onent regulatoyr system wtih BaeR
baeR	STM2131	AAL21035	2224537..2225259	0.432	0.060	0.478	0.042	1.106	0.542	0.012	0.780	0.027	1.438	response regulator in two-onent regulatory system with BaeS (OmpR family)
STM2132	STM2132	pseudogene; frameshift		0.309	0.100	0.158	0.021	0.510	0.705	0.179	0.659	0.153	0.934	
STM2133	STM2133	AAL21036	2225846..2226730	0.211	0.091	0.176	0.018	0.832	0.440	0.093	0.457	0.061	1.038	putative cytoplasmic protein
STM2134	STM2134	AAL21037	2226730..2227446	0.190	0.095	0.162	0.018	0.848	0.606	0.029	0.729	0.079	1.202	putative inner membrane protein
STM2135	STM2135	AAL21038	2227457..2229568	0.201	0.096	0.154	0.031	0.766	0.278	0.042	0.499	0.017	1.795	putative inner membrane protein
yegQ	STM2136	AAL21039	2229684..2231045	0.479	0.135	0.533	0.037	1.114	0.662	0.052	0.594	0.023	0.897	putative protease
STM2137	STM2137	AAL21040	2231496..2232542	0.218	0.081	0.138	0.026	0.636	2.899	0.086	2.283	0.102	0.788	putative cytoplasmic protein
STM2138	STM2138	AAL21041	(2232578..2232994)	0.317	0.027	0.414	0.109	1.308	4.568	0.203	3.942	0.423	0.863	putative cytoplasmic protein
STM2139	STM2139	AAL21042	(2233116..2233451)	0.276	0.046	0.341	0.028	1.237	2.936	0.773	3.233	0.180	1.101	putative inner membrane protein
yegS	STM2140	AAL21043	2234013..2234912	0.413	0.042	0.327	0.046	0.790	0.942	0.016	1.420	0.058	1.508	putative diacylglycerol kinase catalytic domain

fbaB	STM2141	AAL21044	(2234965..2236017)	1.153	0.204	0.490	0.068	0.425	5.027	0.697	5.531	0.282	1.100	3-oxoacyl-[acyl-carrier-protein] synthase I
yegT	STM2142	AAL21045	2236271..2237542	0.339	0.060	0.328	0.033	0.969	0.397	0.151	0.442	0.027	1.114	putative MFS family transport protein
yegU	STM2143	AAL21046	2237539..2238543	0.985	0.116	0.803	0.167	0.815	0.638	0.049	1.087	0.051	1.703	putative glycohydrolase
yegV	STM2144	AAL21047	2238540..2239505	0.732	0.044	0.680	0.194	0.929	0.689	0.255	0.727	0.140	1.056	putative sugar kinase
yegW	STM2145	AAL21048	(2239479..2240225)	1.397	0.166	0.713	0.076	0.511	0.741	0.134	0.724	0.128	0.976	putative regulatory protein, gntR family
thiD	STM2146	AAL21049	(2240261..2241061)	0.530	0.086	0.300	0.004	0.566	0.317	0.108	0.526	0.039	1.660	bifunctional enzyme: hydroxy-phosphomethylpyrimidine kinase (HMP-P kinase); hydroxy-methylpyrimidine kinase (HMP kinase)
thiM	STM2147	AAL21050	(2241048..2241845)	0.718	0.141	0.846	0.122	1.178	0.627	0.596	0.693	0.197	1.105	hydoxyethylthiazole kinase (THZ kinase)
STM2148	STM2148	AAL21051	2242255..2242569	1.812	0.461	0.684	0.120	0.378	1.716	0.131	0.793	0.051	0.462	putative periplasmic protein
stcD	STM2149	AAL21052	(2242832..2243839)	0.250	0.059	0.147	0.025	0.587	1.113	0.075	1.107	0.054	0.994	putative outer membrane lipoprotein
stcC	STM2150	AAL21053	(2243855..2246344)	0.225	0.089	0.145	0.008	0.645	0.872	0.169	0.712	0.030	0.816	paral putative outer membrane protein
stcB	STM2151	AAL21054	(2246358..2247041)	0.180	0.072	0.143	0.018	0.794	0.450	0.033	0.400	0.027	0.890	putative periplasmic chaperone protein
stcA	STM2152	AAL21055	(2247097..2247627)	0.234	0.066	0.326	0.032	1.392	0.579	0.062	0.424	0.035	0.733	paral putative fimbrial-like protein
yehE	STM2153	AAL21056	(2247906..2248187)	0.375	0.074	0.445	0.050	1.188	3.778	0.186	2.756	0.124	0.729	putative outer membrane protein
mrp	STM2154	AAL21057	(2248465..2249574)	3.202	0.642	3.768	0.686	1.177	1.789	0.268	2.737	0.212	1.530	putative ATP-binding protein
metG	STM2155	AAL21058	2249739..2251772	1.393	0.052	2.110	0.236	1.515	1.289	0.122	2.012	0.175	1.561	methionine tRNA synthetase
yehR	STM2156	AAL21059	2252013..2252471	0.226	0.062	0.232	0.019	1.029	0.277	0.036	0.407	0.077	1.469	putative lipoprotein
STM2156A	STM2156A	AAL21060	2252643..2253173					N/A					N/A	hypothetical 16.9 kd lipoprotein precursor
yehS	STM2157	AAL21061	(2253230..2253697)	1.892	0.235	0.456	0.063	0.241	1.669	0.236	0.565	0.048	0.338	putative cytoplasmic protein
yehT	STM2158	AAL21062	(2253744..2254463)	0.903	0.108	0.937	0.049	1.038	0.570	0.041	0.562	0.012	0.986	putative regulator
yehU	STM2159	AAL21063	(2254460..2256145)	1.138	0.084	0.694	0.100	0.610	0.571	0.021	0.484	0.025	0.847	paral putative sensor/kinase in regulatory system
yehV	STM2160	AAL21064	2256368..2257099	0.678	0.042	0.308	0.078	0.454	0.482	0.004	0.592	0.086	1.228	putative transcriptional repressor (MerR family)
STM2161	STM2161	AAL21065	2257159..2257266	2.187	0.293	1.009	0.016	0.461	2.085	3.668	0.838	0.337	0.402	putative inner membrane protein
yehW	STM2162	AAL21066	(2257247..2257978)	1.008	0.047	0.622	0.056	0.618	0.917	0.098	0.742	0.081	0.809	putative ABC-type proline/glycine betaine transport systems, permease onent
yehX	STM2163	AAL21067	(2257962..2258909)	0.951	0.096	0.459	0.094	0.483	1.019	0.234	0.816	0.018	0.801	putative ABC-type proline/glycine betaine transport system, ATPase onent
yehY	STM2164	AAL21068	(2258902..2260071)	1.318	0.147	0.352	0.028	0.267	1.791	0.413	1.392	0.092	0.777	putative ABC-type proline/glycine betaine transport systems, permease onent
yehZ	STM2165	AAL21069	(2260075..2260992)	1.824	0.416	0.571	0.030	0.313	2.072	0.324	1.969	0.126	0.950	putative ABC superfamily (bind_prot) transport protein (possibly glycine betaine choline transport for osmoprotection)
bglX	STM2166	AAL21070	(2261173..2263470)	0.381	0.050	0.716	0.058	1.882	0.511	0.005	0.956	0.037	1.871	beta-D-glucoside glucohydrolase, periplasmic
dld	STM2167	AAL21071	2263737..2265467	1.050	0.089	1.205	0.179	1.148	1.120	0.035	2.144	0.182	1.914	D-lactate dehydrogenase, NADH independent
pbpG	STM2168	AAL21072	(2265525..2266472)	2.852	0.501	1.327	0.151	0.465	2.693	0.262	1.547	0.090	0.574	D-alanyl-D-alanine endopeptidase; penicillin-binding protein 7 and penicillin-binding protein 8
yohC	STM2169	AAL21073	(2266638..2267225)	0.458	0.046	0.295	0.021	0.644	0.399	0.093	0.461	0.028	1.155	paral putative transport protein
yohD	STM2170	AAL21074	2267357..2267953	0.904	0.049	0.230	0.026	0.254	0.609	0.047	0.496	0.037	0.815	putative DedA family, membrane protein

yohF	STM2171	AAL21075	(2268002..2268763)	0.402	0.078	0.212	0.035	0.527	0.354	0.015	0.476	0.031	1.343	putative oxidoreductase
yohG	STM2172	AAL21076	(2268829..2270265)	0.245	0.068	0.089	0.023	0.364	0.256	0.048	0.228	0.026	0.889	putative Outer membrane efflux protein
STM2173	STM2173	AAL21077	2270456..2270653	0.525	0.269	0.220	0.022	0.419	0.373	0.359	0.205	0.053	0.550	putative cytoplasmic protein
yohI	STM2174	AAL21078	(2270724..2271662)	0.451	0.048	0.229	0.032	0.508	0.378	0.038	0.335	0.017	0.888	putative nitrogen regulation protein
STM2175	STM2175	AAL21079	(2271771..2272964)	0.658	0.030	0.480	0.040	0.730	0.439	0.092	0.519	0.021	1.182	putative monooxygenase
STM2176	STM2176	AAL21080	(2272979..2273623)	0.503	0.040	0.360	0.051	0.715	0.291	0.031	0.476	0.045	1.635	putative glutathione S-transferase
STM2177	STM2177	AAL21081	(2273632..2274333)	0.372	0.057	0.270	0.015	0.726	0.254	0.001	0.370	0.059	1.456	putative flutathione S-transferase
STM2178	STM2178	AAL21082	(2274349..2275386)	0.493	0.058	0.258	0.017	0.523	0.288	0.074	0.377	0.029	1.309	putative 1,2-dioxygenase protein
STM2179	STM2179	AAL21083	(2275398..2276756)	0.429	0.072	0.135	0.025	0.315	0.194	0.030	0.229	0.009	1.184	putative sugar transporter
STM2180	STM2180	AAL21084	2276882..2277790	1.277	0.124	0.583	0.029	0.457	0.289	0.015	0.569	0.077	1.973	putative transcriptional regulator, LysR family
yohJ	STM2181	AAL21085	2277922..2278320	0.763	0.065	0.339	0.148	0.444	0.854	0.651	0.445	0.085	0.521	putative effector of murein hydrolase LrgA
yohK	STM2182	AAL21086	2278317..2279012	0.375	0.079	0.410	0.099	1.093	0.294	0.058	0.555	0.048	1.891	putative transmembrane protein
cdd	STM2183	AAL21087	2279166..2280050	0.580	0.061	1.087	0.090	1.875	0.608	0.036	1.713	0.060	2.819	cytidine/deoxycytidine deaminase
sanA	STM2184	AAL21088	2280227..2280946	1.576	0.083	1.619	0.247	1.027	1.526	0.174	2.312	0.102	1.515	vancomycin sensitivity
STM2185	STM2185	AAL21089	2280943..2281188	1.330	0.049	0.611	0.210	0.459	2.101	0.300	1.034	0.238	0.492	putative inner membrane protein
STM2186	STM2186	AAL21090	2281393..2282634	0.343	0.087	1.048	0.077	3.059	2.692	0.308	3.757	0.097	1.396	putative NADPH-dependent glutamate synthase beta chain or related oxidoreductase
yeiA	STM2187	AAL21091	2282628..2283863	0.419	0.047	1.099	0.096	2.623	3.135	0.042	4.219	0.282	1.346	putative dihydropyrimidine dehydrogenase
mglC	STM2188	AAL21092	(2283938..2284948)	1.316	0.400	1.019	0.097	0.775	0.561	0.033	0.885	0.042	1.576	ABC superfamily (membrane), methyl-galactoside transport protein
mglA	STM2189	AAL21093	(2284964..2286484)	2.017	0.460	2.244	0.482	1.112	0.503	0.005	0.855	0.047	1.701	ABC superfamily (atp_bind), galactose (methyl-galactoside) transport protein
mglB	STM2190	AAL21094	(2286618..2287616)	8.599	2.315	7.264	0.885	0.845	0.964	0.030	2.166	0.155	2.248	ABC superfamily (peri_perm), galactose transport protein
galS	STM2191	AAL21095	(2288115..2289137)	1.105	0.101	0.770	0.072	0.697	0.260	0.059	0.761	0.057	2.932	transcriptional repressor of mgl operon (GalR/LacI family)
yeiB	STM2192	AAL21096	(2289287..2290429)	0.756	0.076	0.441	0.097	0.583	0.488	0.014	0.449	0.036	0.922	putative inner membrane protein
folE	STM2193	AAL21097	(2290444..2291112)	0.908	0.032	1.537	0.105	1.692	1.002	0.543	1.350	0.099	1.348	GTP cyclohydrolase I
yeiG	STM2194	AAL21098	2291442..2292179	1.472	0.123	7.126	1.074	4.841	2.388	0.152	12.881	0.856	5.394	putative esterase
STM2195	STM2195	AAL21099	(2292287..2292676)	0.732	0.080	1.177	0.246	1.608	2.708	1.181	1.949	0.103	0.720	putative transcriptional regulator
STM2196	STM2196	AAL21100	(2292681..2294048)	0.381	0.104	0.286	0.031	0.751	1.855	0.049	1.312	0.069	0.707	putative D-serine dehydratase
STM2197	STM2197	AAL21101	2294265..2295152	0.179	0.126	0.152	0.026	0.847	0.374	0.067	0.496	0.020	1.325	putative phosphoserine phosphatase
STM2198	STM2198	AAL21102	2295185..2296507	0.351	0.125	0.144	0.027	0.410	0.570	0.057	0.597	0.040	1.048	putative regulatory protein
cirA	STM2199	AAL21103	(2296551..2298542)	0.250	0.126	0.162	0.010	0.647	0.134	0.044	0.207	0.015	1.541	outer membrane porin, receptor for colicin I, requires TonB
lysP	STM2200	AAL21104	(2298888..2300357)	1.660	0.066	0.493	0.056	0.297	1.406	0.231	0.686	0.056	0.488	APC family, lysine-specific permease
yeiE	STM2201	AAL21105	(2300547..2301410)	1.372	0.048	1.423	0.206	1.037	0.656	0.051	0.994	0.046	1.514	putative transcriptional regulator, LysR family
yeiH	STM2202	AAL21106	2301531..2302580	0.972	0.043	0.884	0.083	0.910	0.465	0.122	1.055	0.054	2.267	putative inner membrane protein

nfo	STM2203	AAL21107	2302659..2303516	0.559	0.046	0.897	0.084	1.606	0.437	0.044	0.845	0.075	1.935	endonuclease IV
fruA	STM2204	AAL21108	(2303581..2305269)					N/A					N/A	Sugar Specific PTS system, fructose-specific transport protein
fruK	STM2205	AAL21109	(2305286..2306224)	0.442	0.095	0.301	0.068	0.681	0.533	0.070	0.618	0.148	1.159	fructose-1-phosphate kinase
fruF	STM2206	AAL21110	(2306224..2307354)	0.389	0.124	0.580	0.148	1.492	0.617	0.144	0.458	0.077	0.742	phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2
setB	STM2207	AAL21111	2307723..2308904	0.302	0.072	0.148	0.020	0.489	0.389	0.016	0.895	3.657	2.304	proton efflux pump
STM2208	STM2208	AAL21112	(2308969..2309634)	0.257	0.081	0.153	0.027	0.594	0.513	0.013	0.433	0.037	0.844	putative inner membrane protein
STM2209	STM2209	AAL21113	(2309636..2309758)	1.584	0.099	0.684	0.080	0.432	1.739	1.151	0.758	0.582	0.436	putative inner membrane protein
STM2210	STM2210	pseudogene; frameshift						N/A					N/A	
yeiP	STM2211	AAL21114	2310493..2311296	2.411	0.182	1.064	0.159	0.441	1.957	0.149	0.897	0.055	0.458	putative elongation factor
yeiR	STM2212	AAL21115	2311509..2312495	0.900	0.040	0.704	0.078	0.783	0.643	0.016	0.830	0.036	1.290	putative cobalamin synthesis protein
yeiU	STM2213	AAL21116	2312525..2313244	3.167	0.141	1.685		0.532	7.444	1.406			0.000	putative permease
spr	STM2214	AAL21117	2313658..2314230	25.902	3.108	15.479	2.380	0.598	15.593	1.085	10.997	0.992	0.705	putative lipoprotein, suppresses thermosensitivity of prc mutants at low osmolality
rtn	STM2215	AAL21118	2314556..2316112	0.853	0.052	0.557	0.048	0.653	0.561	0.015	0.447	0.041	0.797	putative membrane protein involved in resistance to lambda and N4 phages
yejA	STM2216	AAL21119	2316219..2318024	0.370	0.058	0.367	0.054	0.992	0.236	0.004	0.366	0.033	1.551	putative ABC transporter periplasmic binding protein
yejB	STM2217	AAL21120	2318034..2319128	0.705	0.057	0.468	0.143	0.664	0.678	0.118	0.706	0.039	1.041	putative ABC-type dipeptide/oligopeptide/nickel transport systems, permease onent
yejE	STM2218	AAL21121	2319128..2320153	0.493	0.043	0.329	0.028	0.668	0.494	0.078	0.557	0.083	1.127	putative ABC-type dipeptide/oligopeptide/nickel transport systems, permease onent
yejF	STM2219	AAL21122	2320155..2321744	0.521	0.028	0.737	0.076	1.416	0.578	0.057	1.021	0.059	1.766	putative ATPase onent of ABC-type transport system, contain duplicated ATPase domain
yejG	STM2220	AAL21123	(2321748..2322092)	2.570	0.511	1.240	0.249	0.483	4.549	0.839	2.293	0.129	0.504	putative cytoplasmic protein
bcr	STM2221	AAL21124	(2322483..2323673)	0.808	0.098	0.335	0.027	0.415	0.680	0.024	0.411	0.023	0.604	MFS family multidrug transport protein, bicyclomycin resistance protein
rsuA	STM2222	AAL21125	(2323701..2324396)	1.081	0.075	0.756	0.125	0.699	0.724	0.044	0.645	0.036	0.890	16S rRNA pseudouridylate 516 synthase
yejH	STM2223	AAL21126	2324548..2326308	0.600	0.051	0.450	0.037	0.751	0.318	0.011	0.409	0.046	1.285	putative ATP-dependent helicase
rplY	STM2224	AAL21127	2326433..2326717	8.834	1.131	5.020	0.680	0.568	4.642	0.441	2.457	0.173	0.529	50S ribosomal subunit protein L25
STM2225	STM2225	AAL21128	(2326826..2327446)	1.686	0.136	1.052	0.106	0.624	1.393	0.074	0.972	0.028	0.698	putative inner membrane protein
yejK	STM2226	AAL21129	(2327474..2328481)	1.655	0.079	1.277	0.114	0.772	1.807	0.033	1.365	0.070	0.755	nucleotide associated protein, present in spermidine nucleoids
yejL	STM2227	AAL21130	2328661..2328888	5.391	0.671	1.461	0.105	0.271	3.219	0.513	1.304	0.149	0.405	putative cytoplasmic protein
yejM	STM2228	AAL21131	2328920..2330680	3.351	0.359	0.846	0.127	0.252	2.104	0.375	0.996	0.074	0.473	putative hydrolase of alkaline phosphatase superfamily
tRNAPro2	STM2229						N/A					N/A		

STM2230	STM2230	AAL21132	(2330961..2331464)	0.478	0.109	0.246	0.046	0.514	0.422	0.099	0.281	0.014	0.666	putative peptidase
STM2231	STM2231	AAL21133	2331492..2331782	1.088	0.286	1.702	0.609	1.564	1.254	0.382	1.289	0.302	1.028	Homolog of msgA; ssrB-regulated factor
oafA	STM2232	AAL21134	2332130..2333959	2.626	0.469	0.771	0.080	0.294	5.761	0.136	2.189	0.055	0.380	O-antigen five: acetylation of the O-antigen (LPS)
STM2233	STM2233	AAL21135	(2334013..2334456)	0.292	0.102	0.191	0.060	0.655	1.013	0.033	0.599	0.018	0.591	putative cytoplasmic protein
STM2234	STM2234	AAL21136	(2334834..2335361)	0.235	0.080	0.123	0.018	0.523	0.309	0.057	0.605	0.060	1.959	putative tail fiber assembly protein
STM2235	STM2235	AAL21137	(2335364..2336605)	0.187	0.092	0.107	0.010	0.574	0.205	0.069	0.312	0.018	1.519	putative phage protein
STM2236	STM2236	AAL21138	(2336666..2337184)	0.199	0.104	0.109	0.022	0.547	0.205	0.051	0.281	0.027	1.372	putative phage protein
STM2237	STM2237	AAL21139	(2337198..2337527)	0.439	0.076	0.218	0.010	0.497	0.409	0.133	0.419	0.050	1.025	putative inner membrane protein
STM2238	STM2238	AAL21140	2337824..2339155					N/A					N/A	putative phage protein
STM2239	STM2239	AAL21141	(2339184..2339552)	0.404	0.031	0.248	0.010	0.614	0.497	0.196	0.517	0.057	1.040	putative phage protein; homology to antiterminator protein Q of phage P5
STM2240	STM2240	AAL21142	(2339567..2340556)	0.210	0.093	0.135	0.003	0.643	0.291	0.015	0.668	0.072	2.293	putative cytoplasmic protein
sspH2	STM2241	AAL21143	(2340885..2343251)	0.243	0.090	0.212	0.031	0.872	0.463	0.132	1.027	0.072	2.221	Leucine-rich repeat protein, induced by the SPI-2 regulator ssrA/B
STM2242	STM2242	AAL21144	(2343420..2343623)	0.208	0.120	0.090	0.008	0.433	0.383	0.077	0.323	0.062	0.843	putative tail fiber protein of phage
STM2243	STM2243	AAL21145	(2343920..2344711)	0.199	0.107	0.148	0.019	0.743	0.441	0.050	0.595	0.022	1.349	putative tail fiber protein of phage
STM2244	STM2244	AAL21146	2345014..2345217	0.312	0.061	0.215	0.010	0.689	1.732	0.362	1.529	0.215	0.882	homolog of virulence protein MsgA
STM2245	STM2245	AAL21147	(2345409..2345972)					N/A					N/A	putative outer membrane protein
narP	STM2246	AAL21148	2346702..2347349	1.200	0.079	2.776	0.124	2.314	1.192	0.055	1.331	0.014	1.116	response regulator in two-onent regulatory system with NarQ (or NarX)
STM2247	STM2247	AAL21149	1.653	0.138	0.867	0.179	0.525	2.114	0.102	0.892	0.057	0.422	regulatory RNA	
STM2251	STM2251	AAL21153	1.969	0.412	1.727	0.475	0.877	1.476	0.408	1.188	0.342	0.805	signal recognition particle, RNA onent	
STM2253	STM2253	AAL21155	1.257	0.420	0.944	0.083	0.750	1.023	0.750	0.916	0.191	0.895	5S ribosomal RNA	
napC	STM2255	AAL21157	(2353683..2354285)	0.469	0.058			0.000	0.544	0.177			0.000	periplasmic nitrate reductase, cytochrome c-type protein
napB	STM2256	AAL21158	(2354295..2354744)	0.671	0.036	22.150	1.508	33.022	0.858	0.218	1.179	0.031	1.374	periplasmic nitrate reductase, small subunit, cytochrome C550, in lex with NapA
napH	STM2257	AAL21159	(2354860..2355729)	0.470	0.075	11.510	0.823	24.504	0.792	0.128	0.589	0.046	0.744	ferredoxin-type protein: electron transfer
napG	STM2258	AAL21160	(2355716..2356411)					N/A					N/A	ferredoxin-type protein: electron transfer
napA	STM2259	AAL21161	(2356418..2358904)	1.785	0.358	1.202	0.302	0.673	2.376	3.970	1.131	0.515	0.476	periplasmic nitrate reductase, large subunit, in lex with NapB
napD	STM2260	AAL21162	(2358901..2359164)	0.315	0.074	5.605	0.551	17.812	0.126	0.002	0.422	0.106	3.359	periplasmic nitrate reductase
napF	STM2261	AAL21163	(2359154..2359645)	0.378	0.144	3.854	0.675	10.210	0.164	0.014	0.209	0.033	1.270	ferredoxin-type protein: electron transfer
eco	STM2262	AAL21164	2360059..2360553	0.900	0.106	2.696	0.226	2.997	0.461	0.054	0.783	0.027	1.698	ecotin, a serine protease inhibitor
yojI	STM2263	AAL21165	(2360762..2362405)	0.923	0.029	0.251	0.031	0.272	0.406	0.033	0.313	0.035	0.771	putative ABC-type multidrug/protein/lipid transport system, ATPase onent
alkB	STM2264	AAL21166	(2362481..2363131)	1.273	0.038	0.749	0.017	0.588	0.641	0.153	0.661	0.086	1.032	DNA repair system specific for alkylated DNA

ada	STM2265	AAL21167	(2363134..2364195)	1.731	0.104	1.417	0.168	0.819	0.917	0.178	1.156	0.055	1.261	bifunctional: O6-methylguanine-DNA methyltransferase; transcription activator/repressor (AraC/Xyl family)
apbE	STM2266	AAL21168	(2364276..2365328)	1.566	0.054	2.092	0.278	1.336	0.928	0.077	0.887	0.145	0.956	putative thiamine biosynthesis lipoprotein
ompC	STM2267	AAL21169	(2365443..2366579)	49.556	0.655	57.945	3.205	1.169	16.546	1.963	23.201	1.695	1.402	outer membrane protein 1b (ib;c), porin
yojN	STM2269	AAL21170	2367308..2369977	0.848	0.055	0.948	0.098	1.117	0.479	0.109	0.629	0.068	1.312	putative sensor/kinase in regulatory system
rcsB	STM2270	AAL21171	2369994..2370644	4.401	0.704	3.696	0.616	0.840	2.417	0.196	2.525	0.156	1.045	response regulator (positive) in two-onent regulatory system with RcsC (LuxR/UhpA familiy)
rcsC	STM2271	AAL21172	(2370747..2373593)	1.255	0.037	0.676	0.085	0.539	0.743	0.050	0.532	0.035	0.716	sensory histidine kinase in two-onent regulatory system with RcsB, regulates colanic capsule biosynthesis
gyrA	STM2272	AAL21173	(2373711..2376347)	7.091	0.353	5.315	0.636	0.750	5.127	0.292	2.936	0.130	0.573	DNA gyrase, subunit A, type II topoisomerase
STM2273	STM2273	AAL21174	(2376757..2377959)					N/A					N/A	putative dehydratase protein
STM2274	STM2274	AAL21175	(2377974..2379299)	0.493	0.102	0.185	0.022	0.376	0.642	0.129	0.353	0.134	0.550	putative permease
STM2275	STM2275	AAL21176	2379349..2380233	0.521	0.038	0.361	0.026	0.693	1.301	0.107	0.515	0.064	0.396	putative regulatory protein, gntR family
ubiG	STM2276	AAL21177	2380316..2381044	0.999	0.028	1.528	0.149	1.529	0.925	0.085	1.183	0.054	1.279	3-demethylubiquinone-9 3-methyltransferase and 2-octaprenyl-6-hydroxy phenol methylase
nrdA	STM2277	AAL21178	2381400..2383685	1.534	0.109	5.704	0.843	3.719	1.064	0.037	2.296	0.071	2.158	ribonucleoside diphosphate reductase 1, alpha subunit
nrdB	STM2278	AAL21179	2383798..2384928	1.931	0.125	5.251	0.149	2.719	1.002	0.016	1.374	0.150	1.372	ribonucleoside-diphosphate reductase 1, beta subunit
yfaE	STM2279	AAL21180	2384928..2385182	2.483	0.332	3.113	0.506	1.254	1.265	0.349	1.101	0.093	0.871	putative ferredoxin
STM2280	STM2280	AAL21181	(2385184..2386374)	0.552	0.083	0.530	0.104	0.960	0.491	0.153	0.268	0.035	0.545	putative permease
STM2281	STM2281	AAL21182	2386536..2387414	0.920	0.098	1.818	0.175	1.975	0.296	0.036	0.398	0.019	1.345	putative transcriptional regulator, LysR family
glpQ	STM2282	AAL21183	(2387530..2388600)	4.286	0.380	29.336	1.745	6.846	0.209	0.015	1.287	0.061	6.160	glycerophosphodiester phosphodiesterase, periplasmic
glpT	STM2283	AAL21184	(2388605..2389963)	4.849	0.683	18.182	3.773	3.749	0.258	0.027	1.287	0.137	4.999	MFS family, sn-glycerol-3-phosphate transport protein
glpA	STM2284	AAL21185	2390236..2391864	0.393	0.181	3.232	0.306	8.231	0.180	0.018	0.555	0.070	3.082	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit
glpB	STM2285	AAL21186	2391854..2393113	0.464	0.188	6.081	1.176	13.094	0.167	0.005	0.514	0.104	3.070	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit
glpC	STM2286	AAL21187	2393110..2394300	0.292	0.116	5.548	0.763	19.009	0.224	0.024	0.566	0.031	2.524	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit
STM2287	STM2287	AAL21188	2394795..2395748	0.334	0.049	0.422	0.043	1.263	7.474	0.614	4.750	0.384	0.636	putative cytoplasmic protein
STM2288	STM2288	AAL21189	(2395858..2396034)	0.620	0.086	0.390	0.024	0.629	1.267	0.203	1.093	0.112	0.863	putative cytoplasmic protein
STM2289	STM2289	AAL21190	(2396040..2396843)	0.747	0.051	0.523	0.059	0.700	0.696	0.080	0.851	0.027	1.224	putative 2,4-dihydoxyhept-2-ene-1,7-dioic acid aldolase
yfaV	STM2290	AAL21191	(2396869..2398158)	0.419	0.066	0.329	0.040	0.786	0.351	0.000	0.415	0.034	1.182	putative MFS family transport protein
yfaW	STM2291	AAL21192	(2398214..2399431)	0.490	0.104	0.725	0.029	1.480	0.315	0.017	0.315	0.024	0.998	paral putative galactonate dehydratase

yfaX	STM2292	AAL21193	(2399433..2400215)	0.255	0.056	0.250	0.030	0.981	0.140	0.010	0.263	0.021	1.874	putative transcriptional regulator
STM2293	STM2293	AAL21194	(2400465..2401661)					N/A					N/A	putative nucleotide-utilizing enzyme related to molybdopterin-biosynthesis
yfaZ	STM2294	AAL21195	(2401776..2402423)	3.483	0.313	1.031	0.066	0.296	3.157	0.512	1.267	0.077	0.401	putative inner membrane protein
yfaO	STM2295	AAL21196	2402597..2403022	3.588	0.706	0.863	0.114	0.241	1.420	0.124	0.871	0.133	0.613	putative NTP pyrophosphohydrolases including oxidative damage repair enzymes
ais	STM2296	AAL21197	(2403067..2403672)	5.220	0.587	1.015	0.064	0.194	9.466	1.754	2.583	0.106	0.273	aluminum inducible protein
yfbE	STM2297	AAL21198	2403953..2405110	3.744	0.504	3.088	0.515	0.825	6.347	1.023	5.939	0.260	0.936	putative DegT/DnrJ/EryC1/StrS family
pmrF	STM2298	AAL21199	2405113..2406096	3.924	0.434	3.178	0.674	0.810	8.074	2.400	8.697	0.792	1.077	putative glycosyl transferase
yfbG	STM2299	AAL21200	2406093..2408075	2.382	0.253	4.236	0.582	1.779	5.341	0.976	7.098	0.305	1.329	paral putative transformylase
STM2300	STM2300	AAL21201	2408072..2408971	1.619	0.069	2.567	0.107	1.586	3.678	0.326	4.419	0.358	1.201	putative cytoplasmic protein
pqaB	STM2301	AAL21202	2408968..2410614	1.366	0.093	1.051	0.056	0.770	2.909	0.185	1.808	0.196	0.622	putative melittin resistance protein, PqaB, affects polymycin B resistance and lipopolysaccharide synthesis
STM2302	STM2302	AAL21203	2410611..2410946	1.981	0.132	0.893	0.132	0.451	3.107	0.689	1.749	0.087	0.563	putative inner membrane protein
STM2303	STM2303	AAL21204	2410946..2411323	2.025	0.168	1.254	0.224	0.619	3.091	0.451	2.396	0.117	0.775	putative inner membrane protein
pmrD	STM2304	AAL21205	(2411318..2411575)	3.363	0.658	1.979	0.140	0.589	5.948	0.028	3.947	0.253	0.664	polymyxin resistance protein B
menE	STM2305	AAL21206	(2411673..2413040)	1.921	0.218	3.399	0.534	1.769	0.889	0.121	1.072	0.050	1.206	o-succinylbenzoate-CoA ligase
menC	STM2306	AAL21207	(2413037..2413999)	1.919	0.208	4.810	0.991	2.507	0.921	0.114	1.287	0.075	1.397	o-succinylbenzoyl-CoA synthase
menB	STM2307	AAL21208	(2413999..2414856)	2.154	0.197	5.191	0.536	2.410	1.111	0.261	1.583	0.102	1.425	dihydroxynaphtoic acid synthetase
yfbB	STM2308	AAL21209	(2414871..2415629)					N/A					N/A	putative enzyme
menD	STM2309	AAL21210	(2415626..2417296)					N/A					N/A	bifunctional: 2-oxoglutarate decarboxylase; SHCHC synthase
menF	STM2310	AAL21211	(2417382..2418677)	1.198	0.075	1.217	0.059	1.016	0.922	0.138	0.459	0.034	0.498	isochorismate synthase (isochorismate hydroxymutase 2), menaquinone biosynthesis
elaB	STM2311	AAL21212	(2418778..2419089)	2.193	0.705	1.960	0.375	0.894	3.162	0.284	2.309	0.115	0.730	putative inner membrane protein
elaA	STM2312	AAL21213	(2419138..2419599)	0.815	0.015	1.265	0.099	1.552	0.562	0.053	1.058	0.024	1.884	putative acyltransferase
elaC	STM2313	AAL21214	2419660..2420577	0.957	0.065	0.926	0.080	0.968	0.367	0.015	0.453	0.051	1.234	putative metal-dependent hydrolase
STM2314	STM2314	AAL21215	2420643..2421644	2.714	0.138			0.000	0.253	0.010			0.000	putative chemotaxis signal transduction protein
yfbK	STM2315	AAL21216	(2421685..2423466)	0.437	0.060	0.624	0.074	1.427	0.276	0.038	0.332	0.019	1.202	putative von Willebrand factor, vWF type A domain
nuoN	STM2316	AAL21217	(2424354..2425631)	10.530	0.632	7.420	0.832	0.705	4.217	0.612	3.385	0.487	0.803	NADH dehydrogenase I chain N
nuoM	STM2317	AAL21218	(2425818..2427347)	10.806	1.351	8.119	1.392	0.751	3.999	0.766	3.976	0.373	0.994	NADH dehydrogenase I chain M
nuoL	STM2318	AAL21219	(2427661..2429502)	8.571	0.266	8.285	0.754	0.967	4.828	1.087	4.095	0.208	0.848	NADH dehydrogenase I chain L
nuoK	STM2319	AAL21220	(2429499..2429801)	6.682	0.217			0.000	4.184	0.327			0.000	NADH dehydrogenase I chain K
nuoJ	STM2320	AAL21221	(2429798..2430352)	7.142	0.414	7.410	1.130	1.037	3.588	0.530	4.267	0.377	1.189	NADH dehydrogenase I chain J
nuoI	STM2321	AAL21222	(2430363..2430905)	6.713	0.920	9.163	1.430	1.365	3.581	0.014	4.401	0.303	1.229	NADH dehydrogenase I chain I
nuoH	STM2322	AAL21223	(2430920..2431897)	7.418	0.618	5.379	0.559	0.725	4.879	0.703	3.482	0.156	0.714	NADH dehydrogenase I chain H
nuoG	STM2323	AAL21224	(2431894..2434626)	13.653	2.922	15.688	0.919	1.149	6.654	0.950	7.252	1.047	1.090	NADH dehydrogenase I chain G

nuoF	STM2324	AAL21225	(2434651..2435988)	6.558	1.659	18.673	3.241	2.847	2.694	0.343	4.271	0.621	1.586	NADH dehydrogenase I chain F
nuoE	STM2325	AAL21226	(2435985..2436485)	9.261	1.678	17.999	0.398	1.944	4.830	0.233	5.629	0.827	1.165	NADH dehydrogenase I chain E
nuoC	STM2326	AAL21227	(2436488..2438290)	6.753	0.804	15.560	1.412	2.304	3.484	0.262	4.091	0.385	1.174	NADH dehydrogenase I chain C,D
nuoB	STM2327	AAL21228	(2438377..2439039)	12.504	0.327	18.424	1.707	1.473	5.757	0.734	6.078	0.229	1.056	NADH dehydrogenase I chain B
nuoA	STM2328	AAL21229	(2439055..2439498)	19.186	0.917	13.501	1.349	0.704	8.446	1.534	5.807	0.189	0.688	NADH dehydrogenase I chain A
STM2329	STM2329	AAL21230	(2439893..2440045)	2.823	0.281	1.567	0.458	0.555	2.273	0.532	1.004	0.138	0.442	putative cytoplasmic protein
lrhA	STM2330	AAL21231	(2440125..2441063)	1.681	0.057	1.551	0.034	0.923	10.815	0.969	7.101	0.349	0.657	NADH dehydrogenase transcriptional repressor (LysR family)
yfbQ	STM2331	AAL21232	2441995..2443209	0.691	0.053			0.000	0.958	0.034			0.000	putative aminotransferase (ortho), paral putative regulator
STM2332	STM2332	AAL21233	2443303..2443902	2.416	0.339	1.177	0.214	0.487	1.915	0.057	1.000	0.050	0.522	putative hydrolase of HD superfamily
yfbS	STM2333	AAL21234	(2443994..2445820)	1.570	0.232	0.734	0.084	0.467	0.758	0.162	0.405	0.018	0.535	putative response regulator
yfbT	STM2334	AAL21235	(2445897..2446574)	1.836	0.118	2.787	0.267	1.518	0.931	0.118	1.391	0.034	1.493	putative phosphatase
yfbU	STM2335	AAL21236	(2446567..2447061)	1.496	0.078	3.202	0.025	2.141	0.798	0.069	1.540	0.087	1.929	putative cytoplasmic protein
STM2336	STM2336	AAL21237	(2447144..2447599)	3.268	0.583	2.209	0.351	0.676	1.724	0.174	1.160	0.127	0.673	putative cytoplasmic protein
ackA	STM2337	AAL21238	2447939..2449141	1.443	0.042	12.421	0.913	8.607	0.617	0.040	1.412	0.088	2.289	acetate kinase A (propionate kinase 2)
pta	STM2338	AAL21239	2449218..2451362	1.112	0.113	18.538	1.641	16.673	0.570	0.053	1.795	0.108	3.149	phosphotransacetylase
yfcC	STM2339	AAL21240	2451580..2453100	0.506	0.042	0.974	0.104	1.927	0.346	0.135	0.213	0.007	0.616	putative integral membrane protein
STM2340	STM2340	AAL21241	(2453149..2454102)	1.178	0.300	8.842	0.708	7.505	0.537	0.084	0.901	0.011	1.676	putative transketolase
STM2341	STM2341	AAL21242	(2454095..2454925)	1.031	0.151			0.000	0.401	0.090			0.000	putative transketolase
STM2342	STM2342	AAL21243	(2454922..2456313)	1.401	0.429	5.943	0.877	4.241	0.350	0.009	0.569	0.064	1.628	putative inner membrane protein
STM2343	STM2343	AAL21244	(2456334..2456606)	1.237	0.182	4.213	0.437	3.405	0.402	0.066	0.520	0.042	1.292	putative cytoplasmic protein
STM2344	STM2344	AAL21245	(2456687..2457130)	1.713	0.154	2.033	0.144	1.187	0.495	0.046	0.522	0.020	1.053	putative phosphotransferase system
STM2345	STM2345	AAL21246	2457383..2458402	1.416	0.032	0.988	0.159	0.698	0.583	0.034	0.774	0.020	1.327	putative transcriptional regulator
STM2346	STM2346	AAL21247	(2458408..2458962)	4.510	0.336	3.045	0.337	0.675	3.469	0.168	4.509	0.290	1.300	putative NTP pyrophosphohydrolase
yfcE	STM2347	AAL21248	(2459019..2459570)	3.526	0.213	3.712	0.434	1.053	1.946	0.214	4.096	0.241	2.105	putative phosphoesterase
yfcF	STM2348	AAL21249	(2459626..2460270)	0.797	0.047	1.329	0.146	1.668	0.777	0.042	1.654	0.243	2.128	putataive glutathione-S-transferase
yfcG	STM2349	AAL21250	2460413..2461060	0.349	0.083	0.394	0.069	1.128	0.374	0.026	1.262	0.075	3.370	putative glutathione S-transferase
yfcH	STM2350	AAL21251	2461186..2462079	1.303	0.227	0.521	0.025	0.400	0.580	0.029	0.504	0.056	0.870	putative sugar nucleotide epimerase
hisP	STM2351	AAL21252	(2462131..2462907)	1.566	0.664	0.622	0.100	0.397	0.600	0.036	0.662	0.022	1.104	ABC superfamily (atp_bind), histidine and lysine/arginine/ornithine transport protein
hisM	STM2352	AAL21253	(2462918..2463625)	1.249	0.305	0.589	0.116	0.471	0.651	0.038	0.593	0.066	0.911	ABC superfamily (membrane),histidine and lysine/arginine/ornithine transport protein
hisQ	STM2353	AAL21254	(2463622..2464308)	1.202	0.287	0.679	0.055	0.565	0.420	0.047	0.452	0.058	1.074	ABC superfamily (membrane),histidine and lysine/arginine/ornithine transport system
hisJ	STM2354	AAL21255	(2464491..2465273)	4.872	1.419	2.230	0.215	0.458	1.568	0.040	1.152	0.177	0.734	ABC superfamily (bind_prot), histidine transport protein

argT	STM2355	AAL21256	(2465511..2466293)	2.586	0.695	1.987	0.219	0.768	0.384	0.014	0.415	0.022	1.082	ABC superfamily (bind_prot), lysine/arginine/ornithine transport protein
ubiX	STM2356	AAL21257	(2466582..2467151)	2.333	0.319	0.938	0.113	0.402	1.270	0.349	1.049	0.070	0.826	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
STM2357	STM2357	AAL21258	(2467178..2468584)	1.362	0.149	0.538	0.102	0.395	0.691	0.055	0.542	0.025	0.783	putative amino acid transporter
STM2358	STM2358	AAL21259	(2468648..2469751)	0.387	0.083	0.230	0.030	0.594	0.373	0.074	0.389	0.027	1.043	putative cytoplasmic protein
STM2359	STM2359	AAL21260	(2469753..2471174)	0.254	0.096	0.162	0.036	0.635	0.257	0.005	0.280	0.015	1.090	putative amino acid transporter
STM2360	STM2360	AAL21261	(2471265..2472662)	0.180	0.095	0.137	0.020	0.759	0.110	0.007	0.192	0.015	1.738	putative diaminopimelate decarboxylase
STM2361	STM2361	AAL21262	2472873..2474300	0.717	0.044	0.855	0.166	1.193	0.251	0.015	0.593	0.028	2.360	putative regulatory protein
purF	STM2362	AAL21263	(2474336..2475853)	2.598	0.492	1.289	0.134	0.496	1.986	0.209	1.667	0.119	0.839	amidophosphoribosyltransferase (PRPP amidotransferase)
cvpA	STM2363	AAL21264	(2475891..2476379)	5.925	1.219	2.369	0.087	0.400	4.139	0.659	2.965	0.070	0.716	membrane protein required for colicin V production
dedD	STM2364	AAL21265	(2476690..2477364)	5.652	1.229	7.662	0.215	1.356	5.340	0.765	6.723	0.407	1.259	paral putative lipoprotein
folC	STM2365	AAL21266	(2477354..2478622)	5.643	0.967	3.482	0.252	0.617	4.437	0.802	3.889	0.074	0.877	multifunctional folylpolyglutamate synthase; dihydrofolate synthase, also has formylTHF polyglutamate synthase activity
accD	STM2366	AAL21267	(2478690..2479604)	7.614	0.970	6.605	1.083	0.867	5.430	0.431	4.766	0.353	0.878	acetylCoA carboxylase, beta subunit
dedA	STM2367	AAL21268	(2479754..2480413)	2.154	0.213	1.151	0.199	0.534	2.756	0.409	1.398	0.078	0.507	putative DedA family
truA	STM2368	AAL21269	(2480462..2481274)	2.075	0.347	1.633	0.206	0.787	2.647	0.514	2.689	0.148	1.016	pseudouridylate synthase I
usg	STM2369	AAL21270	(2481274..2482287)	3.872	0.508	2.152	0.086	0.556	6.111	1.157	5.145	0.104	0.842	putative aspartate-semialdehyde dehydrogenase
pdxB	STM2370	AAL21271	(2482355..2483491)	5.337	0.790	2.481	0.226	0.465	3.507	0.833	2.867	0.043	0.818	erythronate-4-phosphate dehyrogenase
flk	STM2371	AAL21272	2483595..2484596	1.592	0.129	0.872	0.096	0.548	1.320	0.325	0.800	0.031	0.606	Couples flagellar P- and L-ring assembly to flagellar morphogenesis; cell division
STM2372	STM2372	AAL21273	(2484593..2485771)	1.675	0.176	0.808	0.124	0.483	1.147	0.242	1.535	0.049	1.338	putative transport protein
STM2373	STM2373	AAL21274	(2485951..2486325)	0.768	0.084	0.391	0.067	0.510	0.556	0.065	0.626	0.027	1.126	putative cytoplasmic protein
STM2374	STM2374	AAL21275	2486498..2486746	0.865	0.096	0.710	0.333	0.821	0.758	0.205	0.961	0.087	1.268	putatiave helix-turn-helix regulatory protein
STM2375	STM2375	AAL21276	2486915..2487283	0.275	0.142	0.237	0.041	0.862	0.431	0.176	0.361	0.026	0.838	putative cytoplasmic protein
STM2376	STM2376	AAL21277	2487283..2487801	0.299	0.058	0.293	0.091	0.982	0.368	0.017	0.388	0.009	1.055	putative periplasmic protein
STM2377	STM2377	AAL21278	(2487868..2488524)	0.564	0.081	0.852	0.068	1.510	1.226	0.544	0.507	0.032	0.413	putative inner membrane protein
fabB	STM2378	AAL21279	(2488622..2489836)	1.991	0.365	29.977	2.546	15.058	1.909	0.256	6.561	0.184	3.437	3-oxoacyl-[acyl-carrier-protein] synthase I
STM2379	STM2379	AAL21280	2489936..2491996	1.305	0.049	1.328	0.444	1.017	1.018	0.011	0.926	0.125	0.910	putative peptidase
yfcL	STM2380	AAL21281	(2492048..2492323)	2.988	0.552	0.929	0.107	0.311	1.137	0.087	0.810	0.030	0.712	putative cytoplasmic protein
yfcM	STM2381	AAL21282	(2492356..2492904)	1.318	0.074	0.827	0.055	0.628	1.003	0.299	0.658	0.040	0.655	putative cytoplasmic protein
yfcA	STM2382	AAL21283	(2492904..2493713)	1.038	0.074	0.516	0.093	0.497	0.886	0.046	0.440	0.012	0.497	putative permease
mepA	STM2383	AAL21284	(2493713..2494537)	1.301	0.025	1.815	0.243	1.396	0.937	0.142	1.036	0.060	1.105	murein DD-endopeptidase, penicillin-insensitive
aroC	STM2384	AAL21285	(2494541..2495626)	2.121	0.217	2.326	0.224	1.097	1.394	0.217	1.498	0.186	1.074	chorismate synthase
yfcB	STM2385	AAL21286	(2495662..2496594)	2.505	0.086	1.512	0.153	0.604	2.270	0.250	1.211	0.130	0.534	putative methylase
yfcN	STM2386	AAL21287	2496760..2497311	1.328	0.155	0.697	0.129	0.525	0.826	0.141	0.468	0.071	0.566	putative Smr domain

sixA	STM2387	AAL21288	(2497411..2497896)	10.179	1.622	3.643	0.202	0.358	7.126	2.305	3.936	0.075	0.552	phosphohistidine phosphatase
yfcX	STM2388	AAL21289	(2498105..2500252)	3.243	0.178	5.333		1.644	3.712	13.882	1.626		0.438	paral putative dehydrogenase
yfcY	STM2389	AAL21290	(2500252..2501562)	3.000	0.473	1.826	0.308	0.609	0.287	0.003	0.588	0.036	2.050	paral putative acetyl-CoA acetyltransferase
yfcZ	STM2390	AAL21291	(2501740..2502024)	1.036	0.195	2.724	0.275	2.630	0.456	0.035	0.782	0.047	1.715	putative cytoplasmic protein
fadL	STM2391	AAL21292	2502389..2503702	9.763	1.424	3.822	0.206	0.391	1.033	0.083	1.279	0.049	1.238	transport of long-chain fatty acids; sensitivity to phage T2
vacJ	STM2392	AAL21293	(2503763..2504518)	6.283	0.771	3.677	0.372	0.585	4.612	0.651	2.709	0.154	0.587	lipoprotein precursor
yfdC	STM2393	AAL21294	2504807..2505748					N/A					N/A	putative transport
argW	STM2394						N/A					N/A		
pgtE	STM2395	AAL21295	(2506055..2506993)	0.207	0.090	0.168	0.028	0.814	5.669	0.462	16.459	1.012	2.903	Phosphoglycerate transport: outer membrane protein E
pgtA	STM2396	AAL21296	(2507261..2508508)	0.675	0.033	0.540	0.115	0.800	4.374	1.229	3.293	0.051	0.753	Phosphoglycerate transport: activator
pgtB	STM2397	AAL21297	(2508498..2510504)	0.338	0.049	0.627	0.022	1.855	1.172	0.105	1.909	0.211	1.629	Phosphoglycerate transport: protein for signal transmission
pgtC	STM2398	AAL21298	(2510501..2511694)	0.267	0.133	0.467	0.119	1.752	0.752	0.056	1.411	0.225	1.876	Phosphoglycerate transport: protein for signal transmission
pgtP	STM2399	AAL21299	2512130..2513521	0.227	0.095	0.130	0.013	0.572	0.590	0.028	0.407	0.043	0.688	Phosphoglycerate transport: transporter
STM2400	STM2400	AAL21300	(2513797..2514039)	1.187	0.051	0.373	0.049	0.314	1.112	0.125	0.549	0.064	0.494	putative inner membrane protein
ddg	STM2401	AAL21301	2514561..2515481	0.537	0.022	0.334	0.035	0.622	2.591	0.315	0.397	0.025	0.153	cold shock-induced palmitoleoyl transferase
yfdZ	STM2402	AAL21302	(2516005..2517243)	7.251	1.755	1.916	0.299	0.264	2.822	0.311	1.583	0.210	0.561	putative aminotransferase
glk	STM2403	AAL21303	(2517964..2518929)	5.410	0.517	2.029	0.192	0.375	1.987	0.244	1.537	0.139	0.773	glucokinase
STM2404	STM2404	AAL21304	2519133..2520368	0.585	0.005	0.352	0.033	0.602	0.343	0.016	0.467	0.035	1.362	putative chloride channel permease
STM2405	STM2405	AAL21305	(2520388..2522040)	0.598	0.026	0.327	0.058	0.548	0.294	0.009	0.367	0.089	1.248	putative thiamine pyrophosphate enzymes
STM2406	STM2406	AAL21306	2522220..2523218	0.882	0.031	0.712	0.051	0.807	1.098	0.026	1.086	0.072	0.989	putative oxidoreductase
ypeC	STM2407	AAL21307	2523332..2523658	0.795	0.109	0.604	0.074	0.760	0.749	0.091	0.900	0.067	1.202	putative periplasmic protein
mntH	STM2408	AAL21308	(2523719..2524960)	1.100	0.044	0.345	0.033	0.313	0.529	0.017	0.314	0.018	0.595	Nramp family, manganese/divalent cation transport prortein
nupC	STM2409	AAL21309	2525303..2526505	2.281	0.087	1.355	0.188	0.594	2.468	0.293	2.355	0.112	0.954	NUP family, nucleoside transport
yfeA	STM2410	AAL21310	(2526558..2528747)	0.269	0.073	0.400	0.076	1.483	0.250	0.062	0.356	0.047	1.425	putative Diguanylate cyclase/phosphodiesterase domain 1; Diguanylate cyclase/phosphodiesterase domain 2
alaX	STM2411						N/A					N/A		
alaW	STM2412						N/A					N/A		
yfeC	STM2413	AAL21311	2529353..2529715	1.769	0.066	3.623	0.259	2.048	0.563	0.019	0.540	0.063	0.958	putative negative regulator
yfeD	STM2414	AAL21312	2529717..2530109	2.044	0.224	3.688	0.599	1.804	0.331	0.001	0.590	0.035	1.783	putative negative regulator
gltX	STM2415	AAL21313	(2530163..2531578)	2.139	0.146	4.199	0.427	1.963	1.298	0.135	2.092	0.092	1.612	glutamate tRNA synthetase, catalytic subunit
valU	STM2416						N/A					N/A		
valX	STM2417						N/A					N/A		
valY	STM2418						N/A					N/A		

lysV	STM2419						N/A					N/A		
xapR	STM2420	AAL21314	(2532394..2533278)	0.429	0.038	0.338	0.019	0.789	0.996	0.131	0.536	0.040	0.538	regulator for XapA (LysR family)
xapB	STM2421	AAL21315	(2533547..2534803)	0.189	0.079	0.125	0.017	0.662	0.289	0.023	0.226	0.045	0.783	MFS superfamily, xanthosine permease
xapA	STM2422	AAL21316	(2534858..2535691)	0.139	0.102	0.071	0.010	0.511	0.203	0.041	0.209	0.025	1.029	xanthosine phosphorylase (purine nucleoside phosphorylase)
yfeN	STM2423	AAL21317	2535947..2536708	0.182	0.075	0.104	0.023	0.570	0.215	0.055	0.231	0.044	1.076	putative outer membrane protein
yfeR	STM2424	AAL21318	(2536770..2537696)	0.280	0.093	0.188	0.021	0.673	0.230	0.016	0.287	0.021	1.245	putative transcriptional regulator, LysR family
yfeH	STM2425	AAL21319	2537786..2538784	0.853	0.028	0.379	0.013	0.445	0.509	0.120	0.385	0.021	0.756	putative Na+-dependent transporter
STM2426	STM2426	AAL21320	(2538781..2539008)	1.742	0.351	1.062	0.070	0.610	1.117	0.242	0.825	0.135	0.739	putative cytoplasmic protein
lig	STM2427	AAL21321	(2539001..2541016)	1.162	0.108	1.528	0.165	1.314	0.745	0.127	1.107	0.056	1.486	DNA ligase
zipA	STM2428	AAL21322	(2541088..2542074)					N/A					N/A	cell division protein involved in FtsZ ring
cysZ	STM2429	AAL21323	2542306..2543067	1.877	0.268	1.310	0.028	0.698	1.167	0.158	1.318	0.118	1.130	required for sulfate transport
cysK	STM2430	AAL21324	2543231..2544202	1.354	0.049	2.342	0.488	1.730	2.831	0.168	6.172	0.298	2.180	subunit of cysteine synthase A and O-acetylserine sulfhydrolase A
ptsH	STM2431	AAL21325	2544586..2544843	2.670	0.318	14.637	1.080	5.482	1.963	0.147	5.157	0.258	2.628	PTS family, Hpr protein, phosphohistidinoprotein-hexose phosphotransferase
ptsI	STM2432	AAL21326	2544892..2546619	2.910	0.336	8.277	0.395	2.844	2.552	0.170	5.863	0.271	2.298	General PTS family (Enzyme I) PEP-protein phosphotransferase
crr	STM2433	AAL21327	2546660..2547169	7.859	1.071	9.384	0.422	1.194	5.032	0.235	5.860	0.229	1.165	PTS family, glucose-specific IIA onent
STM2434	STM2434	AAL21328	(2547318..2547557)	1.362	0.073	1.096	0.247	0.805	0.786	0.132	0.584	0.074	0.743	putative cytoplasmic protein
pdxK	STM2435	AAL21329	(2547554..2548420)	0.897	0.039	0.559	0.097	0.623	0.378	0.049	0.544	0.071	1.437	pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase
ptsJ	STM2436	AAL21330	2548503..2549795	0.850	0.063	0.369	0.045	0.434	0.378	0.054	0.521	0.017	1.377	putative regulatory protein, gntR family
yfeJ	STM2437	AAL21331	2549810..2550529	0.626	0.120	0.426	0.072	0.680	0.347	0.040	0.440	0.042	1.267	putative GMP synthase - glutamine amidotransferase domain
yfeK	STM2438	AAL21332	2550588..2550968	0.659	0.074	0.618	0.071	0.937	0.328	0.030	0.323	0.044	0.984	putative periplasmic protein
yfeL	STM2439	AAL21333	2550981..2551520	0.691	0.082	0.694	0.047	1.004	0.698	0.020	0.452	0.027	0.648	putative membrane carboxypeptidase (penicillin-binding protein)
cysM	STM2440	AAL21334	(2551651..2552562)	1.330	0.305	0.487	0.056	0.366	2.456	0.311	1.285	0.071	0.523	cysteine synthase B (O-acetylserine sulfhydrolase B)
cysA	STM2441	AAL21335	(2552630..2553727)	0.403	0.043	0.246	0.020	0.611	3.187	0.592	2.487	0.087	0.780	ABC superfamily (atp_bind), sulfate permease A protein; chromate resistance
cysW	STM2442	AAL21336	(2553717..2554592)	0.291	0.108	0.170	0.047	0.583	2.255	0.186	1.069	0.063	0.474	ABC superfamily (membrane), thiosulfate permease W protein
cysU	STM2443	AAL21337	(2554592..2555425)	0.390	0.072	0.305	0.042	0.783	1.663	0.151	0.908	0.044	0.546	ABC superfamily (membrane), thiosulfate transport protein
cysP	STM2444	AAL21338	(2555425..2556441)	0.440	0.041	0.509	0.050	1.158	1.088	0.043	1.376	0.091	1.265	ABC superfamily (bind_prot), thiosulfate transport protein

uA	STM2445	AAL21339	(2556599..2557390)	14.835	1.465	11.172	0.513	0.753	2.474	0.028	2.334	0.081	0.943	putative oxidoreductase
STM2446	STM2446	AAL21340	(2557628..2558527)	1.711	0.170	2.689	0.316	1.572	0.908	0.044	0.732	0.146	0.806	putative iron-dependent peroxidase
STM2447	STM2447	AAL21341	(2558622..2559197)	1.681	0.233	1.997	0.170	1.188	1.394	0.145	0.910	0.030	0.653	putative outer membrane lipoprotein
yfeZ	STM2448	AAL21342	(2559259..2559708)	0.935	0.035	1.210	0.233	1.294	0.766	0.085	0.836	0.033	1.091	putative inner membrane protein
STM2449	STM2449	AAL21343	(2559695..2560231)	1.306	0.075	1.899	0.177	1.454	0.961	0.144	1.239	0.075	1.289	putative acetyltransferase
amiA	STM2450	AAL21344	2560333..2561202	2.005	0.146	0.740	0.026	0.369	1.108	0.146	0.845	0.023	0.763	N-acetylmuramoyl-l-alanine amidase I
hemF	STM2451	AAL21345	2561205..2562104	1.916	0.055	1.141	0.164	0.595	1.416	0.247	1.227	0.097	0.866	coproporphyrinogen III oxidase
STM2452	STM2452	AAL21346	2562125..2562454	0.358	0.041	0.212	0.013	0.592	0.342	0.038	0.289	0.062	0.845	putative inner membrane protein
STM2453	STM2453	AAL21347	2562583..2563860	0.336	0.116	0.474	0.057	1.412	0.471	0.025	0.609	0.050	1.292	putative cytoplasmic protein
eutR	STM2454	AAL21348	(2564060..2565112)	0.489	0.029	0.360	0.035	0.736	0.358	0.060	0.548	0.311	1.529	putative regulator ethanolamine operon (AraC/XylS family)
eutK	STM2455	AAL21349	(2565160..2565654)	1.473	0.108	0.929	0.155	0.631	1.135	0.220	1.052	0.104	0.927	putative carboxysome structural protein, ethanolamine utilization
eutL	STM2456	AAL21350	(2565667..2566326)	0.956	0.060	0.485	0.077	0.507	0.599	0.105	0.686	0.094	1.145	putative carboxysome structural protein, ethanolamine utilization
eutC	STM2457	AAL21351	(2566336..2567232)	0.501	0.101	0.315	0.064	0.628	0.513	0.090	0.480	0.024	0.936	ethanolamine ammonia-lyase, light chain
eutB	STM2458	AAL21352	(2567251..2568612)	0.368	0.117	0.430	0.076	1.171	0.431	0.096	0.417	0.064	0.967	ethanolamine ammonia-lyase, heavy chain
eutA	STM2459	AAL21353	(2568624..2570027)	0.367	0.134	0.203	0.015	0.553	0.423	0.079	0.383	0.061	0.906	PZ-55 prophage; chaperonin in ethanolamine utilization
eutH	STM2460	AAL21354	(2570024..2571250)	0.426	0.069	0.448	0.064	1.051	0.607	0.042	0.625	0.040	1.030	putative transport protein, ethanolamine utilization
eutG	STM2461	AAL21355	(2571370..2572557)					N/A					N/A	paral putative transport protein in ethanolamine utilization
eutJ	STM2462	AAL21356	(2572547..2573386)	0.322	0.110	0.289	0.041	0.896	0.516	0.015	0.671	0.073	1.302	paral putative heatshock protein (Hsp70)
eutE	STM2463	AAL21357	(2573397..2574800)	0.453	0.076	1.231	0.188	2.718	0.811	0.444	1.338	0.217	1.649	putative aldehyde oxidoreductase in ethanolamine utilization
eutN	STM2464	AAL21358	(2574812..2575111)	0.372	0.121	0.691	0.370	1.858	0.664	0.186	0.606	0.093	0.913	putative detox protein in ethanolamine utilization
eutM	STM2465	AAL21359	(2575212..2575502)	0.443	0.080	0.886	0.195	1.998	0.844	0.138	1.027	0.198	1.216	putative detox protein in ethanolamine utilization
eutD	STM2466	AAL21360	(2575543..2576559)	0.277	0.131	0.255	0.033	0.921	0.343	0.045	0.484	0.047	1.413	putative phosphotransacetylase in ethanolamine utilization
eutT	STM2467	AAL21361	(2576556..2577359)	0.293	0.113	0.274	0.046	0.935	0.284	0.397	0.419	0.014	1.475	putative cobalamin adenosyltransferase, ethanolamine utilization
eutQ	STM2468	AAL21362	(2577356..2578045)	0.290	0.139	0.258	0.032	0.890	0.213	0.032	0.404	0.058	1.900	putative ethanolamine utilization protein
eutP	STM2469	AAL21363	(2578023..2578502)	0.264	0.087	0.245	0.026	0.926	0.225	0.027	0.287	0.040	1.273	putative ethanolamine utilization protein
eutS	STM2470	AAL21364	(2578515..2578850)			0.345	0.075	N/A	0.648		0.306	0.048	0.472	putative carboxysome structural protein, ethanol utilization
tnpA_3	STM2471	AAL21365	(2579331..2579789)					N/A					N/A	transposase for IS200
maeB	STM2472	AAL21366	(2579979..2582258)	12.506	2.454	7.099	1.768	0.568	4.992	0.496	5.660	0.310	1.134	paral putative transferase

talA	STM2473	AAL21367	2582530..2583480	0.635	0.044	0.896	0.073	1.412	0.518	0.043	1.043	0.056	2.013	transaldolase A
tktB	STM2474	AAL21368	2583500..2585500	0.564	0.020	1.611	0.084	2.857	0.612	0.046	1.645	0.116	2.689	transketolase 2, isozyme
STM2475	STM2475	AAL21369	(2585563..2585793)	1.631	0.183	1.855	0.072	1.137	2.503	0.123	1.406	0.268	0.562	putative cytoplasmic protein
ypfG	STM2476	AAL21370	(2585921..2586964)	0.289	0.085	0.278	0.019	0.963	0.292	0.041	0.343	0.019	1.171	putative periplasmic protein
yffH	STM2477	AAL21371	(2587089..2587664)	1.377	0.038	0.504	0.022	0.366	1.374	0.156	0.790	0.079	0.575	putative pyrophosphohydrolase
STM2478	STM2478	AAL21372	2587868..2589166	0.594	0.031	0.297	0.078	0.500	0.855	0.129	0.779		0.911	putative beta-lactamase class C
aegA	STM2479	AAL21373	(2589615..2591576)	0.287	0.128	0.557	0.049	1.941	0.232	0.161	0.244	0.018	1.054	putative oxidoreductase
narQ	STM2480	AAL21374	2591762..2593462	0.243	0.108	0.284	0.032	1.171	0.127	0.034	0.207	0.040	1.633	sensory histidine kinase in two-onent regulatory system with NarP (NarL)
acrD	STM2481	AAL21375	2593647..2596760	0.966	0.347			0.000	1.220	1.258	1.093		0.895	RND family, aminoglycoside/multidrug efflux pump
yffB	STM2482	AAL21376	2597334..2597690	2.939	0.330	2.203	0.132	0.749	3.892	0.976	3.682	0.167	0.946	putative glutaredoxin family
dapE	STM2483	AAL21377	2597694..2598821	3.787	0.532	2.353	0.212	0.621	4.422	1.025	3.119	0.105	0.705	N-succinyl-diaminopimelate deacylase
STM2484	STM2484	AAL21378	2598849..2599049	2.962	0.360	2.168	0.392	0.732	3.039	0.451	1.912	0.168	0.629	putative inner membrane protein
ypfI	STM2485	AAL21379	(2599076..2601094)	2.331	0.238	1.442	0.037	0.619	1.104	0.218	1.186	0.072	1.074	putative acetyltransferase
STM2486	STM2486	AAL21380	(2601110..2601973)	1.782	0.177	0.960	0.197	0.539	0.831	0.184	0.617	0.051	0.742	putative inner membrane protein
purC	STM2487	AAL21381	(2602104..2602817)	3.042	0.057	1.947	0.143	0.640	1.212	0.250	1.430	0.139	1.179	phosphoribosylaminoimidazole-succinocarboxamide synthetase (SAICAR synthetase)
nlpB	STM2488	AAL21382	(2602992..2604026)	22.505	4.052	12.476	2.590	0.554	10.597	2.314	6.510	0.604	0.614	lipoprotein-34
dapA	STM2489	AAL21383	(2604043..2604921)	18.497	3.209	12.798	0.544	0.692	8.425	1.099	5.591	0.545	0.664	dihydrodipicolinate synthase
gcvR	STM2490	AAL21384	2605001..2605639	3.553	0.567	3.751	0.739	1.056	1.033	0.082	1.044	0.082	1.010	transcriptional repressor of gcv operon
b	STM2491	AAL21385	2605639..2606109	3.993	0.427	6.299	0.281	1.578	0.953	0.079	1.734	0.169	1.819	thiol peroxidase, thioredoxin dependent
STM2492	STM2492	AAL21386	(2606156..2606509)	2.044	0.231	2.332	0.160	1.141	0.851	0.106	0.943	0.170	1.108	putative Glycerate kinase
perM	STM2493	AAL21387	(2606696..2607763)	1.005	0.071	0.715	0.143	0.712	0.563	0.039	0.305	0.023	0.543	putative PerM family permease
STM2494	STM2494	AAL21388	2607971..2609434	2.673	0.441	5.373	0.229	2.010	2.377	0.577	2.344	0.194	0.986	putative inner membrane or exported
yfgD	STM2495	AAL21389	2609474..2609833	2.114	0.453	5.698	0.967	2.696	1.514	0.128	1.973		1.303	putative arsenate reductase
yfgE	STM2496	AAL21390	(2609860..2610585)	1.827	0.085	1.455	0.233	0.796	1.025	0.037	0.633	0.034	0.618	putative ATPase involved in DNA replication initiation
uraA	STM2497	AAL21391	(2610656..2611945)	1.198	0.218	1.212	0.190	1.011	0.674	0.112	0.604	0.004	0.896	NCS2 family, uracil transport protein
upp	STM2498	AAL21392	(2612033..2612659)	1.600	0.190	4.586	0.195	2.866	1.069	0.100	1.033	0.140	0.966	uracil phosphoribosyltransferase
purM	STM2499	AAL21393	2613073..2614110	2.722	0.268	1.620	0.231	0.595	1.524	0.172	1.917	0.156	1.258	phosphoribosylaminoimidazole synthetase (AIR synthetase)
purN	STM2500	AAL21394	2614110..2614748	2.273	0.163	0.808	0.069	0.355	1.374	0.043	1.156	0.106	0.841	polyphosphate kinase, onent of RNA degradosome
ppk	STM2501	AAL21395	2614937..2617003	1.606	0.076	1.720	0.095	1.071	0.919	0.048	1.596	0.040	1.737	polyphosphate kinase, onent of RNA degradosome
ppx	STM2502	AAL21396	2617008..2618549	2.266	0.173	1.364	0.153	0.602	1.480	0.272	1.891	0.170	1.278	exopolyphosphatase
STM2503	STM2503	AAL21397	(2618585..2620798)	0.299	0.108	0.214	0.020	0.716	0.343	0.006	0.393	0.026	1.145	putative diguanylate cyclase

STM2504	STM2504	AAL21398	(2620895..2621032)	2.186	1.221	0.684	0.085	0.313	2.313	1.477	0.599	0.157	0.259	putative cytoplasmic protein
STM2505	STM2505	AAL21399	(2621103..2621363)	0.842	0.114	1.588	0.292	1.885	1.713	0.050	1.432	0.095	0.836	putative inner membrane protein
STM2506	STM2506	AAL21400	2621211..2621402	1.131	0.119	1.491	0.130	1.318	1.796	0.298	1.513	0.059	0.842	putative inner membrane protein
STM2507	STM2507	AAL21401	(2621481..2621717)	0.284	0.076			0.000	0.540	0.066			0.000	putative inner membrane protein
STM2508	STM2508	AAL21402	2621943..2622272	0.619	0.056	0.395	0.099	0.638	0.598	0.095	0.340	0.033	0.569	putative cytoplasmic protein
STM2509	STM2509	AAL21403	(2622292..2622648)	0.375	0.137	0.396	0.011	1.055	0.339	0.008	0.314	0.035	0.925	putative IS3-like transposase
guaA	STM2510	AAL21404	(2622805..2624382)	2.210	0.172	4.227	0.748	1.913	1.564	0.139	1.474	0.097	0.943	GMP synthetase
guaB	STM2511	AAL21405	(2624452..2625918)	1.473	0.252	2.176	0.145	1.477	2.500	0.428	1.640	0.060	0.656	IMP dehydrogenase
xseA	STM2512	AAL21406	2626079..2627428	0.940	0.084	0.585	0.118	0.622	1.103	0.238	0.869	0.121	0.788	exonuclease VII, large subunit
shdA	STM2513	AAL21407	(2627589..2633708)					N/A					N/A	similar to the C-terminal region of AIDA; IcsA; subspecies I specific; Peyer's patch colonization and shedding factor
ratB	STM2514	AAL21408	(2634402..2641709)	0.333	0.117	0.604	0.067	1.812	0.234	0.015	0.636	0.043	2.723	putative outer membrane protein
ratA	STM2515	AAL21409	(2641875..2647472)					N/A					N/A	putative outer membrane protein
sinI	STM2516	AAL21410	(2647592..2648551)	0.278	0.102	0.290	0.068	1.042	0.216	0.022	0.314	0.003	1.455	putative outer membrane protein
sinH	STM2517	AAL21411	(2648609..2650801)	0.292	0.036			0.000	15.609				0.000	Similar to E. coli intimin and Y. pestis invasin proteins
yfgJ	STM2518	AAL21412	(2651147..2651368)	0.603	0.133	0.610	0.147	1.012	0.956	0.243	0.633	0.034	0.662	putative cytoplasmic protein
engA	STM2519	AAL21413	(2651457..2652929)	1.042	0.022	1.453	0.118	1.395	1.791	0.255	1.830	0.109	1.022	putative GTP-binding protein
yfgL	STM2520	AAL21414	(2653048..2654226)	16.030	2.226	8.200	1.174	0.512	13.002	1.660	8.810	0.311	0.678	putative serine/threonine protein kinase
yfgM	STM2521	AAL21415	(2654237..2654857)	15.842	2.529	6.205	0.859	0.392	11.809	1.194	6.757	0.426	0.572	putative inner membrane protein
hisS	STM2522	AAL21416	(2654871..2656145)					N/A					N/A	histidine tRNA synthetase
gE	STM2523	AAL21417	(2656256..2657374)	3.342	0.355	4.955	0.293	1.482	3.218	0.388	3.275	0.397	1.018	putative protein, involved in density-dependent regulation of peptidoglycan biosynthesis
yfgA	STM2524	AAL21418	(2657401..2658405)	6.660	1.301	3.928	0.707	0.590	4.659	0.599	3.265	0.180	0.701	paral putative membrane protein
yfgB	STM2525	AAL21419	(2658697..2659863)	5.344	0.229	1.903	0.114	0.356	4.310	0.775	1.867	0.151	0.433	putative Fe-S-cluster redox enzyme
ndk	STM2526	AAL21420	(2660070..2660501)	50.722	7.005	11.126	1.805	0.219	14.602	4.366	7.862	0.536	0.538	nucleoside diphosphate kinase
STM2527	STM2527	AAL21421	(2660622..2661485)	0.716	0.044	0.836	0.079	1.168	0.402	0.015	0.577	0.056	1.437	putative polyferredoxin
STM2528	STM2528	AAL21422	(2661485..2662294)	0.550	0.094	0.499	0.044	0.906	0.467	0.049	0.394	0.013	0.843	putative dimethylsulfoxide reductase
STM2529	STM2529	AAL21423	(2662287..2662916)	0.209	0.098	0.469	0.048	2.247	0.192	0.015	0.325	0.016	1.692	putative anaerobic dimethylsulfoxide reductase
STM2530	STM2530	AAL21424	(2662913..2665318)	0.148	0.104	0.412		2.782	0.185	0.093			0.000	putative anaerobic dimethylsulfoxide reductase
pbpC	STM2531	AAL21425	(2665447..2667762)					N/A					N/A	transglycosylase of penicillin-binding protein 1c
STM2532	STM2532	AAL21426	(2667763..2672697)					N/A					N/A	putative inner membrane lipoprotein
sseA	STM2533	AAL21427	2672906..2673748	6.225	0.630	3.921	0.768	0.630	1.522	0.355	2.234	0.207	1.468	putative sulfurtransferase
STM2534	STM2534	AAL21428	2673995..2674663	0.436	0.094			0.000	1.101	0.026			0.000	putative cytoplasmic protein
sseB	STM2535	AAL21429	(2675232..2676017)	3.380	0.451	2.736	0.368	0.810	1.705	0.247	1.568	0.023	0.919	enhances serine sensitivity
pepB	STM2536	AAL21430	(2676118..2677401)	3.862	0.763	3.269	0.278	0.846	2.876	0.329	2.855	0.224	0.993	putative aminopeptidase
yfhJ	STM2537	AAL21431	(2677648..2677848)	3.901	0.345	2.921	0.439	0.749	3.320	0.139	3.269	0.163	0.985	believed to be involved in assembly of Fe-S clusters

fdx	STM2538	AAL21432	(2677860..2678195)	4.493	0.460	3.813	0.401	0.849	2.992	0.231	4.366	0.662	1.459	[2FE-2S] ferredoxin, electron carrer protein, believed to be involved in assembly of Fe-S clusters
hscA	STM2539	AAL21433	(2678197..2680047)	2.570	0.220	2.271	0.124	0.884	1.924	0.158	2.974	0.178	1.546	chaperone, member of Hsp70 protein family, believed to be involved in assembly of Fe-S clusters
hscB	STM2540	AAL21434	(2680060..2680575)	1.948	0.289	2.163	0.132	1.110	1.385	0.116	3.409	0.333	2.462	co-chaperone protein Hsc20, believed to be involved in assembly of Fe-S clusters
yfhF	STM2541	AAL21435	(2680771..2681094)	1.822	0.183	2.422	0.297	1.329	1.661	0.036	3.471	0.202	2.090	putative regulator
nifU	STM2542	AAL21436	(2681123..2681509)	2.112	0.275	3.148	0.259	1.491	1.937	0.065	5.020	0.281	2.592	NifU homologs involved in Fe-S cluster formation
nifS	STM2543	AAL21437	(2681537..2682751)	1.847	0.167			0.000	2.230	0.128			0.000	putative aminotransferase class-V
yfhP	STM2544	AAL21438	(2682931..2683425)	4.232	0.731	1.272	0.207	0.301	4.429	0.752	5.873	0.249	1.326	believed to be involved in assembly of Fe-S clusters
STM2545	STM2545	AAL21439	(2683585..2684316)	1.674	0.041	2.098	0.126	1.253	1.064	0.135	0.898	0.078	0.844	putative rRNA methylase
suhB	STM2546	AAL21440	2684435..2685238	5.193	0.372	0.920	0.093	0.177	3.915	1.121	0.944	0.099	0.241	inositol monophosphatase
STM2547	STM2547	AAL21441	2685383..2686261	0.520	0.073	0.254	0.035	0.488	0.544	0.056	0.331	0.052	0.609	putative hydrolase
asrA	STM2548	AAL21442	2686443..2687486	0.225	0.101	0.419	0.088	1.864	0.174	0.040	0.335	0.027	1.924	anaerobic sulfide reductase
asrB	STM2549	AAL21443	2687490..2688308	0.360	0.128	0.644	0.108	1.787	0.229	0.167	0.462	0.090	2.013	anaerobic sulfide reductase
asrC	STM2550	AAL21444	2688319..2689332	0.490	0.074	0.703	0.094	1.434	0.381	0.253	0.554	0.104	1.455	anaerobic sulfide reductase
STM2551	STM2551	AAL21445	(2689333..2690319)	1.206	0.154	0.497	0.076	0.412	0.532	0.100	0.495	0.033	0.930	putative inner membrane protein
STM2552	STM2552	AAL21446	(2690310..2690948)	0.548	0.100	0.571	0.090	1.043	0.242	0.040	0.355	0.033	1.470	putative periplasmic or exported protein
csiE	STM2553	AAL21447	2691074..2692351	1.193	0.088	0.925	0.063	0.776	0.471	0.114	0.532	0.026	1.131	stationary phase inducible protein
hcaT	STM2554	AAL21448	(2692346..2693485)	3.494	0.072	0.758	0.150	0.217	2.047	0.525	0.821	0.052	0.401	putative MFS family transport protein
glyA	STM2555	AAL21449	(2693681..2694934)	3.702	0.738	15.312	3.616	4.136	1.651	0.174	3.485	0.622	2.111	serine hydroxymethyltransferase
hmpA	STM2556	AAL21450	2695259..2696449	0.520	0.073	2.362	0.373	4.540	0.235	0.030	0.621	0.043	2.646	dihydropteridine reductase 2 and nitric oxide dioxygenase activity
cadC	STM2557	AAL21451	2696631..2698175	0.651	0.052	0.486	0.055	0.747	0.534	0.014	0.570	0.034	1.067	transcriptional activator of cad operon (OmpR family)
cadB	STM2558	AAL21452	2698536..2699867	0.321	0.119	3.984	0.484	12.419	0.799	0.117	1.771	0.177	2.216	APC family, lysine/cadaverine transport protein
cadA	STM2559	AAL21453	2699950..2702094	0.241	0.093	8.740	0.485	36.235	0.227	0.055	0.736	0.038	3.241	lysine decarboxylase 1
yjdL	STM2560	AAL21454	2702150..2703610	0.578	0.077	1.788	0.137	3.093	0.304	0.021	0.401	0.019	1.321	putative POT family, di-/tripeptide transport protein
glnB	STM2561	AAL21455	(2703659..2703997)	6.312	0.993			0.000	2.723	0.112			0.000	regulatory protein (P-II) for nitrogen assimilation by glutamine synthetase (ATase)
yfhA	STM2562	AAL21456	(2704074..2705411)	1.983	0.194	2.001	0.384	1.009	1.202	0.087	1.407	0.020	1.171	putative transcriptional regulator of two-onent regulator protein (EBP familiiy)
yfhG	STM2563	AAL21457	(2705408..2706172)	2.039	0.316	1.835	0.270	0.900	1.331	0.131	1.762	0.070	1.324	putative transcriptional regulator of two-onent regulator protein (EBP familiiy)
yfhK	STM2564	AAL21458	(2706174..2707616)	1.142	0.062	0.723	0.087	0.634	0.837	0.083	0.797	0.029	0.952	putative sensory kinase in regulatory system

purG	STM2565	AAL21459	(2708254..2712141)	1.281	0.290	1.192	0.037	0.931	0.663	0.046	0.999	0.083	1.506	phosphoribosylformylglycinamidine synthetase
STM2566	STM2566	AAL21460	2712163..2712396	0.358	0.092			0.000	0.427	0.256			0.000	putative periplasmic protein
yfhD	STM2567	AAL21461	2712397..2713941	0.448	0.062	0.348	0.062	0.778	0.296	0.036	0.354	0.008	1.195	putative periplasmic amino acid binding protein
yfhC	STM2568	AAL21462	(2713992..2714543)	1.136	0.125	0.626	0.039	0.551	0.583	0.068	0.805	0.070	1.381	putative Cytosine/adenosine deaminase
yfhB	STM2569	AAL21463	(2714568..2715203)	3.229	0.396	1.435	0.226	0.444	1.697	0.225	2.014	0.083	1.187	putatative phosphoserine phosphatase
STM2570	STM2570	AAL21464	(2715207..2716568)	1.831	0.361	0.744	0.081	0.406	0.454	0.017	0.512	0.031	1.128	putative phosphotransferase system IIB onents
STM2571	STM2571	AAL21465	(2716579..2717472)	1.690	0.189	0.875	0.056	0.518	0.383	0.037	0.526	0.027	1.374	putative aminotransferase
yfhH	STM2572	AAL21466	2717588..2718436	0.448	0.075	0.308	0.015	0.688	0.241	0.013	0.550	0.048	2.276	putative ABC superfamily (membrane) transport protein
STM2573	STM2573	AAL21467	(2718475..2719392)	0.225	0.097	0.202	0.063	0.895	0.858	0.031	1.503	0.071	1.752	putative ketopantoate reductase
STM2574	STM2574	AAL21468	(2719414..2720610)	0.175	0.100	0.119	0.030	0.679	0.325	0.011	0.374	0.049	1.151	putative permease
STM2575	STM2575	AAL21469	2720726..2721652	0.271	0.083	0.211	0.019	0.779	0.392	0.074	0.373	0.017	0.951	putative transcriptional regulator, LysR family
yfhL	STM2576	AAL21470	2721690..2721950	0.643	0.037	0.465	0.029	0.723	1.282	0.355	0.720	0.061	0.561	putative ferredoxin
aS	STM2577	AAL21471	(2722062..2722442)	3.286	0.508	1.662	0.049	0.506	0.771	0.141	0.775	0.036	1.005	holo-[acyl-carrier-protein] synthase, subunit (CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase, phosphopanthetheinyltransferase)
pdxJ	STM2578	AAL21472	(2722442..2723173)	4.759	0.601	3.720	0.330	0.782	1.327	0.186	1.749	0.049	1.318	carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis
recO	STM2579	AAL21473	(2723185..2723913)	1.893	0.119	1.208	0.217	0.638	0.696	0.011	0.482	0.156	0.693	gap repair gene
era	STM2580	AAL21474	(2723925..2724830)	2.828	0.055	2.455	0.201	0.868	1.100	0.060	0.609	0.008	0.554	GTPase believed to be involved in coordination of cell cycle, energy metabolism, cell division
rnc	STM2581	AAL21475	(2724827..2725507)	3.186	0.242	3.129	0.105	0.982	1.286	0.024	0.674	0.052	0.524	RNase III, ds RNA
lepB	STM2582	AAL21476	(2725781..2726755)	1.412	0.177	1.797	0.275	1.272	1.287	0.029	1.551	0.121	1.205	leader peptidase (signal peptidase I), serine protease
lepA	STM2583	AAL21477	(2726772..2728571)					N/A					N/A	GTP-binding elongation factor
gogB	STM2584	AAL21478	2728976..2730469	0.436	0.102	0.270	0.075	0.621	1.232	0.040	2.034	0.043	1.650	Gifsy-1 prophage: leucine-rich repeat protein
STM2585	STM2585	AAL21479	2731356..2731901	0.542	0.113	0.354	0.029	0.654	31.811	2.610	14.563	0.401	0.458	Gifsy-1 prophage: similar to transpose
STM2585A	STM2585A	AAL21480	2733013..2733240					N/A					N/A	Gifsy-1 prophage: Homolog of pagK
STM2586	STM2586	AAL21481	(2733337..2733915)	0.234	0.099	0.134	0.026	0.574	1.619	0.046	0.820	0.029	0.507	Gifsy-1 prophage: similar to phage tail assembly protein
STM2587	STM2587	AAL21482	(2733905..2734729)	0.232	0.122	0.096	0.025	0.415	0.352	0.044	0.329	0.052	0.932	Gifsy-1 prophage: similar to phage tail assembly protein
STM2588	STM2588	AAL21483	(2734726..2737098)					N/A					N/A	Gifsy-1 prophage: similar to tail fiber-like protein
STM2589	STM2589	AAL21484	(2737516..2740794)	0.322	0.083	0.249	0.032	0.773	0.429	0.962	0.392	0.082	0.912	Gifsy-1 prophage: similar to host specificity protein-J in phage lambda
STM2590	STM2590	AAL21485	(2740856..2741503)	0.374	0.160	0.135	0.013	0.362	0.245	0.033	0.285	0.006	1.163	Gifsy-1 prophage: similar to tail assembly protein I in phage lambda
STM2591	STM2591	AAL21486	(2741401..2742000)	0.348	0.094	0.197		0.566	0.229	0.030			0.000	Gifsy-1 prophage: similar to tail assembly protein K in phage lambda

STM2592	STM2592	AAL21487	(2742145..2742843)	0.529	0.087	0.218	0.042	0.413	0.238	0.004	0.230	0.007	0.967	Gifsy-1 prophage: similar to phage tail onent L
STM2593	STM2593	AAL21488	(2742853..2743182)	0.283	0.105	0.176	0.024	0.622	0.171	0.025	0.219	0.017	1.279	Gifsy-1 prophage: similar to phage tail onent M
STM2594	STM2594	AAL21489	(2743185..2746280)	0.216	0.108	0.177	0.024	0.819	0.131	0.090	0.253	0.023	1.936	Gifsy-1 prophage: similar to phage tail onent H
STM2595	STM2595	AAL21490	(2746252..2746590)	0.622	0.229	0.370	0.052	0.594	0.369	0.051	0.526	0.019	1.425	Gifsy-1 prophage: similar to minor tail protein
STM2596	STM2596	AAL21491	(2746587..2746982)	0.294	0.132	0.186	0.034	0.631	0.267	0.052	0.264	0.031	0.987	Gifsy-1 prophage: similar to minor tail protein
STM2597	STM2597	AAL21492	(2747033..2747779)	0.281	0.083	0.281	0.035	0.999	0.236	0.018	0.503	0.027	2.132	Gifsy-1 prophage: similar to major tail protein
STM2598	STM2598	AAL21493	(2747787..2748188)	0.372	0.065	0.287	0.032	0.772	0.232	0.027	0.439	0.020	1.892	Gifsy-1 prophage
STM2599	STM2599	AAL21494	2748177..2749427	1.211	0.066	0.876	0.076	0.723	0.853	0.070	0.831	0.098	0.974	Gifsy-1 prophage
STM2600	STM2600	AAL21495	(2749476..2750054)	0.403	0.107	0.292	0.041	0.725	0.263	0.026	0.321	0.018	1.221	Gifsy-1 prophage: similar to minor tail protein Z
STM2601	STM2601	AAL21496	(2750082..2750465)	0.452	0.143	0.793	0.087	1.754	0.917	2.733	0.801	0.344	0.874	Gifsy-1 prophage: similar to minor capsid protein FII of phage N15
STM2602	STM2602	AAL21497	(2750476..2750835)	0.296	0.080	0.209	0.018	0.706	0.209	0.019	0.269	0.014	1.288	Gifsy-1 prophage: similar to DNA packaging protein gp9 of phage N14
STM2603	STM2603	AAL21498	(2750893..2751921)	0.338	0.093	0.173	0.023	0.512	0.220	0.001	0.248	0.018	1.124	Gifsy-1 prophage: similar to head protein gp7 of phage 21
STM2604	STM2604	AAL21499	(2751976..2752323)	0.439	0.139	0.300	0.026	0.684	0.346	0.021	0.386	0.019	1.115	Gifsy-1 prophage: similar to head protein gpshp of phage 21
STM2605	STM2605	AAL21500	(2752336..2753832)	0.237	0.110	0.156	0.025	0.657	0.285	0.274	0.242	0.006	0.847	Gifsy-1 prophage: similar to head-tail preconnector gp5 of phage 21
STM2606	STM2606	AAL21501	(2753822..2755402)	0.324	0.104	0.148	0.038	0.456	0.227	0.016	0.257	0.012	1.132	Gifsy-1 prophage: similar to head-tail preconnector gp4 of phage 21
STM2607	STM2607	AAL21502	(2755399..2755602)	0.395	0.106	0.189	0.081	0.479	0.314	0.115	0.306	0.027	0.974	Gifsy-1 prophage: similar to head to tail joining protein
STM2608	STM2608	AAL21503	(2755586..2757517)	0.260	0.141	0.121	0.013	0.467	0.171	0.038	0.181	0.010	1.060	Gifsy-1 prophage: similar to terminase large chain gp2 of N15
STM2609	STM2609	AAL21504	(2757539..2758033)	0.248	0.143	0.149	0.021	0.600	0.240	0.147	0.221	0.020	0.921	Gifsy-1 prophage: similar to DNA packaging protein Nu1 of phage 21
STM2610	STM2610	AAL21505	2758320..2758721	0.285	0.103	0.401	0.165	1.407	0.253	0.021	0.361	0.114	1.428	Gifsy-1 prophage
STM2611	STM2611	AAL21506	(2758957..2759409)	0.195	0.117	0.103	0.015	0.531	0.233	0.050	0.283	0.027	1.217	Gifsy-1 prophage
STM2612	STM2612	AAL21507	(2759427..2759879)					N/A					N/A	Gifsy-1 prophage: similar to morphogenesis protein of phage B103
STM2613	STM2613	AAL21508	(2759863..2760192)	0.224	0.086	0.123	0.014	0.547	0.249	0.025	0.276	0.026	1.109	Gifsy-1 prophage
STM2614	STM2614	AAL21509	2760468..2761154	0.206	0.078	0.413	0.040	2.008	0.337	0.019	0.590	0.029	1.752	Gifsy-1 prophage
STM2615	STM2615						N/A					N/A		
STM2616	STM2616	AAL21510	(2762064..2762627)	0.938	0.165	0.350	0.098	0.373	0.399	0.046	0.351	0.040	0.879	Gifsy-1 prophage: similar to antirepressor protein of phage P22
STM2617	STM2617	AAL21511	(2762900..2763577)	0.261	0.079	0.119	0.016	0.457	0.119	0.053	0.185	0.005	1.559	Gifsy-1 prophage: similar to antiterminator Q
STM2618	STM2618	AAL21512	(2763574..2763714)	0.346	0.189	0.201	0.037	0.582	0.383	0.085	0.338	0.022	0.884	Gifsy-1 prophage

STM2619	STM2619	AAL21513	(2763711..2764322)					N/A					N/A	Gifsy-1 prophage
STM2620	STM2620	AAL21514	(2764531..2765133)	0.350	0.073	0.220	0.062	0.629	0.442	0.152	0.418	0.013	0.945	Gifsy-1 prophage
STM2621	STM2621	AAL21515	(2765549..2765782)					N/A					N/A	Gifsy-1 prophage
STM2622	STM2622	AAL21516	(2766074..2766367)					N/A					N/A	Gifsy-1 prophage
STM2623	STM2623	AAL21517	(2766442..2766753)					N/A					N/A	Gifsy-1 prophage
STM2624	STM2624	AAL21518	(2766750..2767097)					N/A					N/A	Gifsy-1 prophage
STM2625	STM2625	AAL21519	(2767108..2767857)					N/A					N/A	Gifsy-1 prophage: similar to dnaC Homolog in S. typhimurium
STM2626	STM2626	AAL21520	(2767860..2768843)					N/A					N/A	Gifsy-1 prophage: similar to replication protein 15
STM2627	STM2627	AAL21521	(2768928..2769302)					N/A					N/A	Gifsy-1 prophage: similar to cI protein in phage N
STM2628	STM2628	AAL21522	2769627..2770037					N/A					N/A	Gifsy-1 prophage
STM2629	STM2629	AAL21523	2770087..2770347					N/A					N/A	Gifsy-1 prophage
STM2630	STM2630	AAL21524	2770340..2770498			0.911	0.277	N/A	1.990		0.633	0.168	0.318	Gifsy-1 prophage
STM2631	STM2631	AAL21525	2770520..2770870					N/A					N/A	Gifsy-1 prophage
STM2632	STM2632	AAL21526	2770997..2773882					N/A					N/A	Gifsy-1 prophage: similar to exodeoxyribonuclease VIII
STM2633	STM2633	AAL21527	2773845..2775002					N/A					N/A	Gifsy-1 prophage: similar to enterohemolysin 1 in E. coli
STM2634	STM2634	AAL21528	2775045..2775284	0.304	0.095	0.200	0.034	0.656	0.384	0.276	0.411	0.084	1.070	putative cytoplasmic protein
STM2635	STM2635	AAL21529	2775325..2775609	0.417	0.077	0.237	0.028	0.569	0.258	0.016	0.303	0.012	1.176	Gifsy-1 prophage: similar to excisionase in phage phi-80
STM2636	STM2636	AAL21530	(2775587..2776816)	0.323	0.098	0.288	0.019	0.890	0.219	0.100	0.254	0.034	1.155	Gifsy-1 prophage: similar to integrase in phage
rseC	STM2637	AAL21531	(2777314..2777793)	3.532	0.676	3.628	0.630	1.027	2.923	0.577	2.008	0.125	0.687	regulator of sigma E (sigma 24) factor
rseB	STM2638	AAL21532	(2777790..2778746)	5.948	1.066	8.716	1.083	1.465	4.752	0.678	4.592	0.318	0.966	anti sigma E (sigma 24) factor, negative regulator
rseA	STM2639	AAL21533	(2778746..2779396)	12.452	1.101	47.772	8.946	3.837	7.594	0.506	12.983	0.424	1.710	anti sigma E (sigma 24) factor, negative regulator
rpoE	STM2640	AAL21534	(2779428..2780003)	25.291	2.944	24.949	5.261	0.986	11.301	0.263	7.962	0.733	0.705	sigma E (sigma 24) factor of RNA polymerase, response to periplasmic stress
nadB	STM2641	AAL21535	2780428..2782050	0.678	0.024	0.506	0.070	0.746	0.329	0.008	0.331	0.041	1.007	quinolinate synthetase, B protein
yfiC	STM2642	AAL21536	(2782035..2782772)	1.536	0.142	0.544	0.071	0.354	0.798	0.136	0.508	0.065	0.637	putative transferase
srmB	STM2643	AAL21537	2782903..2784237	0.751	0.015	1.764	0.103	2.349	0.717	0.042	0.798	0.071	1.114	ATP-dependent RNA helicase
yfiE	STM2644	AAL21538	(2784255..2785154)	0.680	0.015	0.351	0.052	0.516	0.266	0.010	0.328	0.030	1.232	putative transcriptional regulator, LysR family
yfiK	STM2645	AAL21539	2785257..2785844	0.332	0.098	0.546	0.114	1.646	0.240	0.034	0.221	0.018	0.923	paral putative transport protein
yfiD	STM2646	AAL21540	(2785906..2786289)	0.462	0.038	13.108	2.279	28.356	0.332	0.042	0.501	0.085	1.508	putative formate acetyltransferase
ung	STM2647	AAL21541	2786608..2787297	2.170	0.093	1.536	0.255	0.708	0.790	0.006	0.819	0.020	1.037	uracil-DNA-glycosylase

yfiF	STM2648	AAL21542	(2787413..2788450)	2.770	0.385	1.108	0.098	0.400	2.270	0.598	0.974	0.026	0.429	putative tRNA/rRNA methyltransferase
trxC	STM2649	AAL21543	2788654..2789073	4.193	0.738	2.194	0.223	0.523	1.339	0.057	2.166	0.233	1.617	thioredoxin 2, redox factor
yfiP	STM2650	AAL21544	2789146..2789826	0.980	0.020	0.989	0.030	1.009	0.537	0.028	0.707	0.064	1.319	putative cytoplasmic protein
yfiQ	STM2651	AAL21545	2789880..2792540	0.764	0.020	2.274	0.264	2.977	0.335	0.069	0.540	0.020	1.610	putative acetyl-CoA synthetase
pssA	STM2652	AAL21546	2792655..2794010	2.270	0.075	2.275	0.392	1.002	1.688	0.083	1.325	0.082	0.785	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)
yfiM	STM2653	AAL21547	2794055..2794378	1.034	0.048	0.683	0.093	0.660	0.601	0.141	0.590	0.116	0.982	putative outer membrane lipoprotein
kgtP	STM2654	AAL21548	(2794375..2795676)	1.064	0.129	0.700	0.090	0.658	0.426	0.113	0.554	0.094	1.299	MFS family, alpha-ketoglutarate permease
STM2655	STM2655	AAL21549	(2795780..2796235)	1.258	0.094	1.835	0.260	1.459	1.569	0.409	1.999	0.786	1.274	putative cytoplasmic protein
gltW	STM2658						N/A					N/A		
clpB	STM2660	AAL21550	(2802116..2804689)	1.034	0.093	4.316	0.475	4.173	2.179	0.498	8.169	0.171	3.749	ATP-dependent protease, Hsp 100, part of novel multi-chaperone system with DnaK, DnaJ, and GrpE
yfiH	STM2661	AAL21551	(2804819..2805550)	4.990	0.465	2.285	0.116	0.458	5.945	0.851	4.150	0.084	0.698	putative inner membrane protein
rluD	STM2662	AAL21552	(2805547..2806527)	5.944	0.725	2.792	0.278	0.470	9.477	2.319	7.638	0.142	0.806	pseudouridine synthase (pseudouridines 1911, 1915, 1917 in 23S RNA)
yfiO	STM2663	AAL21553	2806659..2807396	18.835	3.384	9.130	1.228	0.485	14.802	1.941	7.767	0.813	0.525	putative lipoprotein
STM2664	STM2664	pseudogene; two in-frame stops relative to E. coli				3.992	1.147	5.671	0.434	1.421	2.103	0.440	2.838	0.255 1.349
yfiA	STM2665	AAL21554	2807668..2808006	21.520	7.610			0.000	4.730	0.078			0.000	ribosome associated factor, stabilizes ribosomes against dissociation
STM2666	STM2666	AAL21555	2808110..2808157					N/A					N/A	hypothetical protein
pheA	STM2667	AAL21556	2808257..2809417	1.240	0.068	1.484	0.054	1.197	0.881	0.135	1.052	0.029	1.194	bifuctional: chorismate mutase P; prephenate dehydratase
STM2668	STM2668	AAL21557	(2809378..2810286)	0.591	0.055	0.324	0.021	0.549	0.711	0.032	0.835	0.021	1.174	putative cytoplasmic protein
tyrA	STM2669	AAL21558	(2810344..2811465)	0.718	0.058	0.708	0.125	0.986	0.848	0.109	1.658	0.084	1.955	bifunctional: chorismate mutase T; prephenate dehydrogenase
aroF	STM2670	AAL21559	(2811475..2812545)	0.952	0.027	0.913	0.176	0.959	1.473	0.221	2.174	0.203	1.476	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase), tyrosine repressible
yfiR	STM2671	AAL21560	2812985..2813503	0.343	0.083	0.523	0.091	1.526	0.548	0.062	0.927	0.081	1.690	putative periplasmic protein
yfiN	STM2672	AAL21561	2813496..2814716	0.425	0.073	0.713	0.048	1.677	0.550	0.039	0.725	0.008	1.316	putative diguanylate cyclase/phosphodiesterase
rplS	STM2673	AAL21562	(2814873..2815220)					N/A					N/A	50S ribosomal subunit protein L19
trmD	STM2674	AAL21563	(2815261..2816028)	9.808	0.386	25.944	3.544	2.645	5.403	0.491	4.280	0.389	0.792	tRNA (guanine-7-)-methyltransferase
rimM	STM2675	AAL21564	(2816073..2816621)	17.635	0.744	19.798	2.393	1.123	14.961	0.175	6.863	0.810	0.459	16S rRNA processing protein
rpsP	STM2676	AAL21565	(2816640..2816888)	22.392	1.074	16.970	2.335	0.758	18.774	1.056	9.691	1.203	0.516	30S ribosomal subunit protein S16
ffh	STM2677	AAL21566	(2817202..2818563)	2.097	0.191	4.075	0.600	1.943	1.337	0.032	1.542	0.048	1.153	4.5S-RNP protein, GTP binding export factor, part of signal recognition particle with 4.5 RNA
corE	STM2678	AAL21567	2818729..2819520	1.028	0.057	0.947	0.130	0.921	0.688	0.045	0.791	0.057	1.149	putative cytochrome c-type biogenesis protein (heme exporter protein C
yfjD	STM2679	AAL21568	2819585..2820826	0.307	0.086	0.772	0.072	2.513	0.233	0.060	0.495	0.049	2.125	putative membrane protein

STM2680	STM2680	AAL21569	2820947..2821552	0.855	0.059	0.801	0.105	0.937	0.669	0.050	0.672	0.138	1.004	putative cytoplasmic protein
grpE	STM2681	AAL21570	(2821587..2822177)	2.219	0.306	5.993	0.346	2.700	1.585	0.191	5.178	0.162	3.268	molecular chaparone; heat shock protein
STM2682	STM2682	AAL21571	(2822174..2822368)	0.959	0.091	1.413	0.305	1.473	0.772	0.117	1.174	0.047	1.521	putative cytoplasmic protein
yfjB	STM2683	AAL21572	2822300..2823178					N/A					N/A	putative kinase
recN	STM2684	AAL21573	2823264..2824925	0.630	0.069	0.728	0.061	1.155	1.395	0.033	0.957	0.037	0.686	protein used in recombination and DNA repair
smpA	STM2685	AAL21574	2825074..2825412	6.445	0.427	4.356	0.768	0.676	3.545	0.106	1.918	0.090	0.541	small membrane protein A
yfjF	STM2686	AAL21575	(2825578..2825868)	1.350	0.057	2.289	0.303	1.696	0.970	0.098	1.253	0.163	1.292	putative cytoplasmic protein
yfjG	STM2687	AAL21576	(2825858..2826334)	2.968	0.403	2.679	0.359	0.903	1.682	0.064	1.463	0.074	0.870	putative Oligoketide cyclase/lipid transport protein
smpB	STM2688	AAL21577	2826484..2826966	5.015	0.676	2.212	0.358	0.441	1.901	0.237	1.452	0.029	0.764	small protein B; putative tmRNA-binding protein
STM2689	STM2689	pseudogene; frameshift; proline/threonine-rich							N/A					N/A
STM2690	STM2690	AAL21578	2839118..2840527	0.419	0.102	0.262	0.013	0.624	0.441	0.029	1.236	0.167	2.804	putative outer membrane efflux protein
STM2691	STM2691	AAL21579	2840524..2842704	0.208	0.138	0.157	0.007	0.755	0.472	0.031	0.734	0.043	1.554	putative ABC transporter transmembrane region
STM2692	STM2692	AAL21580	2842712..2843875	0.958	0.067	1.086	0.082	1.134	1.056	0.155	1.262	0.023	1.195	putative HlyD family secretion protein
STM2694	STM2694	AAL21581	(2844427..2844645)	1.904	0.104	2.936	0.227	1.542	2.138	0.724	2.202	0.285	1.030	Fels-2 prophage: similar to late control gene B in phage
STM2695	STM2695	AAL21582	(2844714..2845814)	0.583	0.100	0.578	0.071	0.992	0.374	0.025	0.541	0.039	1.445	Fels-2 prophage: similar to late control gene in phage
STM2696	STM2696	AAL21583	(2845811..2846296)	0.212	0.105	0.232	0.039	1.095	0.155	0.052	0.296	0.027	1.901	Fels-2 prophage: similar to genes in phage phiCTX
STM2697	STM2697	AAL21584	(2846293..2849100)	0.264	0.108	0.212	0.065	0.803	0.309	1.019	0.218	0.035	0.706	Fels-2 prophage:similar to orfG protein in phage 186
STM2698	STM2698	AAL21585	(2849093..2849212)	0.763	0.191	0.494	0.086	0.647	0.652	0.009	0.504	0.120	0.773	Fels-2 prophage: similar to gpE in phage P2
STM2699	STM2699	AAL21586	(2849227..2849529)	0.235	0.114	0.222	0.049	0.944	0.189	0.071	0.270	0.056	1.427	Fels-2 prophage: similar to genes in P2-like phages
STM2700	STM2700	AAL21587	(2849584..2850099)	0.226	0.094	0.191	0.044	0.846	0.142	0.050	0.186	0.006	1.309	Fels-2 prophage: similar to genes in P2-like phages
STM2701	STM2701	AAL21588	(2850109..2851281)	0.428	0.178	0.267	0.025	0.623	0.223	0.024	0.239	0.019	1.070	Fels-2 prophage: similar to tail sheath proteins in phage P2
STM2702	STM2702	AAL21589	(2851384..2851941)	0.385	0.132	0.170	0.040	0.443	0.283	0.039	0.248	0.036	0.877	Fels-2 prophage: similar to te-specific recombinases, DNA invertase Pin homolog
STM2703	STM2703	AAL21590	2851911..2852990	0.202	0.105	0.109	0.020	0.538	0.288	0.019	0.296	0.011	1.027	Fels-2 prophage: similar to invertase (pin) in phage E14
STM2704	STM2704	AAL21591	2852997..2853404	0.253	0.081	0.149	0.021	0.590	0.804	0.870	0.493	0.016	0.612	Fels-2 prophage: similar to genes in P2-like phages
STM2705	STM2705	AAL21592	(2853408..2854025)	0.240	0.108	0.126	0.008	0.524	0.476	0.147	0.361	0.027	0.759	Fels-2 prophage
STM2706	STM2706	AAL21593	(2853995..2855569)	0.195	0.120	0.106	0.010	0.546	0.165	0.028	0.211	0.013	1.279	Fels-2 prophage: similar to tail fiber protein in phage P2

STM2707	STM2707	AAL21594	(2855566..2856171)	0.276	0.108	0.194	0.026	0.701	0.359	0.460	0.338	0.200	0.940	Fels-2 prophage: similar to tail fiber protein (gpH) in phage P2
STM2708	STM2708	AAL21595	(2856164..2857072)	0.232	0.097	0.108	0.011	0.466	0.190	0.090	0.235	0.045	1.233	Fels-2 prophage: similar to tail fiber protein (gpI) in phage P2
STM2709	STM2709	AAL21596	(2857059..2857418)	0.594	0.342	0.896	0.053	1.508	0.411	0.153	1.029	0.561	2.506	Fels-2 prophage: similar to gpJ, base plate of tail, in phage P2
STM2710	STM2710	AAL21597	(2857415..2857993)	0.354	0.178	0.160	0.032	0.452	0.223	0.008	0.199	0.016	0.891	Fels-2 prophage: similar to gpV, base plate of tail, in phage P2
STM2711	STM2711	AAL21598	(2858062..2858508)	0.296	0.175	0.360	0.035	1.218	0.318	0.458	0.522	0.190	1.642	Fels-2 prophage: similar to gpS for letion of tail, in phage P2
STM2712	STM2712	AAL21599	(2858501..2858932)	0.400	0.118	0.207	0.015	0.517	0.291	0.060	0.229	0.030	0.787	Fels-2 prophage: similar to gpR for letion of tail, in phage P2
STM2713	STM2713	AAL21600	(2858895..2859179)	0.224	0.166	0.437	0.050	1.946	0.298	0.408	0.622	0.376	2.088	Fels-2 prophage: similar to protein from phage CTX
STM2714	STM2714	AAL21601	(2859028..2859456)	0.230	0.131	0.185	0.037	0.803	0.174	0.159	0.387	0.201	2.228	Fels-2 prophage: similar to lysis protein (lysB) in phage P2
STM2715	STM2715	AAL21602	(2859833..2860342)	0.193	0.106	0.132	0.035	0.686	0.155	0.111	0.168	0.038	1.087	Fels-2 prophage: probable prophage lysozyme
STM2716	STM2716	AAL21603	(2860323..2860538)	0.294	0.105	0.201	0.044	0.685	0.226	0.047	0.223	0.019	0.987	Fels-2 prophage: phage-holin analog protein
STM2717	STM2717	AAL21604	(2860542..2860745)	0.320	0.202	0.246	0.022	0.768	0.204	0.007	0.306	0.076	1.501	Fels-2 prophage: similar to gpX in phage P2
STM2718	STM2718	AAL21605	(2860745..2861209)	0.197	0.142	0.177	0.014	0.901	0.225	0.101	0.326	0.149	1.447	Fels-2 prophage: similar to gpQ in phage 186
STM2719	STM2719	AAL21606	(2861303..2861956)	0.254	0.138	0.269	0.036	1.059	0.347	1.106	0.401	0.234	1.154	Fels-2 prophage: similar to gpR in phage 186
STM2720	STM2720	AAL21607	(2861960..2863042)	0.152	0.099	0.198	0.013	1.308	0.095	0.030	0.162	0.024	1.711	Fels-2 prophage: similar to gpN, major capsid, in phage P2
STM2721	STM2721	AAL21608	(2863059..2863892)	0.229	0.112	0.196	0.025	0.858	0.152	0.009	0.216	0.056	1.416	Fels-2 prophage: similar to gpO, capsid scaffold, in phage P2
STM2722	STM2722	AAL21609	2864035..2865801	0.367	0.170	0.099	0.003	0.269	0.232	0.135	0.156	0.013	0.671	Fels-2 prophage: similar to gpP, ATP charging, in phage P2
STM2723	STM2723	AAL21610	2865801..2866841	0.327	0.080	0.175	0.040	0.535	0.411	0.022	0.240	0.012	0.584	Fels-2 prophage: similar to gpQ, portal vector protein, in phage P2
STM2724	STM2724	AAL21611	(2866927..2868678)	4.736	0.433	1.884	0.346	0.398	3.187	0.263	1.765	0.075	0.554	Fels-2 prophage: hypothetical protein
STM2725	STM2725	pseudogene; in-frame stop following codon 22			2.814	0.454	1.172	0.086	0.416	1.311	0.184	0.552	0.109	0.421
STM2726	STM2726	AAL21612	(2868892..2869623)	11.631	1.681	3.001	0.243	0.258	1.916	0.235	0.798	0.047	0.416	Fels-2 prophage: hypothetical protein
STM2727	STM2727	AAL21613	(2869683..2869988)	1.286	0.076	0.526	0.036	0.409	0.899	0.230	0.457	0.097	0.509	Fels-2 prophage: similar to protein in phage 186, and to retron in E coli
STM2728	STM2728	AAL21614	(2869927..2870115)	1.214	0.106	0.434	0.009	0.357	1.198	0.217	0.313	0.035	0.262	Fels-2 prophage: hypothetical protein
STM2729	STM2729	AAL21615	(2870268..2872697)	0.186	0.097	0.085	0.004	0.459	0.085	0.030	0.168	0.004	1.976	Fels-2 prophage: similar to retron in E coli
STM2730	STM2730	AAL21616	(2872688..2873545)	0.155	0.101	0.127	0.025	0.818	0.148	0.051	0.205	0.023	1.386	Fels-2 prophage: similar to retron in E coli
STM2731	STM2731	AAL21617	(2873542..2873769)	0.412	0.098	0.463	0.021	1.125	0.523	0.223	0.698	0.201	1.336	Fels-2 prophage: similar to protein in phage 186

STM2732	STM2732	AAL21618	(2873769..2874002)	0.468	0.158	0.283	0.062	0.604	0.448	0.048	0.318	0.027	0.712	Fels-2 prophage: similar to protein in phage 186
STM2733	STM2733	AAL21619	(2874070..2874411)	0.575	0.126	0.233	0.030	0.405	0.462	0.165	0.278	0.131	0.601	Fels-2 prophage: similar to E. coli retron Ec67
STM2734	STM2734	AAL21620	2874631..2875089	2.140	0.182	0.773	0.076	0.361	2.095	0.415	1.125	0.225	0.537	Fels-2 prophage: hypothetical protein
STM2735	STM2735	AAL21621	(2875037..2875270)	0.579	0.071	0.446	0.044	0.770	0.979	1.050	0.704	0.504	0.719	Fels-2 prophage: hypothetical protein
STM2736	STM2736	AAL21622	(2875278..2875787)	0.407	0.110	0.350	0.031	0.859	0.443	0.101	0.324	0.051	0.731	Fels-2 prophage: similar to retron in E coli and to protein cII of phages
STM2737	STM2737	AAL21623	(2875823..2876062)	0.477	0.072	0.353	0.052	0.740	0.647	0.617	0.403	0.238	0.623	Fels-2 prophage: similar to protein in phage
STM2738	STM2738	AAL21624	2876179..2876811	0.552	0.062	0.702	0.051	1.273	0.408	0.073	0.454	0.019	1.113	Fels-2 prophage: similar to E. coli retron
STM2739	STM2739	AAL21625	2876815..2877840	0.362	0.093	0.525	0.078	1.450	0.204	0.053	0.293	0.025	1.438	Fels-2 prophage: similar to int protein in phage 186
STM2740	STM2740	AAL21626	2878169..2879233	0.263	0.081	0.679	0.046	2.585	0.115	0.029	0.397	0.038	3.446	Fels-2 prophage: similar to int protein in phage 4-57
STM2741	STM2741	AAL21627	2879461..2880054					N/A					N/A	putative periplasmic protein
STM2742	STM2742	AAL21628	2880444..2881637	0.729	0.093	0.352	0.064	0.483	1.486	0.194	0.968	0.049	0.651	putative cytoplasmic protein
STM2743	STM2743	AAL21629	(2881972..2882799)					N/A					N/A	putative cytoplasmic protein
STM2744	STM2744	AAL21630	2883250..2883465	0.390	0.174	0.576	0.038	1.476	0.547	0.331	0.479	0.250	0.877	putative cytoplasmic protein
STM2745	STM2745	AAL21631	2883501..2885570	0.306	0.198	0.143	0.024	0.468	0.273	0.490	0.242	0.032	0.886	putative inner membrane protein
STM2746	STM2746	AAL21632	2886073..2887356	4.137	0.459	1.617	0.151	0.391	1.908	0.268	0.580	0.055	0.304	putative Excinuclease ATPase subunit
STM2747	STM2747	AAL21633	2887401..2888219	3.380	0.334	0.643	0.100	0.190	2.081	0.702	0.562	0.182	0.270	putative cytoplasmic protein
STM2748	STM2748	AAL21634	(2888373..2888729)	1.360	0.096	0.536	0.103	0.394	0.579	0.021	0.444	0.046	0.767	putative transcriptional regulator
STM2749	STM2749	AAL21635	2888824..2889108	1.100	0.102	0.604	0.096	0.549	0.986	1.806	0.452	0.219	0.459	putative cytoplasmic protein
STM2750	STM2750	AAL21636	2889221..2889742	0.267	0.166	0.149	0.007	0.557	0.176	0.097	0.226	0.049	1.283	putative PTS system, glucitol/sorbitol-specific enzyme II
STM2751	STM2751	AAL21637	2889739..2890113	0.291	0.208	0.359	0.015	1.234	0.227	0.309	0.470	0.328	2.072	putative PTS enzyme III glucitol
STM2752	STM2752	AAL21638	2890110..2891090	0.241	0.193	0.115	0.034	0.478	0.136	0.053	0.287	0.080	2.114	putative PTS enzyme III glucitol
STM2753	STM2753	AAL21639	2891101..2892114	0.449	0.129	0.178	0.030	0.396	0.318	0.038	0.228	0.008	0.718	putative dehydrogenase
STM2754	STM2754	AAL21640	2892409..2893611	0.515	0.078	0.580	0.045	1.127	1.086	0.196	0.398	0.032	0.366	putative hexulose 6 phosphate synthase
STM2755	STM2755	AAL21641	(2893685..2894320)	0.251	0.186	0.145	0.025	0.579	0.147	0.022	0.189	0.021	1.286	putative hexulose 6 phosphate synthase
STM2756	STM2756	AAL21642	(2894344..2894907)	0.217	0.152	0.117	0.005	0.539	0.160	0.109	0.253	0.058	1.582	putative sugar phosphate aminotransferase
STM2757	STM2757	AAL21643	(2894907..2895749)	0.194	0.160	0.125	0.008	0.641	0.114	0.073	0.170	0.016	1.487	putative cytoplasmic protein
STM2758	STM2758	AAL21644	(2895879..2897420)	0.198	0.167	0.099	0.018	0.500	0.096	0.059	0.157	0.020	1.637	putative phosphotransferase system IIC onent
STM2759	STM2759	AAL21645	2897643..2899322	0.201	0.159	0.258	0.013	1.286	0.090	0.032	0.213		2.370	putative dipeptide/oligopeptide/nickel ABC-type transport systems, periplasmic onent
STM2760	STM2760	AAL21646	2900439..2901314	0.259	0.135	0.111	0.014	0.430	0.193	0.065	0.191	0.029	0.990	putative integrase
STM2761	STM2761	AAL21647	2901480..2903354	0.417	0.193	0.176	0.114	0.423	0.992	0.076	0.363	0.049	0.366	putative inner membrane protein
STM2762	STM2762	AAL21648	(2903614..2904897)	0.375	0.055	0.112	0.013	0.299	0.834	0.120	0.377	0.036	0.453	putative inner membrane protein
STM2763	STM2763	AAL21649	2905475..2906071	0.644	0.068	0.622	0.055	0.966	0.299	0.013	0.492	0.043	1.646	putative integrase
STM2764	STM2764	AAL21650	(2906452..2906919)	0.286	0.110	0.190	0.064	0.664	0.291	0.038	0.354	0.057	1.218	putative integrase core domain

STM2765	STM2765	AAL21651	(2907066..2907332)	0.510	0.194	0.608	0.073	1.191	0.494	0.009	0.766	0.498	1.552	putative transposase
STM2766	STM2766	AAL21652	(2907785..2908423)	3.015	0.256	0.630	0.117	0.209	2.910	0.547	0.905	0.068	0.311	putative cytoplasmic protein
STM2767	STM2767	AAL21653	(2908420..2910402)	6.765	0.265	1.698	0.338	0.251	5.970	1.112	3.055	0.203	0.512	putative Superfamily I DNA and RNA helicase
STM2768	STM2768	AAL21654	2910681..2910980	0.711	0.119	0.490	0.051	0.689	0.719	0.026	0.514	0.082	0.714	putative transposase
STM2769	STM2769	AAL21655	2910977..2911843	0.474	0.047	0.461	0.097	0.974	0.295	0.060	0.219	0.033	0.743	putative transposase
fljA	STM2770	AAL21656	(2912623..2913162)	1.428	0.111	7.380	0.712	5.167	0.240	0.050	0.408	0.010	1.700	Flagellar synthesis: repressor of fliC
fljB	STM2771	AAL21657	(2913230..2914750)	16.050	0.978	164.070	13.985	10.223	0.265	0.010	1.008	0.020	3.801	Flagellar synthesis: phase 2 flagellin (filament structural protein)
hin	STM2772	AAL21658	2914842..2915414	0.708	0.148	2.019	0.169	2.850	0.492	0.479	0.432	0.038	0.879	H inversion: regulation of flagellar gene expression by site-specific inversion of DNA
iroB	STM2773	AAL21659	2916377..2917492	0.379	0.129	0.369	0.059	0.973	0.146	0.019	0.256	0.021	1.756	putative glycosyl transferase, related to UDP-glucuronosyltransferase
iroC	STM2774	AAL21660	2917573..2921226	0.223	0.095	0.139	0.011	0.625	0.092	0.000	0.221	0.009	2.404	putative ATP binding cassette (ABC) transporter
iroD	STM2775	AAL21661	2921336..2922580	0.281	0.140	0.155	0.017	0.553	0.148	0.045	0.229	0.015	1.550	Similar to enterochelin esterase of E. coli (Fes)
iroE	STM2776	AAL21662	2922612..2923547	0.287	0.148	0.142	0.007	0.494	0.209	0.061	0.193	0.028	0.926	putative hydrolase of the alpha/beta superfamily
iroN	STM2777	AAL21663	(2923589..2925769)	0.165	0.132	0.078	0.016	0.474	0.287	0.054	0.259	0.075	0.903	TonB-dependent siderophore receptor protein
STM2778	STM2778	pseudogene; frameshift		0.263	0.095	0.181	0.021	0.689	3.781	0.585	4.889	0.840	1.293	
STM2779	STM2779	AAL21664	(2926295..2926627)	0.617	0.118	0.419	0.117	0.679	8.715	1.782	13.201	0.435	1.515	putative inner membrane protein
STM2780	STM2780	AAL21665	(2926802..2927854)	0.329	0.094	0.207	0.029	0.629	20.209	1.331	18.792	0.713	0.930	Homolog of pipB, putative pentapeptide repeats (8 copies)
virK	STM2781	AAL21666	2928373..2929302	0.680	0.187	1.185	0.111	1.741	20.400	0.434	24.395	1.236	1.196	virulence gene; homologous sequence to virK in Shigella
mig-14	STM2782	AAL21667	2929595..2930491	2.266	0.114	1.357	0.196	0.599	43.603	4.093	23.014	1.979	0.528	putative transcription activator
nxiA	STM2783	AAL21668	(2931213..2932226)	0.897	0.087	0.395	0.041	0.441	1.092	0.044	1.351	0.077	1.236	putative nickel transporter
tctE	STM2784	AAL21669	(2932359..2933774)	4.437	0.885	3.599	0.645	0.811	0.395	0.027	0.853	0.071	2.158	tricarboxylic transport: regulatory protein
tctD	STM2785	AAL21670	(2933761..2934435)	6.367	0.944	7.606	1.090	1.195	0.386	0.063	0.922	0.064	2.385	tricarboxylic transport: regulatory protein
STM2786	STM2786	AAL21671	2934590..2935567	11.543	5.425	9.010	0.617	0.781	0.298	0.002	0.408	0.095	1.371	tricarboxylic transport
STM2787	STM2787	AAL21672	2935579..2936013	7.241	2.778	4.615	0.468	0.637	0.551	0.139	0.341	0.044	0.619	tricarboxylic transport
STM2788	STM2788	AAL21673	2936024..2937538	4.164	2.191	2.858	0.308	0.686	0.240	0.035	0.387	0.043	1.610	tricarboxylic transport
STM2789	STM2789	AAL21674	2937832..2938818	1.472	0.428	0.932	0.081	0.633	0.428	0.017	1.852	0.124	4.331	putative cytoplasmic protein
ygaF	STM2790	AAL21675	2938844..2940112	1.220	0.403	0.569	0.082	0.467	0.386	0.024	1.570	0.034	4.068	paral putative sarcosine oxidase-like protein
gabD	STM2791	AAL21676	2940134..2941582	0.654	0.162	0.279	0.055	0.427	0.440	0.059	1.541	0.083	3.503	succinate-semialdehyde dehydrogenase I, NADP-dependent
gabT	STM2792	AAL21677	2941597..2942880	0.628	0.104	0.200	0.030	0.319	0.556	0.070	1.570	0.092	2.824	4-aminobutyrate aminotransferase
gabP	STM2793	AAL21678	2943010..2944410	0.430	0.050	0.161	0.045	0.376	0.270	0.050	0.431	0.024	1.594	APC family, gamma-aminobutyrate transport protein, RpoS dependent
ygaE	STM2794	AAL21679	2944452..2945129	0.585	0.082	0.252	0.026	0.432	0.742	0.016	0.824	0.042	1.111	putative transcriptional repressor (GntR familiy)
ygaU	STM2795	AAL21680	(2945151..2945600)	0.656	0.080	0.395	0.041	0.602	3.803	0.392	4.216	0.159	1.108	putative LysM domain

yqaE	STM2796	AAL21681	(2945700..2945858)	0.964	0.104	0.356	0.007	0.369	3.761	0.400	0.992	0.104	0.264	putative YqaE family transport protein
STM2797	STM2797	AAL21682	2946041..2946340	0.427	0.051	0.300	0.048	0.702	0.655	0.080	0.542	0.042	0.828	putative regulatory protein, arsR family
ygaP	STM2798	AAL21683	2946350..2946877	0.652	0.097	0.511	0.067	0.784	1.146	0.224	0.876	0.050	0.764	putative rhodanese-related sulfurtransferase
stpA	STM2799	AAL21684	(2947225..2947626)	2.944	0.235	5.112	0.533	1.736	44.223	1.648	27.798	1.577	0.629	DNA-binding protein with chaperone activity
STM2800	STM2800	AAL21685	2948325..2948774	1.217	0.039	1.294	0.125	1.063	1.277	0.039	1.158	0.057	0.907	putative inner membrane protein
ygaC	STM2801	AAL21686	(2948809..2949159)	0.897	0.048	0.657	0.039	0.732	0.903	0.156	0.700	0.079	0.775	putative cytoplasmic protein
ygaM	STM2802	AAL21687	2949309..2949647	2.442	0.798	0.739	0.099	0.303	3.047	0.373	1.534	0.068	0.503	putative inner membrane protein
STM2803	STM2803	AAL21688	(2949731..2951065)	0.866	0.046	0.305	0.022	0.353	0.381	0.022	0.566	0.036	1.487	putative regulatory protein, gntR family
STM2804	STM2804	AAL21689	2951154..2951585	0.307	0.045	0.169	0.015	0.550	0.144	0.032	0.255	0.003	1.771	putative cytoplasmic protein
nrdH	STM2805	AAL21690	2951857..2952102	0.806	0.119	0.771	0.144	0.957	0.489	0.046	0.455	0.050	0.931	glutaredoxin-like protein; hydrogen donor
nrdI	STM2806	AAL21691	2952099..2952509	0.371	0.169	0.165	0.010	0.446	0.438	0.661	0.341	0.030	0.779	stimulates ribonucleotide reduction
nrdE	STM2807	AAL21692	2952482..2954626	0.265	0.115	0.140	0.017	0.527	0.185	0.044	0.254	0.008	1.375	ribonucleoside diphosphate reductase 2, alpha subunit
nrdF	STM2808	AAL21693	2954637..2955596	0.466	0.084	0.217	0.014	0.465	0.401	0.028	0.454	0.047	1.133	ribonucleoside-diphosphate reductase 2, beta subunit
proV	STM2809	AAL21694	2955951..2957153	3.783	0.645	0.913	0.174	0.241	5.537	0.755	5.302	0.265	0.958	ABC superfamily (atp_bind), glycine/betaine/proline transport protein
proW	STM2810	AAL21695	2957146..2958210	7.507	1.736	1.095	0.107	0.146	13.180	3.318	12.100	0.960	0.918	ABC superfamily (membrane), glycine/betaine/proline transport protein
proX	STM2811	AAL21696	2958280..2959275	3.077	0.820	1.054	0.157	0.342	4.287	0.228	4.561	0.395	1.064	ABC superfamily (bind_prot), glycine/betaine/proline transport protein
STM2812	STM2812	AAL21697	2959440..2960624	1.534	0.655	1.204	0.157	0.784	1.874	0.772			0.000	putative inner membrane protein
emrR	STM2813	AAL21698	2961121..2961651	3.929	0.402	3.283	0.537	0.836	1.481	0.036	1.491	0.056	1.006	transcriptional repressor of emrAB operon (MarR family)
emrA	STM2814	AAL21699	2961778..2962950	0.706	0.107	1.816	0.292	2.571	0.378	0.065	0.633	0.045	1.675	multidrug resistance secretion protein
emrB	STM2815	AAL21700	2962967..2964505	0.631	0.065	0.625	0.045	0.991	0.519	0.160	0.399	0.066	0.769	putative MFS superfamily, multidrug transport protein
STM2816	STM2816	AAL21701	(2964554..2965924)	0.299	0.090	0.273	0.028	0.912	0.329	0.013	0.505	0.023	1.535	putative glycoporin
luxS	STM2817	AAL21702	(2966270..2966785)	4.012	0.771	3.505	0.523	0.874	1.997	0.222	3.344	0.352	1.674	quorum sensing protein, produces autoinducer - acyl-homoserine lactone-signaling molecules
gshA	STM2818	AAL21703	(2966935..2968491)	1.890	0.180	2.349	0.211	1.243	1.062	0.033	1.095	0.134	1.031	gamma-glutamate-cysteine ligase
yqaA	STM2819	AAL21704	(2968568..2968993)	2.515	0.263	1.775	0.318	0.706	1.027	0.183	0.799	0.043	0.777	putative inner membrane protein
yqaB	STM2820	AAL21705	(2968990..2969556)	5.383	0.454	2.764	0.113	0.513	2.240	0.280	1.623	0.124	0.725	putative phosphoglucomutase
STM2821	STM2821						N/A					N/A		
STM2822	STM2822						N/A					N/A		
STM2823	STM2823						N/A					N/A		
STM2824	STM2824						N/A					N/A		
STM2825	STM2825						N/A					N/A		

csrA	STM2826	AAL21706	(2970951..2971136)	10.800	3.393	4.701	0.498	0.435	6.041	0.416	3.029	0.148	0.501	carbon storage regulator
alaS	STM2827	AAL21707	(2971371..2974001)	2.471	0.122	8.463	0.509	3.425	1.392	0.017	2.467	0.320	1.773	alanyl-tRNA synthetase
oraA	STM2828	AAL21708	(2974237..2974737)	0.739	0.035	1.445	0.073	1.955	0.677	0.012	0.843	0.221	1.245	regulator
recA	STM2829	AAL21709	(2974854..2975915)	3.998	0.437	7.192	0.397	1.799	4.404	0.027	6.971	0.542	1.583	DNA strand exchange and recombination protein with proteiase and nuclease activity
ygaD	STM2830	AAL21710	(2976000..2976497)	1.984	0.079	1.922	0.267	0.969	1.258	0.014	2.031	0.073	1.615	putative cytoplasmic protein
mltB	STM2831	AAL21711	(2976975..2978054)	1.884	0.101	0.668	0.039	0.355	1.159	0.091	1.006	0.040	0.868	membrane-bound lytic murein transglycosylase B
srlA	STM2832	AAL21712	2978308..2978871	2.255	0.380	0.903	0.100	0.400	0.382	0.074	0.292	0.041	0.764	PTS family, glucitol/sorbitol-specific enzyme IIC onent,one of two IIC onents
srlE	STM2833	AAL21713	2978868..2979839	2.163	0.610	1.803	0.218	0.834	0.265	0.006	0.369	0.034	1.395	PTS family, glucitol/sorbitol-specific IIB onent, one of two IIC onents
slrB	STM2834	AAL21714	2979851..2980213	2.251	0.472	1.486	0.079	0.660	0.422	0.028	0.434	0.022	1.028	PTS family, glucitol/sorbitol-specific
srlD	STM2835	AAL21715	2980225..2981004	3.109	0.339	1.604	0.173	0.516	0.411	0.076	0.512	0.073	1.247	glucitol (sorbitol)-6-phosphate dehydrogenase
gutM	STM2836	AAL21716	2981080..2981439					N/A					N/A	putative glucitol (srl) operon regulatory protein
srlR	STM2837	AAL21717	2981637..2982410	3.017	0.241	2.653	0.249	0.879	0.778	0.020	1.198	0.066	1.540	transcriptional repressor for glucitol operon (DeoR family)
gutQ	STM2838	AAL21718	2982442..2983368	4.031	0.675	2.590	0.372	0.642	1.025	0.034	1.695	0.110	1.654	putative polysialic acid capsule expression protein
ygaA	STM2839	AAL21719	(2983365..2984885)	0.511	0.034	0.522	0.066	1.023	0.240	0.020	0.462	0.017	1.927	putative regulator (EBP family)
STM2840	STM2840	AAL21720	2985071..2986510	0.383	0.090	0.174	0.037	0.454	0.240	0.122	0.239	0.015	0.994	putative flavoprotein
ygbD	STM2841	AAL21721	2986507..2987640	0.382	0.075	0.239	0.022	0.627	0.144	0.011	0.272	0.021	1.887	putative oxidoreductase
hypF	STM2842	AAL21722	(2987737..2989977)	1.085	0.101	0.689	0.013	0.635	0.701	0.083	0.856	0.077	1.222	hydrogenase maturation protein
hydN	STM2843	AAL21723	(2990123..2990668)	0.393	0.059	0.181	0.006	0.459	0.327	0.190	0.277	0.038	0.848	electron transport protein (FeS senter) from formate to hydrogen
STM2844	STM2844	AAL21724	(2990869..2991678)	0.272	0.129	0.175	0.030	0.644	0.181	0.006	0.328	0.005	1.814	putative periplasmic or exported protein
hycI	STM2845	AAL21725	(2991705..2992175)	0.246	0.086	0.196	0.017	0.797	0.217	0.071	0.530	0.017	2.443	protease involved in processing C-terminal end of HycE
hycH	STM2846	AAL21726	(2992168..2992578)	0.347	0.147	0.306	0.066	0.882	0.373	0.175	0.607	0.082	1.628	processing of HycE (part of the FHL lex)
hycG	STM2847	AAL21727	(2992575..2993342)	0.255	0.129	0.301	0.053	1.179	0.242	0.010	0.852	0.035	3.515	hydrogenase activity
hycF	STM2848	AAL21728	(2993342..2993884)	0.265	0.100	0.429	0.024	1.620	0.251	0.060	0.840	0.116	3.353	hydrogenase 3, putative quinone oxidoreductase
hycE	STM2849	AAL21729	(2993894..2995603)	0.247	0.138	0.250	0.049	1.013	0.226	0.274	0.408	0.019	1.810	hydrogenase 3, large subunit (part of FHL lex)
hycD	STM2850	AAL21730	(2995621..2996544)	0.308	0.175	0.180	0.015	0.585	0.209	0.100	0.235	0.034	1.123	hydrogenase 3, membrane subunit (part of FHL lex)
hycC	STM2851	AAL21731	(2996547..2998373)	0.224	0.116	0.137	0.009	0.613	0.094	0.019	0.272	0.018	2.899	hydrogenase 3, membrane subunit (part of FHL lex)
hycB	STM2852	AAL21732	(2998373..2998981)	0.209	0.132	0.231	0.022	1.106	0.146	0.048	0.417	0.085	2.858	hydrogenase-3, iron-sulfur subunit (part of FHL lex)

hycA	STM2853	AAL21733	(2999127..2999588)	0.174	0.099	0.242	0.044	1.394	0.126	0.052	0.261	0.019	2.081	transcriptional repressor of hyc and hyp operons
hypA	STM2854	AAL21734	2999798..3000154	0.465	0.171	1.579	0.300	3.395	0.438	0.176	0.404	0.083	0.922	guanine-nucleotide binding protein in formate-hydrogenlyase system, functions as nickel donor for HycE of hydrogenlyase 3
hypB	STM2855	AAL21735	3000223..3001095	0.735	0.050	7.116	1.161	9.681	1.417	0.324	4.139	0.433	2.921	hydrogenase-3 accessory protein, assembly of metallocenter
hypC	STM2856	AAL21736	3001086..3001358	0.735	0.086	4.960	0.571	6.746	1.986	0.357	3.258	0.437	1.640	putative hydrogenase expression/formation protein
hypD	STM2857	AAL21737	3001358..3002476	0.832	0.048	4.234	0.350	5.089	1.848	0.501	2.992	0.106	1.619	putative hydrogenase expression/formation protein
hypE	STM2858	AAL21738	3002515..3003483	0.955	0.041	4.277	0.182	4.477	1.450	0.232	2.883	0.144	1.988	putative hydrogenase expression/formation protein
fhlA	STM2859	AAL21739	3003702..3005780	0.383	0.060	0.731	0.078	1.906	0.274	0.018	0.412	0.017	1.499	formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons (EBP family)
ygbA	STM2860	AAL21740	(3005842..3006186)	0.310	0.100	0.321	0.065	1.035	0.215	0.106	0.314	0.054	1.463	putative cytoplasmic protein
sitA	STM2861	AAL21741	3006368..3007285	0.794	0.049	0.245	0.040	0.309	0.374	0.059	0.511	0.031	1.368	Salmonella iron transporter: fur regulated
sitB	STM2862	AAL21742	3007282..3008103	0.659	0.032	0.295	0.054	0.447	0.367	0.016	0.536	0.021	1.461	Salmonella iron transporter: fur regulated
sitC	STM2863	AAL21743	3008100..3008960	0.472	0.122	0.245	0.034	0.519	0.365	0.051	0.424	0.035	1.162	Salmonella iron transporter: fur regulated
sitD	STM2864	AAL21744	3008951..3009799	0.501	0.115	0.726	0.081	1.449	0.715	0.051	0.876	0.048	1.225	Salmonella iron transporter: fur regulated
avrA	STM2865	AAL21745	(3009898..3010806)	0.289	0.076	4.456	0.411	15.427	4.691	0.117	8.791	0.135	1.874	putative inner membrane protein
sprB	STM2866	AAL21746	(3010967..3011722)	0.642	0.083	9.709	1.543	15.118	7.763	0.482	15.081	1.148	1.943	transcriptional regulator
hilC	STM2867	AAL21747	(3012107..3012994)	1.565	0.057	10.201	1.194	6.519	10.217	0.957	8.792	0.350	0.861	bacterial regulatory helix-turn-helix proteins, araC family
STM2868	STM2868	AAL21748	(3013339..3013791)	0.821	0.111	8.182	0.663	9.962	6.631	1.004	10.246	1.068	1.545	putative cytoplasmic protein
orgA	STM2869	AAL21749	(3013788..3014468)	1.194	0.042	9.223	1.044	7.725	10.311	0.394	13.633	1.129	1.322	putative flagellar biosynthesis/type III secretory pathway protein
STM2870	STM2870	AAL21750	(3014425..3015024)					N/A					N/A	putative inner membrane protein
prgK	STM2871	AAL21751	(3014996..3015754)	1.352	0.098	29.425	3.007	21.771	9.844	0.370	27.172	1.740	2.760	cell invasion protein; lipoprotein, may link inner and outer membranes
prgJ	STM2872	AAL21752	(3015751..3016056)	0.718	0.083	29.962	2.184	41.755	6.349	0.413	21.266	2.446	3.349	cell invasion protein; cytoplasmic
prgI	STM2873	AAL21753	(3016075..3016317)	0.849	0.114	35.734	1.989	42.110	6.875	0.362	24.601	2.802	3.578	cell invasion protein; cytoplasmic
prgH	STM2874	AAL21754	(3016342..3017520)	0.296	0.093	8.401	1.017	28.427	1.910	0.190	4.325	0.435	2.264	cell invasion protein
hilD	STM2875	AAL21755	3017836..3018765	0.884	0.058	13.267	1.254	15.015	5.242	0.113	5.801	0.189	1.107	regulatory helix-turn-helix proteins, araC family
hilA	STM2876	AAL21756	3019856..3021517	0.405	0.076	7.306	0.880	18.021	0.789	0.075	1.563	0.112	1.980	invasion genes transcription activator
iagB	STM2877	AAL21757	3021535..3022017	0.363	0.134	5.092	1.074	14.030	1.806	0.096	2.259	0.196	1.251	cell invasion protein
sptP	STM2878	AAL21758	(3022071..3023702)	1.015	0.029	3.008	0.272	2.964	14.016	0.018	25.303	1.637	1.805	protein tyrosine phosphate
si	STM2879	AAL21759	(3023689..3024081)	1.854	0.207	3.922	0.365	2.116	42.639	3.212	47.079	3.359	1.104	chaparone, related to virulence
STM2880	STM2880	AAL21760	(3024108..3024368)	1.823	0.167	2.917	0.167	1.600	41.963	8.129	44.341	2.808	1.057	putative cytoplasmic protein
ia	STM2881	AAL21761	(3024412..3024660)	1.006	0.054	2.955	0.390	2.937	14.098	0.393	25.286	1.260	1.794	putative acyl carrier protein

sipA	STM2882	AAL21762	(3024679..3026736)	0.407	0.042	4.194	0.459	10.304	3.909	0.109	19.185	1.882	4.908	cell invasion protein
sipD	STM2883	AAL21763	(3026755..3027786)	0.604	0.087	6.629	0.721	10.969	5.506	0.307	23.518	1.585	4.271	cell invasion protein
sipC	STM2884	AAL21764	(3027857..3029086)	0.864	0.083	8.653	1.787	10.019	8.971	0.288	53.896	4.859	6.008	cell invasion protein
sipB	STM2885	AAL21765	(3029114..3030895)	1.431	0.235	7.683	1.230	5.371	9.000	0.908	35.331	4.472	3.926	cell invasion protein
sicA	STM2886	AAL21766	(3030898..3031395)	0.396	0.055	5.224	0.529	13.187	3.798	0.347	14.540	0.749	3.829	surface presentation of antigens; secretory proteins
spaS	STM2887	AAL21767	(3031533..3032603)	0.233	0.103	1.099	0.118	4.719	1.570	0.093	2.276	0.322	1.450	surface presentation of antigens; secretory proteins
spaR	STM2888	AAL21768	(3032590..3033381)	0.318	0.170	1.559	0.244	4.908	3.600	0.430	4.603	0.568	1.279	surface presentation of antigens; secretory proteins
spaQ	STM2889	AAL21769	(3033385..3033645)	0.722	0.165	2.205	0.209	3.055	7.822	2.860	6.740	0.525	0.862	surface presentation of antigens; secretory proteins
spaP	STM2890	AAL21770	(3033671..3034345)	0.501	0.129	3.125	0.421	6.231	6.268	0.574	7.869	0.961	1.256	surface presentation of antigens; secretory proteins
spaO	STM2891	AAL21771	(3034335..3035246)	1.566	0.793	5.178	2.372	3.305	13.409	37.643	8.359	1.090	0.623	surface presentation of antigens; secretory proteins
invJ	STM2892	AAL21772	(3035246..3036256)	0.297	0.071	8.546	1.023	28.808	2.291	0.241	9.615	1.042	4.197	surface presentation of antigens; secretory proteins
invI	STM2893	AAL21773	(3036256..3036699)	0.284	0.103	8.481	0.653	29.835	1.426	0.222	4.852	0.899	3.402	surface presentation of antigens; secretory proteins
invC	STM2894	AAL21774	(3036677..3037972)	0.691	0.098	9.746	2.229	14.113	6.150	0.903	9.967	0.783	1.621	surface presentation of antigens; secretory proteins
invB	STM2895	AAL21775	(3037969..3038376)	0.764	0.061	7.005	0.393	9.173	7.102	0.022	9.270	0.601	1.305	surface presentation of antigens; secretory proteins
invA	STM2896	AAL21776	(3038400..3040457)	0.516	0.134	3.477	0.271	6.737	5.055	0.887	4.450	0.596	0.880	invasion protein
invE	STM2897	AAL21777	(3040482..3041600)	0.340	0.076	3.905	0.188	11.481	2.619	0.069	4.127	0.375	1.576	invasion protein
invG	STM2898	AAL21778	(3041597..3043285)	0.359	0.081	6.203	0.382	17.267	1.950	0.135	4.286	0.210	2.198	invasion protein; outer membrane
invF	STM2899	AAL21779	(3043282..3043932)	0.602	0.122	9.101	1.013	15.120	3.545	0.468	6.536	0.455	1.844	invasion protein
invH	STM2900	AAL21780	3044389..3044832	0.414	0.058	2.863	0.489	6.908	7.185	0.103	3.873	0.089	0.539	invasion protein
STM2901	STM2901	AAL21781	3045263..3045712	1.173	0.065	0.813	0.062	0.693	1.198	0.239	1.080	0.046	0.901	putative cytoplasmic protein
STM2902	STM2902	AAL21782	3045697..3046044	1.094	0.193	0.873	0.059	0.798	1.592	0.115	1.259	0.130	0.791	putative cytoplasmic protein
STM2903	STM2903	AAL21783	(3046317..3046643)	0.718	0.061	0.509	0.060	0.709	1.742	0.013	0.873	0.137	0.501	putative cytoplasmic protein
STM2904	STM2904	AAL21784	3047332..3047622	0.473	0.051	1.076	0.205	2.272	0.644	0.315	0.733	0.077	1.138	putative ABC-type transport system
STM2905	STM2905	AAL21785	3047619..3048146	0.361	0.091	0.609	0.122	1.687	0.363	0.034	0.431	0.056	1.188	putative acetyltransferase
STM2906	STM2906	AAL21786	(3048219..3048407)	0.351	0.137			0.000	0.653	0.037			0.000	putative cytoplasmic protein
pphB	STM2907	AAL21787	3048771..3049427	0.491	0.106	0.228	0.030	0.465	3.099	0.476	0.773	0.090	0.249	serine/threonine specific protein phosphatase 2
STM2908	STM2908	AAL21788	(3049599..3050120)	0.364	0.099	0.311		0.854	0.483	0.034	0.364		0.754	putative cytoplasmic protein

mutS	STM2909	AAL21789	3050279..3052846	1.078	0.067	1.801	0.196	1.670	0.832	0.066	1.554	0.124	1.868	methyl-directed mismatch repair, recognize exocyclic adducts of guanosine
STM2910	STM2910	AAL21790	(3052902..3053282)	0.446	0.134	0.252	0.015	0.565	0.286	0.124	0.286	0.029	0.999	putative cytoplasmic protein
STM2911	STM2911	AAL21791	(3053279..3054487)	0.339	0.135	0.138	0.014	0.407	0.145	0.012	0.199	0.010	1.370	putative permease
STM2912	STM2912	AAL21792	3054575..3055507	0.377	0.123	0.180	0.069	0.479	0.156	0.019	0.197	0.022	1.266	putative transcriptional regulators, LysR family
STM2913	STM2913	AAL21793	(3055549..3057045)	0.747	0.108	1.027	0.046	1.375	0.279	0.006	0.347	0.017	1.245	putative permease
STM2914	STM2914	AAL21794	(3057042..3057992)	0.289	0.086	1.463	0.104	5.060	0.163	0.005	0.228	0.031	1.403	putative nucleoside-diphosphate-sugar epimerase
ygbM	STM2915	AAL21795	(3058032..3058808)	0.395	0.145	3.422	0.605	8.669	0.152	0.035	0.257	0.021	1.696	putative endonuclease
ygbL	STM2916	AAL21796	(3058813..3059451)	0.276	0.100	2.977	0.512	10.785	0.153	0.064	0.246	0.024	1.608	putative fuculose phosphate aldolase
ygbK	STM2917	AAL21797	(3059448..3060710)	0.430	0.112	5.377	0.317	12.504	0.151	0.030	0.336	0.024	2.227	paral putative tRNA synthase
ygbJ	STM2918	AAL21798	(3060704..3061627)	0.450	0.109	4.859	0.914	10.789	0.223	0.203	0.274	0.016	1.230	3-hydroxyisobutyrate dehydrogenase
ygbI	STM2919	AAL21799	3061824..3062588	1.079	0.071	0.949	0.184	0.879	0.394	0.008	0.436	0.051	1.106	putative regulatory protein, deoR family
STM2920	STM2920	AAL21800	(3062607..3063011)	1.132	0.023	0.759	0.058	0.670	0.499	0.069	0.714	0.066	1.430	putative transcriptional regulator
STM2921	STM2921	AAL21801	3063182..3063775	0.338	0.146	0.212	0.071	0.627	0.185	0.043	0.303	0.089	1.638	putative flavoprotein
STM2922	STM2922	AAL21802	3063775..3065202	0.629	0.622	0.657		1.046	0.270	0.085			0.000	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylase
STM2923	STM2923	AAL21803	3065213..3065449	1.306	0.220	1.410	0.277	1.080	0.774	0.141	0.500	0.073	0.646	putative cytoplasmic protein
rpoS	STM2924	AAL21804	(3065494..3066486)	5.709	1.421	14.155	1.668	2.480	3.559	0.460	4.535	0.171	1.274	sigma S (sigma 38) factor of RNA polymerase, major sigmafactor during stationary phase
nlpD	STM2925	AAL21805	(3066549..3067682)	9.802	2.551	13.078	0.988	1.334	7.588	0.249	7.280	0.685	0.959	lipoprotein
pcm	STM2926	AAL21806	(3067858..3068484)	4.995	0.358	2.439	0.403	0.488	2.729	0.648	2.466	0.117	0.903	L-isoaspartate protein carboxylmethyltransferase type II
surE	STM2927	AAL21807	(3068478..3069239)	5.807	0.482	3.183	0.185	0.548	3.451	0.444	2.392	0.301	0.693	survival protein, protein damage control
ygbO	STM2928	AAL21808	(3069220..3070269)	7.195	1.205	3.725	0.198	0.518	4.005	0.725	2.638		0.659	paral putative hydrogenase subunit
ispF	STM2929	AAL21809	(3070266..3070745)	5.791	0.855	2.535	0.238	0.438	3.194	0.683	2.074	0.340	0.649	2C-methyl-d-erythritol-2,4-cyclodiphosphate synthase
ispD	STM2930	AAL21810	(3070745..3071455)	4.692	0.354	17.957		3.827	2.692	0.468			0.000	4-phosphocytidyl-2C-methyl-D-erythritol synthase
ygbQ	STM2931	AAL21811	(3071474..3071785)	9.141	1.190	2.925	0.437	0.320	4.794	0.746	2.286	0.187	0.477	putative Septum formation initiator
ygbE	STM2932	AAL21812	(3071976..3072332)	2.958	0.200	0.632	0.071	0.214	5.045	1.136	1.408	0.224	0.279	putative inner membrane protein
cysC	STM2933	AAL21813	(3072350..3072955)	0.686	0.018	0.345	0.030	0.502	2.523	0.406	1.676	0.149	0.664	adenosine 5'-phosphosulfate kinase
cysN	STM2934	AAL21814	(3072942..3074381)	0.402	0.070	0.274	0.025	0.681	1.768	0.226	1.647	0.078	0.932	ATP-sulfurylase, subunit 1 (ATP:sulfate adenylyltransferase)
cysD	STM2935	AAL21815	(3074391..3075299)	0.441	0.160	0.313	0.136	0.709	1.901	0.140	1.386	0.025	0.729	ATP-sulfurylase, subunit 1 (ATP:sulfate adenylyltransferase)
iap	STM2936	AAL21816	3075550..3076596	0.429	0.115	0.438	0.084	1.020	0.749	0.057	0.758	0.052	1.012	aminopeptidase in alkaline phosphatase isozyme conversion

ygbF	STM2937	AAL21817	(3078244..3078540)	0.428	0.100	0.394	0.022	0.921	1.103	0.085	0.398	0.053	0.361	putative inner membrane protein
STM2938	STM2938	AAL21818	(3078537..3079457)	0.502	0.060	0.451	0.037	0.898	1.552	0.267	0.690	0.068	0.445	putative cytoplasmic protein
ygcH	STM2939	AAL21819	(3079454..3080104)	0.497	0.104	0.569	0.076	1.145	2.121	0.589	1.292	0.065	0.609	putative cytoplasmic protein
STM2940	STM2940	AAL21820	(3080086..3080832)	0.476	0.069	0.679	0.011	1.426	2.766	0.771	1.614	0.085	0.583	putative cytoplasmic protein
yghJ	STM2941	AAL21821	(3080843..3081901)	0.364	0.096	0.848	0.088	2.334	2.496	0.152	1.926	0.076	0.772	putative cytoplasmic protein
STM2942	STM2942	AAL21822	(3081915..3082475)	0.378	0.113	0.682	0.073	1.802	1.558	0.165	1.076	0.082	0.691	putative transposase
STM2943	STM2943	AAL21823	(3082472..3084028)	0.250	0.120	0.329	0.030	1.314	1.119	0.024	0.799	0.124	0.714	putative cytoplasmic protein
ygcB	STM2944	AAL21824	(3084040..3086703)	0.252	0.123	0.176	0.022	0.699	0.961	0.005	0.673	0.026	0.700	putative helicase
sopD	STM2945	AAL21825	3087148..3088101	0.291	0.064	0.293	0.083	1.008	12.104	1.309	6.156	0.408	0.509	secreted protein in the Sop family; transferred to eukaryotic cells
cysH	STM2946	AAL21826	(3088189..3088923)	0.184	0.115	0.165	0.011	0.896	0.994	0.011	1.191	0.081	1.198	3'-phosphoadenosine 5'-phosphosulfate (PAPS) reductase
cysI	STM2947	AAL21827	(3088999..3090711)					N/A					N/A	sulfite reductase, alpha subunit, NADPH dependent
cysJ	STM2948	AAL21828	(3090711..3092510)	0.295	0.076	0.275	0.039	0.933	1.522	0.122	1.729	0.137	1.136	sulfite reductase, beta (flavoprotein) subunit
ptpS	STM2949	AAL21829	3092934..3093296	1.059	0.060	0.436	0.031	0.412	1.090	0.102	0.492	0.026	0.452	putative synthase
STM2950	STM2950	AAL21830	(3093384..3094181)	0.476	0.086	0.426	0.057	0.896	0.302	0.038	0.222	0.016	0.736	putative metal-dependent hydrolases of the beta-lactamase superfamily II
ygcF	STM2951	AAL21831	(3096557..3097228)	3.879	0.132	1.340	0.253	0.345	2.384	0.324	1.007	0.044	0.423	putative Organic radical activating enzymes
eno	STM2952	AAL21832	(3097364..3098662)	6.485	0.430	20.451	2.844	3.154	2.050	0.267	4.833	0.909	2.358	enolase
pyrG	STM2953	AAL21833	(3098745..3100382)	6.770	0.413	7.140	0.941	1.055	3.696	0.062	2.294	0.134	0.621	CTP synthetase
mazG	STM2954	AAL21834	(3100610..3101410)	0.563	0.072	1.412	0.114	2.510	0.668	0.072	1.280	0.104	1.914	putative pyrophosphatase
STM2955	STM2955	AAL21835	(3102440..3102796)	1.055	0.109	0.768	0.080	0.728	1.603	0.016	1.530	0.112	0.955	putative transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain and a metal-binding domain
relA	STM2956	AAL21836	(3102880..3105114)	3.157	0.426	2.405	0.230	0.762	3.667	0.816	6.005	0.526	1.637	(p)ppGpp synthetase I (GTP pyrophosphokinase)
ygcA	STM2957	AAL21837	(3105166..3106461)	3.572	0.243	1.430	0.148	0.400	6.820	1.481	5.316	0.332	0.779	putative RNA methyltransferase
barA	STM2958	AAL21838	3106519..3109275	0.386	0.112	0.458	0.031	1.185	0.274	0.039	0.371	0.021	1.354	sensory histidine kinase
STM2959	STM2959	AAL21839	(3109319..3110461)	0.524	0.094	0.865	0.054	1.649	0.265	0.008	0.460	0.019	1.740	putative glycerate kinase 2
gudD	STM2960	AAL21840	(3110539..3111879)	0.492	0.110	1.625	0.271	3.305	0.145	0.011	0.364	0.030	2.507	d-glucarate dehydratase
ygcY	STM2961	AAL21841	(3111900..3113240)	0.709	0.093	1.680	0.247	2.369	0.270	0.039	0.304	0.017	1.126	putative d-glucarate dehydratase
gudT	STM2962	AAL21842	(3113237..3114595)	0.304	0.116	0.928	0.121	3.052	0.080	0.002	0.165	0.022	2.051	putative MFS superfamily, D-glucarate permease
STM2963	STM2963	AAL21843	(3115076..3115525)	3.195	0.682	1.949	0.066	0.610	0.870	0.050	0.961	0.094	1.105	putative MFS superfamily, D-glucarate permease
yqcB	STM2964	AAL21844	(3115544..3116326)	1.709	0.018	1.448	0.137	0.847	1.025	0.113	0.795	0.009	0.776	putative synthase
yqcC	STM2965	AAL21845	(3116326..3116655)	2.810	0.295	2.722	0.174	0.969	2.358	1.109	0.976	0.065	0.414	putative cytoplasmic protein
syd	STM2967	AAL21846	(3117267..3117812)	1.914	0.101	1.395	0.276	0.729	1.011	0.046	0.630	0.042	0.623	interacts with secY

yqcD	STM2968	AAL21847	3117881..3118729	1.289	0.037	1.431	0.167	1.110	0.639	0.040	0.809	0.049	1.265	putative GTP cyclohydrolase I
ygdH	STM2969	AAL21848	3118842..3120206	12.635	2.548	6.153	0.757	0.487	2.770	0.344	2.962	0.304	1.069	putative nucleotide binding
sdaC	STM2970	AAL21849	3120771..3122060	9.430	0.093	25.600	0.717	2.715	3.436	0.235	7.986	0.551	2.324	putative HAAAP family, serine transport protein
sdaB	STM2971	AAL21850	3122119..3123486	11.683	0.806	15.884	1.778	1.360	3.286	0.203	3.090	0.031	0.940	L-serine dehydratase (L-threonine deaminase 2)
exo	STM2972	AAL21851	3123597..3124412	1.529	0.087	1.119	0.142	0.732	0.730	0.113	0.609	0.042	0.835	exonuclease IX, 5'-3' exonuclease
fucO	STM2973	AAL21852	(3124504..3125652)	0.343	0.119	0.330	0.040	0.962	0.468	0.033	0.776	0.131	1.656	L-1,2-propanediol oxidoreductase
fucA	STM2974	AAL21853	(3125669..3126316)	0.370	0.065	0.542	0.057	1.464	0.336	0.019	1.004	0.102	2.989	L-fuculose-1-phosphate aldolase
fu	STM2975; pseudogene; frameshift; fucose permease					0.326	0.141	0.333	0.054	1.021	0.573	0.081	1.507	0.094 2.629
fucI	STM2976	AAL21854	3128220..3129995	0.487	0.136	1.050	0.153	2.158	0.797	0.043	2.238	0.094	2.806	L-fucose isomerase
fucK	STM2977	AAL21855	3130096..3131514	0.437	0.089	0.770	0.085	1.761	0.730	0.068	1.311	0.191	1.796	L-fuculokinase
fucU	STM2978	AAL21856	3131516..3131938	0.593	0.079	0.645	0.069	1.088	0.732	0.020	0.940	0.016	1.285	conserved protein of fucose operon
fucR	STM2979	AAL21857	3131996..3132706	2.152	0.081	1.226	0.147	0.570	0.749	0.051	0.781	0.031	1.043	positive regulator of the fuc operon (DeoR family)
ygdE	STM2980	AAL21858	(3132765..3133865)					N/A					N/A	putative SAM-dependent methyltransferase
ygdD	STM2981	AAL21859	(3133858..3134253)	1.364	0.112	0.670	0.096	0.491	2.823	0.393	1.937	0.150	0.686	putative small membrane protein
gcvA	STM2982	AAL21860	(3134272..3135189)	1.341	0.034	1.027	0.012	0.766	1.980	0.022	1.554	0.026	0.785	regulator of gcv operon (LysR family)
ygdI	STM2983	AAL21861	(3135536..3135763)	3.953	0.918	1.996	0.279	0.505	7.238	0.119	2.911	0.217	0.402	putative lipoprotein
csdA	STM2984	AAL21862	3135956..3137161	1.362	0.041	0.717	0.085	0.527	1.054	0.046	0.862	0.087	0.817	putative selenocysteine lyase
ygdK	STM2985	AAL21863	3137161..3137604	0.418	0.073	0.418	0.030	0.998	0.424	0.049	0.540	0.066	1.273	putative SufE protein probably involved in Fe-S center assembly
STM2986	STM2986	AAL21864	3137904..3138791	0.314	0.076	0.241	0.040	0.767	0.580	0.123	0.576	0.022	0.992	putative integral membrane protein
ygdL	STM2987	AAL21865	(3138843..3139649)	2.216	0.170	1.003	0.053	0.453	2.229	0.361	1.465	0.081	0.657	paral putative enzyme
mltA	STM2988	AAL21866	(3139759..3140856)	2.469	0.207	1.279	0.056	0.518	2.196	0.356	1.311	0.044	0.597	membrane-bound lytic murein transglycosylase A
metZ	STM2989						N/A					N/A		
metW	STM2990						N/A					N/A		
amiC	STM2991	AAL21867	(3141356..3142609)	2.471	0.328	1.314	0.161	0.532	2.043	0.331	1.839	0.125	0.900	N-acetylmuramoyl-L-alanine amidase
argA	STM2992	AAL21868	3142842..3144173	0.464	0.084	0.255	0.041	0.550	0.352	0.025	0.634	0.043	1.802	N-alpha-acetylglutamate synthase (amino-acid acetyltransferase)
recD	STM2993	AAL21869	(3144276..3146111)	2.365	0.381	1.261	0.215	0.533	1.594	0.462	1.506	0.097	0.945	exonuclease V, alpha chain
recB	STM2994	AAL21870	(3146108..3149653)	1.283	0.294	1.833	0.437	1.429	1.203	4.133	1.490	0.409	1.238	exonuclease V, beta chain
ptr	STM2995	AAL21871	(3149646..3152534)	1.493	0.210	0.983	0.036	0.658	1.145	0.037	0.808	0.100	0.705	protease III
recC	STM2996	AAL21872	(3152712..3156083)	0.967	0.038	0.697	0.128	0.721	0.612	0.044	0.609		0.996	exonuclease V, subunit
ppdC	STM2997	AAL21873	(3156099..3156419)	0.647	0.075	0.385	0.060	0.595	0.472	0.140	0.371	0.042	0.786	prepilin peptidase dependent protein C, putative onent in type IV pilin biogenesis
ygdB	STM2998	AAL21874	(3156404..3156811)	0.689	0.126	0.287	0.015	0.416	0.463	0.144	0.336	0.037	0.725	putative periplasmic protein
ppdB	STM2999	AAL21875	(3156808..3157371)	0.392	0.116	0.263	0.055	0.671	0.172	0.017	0.279	0.008	1.626	prepilin peptidase dependent protein B, putative onent in type IV pilin biogenesis

ppdA	STM3000	AAL21876	(3157362..3157832)	0.598	0.093	0.774	0.177	1.294	0.311	0.025	0.512	0.066	1.648	prepilin peptidase dependent protein A, putative onent in type IV pilin biogenesis
thyA	STM3001	AAL21877	(3158017..3158811)	3.562	0.192	3.028	0.205	0.850	3.900	0.373	2.421	0.192	0.621	thymidylate synthetase
lgt	STM3002	AAL21878	(3158818..3159693)	5.698	0.211	1.655	0.256	0.290	5.780	1.619	1.465	0.189	0.254	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase
ptsP	STM3003	AAL21879	(3159909..3162155)	2.556	0.312	2.706	0.251	1.059	2.534	0.187	2.107	0.078	0.831	General PTS system, enzyme I, transcriptional regulator with NPR and NTR proteins
ygdP	STM3004	AAL21880	(3162168..3162698)	3.374	0.575	3.015	0.164	0.894	2.648	0.046	3.675	0.233	1.388	putative invasion protein; NTP pyrophosphohydrolase
mutH	STM3005	AAL21881	3163381..3164076	1.284	0.067	0.941	0.126	0.733	0.665	0.044	0.598	0.049	0.900	methyl-directed mismatch repair protein
ygdQ	STM3006	AAL21882	3164258..3164971	1.627	0.282	0.521	0.105	0.320	3.337	0.706	0.908	0.030	0.272	putative integral membrane transport protein
ygdR	STM3007	AAL21883	3165141..3165359	1.813	0.236	0.890	0.155	0.491	0.649	0.092	0.494	0.042	0.761	putative POT family, peptide transport protein
tas	STM3008	AAL21884	3165550..3166590	1.034	0.011	1.155	0.130	1.117	0.710	0.081	0.888	0.099	1.250	putative aldo/keto reductase
ygeD	STM3009	AAL21885	(3166677..3167879)	2.091	0.072	0.777	0.033	0.372	1.342	0.104	0.818	0.089	0.609	putative efflux protein, resistance protein
aas	STM3010	AAL21886	(3167872..3170031)	1.779	0.109	0.910	0.064	0.512	1.134	0.065	0.890	0.049	0.784	bifunctional: 2-acylglycerophospho-ethanolamine acyl transferase; acyl-acyl carrier protein synthetase
galR	STM3011	AAL21887	3170624..3171652	1.519	0.092	1.306	0.067	0.859	0.491	0.061	0.932	0.069	1.900	transcriptional repressor of galETK operon (GalR/LacI family)
STM3012	STM3012	AAL21888	3171663..3172685	1.126	0.063	0.907	0.113	0.806	0.440	0.063	0.936	0.050	2.129	putative transcriptional regulator
lysA	STM3013	AAL21889	(3172695..3173957)	1.040	0.040	0.324	0.066	0.312	0.718	0.224	0.644	0.030	0.898	diaminopimelate decarboxylase
lysR	STM3014	AAL21890	3174075..3175010	0.455	0.097	0.433	0.030	0.952	0.284	0.012	0.439	0.006	1.544	positive transcriptional regulator (LysR family)
ygeA	STM3015	AAL21891	(3174982..3175689)	0.609	0.069	0.717	0.116	1.176	0.359	0.143	0.493	0.048	1.372	putative aspartate racemase
araE	STM3016	AAL21892	(3175802..3177220)	0.335	0.112	0.200	0.043	0.598	0.160	0.058	0.257	0.011	1.611	MFS family, L-arabinose: proton symport protein (low-affinity transporter)
kduD	STM3017	AAL21893	(3177574..3178335)	0.398	0.076	0.354	0.064	0.888	0.191	0.017	0.341	0.038	1.786	2-deoxy-D-gluconate 3-dehydrogenase
kduI	STM3018	AAL21894	(3178392..3179228)	0.479	0.089	0.349	0.019	0.728	0.204	0.011	0.282	0.029	1.385	putative pectin degrading enzyme 5-keto 4-deoxyuronate isomerase
yqeF	STM3019	AAL21895	(3179658..3180836)	12.283	3.486	4.029	0.727	0.328	1.330	0.213	1.463	0.161	1.100	putative acetyl-CoA acetyltransferase
STM3020	STM3020	AAL21896	(3180959..3181822)	1.106	0.043	0.502	0.018	0.454	0.493	0.183	0.526	0.040	1.068	putative transcriptional regulator, LysR family
STM3021	STM3021	AAL21897	3181899..3182381	0.886	0.043	0.280	0.050	0.316	0.575	0.135	0.368	0.019	0.640	putative inner membrane protein
STM3022	STM3022	AAL21898	3182523..3183752	1.329	0.155	0.338	0.066	0.254	1.348	0.248	0.565	0.010	0.419	putative transport protein
yohL	STM3023	AAL21899	(3183783..3184055)	0.644	0.061	0.374	0.085	0.582	0.624	0.314	0.348	0.023	0.557	putative cytoplasmic protein
yohM	STM3024	AAL21900	3184177..3185043	0.415	0.142	0.301	0.057	0.725	0.245	0.070	0.267	0.017	1.092	putative inner membrane protein
STM3025	STM3025	AAL21901	(3185253..3186011)	0.415	0.182	0.212	0.013	0.512	1.117	0.077	1.519	0.060	1.359	putative cytoplasmic protein
STM3026	STM3026	AAL21902	(3186654..3187730)	0.361	0.057	0.094	0.028	0.261	0.478	0.045	0.501	0.033	1.049	putative outer membrane protein
stdC	STM3027	AAL21903	(3187727..3188470)	0.263	0.182	0.235	0.037	0.892	0.245	0.028	0.334	0.031	1.368	putative fimbrial chaparone protein
stdB	STM3028	AAL21904	(3188511..3191000)	0.207	0.132	0.100	0.019	0.483	0.205	0.070	0.224	0.010	1.094	putative outer membrane usher protein
stdA	STM3029	AAL21905	(3191120..3191830)	0.214	0.099	0.148	0.016	0.693	0.378	0.039	0.366	0.022	0.967	putative fimbrial-like protein

STM3030	STM3030	AAL21906	(3192423..3193055)	0.328	0.097	0.272	0.020	0.829	5.539	0.682	3.745	0.138	0.676	putative periplasmic protein
STM3031	STM3031	AAL21907	(3193102..3193638)	0.392	0.075	0.235	0.050	0.599	4.513	0.115	3.194	0.137	0.708	ail and ompX Homolog
tnpA_4	STM3032	AAL21908	(3194318..3194776)					N/A					N/A	transposase for IS200
STM3033	STM3033	AAL21909	(3195156..3195554)	3.299	0.551	1.602	0.283	0.486	1.748	0.333	1.853	0.134	1.061	putative nucleic acid-binding protein, contains PIN domain
STM3034	STM3034	AAL21910	(3195554..3195781)	3.900	0.493	1.411	0.053	0.362	2.206	0.492	1.461	0.096	0.662	putative cytoplasmic protein
STM3035	STM3035	AAL21911	3195958..3196209	0.658	0.058	0.382	0.042	0.580	0.521	0.150	0.514	0.075	0.987	putative periplasmic protein
STM3036	STM3036	AAL21912	3196484..3197290	0.389	0.115	0.273	0.063	0.703	0.814	0.096	3.771	0.043	4.633	putative inner membrane protein
glyU	STM3037						N/A					N/A		
STM3038	STM3038	AAL21913	(3197575..3198333)	0.809	0.038	1.300	0.131	1.607	0.487	0.053	0.918	0.044	1.886	putative metalloendopeptidase
idi	STM3039	AAL21914	3198598..3199143	1.053	0.037	2.306	0.097	2.190	0.601	0.060	1.276	0.157	2.124	isopentenyldiphosphate isomerase
lysS	STM3040	AAL21915	(3199219..3200736)	3.568	0.126	9.647	0.660	2.703	2.579	0.114	4.396	0.302	1.705	lysine tRNA synthetase, constitutive
prfB	STM3041	AAL21916	(3200746..3201627)	2.238	0.092	4.898	1.207	2.189	1.526	0.104	2.469	0.144	1.618	peptide chain release factor RF-2
recJ	STM3042	AAL21917	(3201949..3203682)	1.930	0.105	1.861	0.356	0.964	1.675	0.088	1.683	0.194	1.005	ssDNA exonuclease, 5' --> 3' specific, Mg dependent
dsbC	STM3043	AAL21918	(3203688..3204401)	1.264	0.055	2.333	0.292	1.846	0.798	0.058	1.735	0.204	2.175	protein disulfide isomerase II
xerD	STM3044	AAL21919	(3204425..3205321)					N/A					N/A	recombinase, site-specific
fldB	STM3045	AAL21920	3205434..3205955	1.910	0.077	1.682	0.137	0.881	0.823	0.028	0.918	0.077	1.116	flavodoxin 2
ygfX	STM3046	AAL21921	(3206008..3206421)	3.976	0.369	2.010	0.128	0.506	1.318	0.123	1.175	0.111	0.891	putative inner membrane protein
ygfY	STM3047	AAL21922	(3206402..3206668)	7.592	1.156	2.123	0.083	0.280	2.280	0.484	1.453	0.104	0.637	putative cytoplasmic protein
ygfZ	STM3048	AAL21923	3206918..3207898	1.746	0.076	4.012	0.191	2.298	1.205	0.030	4.732	0.397	3.927	putative aminomethyltransferase
yqfA	STM3049	AAL21924	(3208014..3208673)	1.492	0.153	1.097	0.127	0.735	2.117	0.525	1.832	0.095	0.865	putative hemolysin
yqfB	STM3050	AAL21925	(3208837..3209148)	1.252	0.091	1.136	0.228	0.908	0.757	0.024	0.917	0.017	1.211	putative cytoplasmic protein
bglA	STM3051	AAL21926	3209307..3210740	1.349	0.032	0.856	0.121	0.634	0.926	0.042	1.474	0.056	1.592	6-phospho-beta-glucosidase A
STM3052	STM3052	AAL21927	(3210788..3211681)	0.345	0.085	0.332	0.059	0.962	0.368	0.006	0.367	0.039	0.998	putative outer membrane protein
gcvP	STM3053	AAL21928	(3212137..3215010)	10.031	1.407	16.342	2.265	1.629	5.676	0.661	10.679	1.816	1.882	glycine cleavage lex protein P, glycine decarboxylase
gcvH	STM3054	AAL21929	(3215173..3215562)	22.425	2.959			0.000	12.990	1.230			0.000	glycine cleavage lex protein H, carrier of aminomethyl moiety via covalently bound lipoyl cofactor
gcvT	STM3055	AAL21930	(3215588..3216682)	10.555	0.911	26.895	6.568	2.548	7.360	0.526	14.442	0.428	1.962	glycine cleavage lex protein T, aminomethyltransferase, tetrahydrofolate-dependent
visC	STM3056	AAL21931	(3217137..3218339)	2.936	0.461	2.184	0.101	0.744	1.467	0.315	1.756	0.173	1.197	putative monooxygenase
ubiH	STM3057	AAL21932	(3218465..3219643)	5.350	0.692	3.116	0.239	0.582	2.806	0.879	2.838	0.106	1.011	2-octaprenyl-6-methoxyphynol hydroxylase
pepP	STM3058	AAL21933	(3219640..3220956)	7.281	0.864	3.880	0.293	0.533	3.905	0.852	3.190	0.272	0.817	proline aminopeptidase P II
ygfB	STM3059	AAL21934	(3220982..3221566)					N/A					N/A	putative cytoplasmic protein
ygfE	STM3060	AAL21935	3221727..3222056	10.079	2.186			0.000	3.754	0.138			0.000	putative cytoplasmic protein
ygfA	STM3061	AAL21936	3222350..3222898	1.362	0.103	1.034	0.077	0.759	0.715	0.007	0.757	0.067	1.058	putative ligase
serA	STM3062	AAL21937	(3223279..3224511)	1.198	0.141	1.347	0.063	1.124	0.811	0.075	1.965	0.157	2.421	D-3-phosphoglycerate dehydrogenase

rpiA	STM3063	AAL21938	(3224777..3225436)					N/A					N/A	ribosephosphate isomerase, constitutive
iciA	STM3064	AAL21939	3225590..3226483	0.607	0.077	0.669	0.105	1.101	0.579	0.256	0.644	0.032	1.113	inhibitor of replication initiation, also transcriptional regulator of dnaA and argK (LysR family)
yggE	STM3065	AAL21940	(3226749..3227495)	2.665	0.376	1.759	0.154	0.660	4.762	0.376	5.740	0.839	1.205	putative periplasmic immunogenic protein
yggA	STM3066	AAL21941	(3227589..3228224)	0.456	0.101	0.646	0.154	1.417	0.647	0.086	0.576	0.050	0.890	putative LYSE family, amino acid transport protein
yggB	STM3067	AAL21942	(3228424..3229284)	0.932	0.191	1.367	0.187	1.466	1.215	0.096	1.844	0.307	1.518	putative membrane protein, involved in stability of MscS mechanosensitive channel
fba	STM3068	AAL21943	(3229511..3230590)	9.312	0.722	23.558	3.129	2.530	4.230	0.360	7.157	0.450	1.692	fructose-bisphosphate aldolase
pgk	STM3069	AAL21944	(3230692..3231855)	3.760	0.209	21.147	4.722	5.625	2.173	0.300	6.680	0.188	3.074	phosphoglycerate kinase
epd	STM3070	AAL21945	(3231877..3232923)	8.131	2.502	8.242	1.209	1.014	4.353	0.445	3.861	0.772	0.887	D-erythrose 4-phosphate dehydrogenase
STM3071	STM3071	AAL21946	3233297..3233722	0.505	0.146	0.908	0.156	1.798	0.246	0.078	0.462	0.053	1.876	putative DNA-binding protein
STM3072	STM3072	AAL21947	3233748..3234326	0.360	0.158			0.000	0.225	0.090			0.000	putative inner membrane protein
STM3073	STM3073	AAL21948	3234327..3235034	0.452	0.090	0.593	0.033	1.313	0.249	0.091	0.305	0.019	1.226	putative ABC-type cobalt transport system, permease onent CbiQ and related transporter
STM3074	STM3074	AAL21949	3235022..3235699	0.525	0.076	0.621	0.061	1.183	0.215	0.008	0.323	0.043	1.501	putative ABC-type cobalt transport system, ATPase onent
STM3075	STM3075	AAL21950	3235693..3236349	0.615	0.074	0.850	0.260	1.382	0.265	0.052	0.513	0.046	1.937	putative ABC-type cobalt transport system, ATPase onent
tktA	STM3076	AAL21951	(3236393..3238384)	4.252	0.173	26.347	2.234	6.196	1.849	0.158	5.139	0.276	2.780	transketolase 1 isozyme
yggG	STM3077	AAL21952	3238660..3239418	1.781	0.144	1.838	0.443	1.032	1.529	0.097	1.418	0.152	0.928	putative Zn-dependent proteases with possible chaperone function
speB	STM3078	AAL21953	(3239519..3240439)	9.612	0.958	2.413	0.144	0.251	8.054	1.066	3.701	0.258	0.459	agmatinase
STM3079	STM3079	AAL21954	(3240644..3241600)	0.575	0.071	0.242	0.034	0.422	1.176	0.031	0.961	0.198	0.817	putative hydrolase or acyltransferase
STM3080	STM3080	AAL21955	(3241814..3242287)	0.448	0.060	0.204	0.025	0.455	0.954	0.019	0.526	0.120	0.551	putative mannitol dehydrogenase
STM3081	STM3081	AAL21956	(3242326..3243333)	0.215	0.086	0.429	0.092	2.001	0.244	0.107	0.443	0.021	1.814	putative malate/L-lactate dehydrogenase
STM3082	STM3082	AAL21957	(3243347..3244363)	0.342	0.114	0.216	0.021	0.632	0.278	0.076	0.293	0.028	1.053	putative zinc-binding dehydrogenase
STM3083	STM3083	AAL21958	(3244366..3245838)	0.168	0.113	0.149	0.017	0.888	0.086	0.031	0.220	0.015	2.555	putative Mannitol dehydrogenase
STM3084	STM3084	AAL21959	(3247098..3247898)	0.616	0.048	1.413	0.205	2.293	0.426	0.245	0.656	0.040	1.542	putative regulatory protein, gntR family
STM3085	STM3085	AAL21960	(3248052..3248783)	0.285	0.093	0.299	0.062	1.049	1.408	0.613	1.004	0.156	0.713	putative outer membrane lipoprotein
speA	STM3086	AAL21961	(3248927..3250903)					N/A					N/A	arginine decarboxylase
yqgB	STM3087	AAL21962	(3250912..3251043)	4.148	0.323	3.792	0.306	0.914	3.899	0.105			0.000	putative inner membrane protein
yqgC	STM3088	AAL21963	3251177..3251341	3.349	0.374	1.262	0.018	0.377	3.913	0.243	1.613	0.091	0.412	putative cytoplasmic protein
yqgD	STM3089	AAL21964	(3251338..3251637)	1.544	0.091	0.773	0.102	0.500	1.531	0.402	0.758	0.072	0.495	putative inner membrane protein
metK	STM3090	AAL21965	3251693..3252847	6.648	0.527	2.643	0.535	0.398	2.068	0.179	2.856	0.084	1.381	methionine adenosyltransferase 1 (AdoMet synthetase)
galP	STM3091	AAL21966	3253339..3254733	1.257	0.050	0.636	0.109	0.506	2.357	0.318	3.056	0.058	1.297	MFS family, galactose:proton symporter
sprT	STM3092	AAL21967	3254812..3255309	0.841	0.107	0.469	0.044	0.557	0.487	0.082	0.509	0.024	1.043	putative cytoplasmic protein

endA	STM3093	AAL21968	3255404..3256111	1.659	0.114	0.591	0.056	0.356	1.123	0.119	0.686	0.157	0.611	DNA-specific endonuclease I
yggJ	STM3094	AAL21969	3256140..3256919	2.748	0.144	1.863	0.146	0.678	1.480	0.215	1.691	0.057	1.143	putative cytoplasmic protein
gshB	STM3095	AAL21970	3256939..3257886	2.119	0.199	2.631	0.306	1.241	1.001	0.022	1.725	0.180	1.724	glutathione synthetase
yqgE	STM3096	AAL21971	3258102..3258665	0.863	0.026	1.349	0.135	1.563	0.553	0.092	0.784	0.095	1.418	putative transcriptional regulator
yqgF	STM3097	AAL21972	3258665..3259081	0.724	0.130	1.020	0.162	1.408	0.387	0.076	0.522	0.027	1.349	putative endonuclease involved in recombination
STM3098	STM3098	AAL21973	(3259128..3259814)	0.675	0.053	0.279	0.045	0.414	0.457	0.049	0.435	0.009	0.952	putative transcriptional regulator
yggR	STM3099	AAL21974	(3259946..3260926)	0.424	0.098	0.256	0.038	0.602	0.176	0.049	0.259	0.016	1.471	putative protein transport
yggS	STM3100	AAL21975	3260944..3261648	1.868	0.361	1.034	0.143	0.553	1.870	0.148	1.581	0.243	0.846	putative enzyme with a TIM-barrel fold
yggT	STM3101	AAL21976	3261667..3262233	1.738	0.063	1.748	0.122	1.005	1.811	0.074	1.302	0.112	0.719	putative integral membran resistance protein
yggU	STM3102	AAL21977	3262230..3262520	2.037	0.202	4.062	0.494	1.994	2.057	0.310	3.876	0.930	1.884	putative cytoplasmic protein
yggV	STM3103	AAL21978	3262528..3263121	2.316	0.069			0.000	2.203	0.064			0.000	putative Xanthosine triphosphate pyrophosphatase
yggW	STM3104	AAL21979	3263114..3264250	1.142	0.060	1.514	0.290	1.326	0.703	0.071	0.781	0.037	1.111	putative oxidase
yggM	STM3105	AAL21980	(3264341..3265348)	0.609	0.067	1.452	0.323	2.383	0.165	0.060			0.000	putative periplasmic protein
ansB	STM3106	AAL21981	(3265481..3266527)	6.143	0.748	30.756	1.853	5.007	0.387	0.088	0.470	0.056	1.214	periplasmic L-asparaginase II
yggN	STM3107	AAL21982	(3266716..3267435)	8.836	3.378	9.068	0.345	1.026	4.754	0.544	4.008	0.314	0.843	putative periplasmic protein
yggL	STM3108	AAL21983	(3267485..3267811)	3.465	0.323	4.883	0.167	1.409	2.745	0.430	2.794	0.495	1.018	putative cytoplasmic protein
yggH	STM3109	AAL21984	(3267811..3268530)	2.248	0.122	1.871	0.363	0.832	2.208	0.196	1.682	0.161	0.762	putative S-adenosylmethionine-dependent methyltransferase
mutY	STM3110	AAL21985	3268685..3269737	3.346	0.404	1.453	0.255	0.434	2.673	0.392	1.555	0.210	0.582	adenine DNA glycosylase
yggX	STM3111	AAL21986	3269765..3270040	3.936	0.807	2.833	0.462	0.720	3.852	0.410	5.186	0.850	1.347	putative cytoplasmic protein
mltC	STM3112	AAL21987	3270153..3271238	1.068	0.051	1.326	0.151	1.241	1.025	0.066	1.103	0.073	1.076	membrane-bound lytic murein transglycosylase C
nupG	STM3113	AAL21988	3271455..3272711	0.748	0.099	1.763	0.252	2.357	0.232	0.019	0.393	0.034	1.694	MFS family, nucleoside transport
speC	STM3114	AAL21989	(3272773..3274908)	0.828	0.105	0.574	0.108	0.693	0.699	0.112	0.395	0.048	0.566	ornithine decarboxylase isozyme
yqgA	STM3115	AAL21990	3275333..3276040	0.860	0.063	0.214	0.008	0.248	0.637	0.189	0.384	0.050	0.603	putative inner membrane protein
pheV	STM3116						N/A					N/A		
STM3117	STM3117	AAL21991	(3276380..3276814)	0.524	0.029	0.228	0.028	0.434	1.269	0.199	0.980	0.079	0.772	putative lactoylglutathione lyase
STM3118	STM3118	AAL21992	(3276825..3278150)	0.266	0.107	0.216	0.034	0.812	0.430	0.258	0.323	0.016	0.751	putative acetyl-CoA hydrolase
STM3119	STM3119	AAL21993	(3278175..3278702)	0.329	0.128	0.410	0.063	1.245	0.296	0.148	0.439	0.028	1.483	putative monoamine oxidase
STM3120	STM3120	AAL21994	(3278726..3279568)	0.370	0.113	0.251	0.023	0.679	0.313	0.110	0.311	0.050	0.992	putative transcriptional regulator, LysR family
STM3121	STM3121	AAL21995	3279660..3280538	0.543	0.095	0.288	0.056	0.530	0.506	0.040	0.399	0.047	0.788	putative transcriptional regulator, LysR family
STM3122	STM3122	AAL21996	(3280586..3282325)	0.283	0.121	0.203	0.015	0.718	0.155	0.177	0.245	0.026	1.577	putative arylsulfatase
STM3123	STM3123	AAL21997	(3282394..3283578)	0.303	0.131	0.174		0.575	0.229	0.049	0.248		1.082	putative arylsulfatase regulator
STM3124	STM3124	AAL21998	3284090..3284773	4.293	0.596	0.941	0.064	0.219	0.510	0.037	0.627	0.067	1.228	putative response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain
STM3125	STM3125	AAL21999	(3284877..3285434)	0.517	0.120	0.210	0.019	0.407	0.325	0.032	0.412	0.046	1.269	putative cytoplasmic protein
STM3126	STM3126	AAL22000	(3285412..3286911)	0.305	0.132	0.151	0.016	0.495	0.327	0.027	0.296	0.052	0.903	putative amino acid transporter

STM3127	STM3127	AAL22001	(3287120..3287494)	0.509	0.079	0.271	0.058	0.532	0.983	0.131	0.532	0.046	0.541	putative cytoplasmic protein
STM3128	STM3128	AAL22002	(3287509..3288810)	0.186	0.102	0.108	0.022	0.581	0.231	0.004	0.260	0.021	1.125	putative oxidoreductase
STM3129	STM3129	AAL22003	3288972..3290456	0.266	0.135	0.204	0.044	0.765	0.175	0.056	0.322	0.020	1.834	putative NAD-dependent aldehyde dehydrogenase
STM3130	STM3130	AAL22004	(3290592..3290972)	0.310	0.110	0.363	0.044	1.171	0.432	0.046	0.509	0.057	1.176	putative cytoplasmic protein
STM3131	STM3131	AAL22005	(3290972..3291457)	0.266	0.096	0.498	0.104	1.872	0.613	0.069	0.688	0.038	1.122	putative cytoplasmic protein
STM3132	STM3132	AAL22006	(3292183..3293106)	0.212	0.115	0.284	0.054	1.338	5.067	0.430	10.019	0.908	1.977	putative xylanase/chitin deacetylase
STM3133	STM3133	AAL22007	(3293145..3294023)	0.313	0.115	0.178	0.027	0.570	3.402	0.129	4.572	0.555	1.344	putative amidohydrolase
STM3134	STM3134	AAL22008	(3294419..3295723)	0.888	0.077	1.877	0.053	2.113	0.226	0.110	0.520	0.028	2.303	putative permease
STM3135	STM3135	AAL22009	3296128..3297312					N/A					N/A	putative mannonate hydrolase
STM3136	STM3136	AAL22010	3297423..3298895	0.580	0.027			0.000	0.174	0.039			0.000	putative D-mannonate oxidoreductase
STM3137	STM3137	AAL22011	3298907..3300319	0.891	0.093	2.997	0.625	3.362	0.370	0.014	0.577	0.034	1.560	putative uronate isomerase
STM3138	STM3138	AAL22012	(3300619..3301677)	0.485	0.033	8.742	0.466	18.042	2.462	0.201	1.813	0.162	0.736	putative methyl-accepting chemotaxis protein
gsp	STM3139	AAL22013	(3302347..3304203)	0.686	0.076	1.740	0.123	2.538	0.544	0.070	1.268	0.050	2.331	bifunctional: glutathionylspermidine synthetase; glutathionylspermidine amidase
yghU	STM3140	AAL22014	3304430..3305296	2.252	0.150	0.775	0.068	0.344	1.931	0.604	1.452	0.080	0.752	putative glutathione S-transferase
STM3141	STM3141	AAL22015	(3305364..3306074)	0.822	0.043	0.392	0.074	0.476	0.386	0.027	0.515	0.025	1.337	molybdenum-binding periplasmic protein
STM3142	STM3142	AAL22016	(3306074..3307126)	0.313	0.141	0.309	0.112	0.988	0.158	0.034	0.185	0.006	1.166	putative ferrichrome-binding periplasmic protein
hybG	STM3143	AAL22017	(3307202..3307450)	0.510	0.012	1.573	0.217	3.083	0.380	0.025	0.488	0.061	1.282	hydrogenase-2 operon protein
hybF	STM3144	AAL22018	(3307478..3307819)	0.872	0.061	2.763	0.099	3.168	0.749	0.051	0.762	0.039	1.017	putative hydrogenase expression/formation protein
hybE	STM3145	AAL22019	(3307812..3308300)	0.879	0.058	3.612	0.637	4.108	0.490	0.034	0.584	0.019	1.192	putative hydrogenase
hybD	STM3146	AAL22020	(3308293..3308787)	1.239	0.098	7.581	0.710	6.118	0.700	0.105	1.060	0.014	1.516	putative processing element for hydrogenase-2
hybC	STM3147	AAL22021	(3308787..3310490)	0.856	0.048	7.808	0.298	9.122	0.500	0.025	1.002	0.088	2.003	hydrogenase-2, large subunit
hybB	STM3148	AAL22022	(3310487..3311665)	0.464	0.103	4.083	0.209	8.804	0.242	0.024	0.290	0.036	1.199	putative cytochrome Ni/Fe onent of hydrogenase-2
hybA	STM3149	AAL22023	(3311655..3312641)	0.366	0.108	5.160	0.765	14.085	0.154	0.036	0.428	0.029	2.776	function unknown, intitally thought to be hydrogenase-2 small subunit which now identified as hybO
hypO	STM3150	AAL22024	(3312644..3313762)	0.453	0.152	6.866	1.287	15.156	0.180	0.037	0.381	0.016	2.109	putative Ni/Fe hydrogenases, small subunit
yghW	STM3151	AAL22025	(3313952..3314239)	0.511	0.098	0.906	0.113	1.773	0.229	0.021	0.176	0.040	0.770	putative cytoplasmic protein
STM3152	STM3152	AAL22026	(3314324..3315967)	2.536	0.214	3.349	0.219	1.320	0.319	0.015	0.370	0.017	1.162	putative methyl-accepting chemotaxis protein
yqhA	STM3153	AAL22027	(3316274..3316768)	1.299	0.060	0.947	0.017	0.729	1.982	0.333	1.064	0.046	0.537	putative membrane-associated protein
STM3154	STM3154	AAL22028	(3317048..3317563)	0.868	0.055	1.140	0.192	1.313	4.579	0.139	2.559	0.185	0.559	putative ATP-dependent RNA helicase-like protein
STM3155	STM3155	AAL22029	3317655..3318065	0.936	0.041	1.674	0.181	1.789	3.782	0.157	2.668	0.098	0.705	putative cytoplasmic protein
STM3156	STM3156	AAL22030	3318052..3318456	0.976	0.061	1.678	0.167	1.720	4.164	0.195	2.740	0.205	0.658	putative cytoplasmic protein
yghA	STM3157	AAL22031	3318580..3319464	2.274	0.502	1.805	0.265	0.794	9.754	1.978	13.902	0.790	1.425	putative oxidoreductase

exbD	STM3158	AAL22032	(3319577..3320002)	1.274	0.036	0.499	0.031	0.392	0.995	0.068	1.431	0.064	1.438	uptake of enterochelin; tonB-dependent uptake of B colicins
exbB	STM3159	AAL22033	(3320009..3320743)	1.660	0.064	0.400	0.046	0.241	0.662	0.004	0.875	0.059	1.323	uptake of enterochelin; tonB-dependent uptake of B colicins
STM3160	STM3160	AAL22034	(3320736..3320885)	0.926	0.052	0.320	0.026	0.346	0.677	0.248	0.403	0.066	0.595	putative inner membrane protein
metC	STM3161	AAL22035	3320995..3322182	0.512	0.136	0.585	0.075	1.142	0.233	0.027	0.396	0.020	1.703	cystathionine beta-lyase (beta-cystathionase)
yghB	STM3162	AAL22036	3322322..3322981	0.972	0.191			0.000	1.350	0.064			0.000	putative DedA family, membrane protein
yqhC	STM3163	AAL22037	(3323045..3323962)	0.678	0.075	0.431	0.081	0.637	0.310	0.019	0.420	0.065	1.357	putative transcriptional regulator (AraC/XylS family)
yqhD	STM3164	AAL22038	3324137..3325300	0.387	0.110	0.852	0.106	2.204	0.231	0.058	0.638	0.030	2.756	putative alcohol dehydrogenase
yqhE	STM3165	AAL22039	3325406..3326233	1.219	0.136	0.891	0.038	0.731	1.073	0.117	1.842	0.366	1.718	2,5-diketo-D-gluconate reductase A
STM3166	STM3166	AAL22040	3326399..3327883	0.337	0.113	0.137	0.021	0.407	0.363	0.155	0.297	0.012	0.819	putative cation transporter
STM3167	STM3167	AAL22041	3327928..3328383	1.706	0.128	0.713	0.095	0.418	0.723	0.020	0.578	0.066	0.800	putative diadenosine tetraphosphate (Ap4A) hydrolase
ygiR	STM3168	AAL22042	(3328938..3331109)	0.947	0.145	0.462	0.039	0.487	1.198	0.216	0.590	0.018	0.493	putative Fe-S oxidoreductase family 2
STM3169	STM3169	AAL22043	3331597..3332580	0.208	0.141	0.263	0.031	1.263	0.154	0.058	0.233	0.019	1.512	putative dicarboxylate-binding periplasmic protein
STM3170	STM3170	AAL22044	3332622..3333104	0.259	0.169	0.196	0.009	0.757	0.276	0.078	0.250	0.006	0.903	putative inner membrane protein
ygiK	STM3171	AAL22045	3333115..3334422	0.529	0.083	0.340	0.086	0.643	0.868	0.167	0.424	0.021	0.488	putative integral membrane protein, possible transporter
sufI	STM3172	AAL22046	(3334467..3335879)	4.486	0.612	1.984	0.069	0.442	2.479	0.086	1.694	0.148	0.683	suppressor of ftsI, putative periplasmic protein
plsC	STM3173	AAL22047	(3335953..3336690)	3.083	0.405	0.832	0.279	0.270	1.953	0.302	1.083	0.354	0.554	1-acyl-sn-glycerol-3-phosphate acyltransferase
parC	STM3174	AAL22048	(3336947..3339205)					N/A					N/A	DNA topoisomerase IV, subunit A
STM3175	STM3175	AAL22049	(3339316..3340182)	2.057	0.111	1.005	0.123	0.488	0.427	0.042	0.501	0.055	1.173	putative bacterial regulatory helix-turn-helix proteins, araC family
ygiW	STM3176	AAL22050	(3340254..3340646)	4.432	0.614	5.783	0.597	1.305	0.804	0.104	1.104	0.059	1.373	putative outer membrane protein
qseB	STM3177	AAL22051	3340798..3341457	1.058	0.033	0.482	0.057	0.456	0.596	0.076	0.603	0.032	1.013	
qseC	STM3178	AAL22052	3341454..3342803	0.520	0.066	0.351	0.056	0.674	0.373	0.063	0.441	0.014	1.182	
mdaB	STM3179	AAL22053	3342910..3343491	0.446	0.080	0.940	0.047	2.107	0.211	0.033	0.614	0.021	2.903	NADPH specific quinone oxidoreductase (drug modulator)
ygiN	STM3180	AAL22054	3343523..3343837	1.138	0.047	1.447	0.222	1.272	0.567	0.151	0.771	0.034	1.361	putative cytoplasmic protein
parE	STM3181	AAL22055	(3343962..3345854)	2.079	0.173	1.854	0.306	0.892	1.370	0.080	1.171	0.117	0.855	DNA topoisomerase IV, subunit B
yqiA	STM3182	AAL22056	(3345882..3346463)	1.269	0.031	1.936	0.099	1.525	0.765	0.064	1.002	0.032	1.309	putative esterase
icc	STM3183	AAL22057	(3346463..3347290)	1.474	0.120	4.067	0.588	2.759	0.742	0.031	1.636	0.094	2.205	cyclic 3',5'-adenosine monophosphate phosphodiesterase
yqiB	STM3184	AAL22058	(3347315..3347737)	0.548	0.076	1.434	0.266	2.616	0.454	0.081	1.172	0.024	2.580	putative cytoplasmic protein
yqiE	STM3185	AAL22059	(3347734..3348366)	0.430	0.095	1.060	0.185	2.463	0.308	0.031	0.722	0.106	2.346	putative resistance protein

tolC	STM3186	AAL22060	3348567..3350042	1.084	0.111	4.832	0.413	4.457	1.118	0.067	4.142	0.192	3.705	outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes, role in organic solvent tolerance
ygiB	STM3187	AAL22061	3350255..3350926	11.140	2.842	7.516	0.486	0.675	6.353	1.582	5.556	0.204	0.875	putative inner membrane protein
ygiC	STM3188	AAL22062	3350932..3352095	7.170	1.469	4.552	0.877	0.635	3.758	0.253	1.657	0.132	0.441	putative glutathionylspermidine synthase
ygiD	STM3189	AAL22063	(3352157..3352987)	1.286	0.198	0.580	0.041	0.451	0.530	0.033	0.386	0.057	0.727	putative cytoplasmic protein
ygiE	STM3190	AAL22064	3353086..3353859	1.958	0.160	0.539	0.050	0.276	0.857	0.039	0.740	0.036	0.863	putative divalent heavy-metal cations transporter
STM3191	STM3191	AAL22065	3354502..3355467	0.197	0.144	0.151	0.030	0.765	0.470	0.089	0.879	0.047	1.868	putative arylsulfate sulfotransferase
STM3192	STM3192	AAL22066	3355503..3356297	0.229	0.100	0.122	0.017	0.531	0.373	0.036	0.377	0.035	1.013	putative arylsulfate sulfotransferase
STM3193	STM3193	AAL22067	3356317..3356988	0.285	0.104	0.204	0.019	0.717	0.409	0.016	0.556	0.031	1.360	putative thiol-disulfide isomerase and thioredoxin
STM3194	STM3194	AAL22068	3357003..3357680	0.538	0.092	0.190	0.049	0.354	0.643	0.022	0.443	0.055	0.689	putative disulfide isomerase
ribB	STM3195	AAL22069	(3357851..3358504)	4.543	1.367	0.989	0.059	0.218	3.204	0.365	3.339	0.155	1.042	3,4 dihydroxy-2-butanone-4-phosphate synthase
yqiC	STM3196	AAL22070	3358881..3359240	0.917	0.062	0.870	0.084	0.949	0.515	0.021	0.535	0.027	1.039	putative cytoplasmic protein
glgS	STM3197	AAL22071	(3359314..3359523)	0.652	0.064	0.531	0.096	0.814	0.464	0.054	0.436	0.039	0.940	glycogen biosynthesis, rpoS dependent
STM3198	STM3198	AAL22072	3359781..3360401	0.406	0.127	0.225	0.031	0.553	0.272	0.058	0.361	0.038	1.325	putative inner membrane protein
yqiK	STM3199	AAL22073	3360420..3362099	0.352	0.086	0.237	0.026	0.674	0.228	0.030	0.315	0.046	1.383	paral putative membrane protein
rfaE	STM3200	AAL22074	(3362559..3363992)	4.307	0.581	2.220	0.060	0.515	2.397	0.481	1.838	0.092	0.767	bifunctional; putative sugar nucleotide transferase domain of ADP-L-glycero-D-manno-heptose synthase
glnE	STM3201	AAL22075	(3364040..3366883)					N/A					N/A	adenylyl transferase for glutamine synthetase, regulates P-II (GlnB) and GlnK
ygiF	STM3202	AAL22076	(3367001..3368302)	1.087	0.075	1.490	0.038	1.370	0.583	0.079	1.347	0.176	2.309	putative cytoplasmic protein
ygiM	STM3203	AAL22077	3368544..3369158	9.662	1.177	27.198	5.746	2.815	2.815	0.077	4.165	0.344	1.480	putative SH3 domain protein
cca	STM3204	AAL22078	3369221..3370462	2.577	0.408	4.330	0.526	1.680	0.950	0.070	1.050	0.070	1.105	tRNA nucleotidyl transferase
bacA	STM3205	AAL22079	(3370567..3371391)	2.831	0.195	0.967	0.080	0.342	3.378	0.905	1.175	0.175	0.348	bacitracin resistance; possibly phosphorylates undecaprenol
folB	STM3206	AAL22080	(3371486..3371848)	1.188	0.051	0.647	0.032	0.545	2.269	0.285	1.304	0.134	0.575	dihydroneopterin aldolase, also has dihydroneopterin triphosphate 2'-epimerase activity
ygiH	STM3207	AAL22081	3371952..3372563	2.503	0.094	0.846	0.029	0.338	1.366	0.393	1.141	0.116	0.835	putative inner membrane protein
g	STM3208	AAL22082	(3372814..3373827)	2.182	0.060	1.295	0.011	0.593	1.846	0.235	1.110	0.059	0.601	putative O-sialoglycoprotein endopeptidase
rpsU	STM3209	AAL22083	3374055..3374270	18.367	4.224	9.918	0.804	0.540	9.813	0.665	3.808	0.330	0.388	30S ribosomal subunit protein S21
dnaG	STM3210	AAL22084	3374506..3376251	1.396	0.497	2.081	0.369	1.490	2.014	0.604	1.207	0.130	0.599	DNA biosynthesis; DNA primase
rpoD	STM3211	AAL22085	3376266..3378248	3.659	0.342	8.011	1.292	2.189	3.312	0.133	6.161	0.156	1.860	sigma D (sigma 70) factor of RNA polymerase, major sigma factor during exponential growth
mug	STM3212	AAL22086	(3378372..3378878)	1.358	0.161	1.074	0.117	0.791	0.887	0.097	0.783	0.069	0.884	DNA glycosylase, G/U mismatch specific
ileX	STM3213						N/A					N/A		
yqjH	STM3214	AAL22087	(3379159..3379926)	1.603	0.224	0.544	0.120	0.340	0.377	0.004	0.588	0.086	1.561	putative transporter
yqjI	STM3215	AAL22088	3380158..3380805	1.645	0.145	2.001	0.363	1.217	0.580	0.125	0.567	0.033	0.977	putative transcriptional regulator
STM3216		AAL22089	(3380802..3382367)	1.056	0.019	21.944	1.443	20.784	0.248	0.024	0.355	0.023	1.430	putative methyl-accepting chemotaxis protein

aer	STM3217	AAL22090	(3382755..3384275)	1.311	0.129	8.341	1.425	6.362	0.167	0.017	0.269	0.023	1.606	aerotaxis sensor receptor, senses cellular redox state or proton motive force
oat	STM3218	AAL22091	3384795..3386084	0.489	0.126	0.459	0.033	0.938	0.483	0.038	0.728		1.507	putative acetylornithine aminotransferase
fadH	STM3219	AAL22092	3386255..3388273	2.834	0.537	0.965	0.068	0.341	0.590	0.034	0.871	0.058	1.477	2,4-dieonyl-coa reductase
ygjO	STM3220	AAL22093	(3388354..3389490)	1.737	0.133	0.474	0.081	0.273	1.120	0.057	0.395	0.013	0.352	paral putative methyltransferase
ygjP	STM3221	AAL22094	3389576..3390073	1.049	0.041	0.594	0.051	0.566	0.666	0.032	0.503	0.032	0.755	putative metal-dependent hydrolase
ygjQ	STM3222	AAL22095	3390225..3390917	0.612	0.130	0.356	0.093	0.582	0.341	0.034	0.280	0.043	0.822	putative integral membrane protein
ygjR	STM3223	AAL22096	3391006..3392004	1.855	0.104	2.209	0.166	1.191	0.357	0.010	0.723	0.070	2.026	putative dehydrogenase
ygjT	STM3224	AAL22097	3392277..3393245	1.103	0.031	0.730	0.158	0.662	0.630	0.143	0.426	0.020	0.676	putative resistance protein
ygjU	STM3225	AAL22098	3393500..3394744	2.600	0.413	4.973	0.121	1.913	0.266	0.023	0.502	0.057	1.889	putative dicarboxylate permease
yqjA	STM3226	AAL22099	3395194..3395856	1.958	0.141	1.199	0.281	0.612	2.326	0.364	2.023	0.195	0.870	putative DedA family, membrane protein
yqjB	STM3227	AAL22100	3395860..3396243	1.520	0.077	1.454	0.134	0.957	1.563	0.084	1.645	0.101	1.053	putative outer membrane protein
yqjC	STM3228	AAL22101	3396388..3396756	2.228	0.382	3.430	0.255	1.539	2.568	0.292	4.092	0.216	1.593	putative periplasmic protein
yqjD	STM3229	AAL22102	3396798..3397103	5.497	0.867	6.754	0.594	1.229	5.257	1.478	7.381	0.316	1.404	putative inner membrane protein
yqjE	STM3230	AAL22103	3397106..3397504	7.824	1.748	9.172	1.780	1.172	7.605	1.628	9.369	0.993	1.232	putative inner membrane protein
yqjK	STM3231	AAL22104	3397501..3397800	2.171	0.340	2.082	0.251	0.959	2.615	0.417	2.801	0.174	1.071	putative inner membrane protein
yqjF	STM3232	AAL22105	3397945..3398430	0.603	0.080	0.350	0.127	0.581	0.428	0.033			0.000	putative membrane-associated protein
yqjG	STM3233	AAL22106	3398498..3399484	1.125	0.068	0.579	0.062	0.514	0.920	0.076	0.860	0.085	0.935	putative glutathione S-transferase
yhaH	STM3234	AAL22107	3399608..3399973	2.406	0.145	1.419	0.256	0.590	1.583	0.106	1.364	0.043	0.861	putative inner membrane protein
yhaJ	STM3235	AAL22108	(3400012..3400908)	1.422	0.056	1.093	0.076	0.769	0.699	0.044	0.876	0.030	1.253	putative transcriptional regulator, LysR family
yhaK	STM3236	AAL22109	3401013..3401714	0.545	0.161	0.390	0.065	0.716	0.197	0.012	0.324	0.029	1.643	putative cytoplasmic protein
yhaL	STM3237	AAL22110	3401738..3401902	2.785	0.543	2.269	0.562	0.815	0.479	0.021	0.701	0.127	1.462	putative cytoplasmic protein
yhaN	STM3238	AAL22111	(3402015..3403325)	0.569	0.096	0.639	0.042	1.122	0.606	0.139	0.801	0.040	1.322	putative inner membrane protein
yhaO	STM3239	AAL22112	(3403351..3404682)	0.278	0.148	0.350	0.019	1.259	0.248	0.006	0.237	0.051	0.957	putative HAAAP family transport protein
tdcG	STM3240	AAL22113	(3404998..3406362)	0.592	0.166	1.008	0.052	1.703	0.852	0.160	0.849	0.036	0.996	L-serine deaminase
tdcE	STM3241	AAL22114	(3406432..3408726)	0.356	0.136	2.890	0.099	8.122	1.391	0.090	1.358		0.976	pyruvate formate-lyase 4/ 2-ketobutyrate formate-lyase
tdcD	STM3242	AAL22115	(3408760..3409968)	0.249	0.152	3.036	0.196	12.184	1.042	0.213	1.200	0.115	1.151	propionate kinase/acetate kinase II, anaerobic
tdcC	STM3243	AAL22116	(3410034..3411365)	0.315	0.129	3.697	0.184	11.721	1.166	0.073	2.231	0.144	1.914	HAAAP family, L-threonine/ L-serine permease, anaerobically inducible
tdcB	STM3244	AAL22117	(3411386..3412375)	0.401	0.111	3.745	0.617	9.332	1.476	0.064	2.254	0.156	1.527	threonine dehydratase, catabolic
tdcA	STM3245	AAL22118	(3412473..3413411)	0.805	0.155	0.861	0.163	1.070	1.584	0.332	1.610	0.182	1.017	transcriptional activator of tdc operon (LysR family)
garK	STM3247	AAL22119	(3415210..3416355)	0.964	0.056	1.877	0.197	1.946	0.923	0.094	0.786	0.025	0.852	glycerate kinase
garR	STM3248	AAL22120	(3416453..3417343)	5.896	0.438	4.602	0.785	0.781	2.310	0.586	2.977	0.155	1.289	tartronate semialdehyde reductase (TSAR)
garL	STM3249	AAL22121	(3417369..3418139)	1.489	0.057	3.379	0.078	2.269	1.700	0.257	1.701	0.184	1.001	2-Dehydro-3-Deoxy-Galactarate Aldolase
garD	STM3250	AAL22122	3418669..3420240	0.628	0.138	1.465	0.122	2.333	0.663	0.127	0.945	0.067	1.427	galactarate dehydrogenase
STM3251	STM3251	AAL22123	(3420480..3421427)	1.411	0.119	0.749	0.042	0.531	0.470	0.013	0.628	0.029	1.336	putative sugar kinase, ribokinase family

agaR	STM3252	AAL22124	(3421438..3422271)	2.311	0.092	0.923	0.162	0.400	0.616	0.059	0.617	0.036	1.001	aga operon transcriptional repressor (DeoR family)
STM3253	STM3253	AAL22125	3422605..3423459	1.926	0.142	0.221	0.039	0.115	0.184	0.024	0.223	0.037	1.213	putative fructose/tagatose biphosphate aldolase
STM3254	STM3254	AAL22126	3423470..3424384	1.319	0.029	0.196	0.014	0.148	0.203	0.199	0.273	0.013	1.346	putative fructose-1-phosphate kinase
STM3255	STM3255	AAL22127	3424411..3425838	1.118	0.076	0.121	0.004	0.108	0.511	0.077	0.494	0.014	0.966	putative phosphotransferase system fructose-specific onent IIB
STM3256	STM3256	AAL22128	3425825..3426631	0.704	0.053	0.119	0.029	0.169	0.289	0.062	0.325	0.070	1.127	putative phosphotransferase system mannitol/fructose-specific IIA domain
STM3257	STM3257	AAL22129	3426829..3428100	0.433	0.104	0.227	0.019	0.525	0.113	0.015	0.518	0.768	4.572	putative tagatose 6-phosphate kinase 1
STM3258	STM3258	AAL22130	3428115..3428579	0.442	0.065	0.285	0.045	0.644	0.245	0.086	0.345	0.038	1.408	Sugar specific-family of transport protein, galactitol-specific enzyme IIA of phosphotransferase system
STM3259	STM3259	AAL22131	3428610..3428894	1.148	0.155	0.542	0.093	0.472	0.868	0.186	0.562	0.071	0.647	PTS family galactitol-specific enzyme IIB
STM3260	STM3260	AAL22132	3428898..3430271	0.444	0.100	0.205	0.022	0.462	0.148	0.018	0.232	0.003	1.574	PTS family galactitol-specific enzyme IIC
STM3261	STM3261	AAL22133	3430315..3431358	0.427	0.132			0.000	0.141	0.049			0.000	galactitol-1-phosphate dehydrogenase
STM3262	STM3262	AAL22134	3431469..3432242	1.046	0.109	3.145	0.579	3.006	0.353	0.031	0.623	0.054	1.764	transcriptional regulator of sugar metabolism
yraL	STM3263	AAL22135	(3432400..3433263)	0.665	0.071	0.723	0.140	1.088	0.343	0.003	0.485	0.040	1.413	putative methyltransferase
yraM	STM3264	AAL22136	3433327..3435369	1.902	0.173	1.979	0.238	1.041	1.460	0.092	2.362	0.733	1.618	paral putative transglycosylase
yraN	STM3265	AAL22137	3435327..3435722	1.666	0.096	1.509	0.321	0.905	1.247	0.028	1.271	0.180	1.020	putative endonuclease
yraO	STM3266	AAL22138	3435744..3436334	2.178	0.228	3.636	0.270	1.670	2.426	0.272	3.547	0.202	1.462	putative phosphoheptose isomerase
yraP	STM3267	AAL22139	3436344..3436919	1.579	0.231	9.546	0.220	6.044	1.559	0.074	6.082	0.831	3.902	paral putative periplasmic protein
yraR	STM3268	AAL22140	(3436986..3437654)	0.786	0.056	0.791	0.111	1.007	0.713	0.098	1.010	0.044	1.417	putative nucleoside-diphosphate-sugar epimerase
yhbO	STM3269	AAL22141	3437752..3438270	1.335	0.114	0.782	0.130	0.585	3.059	0.311	2.893	0.234	0.946	putative intracellular proteinase
yhbP	STM3270	AAL22142	(3438250..3438693)	0.616	0.071	0.572	0.040	0.930	0.513	0.046	0.541	0.064	1.054	putative cytoplasmic protein
yhbQ	STM3271	AAL22143	3438731..3439048	1.151	0.221	1.086	0.213	0.944	0.485	0.127	0.700	0.095	1.445	putative cytoplasmic protein
yhbS	STM3272	AAL22144	(3439035..3439538)	4.040	0.620	4.068	0.372	1.007	1.491	0.379	1.796	0.175	1.205	putative ABC superfamily (membrane) transport protein
yhbT	STM3273	AAL22145	(3439532..3440056)	3.487	0.310	4.700	0.530	1.348	1.336	0.055	2.043	0.297	1.530	putative lipid carrier protein
yhbU	STM3274	AAL22146	3440273..3441268	0.337	0.164	1.639	0.121	4.858	1.017	59.712	0.308	0.028	0.303	putative protease
yhbV	STM3275	AAL22147	3441259..3442155	0.300	0.153	1.627		5.426	0.189	0.075			0.000	putative protease
yhbW	STM3276	AAL22148	3442333..3443340	0.934	0.051	0.737	0.107	0.789	0.611	0.050	0.917	0.084	1.499	putative alkanal monooxygenase
STM3277	STM3277	AAL22149	(3443318..3444037)	0.214	0.139	0.102	0.010	0.479	0.242	0.003	0.242	0.032	1.000	putative inner membrane protein
STM3278	STM3278	AAL22150	3444196..3444726	0.268	0.135	0.155	0.005	0.578	0.376	0.020	0.275	0.028	0.731	putative cytoplasmic protein
mtr	STM3279	AAL22151	(3444787..3446031)	0.838	0.178	0.236	0.059	0.282	0.518	0.041	0.320	0.021	0.618	HAAAP family, tryptophan-specific transport protein
deaD	STM3280	AAL22152	(3446185..3448125)	3.235	0.727	1.048	0.282	0.324	4.561	0.242	0.520		0.114	cysteine sulfinate desulfinase
nlpI	STM3281	AAL22153	(3448253..3449137)	16.051	0.763	6.942	0.949	0.433	9.002	0.616	2.058	0.072	0.229	lipoprotein, cell division

pnp	STM3282	AAL22154	(3449247..3451382)	4.560	0.494	8.861	0.984	1.943	4.659	0.381	4.414	0.678	0.947	polynucleotide phosphorylase, member of mRNA degradosome
rpsO	STM3283	AAL22155	(3451624..3451893)	15.559	2.011			0.000	8.748	0.965			0.000	30S ribosomal subunit protein S15
truB	STM3284	AAL22156	(3452044..3452988)	6.414	0.205	3.029	0.285	0.472	3.660	0.588	2.516	0.124	0.688	tRNA pseudouridine 5S synthase
rbfA	STM3285	AAL22157	(3452988..3453389)	4.248	0.278	2.280	0.303	0.537	2.798	0.069	2.126	0.145	0.760	ribosome-binding factor, role in processing of 10S rRNA
infB	STM3286	AAL22158	(3453610..3456288)	3.748	0.379	8.421	0.525	2.247	2.621	0.120	4.814	0.789	1.836	protein chain initiation factor IF-2
nusA	STM3287	AAL22159	(3456313..3457815)	4.767	0.131	7.805	0.278	1.637	3.721	0.056	3.983	0.544	1.070	transcription pausing; L factor
yhbC	STM3288	AAL22160	(3457843..3458265)	3.373	0.062	4.024	0.339	1.193	2.811	0.143	3.136	0.122	1.116	putative cytoplasmic protein
metY	STM3289						N/A					N/A		
argG	STM3290	AAL22161	3458857..3460266	0.461	0.145	0.602		1.305	0.243	0.079	0.370		1.519	argininosuccinate synthetase
STM3291	STM3291	AAL22162	(3460352..3461416)	0.720	0.112	0.354	0.056	0.491	0.407	0.012	0.319	0.028	0.783	putative cytoplasmic protein
leuU	STM3292						N/A					N/A		
secG	STM3293	AAL22163	(3461852..3462184)	16.389	2.754	5.311	0.601	0.324	11.102	1.276	3.919	0.278	0.353	preprotein translocase IISP family, auxillary membrane onent
mrsA	STM3294	AAL22164	(3462407..3463744)	8.246	1.432	5.403	0.510	0.655	2.821	0.287	2.825	0.081	1.001	phosphoglucosamine mutase
folP	STM3295	AAL22165	(3463737..3464585)	3.671	0.590	2.653	0.486	0.723	1.561	0.002	1.203	0.140	0.771	7,8-dihydropteroate synthase
hflB	STM3296	AAL22166	(3464690..3466624)	33.023	7.387	15.133	2.260	0.458	19.949	3.295	15.380	0.736	0.771	ATP-dependent zinc-metallo protease
ftsJ	STM3297	AAL22167	(3466728..3467354)	9.929	1.349	4.793	0.499	0.483	11.219	0.278	7.221	0.278	0.644	23S rRNA methyltransferase
yhbY	STM3298	AAL22168	3467442..3467774	7.098	1.266	3.257	0.262	0.459	5.337	0.620	1.853	0.331	0.347	putative RNA-binding protein containing KH domain
greA	STM3299	AAL22169	(3467930..3468406)	6.735	1.459			0.000	5.561	0.181			0.000	transcription elongation factor, cleaves 3' nucleotide of paused mRNA
dacB	STM3300	AAL22170	3468654..3470087	2.519	0.291	1.399	0.152	0.555	1.861	0.335	1.593	0.136	0.856	D-alanyl-D-alanine carboxypeptidase, penicillin-binding protein 4
yhbZ	STM3301	AAL22171	(3470219..3471391)	0.991	0.164	0.990	0.074	0.999	0.847	0.040	0.694	0.012	0.820	putative GTP-binding protein
yhbE	STM3302; pseudogene; frameshift relative to E. coli					2.094	0.339	0.931	0.136	0.445	2.095	0.352	0.738	0.045 0.352
rpmA	STM3303	AAL22172	(3472501..3472758)	11.050	1.162	12.888	1.866	1.166	7.782	0.468	6.306	0.563	0.810	50S ribosomal subunit protein L27
rplU	STM3304	AAL22173	(3472778..3473089)	31.617	1.550	24.466	3.309	0.774	23.308	2.650	10.912	0.783	0.468	50S ribosomal subunit protein L21
ispB	STM3305	AAL22174	3473347..3474318	3.364	0.141	2.549	0.244	0.758	1.471	0.045	1.359	0.060	0.924	octaprenyl diphosphate synthase
nlp	STM3306	AAL22175	3474550..3474837	1.176	0.110	0.776	0.104	0.660	0.622	0.088	0.594	0.060	0.956	regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu
murA	STM3307	AAL22176	(3474895..3476154)	4.393	0.826	2.326	0.215	0.530	2.555	0.349	2.025	0.277	0.793	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
yrbA	STM3308	AAL22177	(3476208..3476501)	3.731	0.910	1.522	0.193	0.408	2.291	0.138	1.239	0.080	0.541	putative transcriptional regulator (BolA family)
yrbB	STM3309	AAL22178	(3476650..3476946)	4.383	1.059	3.297	0.372	0.752	2.949	0.387	2.720	0.248	0.922	putative STAS domain
yrbC	STM3310	AAL22179	(3476946..3477581)	2.786	0.115			0.000	2.421	0.211			0.000	putative ABC superfamily (atp&memb), transport protein

yrbD	STM3311	AAL22180	(3477600..3478151)	1.525	0.132	1.801	0.249	1.181	1.031	0.074	1.465	0.047	1.420	putative ABC superfamily (bind_prot) transport protein
yrbE	STM3312	AAL22181	(3478156..3478938)	1.612	0.060	1.294	0.048	0.803	1.332	0.109	1.338	0.069	1.005	putative ABC superfamily (membr) transport protein
yrbF	STM3313	AAL22182	(3478946..3479758)	6.661	1.067	6.378	0.670	0.958	1.406	0.318	3.127	0.174	2.224	putative ABC superfamily (atp_bind) transport protein
yrbG	STM3314	AAL22183	3479971..3480948	2.687	0.113	1.155	0.071	0.430	1.429	0.340	1.036	0.048	0.725	putative CacA family, Na:Ca transport protein
yrbH	STM3315	AAL22184	3480962..3481948	2.930	0.291	1.952	0.354	0.666	1.729	0.222	1.720	0.053	0.995	putative polysialic acid capsule expression protein
yrbI	STM3316	AAL22185	3481969..3482535					N/A					N/A	putative protein of HAD superfamily, CMP-Neu5Ac homologs
yrbK	STM3317	AAL22186	3482532..3483107	1.600	0.090	2.587	0.567	1.617	1.170	0.098	2.149	0.073	1.837	putative inner membrane protein
yhbN	STM3318	AAL22187	3483076..3483630	2.376	0.408	4.208	0.512	1.771	1.292	0.053	2.911	0.193	2.254	putative ABC superfamily (bind_prot) transport protein
yhbG	STM3319	AAL22188	3483637..3484362	2.041	0.109	3.774	0.213	1.849	1.274	0.060	2.140	0.108	1.681	putative ABC superfamily (atp_bind) transport protein
rpoN	STM3320	AAL22189	3484410..3485843	2.663	0.288	3.629	0.639	1.362	1.882	0.205	2.844	0.102	1.511	sigma N (sigma 54) factor of RNA polymerase, pleiotrophic functions (nitrogen metabolism, formate degradation, phage shock response)
yhbH	STM3321	AAL22190	3485866..3486153	7.087	2.724	21.335	4.440	3.010	2.989	0.192	8.889	0.320	2.974	putative sigma N modulation factor
ptsN	STM3322	AAL22191	3486271..3486762	2.060	0.337	7.779	0.917	3.775	1.280	0.119	3.427	0.492	2.676	sugar specific PTS family, enzyme IIA, also regulates N metabolism
yhbJ	STM3323	AAL22192	3486808..3487662	1.046	0.015	3.392	0.703	3.244	0.715	0.013	2.015	0.213	2.816	putative P-loop-containing kinase
ptsO	STM3324	AAL22193	3487659..3487931	0.733	0.114	1.478	0.097	2.016	0.584	0.148	0.868	0.133	1.486	NPr, phosphocarrier protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I
yrbL	STM3325	AAL22194	3488180..3488812	0.735	0.042	0.725	0.068	0.986	0.335	0.019	0.438	0.041	1.307	putative cytoplasmic protein
mtgA	STM3326	AAL22195	(3488887..3489615)	5.465	0.491	2.415	0.335	0.442	1.631	0.483	1.199	0.094	0.735	peptidoglycan transglycosylase, biosynthetic
yhbL	STM3327	AAL22196	(3489612..3490265)	6.471	1.567	4.974	0.440	0.769	2.705	0.695	2.711	0.159	1.002	sigma cross-reacting protein 27A (SCRP-27A)
arcB	STM3328	AAL22197	(3490492..3492828)	1.964	0.209	1.288	0.137	0.656	0.799	0.153	0.839	0.046	1.050	sensory histidine kinase in two-onent regulatory system with ArcA, senses redox conditions
yhcC	STM3329	AAL22198	(3492922..3493851)	0.471	0.113	0.290	0.034	0.616	0.162	0.020	0.235	0.026	1.453	putative FeS oxidoreductase
gltB	STM3330	AAL22199	3494523..3498983					N/A					N/A	glutamate synthase, large subunit
gltD	STM3331	AAL22200	3498993..3500411	0.464	0.140	0.592	0.078	1.277	0.260	0.028	0.471	0.028	1.812	glutamate synthase, small subunit
yhcG	STM3332	AAL22201	3500618..3501721	0.978	0.118	0.697	0.123	0.712	0.631	0.016	0.639	0.112	1.012	putative cytoplasmic protein
STM3333	STM3333	AAL22202	3501838..3503091	1.533	0.309	0.477	0.077	0.311	0.408	0.051	0.376	0.015	0.921	putative purine-cytosine permease
STM3334	STM3334	AAL22203	3503078..3504358	1.940	0.131	2.196	0.087	1.132	0.500	0.011	0.947	0.033	1.893	putative cytosine deaminase
yhcH	STM3335	AAL22204	(3504441..3504908)	5.045	1.822	12.595	1.721	2.496	0.510	0.085	2.975	0.151	5.832	putative cytoplasmic protein
nanK	STM3336	AAL22205	(3504905..3505780)	2.997	0.640	13.293	1.622	4.435	0.300	0.074	2.907	0.125	9.686	putative ManNAc kinase
nanE	STM3337	AAL22206	(3505777..3506466)	8.071	1.470	17.149	1.556	2.125	0.414	0.061	5.255	0.234	12.692	putative ManNAc-6P epimerase

nanT	STM3338	AAL22207	(3506513..3508003)	10.446	1.045	10.497	1.510	1.005	0.267	0.048	3.917	0.232	14.645	MFS family, sialic acid transport protein
nanA	STM3339	AAL22208	(3508119..3509012)	17.210	1.144	22.543	2.127	1.310	0.279	0.032	5.073	0.317	18.205	N-acetylneuraminate lyase (aldolase)
yhcK	STM3340	AAL22209	(3509147..3509938)	2.653	0.259			0.000	1.101	0.050	1.178		1.070	putative regulatory protein, gntR family
sspB	STM3341	AAL22210	(3510047..3510547)	18.317	2.188	6.439	0.993	0.352	8.776	1.616	4.011	0.257	0.457	stringent starvation protein B
sspA	STM3342	AAL22211	(3510553..3511191)	17.106	1.371	9.255	1.406	0.541	8.812	0.973	5.867	0.218	0.666	stringent starvation protein A, regulator of transcription
STM3343	STM3343	AAL22212	(3511454..3512206)	1.707	0.146	1.598	0.071	0.936	0.913	0.097	0.822	0.039	0.901	putative cytoplasmic protein
rpsI	STM3344	AAL22213	(3512406..3512798)	20.109	0.705	23.063	2.204	1.147	10.649	1.444	7.592	0.476	0.713	30S ribosomal subunit protein S9
rplM	STM3345	AAL22214	(3512814..3513242)	34.888	1.676	35.258	5.201	1.011	19.732	2.066	12.541	0.275	0.636	50S ribosomal subunit protein L13
yhcM	STM3346	AAL22215	(3513545..3514669)	4.598	0.825	1.664	0.294	0.362	1.775	0.055	0.973	0.018	0.548	putative ATPase
yhcB	STM3347	AAL22216	3514856..3515260	10.586	1.559	6.321	0.359	0.597	3.176	0.292	2.700	0.194	0.850	putative periplasmic protein
degQ	STM3348	AAL22217	3515417..3516784	2.958	0.458	3.412	0.185	1.154	1.351	0.071	1.909	0.172	1.413	serine endoprotease
degS	STM3349	AAL22218	3516877..3517947	1.171	0.015	0.918	0.086	0.784	0.839	0.082	0.892	0.041	1.063	periplasmic serine endoprotease
STM3350	STM3350	AAL22219	(3517981..3518712)	0.792	0.154	0.616	0.127	0.778	0.934	0.095	0.903	0.037	0.967	putative inner membrane protein
oadB	STM3351	AAL22220	(3518732..3520033)					N/A					N/A	putative sodium ion pump oxaloacetate decarboxylase beta chain
oadA	STM3352	AAL22221	(3520046..3521821)					N/A					N/A	putative sodium ion pump oxaloacetate decarboxylase alpha chain
oadG	STM3353	AAL22222	(3521837..3522091)	0.367	0.166	0.560	0.041	1.525	0.891	0.442	0.724	0.250	0.812	putative sodium ion pump oxaloacetate decarboxylase gamma chain
STM3354	STM3354	AAL22223	(3522247..3522864)	0.479	0.091	0.320	0.041	0.667	0.262	0.027	0.351	0.037	1.343	putative tartrate dehydratase beta subunit
STM3355	STM3355	AAL22224	(3522864..3523763)	0.266	0.168	0.162	0.027	0.608	0.110	0.016	0.227	0.020	2.065	putative tartrate dehydratase alpha subunit
STM3356	STM3356	AAL22225	(3523796..3525064)	0.323	0.172	0.203	0.026	0.627	0.133	0.039	0.241	0.009	1.812	putative cation transporter
STM3357	STM3357	AAL22226	(3525275..3525940)	1.394	0.085	1.056	0.173	0.758	0.466	0.029	0.456	0.033	0.977	putative regulatory protein, gntR family
STM3358	STM3358	AAL22227	(3525927..3526556)	3.083	0.174	3.279	0.194	1.064	1.024	0.130	1.285	0.082	1.255	putative regulatory protein, gntR family
mdh	STM3359	AAL22228	(3526676..3527614)	29.354	3.670	34.716	4.729	1.183	7.474	0.470	14.972	0.897	2.003	malate dehydrogenase
argR	STM3360	AAL22229	3528028..3528498	3.325	0.270	2.871	0.621	0.863	1.180	0.100	0.935	0.121	0.793	repressor of arg regulon (ArgR familiy)
yhcN	STM3361	AAL22230	3528863..3529126	0.938	0.063	0.679	0.082	0.724	0.506	0.017	0.543	0.010	1.073	putative outer membrane protein
STM3362	STM3362	AAL22231	3529230..3529496	1.150	0.089	0.519	0.077	0.452	0.633	0.041	0.468	0.059	0.740	putative periplasmic protein
yhcO	STM3363	AAL22232	(3529556..3529828)	0.871	0.090	0.389	0.062	0.447	0.538	0.096	0.490	0.055	0.912	putative cytoplasmic protein
yh	STM3364	AAL22233	(3530000..3531967)	0.465	0.170	0.205	0.035	0.441	0.213	0.049	0.220	0.018	1.033	putative inner membrane protein
yhcQ	STM3365	AAL22234	(3531973..3532905)	0.483	0.112	0.269	0.040	0.558	0.211	0.012	0.453	0.038	2.151	putative membrane located multidrug resistance protein
yhcR	STM3366	AAL22235	(3532913..3533116)	0.504	0.093	0.396	0.051	0.786	0.275	0.105	0.438	0.060	1.590	putative inner membrane protein
qseA	STM3367	AAL22236	3533298..3534227	1.066	0.033	0.516	0.082	0.484	0.533	0.081	0.542	0.019	1.017	
tldD	STM3368	AAL22237	(3534350..3535795)	7.990	2.099	1.686	0.331	0.211	3.458	0.831	1.999	0.202	0.578	suppresses inhibitory activity of CsrA
yhdP	STM3369	AAL22238	(3535940..3539740)	0.918	0.127	0.617	0.160	0.672	0.771	0.180	0.778	0.105	1.009	paral putative protease
cafA	STM3370	AAL22239	(3539847..3541316)	2.213	0.342	1.438	0.141	0.650	2.533	0.288	1.806	0.127	0.713	RNase G

yhdE	STM3371	AAL22240	(3541306..3541899)	5.216	0.972	1.848	0.104	0.354	4.062	0.868	2.221	0.238	0.547	putative inhibitor of septum formation
mreD	STM3372	AAL22241	(3541908..3542399)	4.009	0.592	0.709	0.064	0.177	3.527	1.197	0.743	0.059	0.211	rod shape-determining protein
mreC	STM3373	AAL22242	(3542399..3543451)	5.164	0.369	2.889	0.590	0.559	5.937	2.648	2.203	0.850	0.371	rod shape-determining protein
mreB	STM3374	AAL22243	(3543516..3544559)	12.999	1.509	6.906	1.029	0.531	9.933	1.188	5.109	0.311	0.514	rod shape-determining protein; HSP70 class molecular chaperones involved in cell morphogenesis
yhdA	STM3375	AAL22244	(3544867..3546807)	1.614	0.148	1.146	0.111	0.710	0.861	0.092	0.605	0.041	0.702	putative diguanylate cyclase
yhdH	STM3376	AAL22245	3547011..3547985	3.770	0.648	2.776	0.147	0.736	1.265	0.146	1.374	0.017	1.086	putative oxidoreductase
STM3377	STM3377	AAL22246	3548098..3549102	0.687	0.026	0.891	0.064	1.297	0.394	0.061	0.925	0.165	2.344	putative nitrate reductase
STM3378	STM3378	AAL22247	3549103..3549702	1.723	0.187	1.112	0.202	0.645	0.781	0.114	1.147	0.051	1.468	putative inner membrane protein
accB	STM3379	AAL22248	3550095..3550565	5.961	0.480	7.571	1.263	1.270	3.276	0.101	4.394	0.534	1.341	acetylCoA carboxylase, BC subunit, carrier of biotin
accC	STM3380	AAL22249	3550576..3551925	5.782	0.809	5.398	0.775	0.933	3.435	0.126	4.312	0.322	1.255	acetyl CoA carboxylase, biotin carboxylase subunit
yhdT	STM3381	AAL22250	3552034..3552276	0.862	0.113	0.522	0.097	0.606	0.677	0.101	0.447	0.057	0.660	putative inner membrane protein
panF	STM3382	AAL22251	3552266..3553717	0.905	0.163	0.600	0.038	0.663	0.651	0.098	0.465	0.054	0.714	SSS family, sodium/pantothenate symporter
prmA	STM3383	AAL22252	3553729..3554610	0.898	0.146	1.114	0.132	1.240	0.512	0.023	0.643	0.015	1.256	methylation of 50S ribosomal subunit protein L11
yhdG	STM3384	AAL22253	3555271..3556236	2.429	0.358	2.145	0.142	0.883	2.144	0.246	1.102	0.136	0.514	putative TIM-barrel enzyme, possibly dehydrogenase
fis	STM3385	AAL22254	3556262..3556558	3.797	0.416	2.623	0.249	0.691	3.059	0.175	1.304	0.077	0.426	site-specific DNA inversion stimulation factor
yhdJ	STM3386	AAL22255	3556644..3557528	0.379	0.112	0.256	0.031	0.676	0.283	0.056	0.236	0.016	0.833	putative methyltransferase
yhdU	STM3387	AAL22256	3557611..3557775	0.936	0.137	0.375	0.069	0.401	0.773	0.010	0.478	0.232	0.618	putative periplasmic protein
STM3388	STM3388	AAL22257	3557926..3560025	0.352	0.126	0.151	0.029	0.429	0.397	0.012	0.291	0.011	0.732	putative membrane domain involved in signal transduction; Diguanylate cyclase/phosphodiesterase domain 1; Diguanylate cyclase/phosphodiesterase domain 2
envR	STM3389	AAL22258	(3560028..3560690)	0.356	0.096	0.197	0.059	0.555	3.292	0.123	1.008	0.029	0.306	transcriptional repressor for envCD (acrEF) (TetR/AcrR family)
acrE	STM3390	AAL22259	3561104..3562261	0.229	0.113	0.207	0.039	0.905	0.777	0.056	0.718	0.041	0.925	transmembrane protein affecting septum formation and cell membrane permeability
acrF	STM3391	AAL22260	3562273..3565386	0.435	0.095	0.497	0.015	1.143	0.865	0.320	0.829	0.157	0.958	RND family, multidrug transport protein, acriflavin resistance protein F
yhdV	STM3392	AAL22261	3565622..3565843	1.384	0.041	1.200	0.218	0.867	2.326	0.141	1.966	0.164	0.845	putative outer membrane lipoprotein
thrV	STM3394						N/A					N/A		
STM3397	STM3397						N/A					N/A		
yrdA	STM3399	AAL22262	3572482..3573036	5.166	0.710	3.304	0.273	0.640	4.351	0.091	3.618	0.702	0.832	putative ferripyochelin binding protein
yrdB	STM3400	AAL22263	(3573012..3573269)	2.068	0.157	1.959	0.084	0.947	1.755	0.137	2.103	0.257	1.198	putative periplasmic protein
aroE	STM3401	AAL22264	(3573266..3574084)	1.397	0.048	2.016	0.185	1.443	1.294	0.035	1.876	0.187	1.450	dehydroshikimate reductase
yrdC	STM3402	AAL22265	(3574089..3574661)	1.529	0.115	1.786	0.352	1.168	1.258	0.054	1.615	0.162	1.283	putative translation factor

yrdD	STM3403	AAL22266	(3574666..3575208)	3.638	0.501	2.088	0.321	0.574	1.884	0.128	1.603	0.207	0.851	putative DNA topoisomerase
smg	STM3404	AAL22267	(3575235..3575708)	5.441	0.660	4.594	0.434	0.844	2.529	0.157	2.931	0.095	1.159	putative cytoplasmic protein
smf	STM3405	AAL22268	(3575680..3576804)	1.378	0.093	1.415	0.236	1.027	0.467	0.013	0.867	0.037	1.854	putative protein involved in DNA uptake
def	STM3406	AAL22269	3576936..3577445	1.761	0.089	3.945	0.638	2.241	0.999	0.117	1.468	0.057	1.470	peptide deformylase
fmt	STM3407	AAL22270	3577461..3578408	1.597	0.098	2.391	0.192	1.497	1.014	0.110	1.546	0.068	1.524	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase
sun	STM3408	AAL22271	3578460..3579749	0.566	0.154	1.055	0.268	1.865	0.472	0.110	0.542	0.094	1.149	putative rRNA methylase
trkA	STM3409	AAL22272	3579771..3581147	0.815	0.089	1.181	0.064	1.450	0.600	0.083	0.796	0.094	1.327	Trk system transport of potassium
mscL	STM3410	AAL22273	3581289..3581702	5.685	1.130	1.742	0.182	0.306	4.594	0.578	3.179	0.286	0.692	mechanosensitive channel
STM3411	STM3411	AAL22274	(3581638..3581907)	1.603	0.254	0.974	0.095	0.608	1.648	0.154	1.775	0.087	1.077	putative cytoplasmic protein
zntR	STM3412	AAL22275	(3581965..3582390)	1.311	0.038	1.614	0.154	1.231	1.092	0.073	2.093	0.079	1.917	Zn(II)-responsive transcriptional regulator (MerR family)
yhdN	STM3413	AAL22276	(3582401..3582769)	1.004	0.018	1.864	0.265	1.857	0.772	0.163	1.300	0.106	1.685	putative cytoplasmic protein
rplQ	STM3414	AAL22277	(3582877..3583260)	9.332	2.213	26.586	4.191	2.849	4.612	0.106	6.731	0.313	1.459	50S ribosomal subunit protein L17
rpoA	STM3415	AAL22278	(3583301..3584290)	14.694	2.512	68.896	4.106	4.689	6.370	0.403	14.900	1.541	2.339	RNA polymerase, alpha subunit
rpsD	STM3416	AAL22279	(3584316..3584936)	15.324	1.948	63.666	5.165	4.155	7.750	0.262	13.046	0.904	1.683	30S ribosomal subunit protein S4
rpsK	STM3417	AAL22280	(3584970..3585359)	18.190	1.443	48.981	5.173	2.693	9.332	0.362	13.059	0.781	1.399	30S ribosomal subunit protein S11
rpsM	STM3418	AAL22281	(3585376..3585732)	30.471	3.056	65.040	4.860	2.134	18.251	0.960	19.248	0.753	1.055	30S ribosomal subunit protein S13
rpmJ	STM3419	AAL22282	(3585879..3585995)	42.236	4.814	46.650	5.973	1.104	26.807	2.197	22.349	2.788	0.834	50S ribosomal subunit protein X
secY	STM3420	AAL22283	(3586027..3587358)	40.370	2.595	35.353	3.023	0.876	28.073	0.182	17.912	1.970	0.638	preprotein translocase of IISP family, membrane subunit, putative ATPase
rplO	STM3421	AAL22284	(3587366..3587800)	29.488	2.330	57.359	7.679	1.945	13.368	0.405	15.939	0.728	1.192	50S ribosomal subunit protein L15
rpmD	STM3422	AAL22285	(3587804..3587983)	20.425	1.666	59.032	9.186	2.890	9.927	0.734	12.041	0.476	1.213	50S ribosomal subunit protein L30
rpsE	STM3423	AAL22286	(3587987..3588490)	12.001	0.538	58.561	9.781	4.880	7.947	0.711	14.066	1.392	1.770	30S ribosomal subunit protein S5
rplR	STM3424	AAL22287	(3588505..3588858)	12.407	0.302	64.233	2.185	5.177	9.360	0.750	15.500	1.420	1.656	50S ribosomal subunit protein L18
rplF	STM3425	AAL22288	(3588868..3589401)	15.869	0.337	50.203	5.416	3.164	17.833	1.175	22.615	1.201	1.268	50S ribosomal subunit protein L6
rpsH	STM3426	AAL22289	(3589414..3589806)	14.287	0.195	50.002	3.547	3.500	14.814	0.410	18.755	1.331	1.266	30S ribosomal subunit protein S8, and regulator
rpsN	STM3427	AAL22290	(3589840..3590145)	14.352	0.700	67.823	7.625	4.726	15.618	1.074	20.317	1.653	1.301	30S ribosomal subunit protein S14
rplE	STM3428	AAL22291	(3590160..3590699)	15.292	1.639	58.105	5.798	3.800	15.246	2.087	16.066	1.106	1.054	50S ribosomal subunit protein L5
rplX	STM3429	AAL22292	(3590714..3591028)	29.948	1.561	65.892	9.594	2.200	17.129	2.615	16.315	1.591	0.952	50S ribosomal subunit protein L24
rplN	STM3430	AAL22293	(3591039..3591410)	31.141	2.200	41.677	4.188	1.338	21.224	1.307	16.317	1.063	0.769	50S ribosomal subunit protein L14
rpsQ	STM3431	AAL22294	(3591574..3591828)	18.690	6.187	33.479	2.912	1.791	12.527	0.417	14.252	0.589	1.138	30S ribosomal subunit protein S17
rpmC	STM3432	AAL22295	(3591828..3592019)	36.706	7.597	61.883	5.368	1.686	21.857	1.563	23.169	1.164	1.060	50S ribosomal subunit protein L29
rplP	STM3433	AAL22296	(3592019..3592429)	53.458	11.571	77.145	11.701	1.443	24.670	1.200	33.392	2.650	1.354	50S ribosomal subunit protein L16
rpsC	STM3434	AAL22297	(3592442..3593143)	32.917	3.568	53.816	4.988	1.635	16.370	2.008	22.001	2.403	1.344	30S ribosomal subunit protein S3
rplV	STM3435	AAL22298	(3593161..3593493)	25.657	0.841	60.953	5.094	2.376	13.374	0.303	17.911	1.040	1.339	50S ribosomal subunit protein L22
rpsS	STM3436	AAL22299	(3593508..3593786)	19.395	0.443	52.855	7.067	2.725	11.485	1.732	12.225	0.689	1.064	30S ribosomal subunit protein S19
rplB	STM3437	AAL22300	(3593803..3594624)	22.009	1.670	70.832	12.233	3.218	11.563	1.215	18.979	1.620	1.641	50S ribosomal subunit protein L2

rplW	STM3438	AAL22301	(3594642..3594944)	20.391	0.986	57.369	6.590	2.813	12.797	3.256	19.618	1.623	1.533	50S ribosomal subunit protein L23
rplD	STM3439	AAL22302	(3594941..3595546)	23.495	0.703	58.527	10.808	2.491	16.170	1.923	15.660	1.347	0.968	50S ribosomal subunit protein L4, regulates expression of S10 operon
rplC	STM3440	AAL22303	(3595557..3596186)	48.564	2.601	53.825	5.028	1.108	35.339	1.663	17.893	0.612	0.506	50S ribosomal subunit protein L3
rpsJ	STM3441	AAL22304	(3596219..3596530)	43.815	0.508	35.948	3.543	0.820	35.095	2.108	11.738	0.522	0.334	30S ribosomal subunit protein S10
hopD	STM3442	AAL22305	3596910..3597377	1.572	0.158	2.031	0.273	1.292	1.631	0.382	1.655	0.119	1.015	leader peptidase HopD
bfr	STM3443	AAL22306	(3597374..3597850)	3.159	0.550	2.689	0.382	0.851	3.643	0.380	3.813	0.142	1.047	bacterioferrin, an iron storage homoprotein
bfd	STM3444	AAL22307	(3597923..3598117)	3.074	0.259	4.786	0.193	1.557	1.922	0.237	1.981	0.126	1.031	regulatory or redox onent lexing with Bfr, in iron storage and mobility
tufA	STM3445	AAL22308	(3598302..3599486)	38.391	4.442	94.246	4.902	2.455	19.871	0.667	33.978	1.916	1.710	protein chain elongation factor EF-Tu (duplicate of tufB)
fusA	STM3446	AAL22309	(3599558..3601672)	10.890	1.965	45.514	8.545	4.180	6.112	0.165	13.579	1.633	2.222	protein chain elongation factor EF-G, GTP-binding
rpsG	STM3447	AAL22310	(3601769..3602239)	15.176	1.259	31.653	4.308	2.086	10.770	0.590	10.291	0.734	0.956	30S ribosomal subunit protein S7, initiates assembly
rpsL	STM3448	AAL22311	(3602335..3602709)	14.576	1.196	24.107	2.235	1.654	12.239	0.982	8.759	0.814	0.716	30S ribosomal subunit protein S12
yheL	STM3449	AAL22312	(3602835..3603122)	3.335	0.498	3.389	0.540	1.016	2.162	0.185	2.933	0.067	1.357	putative oxidation of intracellular sulfur
yheM	STM3450	AAL22313	(3603130..3603486)	4.037	0.695	2.622	0.410	0.650	2.280	0.249	1.998	0.112	0.876	putative oxidation of intracellular sulfur
yheN	STM3451	AAL22314	(3603486..3603872)	6.478	1.055	3.988	0.560	0.616	3.228	0.388	2.819	0.124	0.873	putative ACR involved in intracellular sulfur reduction
yheO	STM3452	AAL22315	(3603872..3604594)	6.643	0.781	4.522	0.268	0.681	3.250	0.111	2.607	0.098	0.802	putative regulator
fkpA	STM3453	AAL22316	(3604871..3605689)	12.122	1.242	16.196	1.548	1.336	8.628	1.245	8.659	1.315	1.004	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
slyX	STM3454	AAL22317	3605909..3606127	4.000	0.925	3.401	0.630	0.850	2.576	0.461	1.643	0.238	0.638	putative cytoplasmic protein
slyD	STM3455	AAL22318	(3606315..3606905)	8.886	0.928	13.825	1.308	1.556	4.264	0.059	6.148	0.334	1.442	FKBP-type peptidyl prolyl cis-trans isomerase (rotamase)
yheV	STM3456	AAL22319	(3607000..3607200)	1.287	0.102	2.472	0.291	1.921	0.925	0.025	2.010	0.290	2.173	putative cytoplasmic protein
kefB	STM3457	AAL22320	(3607211..3609016)	1.207	0.068	0.673	0.266	0.558	1.029	0.133	1.121	0.107	1.089	A2 family, K+:H+ antiporter
yheR	STM3458	AAL22321	(3609016..3609567)	2.657	0.407	0.806	0.080	0.304	1.803	0.457	1.936	0.070	1.074	putative NAD(P)H oxidoreductase
yheS	STM3459	AAL22322	3609833..3611740					N/A					N/A	putative ATPase onent of ABC transporter with duplicated ATPase domain
STM3460	STM3460	pseudogene; in-frame stop following codon 15			1.471	0.131	1.426	0.098	0.970	0.894	0.079	0.650	0.106	0.727
STM3461	STM3461	AAL22323	(3612126..3612437)	1.189	0.126	3.035	0.114	2.553	0.332	0.058	0.838	0.090	2.522	putative cytoplasmic protein
yheT	STM3462	AAL22324	3612635..3613702	1.264	0.077	1.456	0.161	1.152	1.143	0.016	3.510	0.016	3.071	putative hydrolase. Alpha/beta-hydrolase fold
yheU	STM3463	AAL22325	3613710..3613916	1.633	0.065	1.405		0.860	1.436	0.027	2.720		1.894	putative cytoplasmic protein
prkB	STM3464	AAL22326	3613968..3614837	2.661	0.369	1.777	0.312	0.668	1.585	0.344	2.296	0.186	1.449	putative phosphoribulokinase
yhfA	STM3465	AAL22327	(3614933..3615337)	4.026	0.207	3.089	0.469	0.767	0.963	0.062	1.106	0.057	1.148	putative inner membrane protein

crp	STM3466	AAL22328	3615645..3616277	3.647	0.350	14.241	1.516	3.905	0.855	0.111	2.146	0.086	2.510	catabolite activator protein (CAP), cyclic AMP receptor protein (CRP family)
yhfK	STM3467	AAL22329	3616326..3618413	0.908	0.023	1.470	0.090	1.618	0.330	0.008	0.807	0.063	2.447	putative inner membrane protein
argD	STM3468	AAL22330	(3618456..3619673)	0.468	0.091	0.596	0.074	1.274	0.318	0.015	1.240	0.095	3.896	acetylornithine transaminase (NAcOATase and DapATase)
pabA	STM3469	AAL22331	(3619759..3620322)	0.978	0.126	0.639	0.092	0.654	0.557	0.081	0.680	0.073	1.222	p-aminobenzoate synthetase, onent II
fic	STM3470	AAL22332	(3620354..3620956)	0.741	0.096	0.450	0.074	0.608	0.723	0.045	0.648	0.045	0.897	putative cell filamentation protein, stationary phase induced gene, affects cell division
yhfG	STM3471	AAL22333	(3620946..3621113)	1.132	0.053	0.680	0.144	0.600	1.351	0.109	1.164	0.096	0.862	putative cytoplasmic protein
ppiA	STM3472	AAL22334	(3621222..3621794)	4.706	0.322	2.354	0.278	0.500	6.232	0.292	4.343	0.290	0.697	peptidyl-prolyl cis-trans isomerase A (rotamase A)
yhfC	STM3473	AAL22335	3622071..3623252	0.411	0.146	0.173	0.012	0.421	0.353	0.028	0.345	0.020	0.976	putative MFS family transport protein
nirB	STM3474	AAL22336	3623515..3626058	0.205	0.132	0.565	0.160	2.755	0.110	0.041	0.307	0.036	2.783	nitrite reductase, large subunit
nirD	STM3475	AAL22337	3626055..3626381	0.419	0.124	0.476	0.095	1.137	0.150	0.022	0.232	0.023	1.549	nitrite reductase, small subunit
nirC	STM3476	AAL22338	3626647..3627456	0.240	0.156	0.212	0.030	0.881	0.118	0.020	0.206	0.020	1.749	FNT family, nitrite transport protein
cysG	STM3477	AAL22339	3627468..3628841	0.655	0.034	1.129	0.063	1.723	0.393	0.021	0.679	0.041	1.729	siroheme synthase, catalyses four separate reactions that are required for the transformation of uroporphyrinogen III into siroheme
bigA	STM3478	AAL22340	3629167..3635028	0.284	0.184	0.144	0.018	0.506	0.196	0.063	0.316	0.081	1.607	putative surface-exposed virulence protein
tnpA_5	STM3479	AAL22341	(3635160..3635618)					N/A					N/A	transposase for IS200
yhfL	STM3480	AAL22342	3635932..3636102	1.205	0.105	0.949	0.066	0.787	1.139	0.017	1.027	0.120	0.902	putative outer membrane lipoprotein
trpS	STM3481	AAL22343	(3636247..3637251)	7.076	0.830	3.957	0.630	0.559	4.134	0.254	3.459	0.218	0.837	tryptophan tRNA synthetase
gph	STM3482	AAL22344	(3637244..3638002)	6.908	0.516	3.902	0.385	0.565	3.928	0.619	2.838	0.136	0.722	phosphoglycolate phosphatase
rpe	STM3483	AAL22345	(3637995..3638672)	3.684	0.250	3.700	0.467	1.004	1.914	0.177	2.395	0.157	1.251	D-ribulose-5-phosphate 3-epimerase
dam	STM3484	AAL22346	(3638690..3639526)	4.530	0.330	2.403	0.186	0.531	2.728	0.178	1.546	0.146	0.567	DNA adenine methylase
damX	STM3485	AAL22347	(3639707..3640984)	4.188	0.327	5.337	0.229	1.274	2.636	0.114	5.036	0.773	1.911	membrane protein
aroB	STM3486	AAL22348	(3641082..3642170)	3.996	0.417	3.652	0.565	0.914	2.830	0.061	2.412	0.321	0.852	dehydroquinate synthase
aroK	STM3487	AAL22349	(3642227..3642748)	6.085	0.284	4.484	0.805	0.737	3.372	0.232	2.912	0.075	0.864	shikimate kinase I
hofQ	STM3488	AAL22350	(3643213..3644451)	0.634	0.114	0.486	0.095	0.766	0.301	0.043	0.494	0.091	1.644	putative transport protein, possibly in biosynthesis of type IV pilin
yrfA	STM3489	AAL22351	(3644366..3644767)	0.446	0.130	0.244	0.029	0.547	0.165	0.009	0.325	0.065	1.972	putative inner membrane protein
yrfB	STM3490	AAL22352	(3644757..3645230)	0.550	0.148	0.225	0.026	0.410	0.160	0.032	0.310	0.071	1.937	putative inner membrane protein
yrfC	STM3491	AAL22353	(3645214..3645753)	0.567	0.106	0.391	0.518	0.689	0.368	0.292	0.345	0.033	0.938	putative inner membrane protein
yrfD	STM3492	AAL22354	(3645753..3646532)	0.522	0.107	0.276	0.034	0.528	0.134	0.010	0.386	0.066	2.877	putative periplasmic protein
mrcA	STM3493	AAL22355	3646629..3649205					N/A					N/A	transpeptidase of penicillin-binding protein 1a (peptidoglycan synthetase)
yrfE	STM3494	AAL22356	(3649301..3649897)	1.964	0.108	1.183	0.162	0.602	1.188	0.102	0.971	0.064	0.818	putative NTP pyrophosphohydrolase
yrfF	STM3495	AAL22357	3650187..3652319	1.133	0.054	1.355	0.084	1.196	0.297	0.024	0.867	0.080	2.916	putative inner membrane protein
yrfG	STM3496	AAL22358	3652384..3653052	1.168	0.093	0.938	0.143	0.803	1.687	0.065	2.357	0.052	1.397	putative hydrolase

yrfH	STM3497	AAL22359	3653063..3653464	1.130	0.035	1.095	0.149	0.969	1.716	0.203	2.759	0.393	1.608	heat shock protein, predicted small RNA-binding protein
yrfI	STM3498	AAL22360	3653483..3654367	1.340	0.059	1.519	0.080	1.134	1.797	0.050	4.289	0.302	2.386	heat shock protein 33, redox regulated chaparone
yhgE	STM3499	AAL22361	(3654477..3656186)	0.477	0.147	0.503	0.117	1.054	0.353	0.040	0.446	0.043	1.264	putative inner membrane protein
pckA	STM3500	AAL22362	3656566..3658182	16.454	2.179	62.680	5.922	3.809	4.740	0.226	11.588	0.993	2.444	phosphoenolpyruvate carboxykinase
envZ	STM3501	AAL22363	(3658257..3659609)	5.775	0.702	2.634	0.221	0.456	6.008	1.053	2.918	0.330	0.486	sensory histidine kinase in two-onent regulatory system with OmpR
ompR	STM3502	AAL22364	(3659606..3660325)	7.176	0.449	5.249	0.224	0.732	6.933	0.387	7.772	0.637	1.121	response regulator in two-onent regulatory system with EnvZ, affecting transcription of ompC and ompF (OmpR family)
greB	STM3503	AAL22365	3660551..3661024	0.924	0.069	0.865	0.109	0.936	0.605	0.019	0.630	0.080	1.041	transcription elongation factor and transcript cleavage
yhgF	STM3504	AAL22366	3661126..3663453	0.592	0.072	0.473	0.056	0.799	0.985	0.343	0.677	0.047	0.688	paral putative RNase R
feoA	STM3505	AAL22367	3663890..3664117	6.831	7.431	0.468	0.070	0.069	0.854		0.899	0.114	1.052	ferrous iron transport protein A
feoB	STM3506	AAL22368	3664136..3666454	0.831	0.101	0.401	0.047	0.482	2.024	0.376	1.384	0.036	0.684	FeoB family, ferrous iron transport protein B
yhgG	STM3507	AAL22369	3666467..3666703	1.333	0.063	0.371	0.027	0.278	1.787	0.570	1.005	0.050	0.563	putative cytoplasmic protein
STM3508	STM3508	AAL22370	3666938..3667852	0.706	0.050	0.537	0.022	0.761	0.332	0.012	0.412	0.050	1.241	putative cytoplasmic protein
bioH	STM3509	AAL22371	(3667888..3668658)	2.986	0.545	0.848	0.070	0.284	0.995	0.277	1.077	0.133	1.082	putative hydrolase, biotin biosynthesis; reaction prior to pimeloyl CoA
yhgH	STM3510	AAL22372	3668696..3669379	1.196	0.022	0.601	0.116	0.503	0.704	0.035	0.986	0.025	1.401	putative amidophosphoribosyltransferase
yhgI	STM3511	AAL22373	3669438..3670013	6.073	0.565	1.723	0.190	0.284	4.706	0.620	2.866	1.546	0.609	putative Thioredoxin-like proteins and domain
gntT	STM3512	AAL22374	3670390..3671706	0.885	0.107	0.377	0.053	0.426	0.242	0.040	0.316	0.014	1.307	GntP family, high-affinity gluconate permease in GNT I system
malQ	STM3513	AAL22375	(3671825..3673903)					N/A					N/A	4-alpha-glucanotransferase (amylomaltase)
malP	STM3514	AAL22376	(3673913..3676306)					N/A					N/A	maltodextrin phosphorylase
malT	STM3515	AAL22377	3676900..3679605	9.536	1.549	4.160	0.597	0.436	1.813	0.307	2.880	0.230	1.588	transcriptional activator of the mal genes, binds inducer (maltotriose) and ATP (LysR familiy)
STM3516	STM3516	AAL22378	(3679693..3679968)	2.879	0.327	0.805	0.064	0.280	0.944	0.169	0.698	0.021	0.740	putative cytoplasmic protein
STM3517	STM3517	AAL22379	(3679971..3680231)	2.125	0.035	0.776	0.206	0.365	0.931	0.057	0.594	0.045	0.638	putative DNA-damage-inducibile protein, resembles dinJ
rtcA	STM3518	AAL22380	(3680340..3681359)	0.859	0.082	1.028	0.072	1.196	0.480	0.004	0.877	0.208	1.826	RNA 3'-terminal phosphate cyclase (with b3419)
rtcB	STM3519	AAL22381	(3681363..3682580)	0.522	0.149	0.811	0.162	1.554	0.352	0.011	0.529	0.057	1.503	putative cytoplasmic protein
STM3520	STM3520	pseudogene; tRNA						N/A					N/A	
STM3521	STM3521	AAL22382	(3683125..3684678)	0.422	0.155	0.397	0.022	0.942	0.861	0.121	0.817	0.085	0.948	putative ribonucleoprotein related-protein
rtcR	STM3522	AAL22383	3684868..3686451	0.947	0.069	0.623	0.111	0.658	0.379	0.047	0.633	0.039	1.672	sigma N (sigma 54)-dependent regulator of rtcBA expression (EBP familiy)
glpR	STM3523	AAL22384	(3686448..3687206)	2.377	0.171	2.240	0.153	0.942	1.102	0.131	2.554	0.759	2.317	transcriptional repressor of the glp operon (DeoR family)

glpG	STM3524	AAL22385	(3687300..3688130)	2.040	0.212	1.270	0.117	0.622	1.147	0.256	1.052	0.082	0.917	protein of glp regulon
glpE	STM3525	AAL22386	(3688206..3688532)	1.973	0.118	0.968	0.094	0.491	0.831	0.101	1.435	0.134	1.727	thiosulfate/cyanide sulfurtransferase (rhodanese)
glpD	STM3526	AAL22387	3688731..3690239	0.650	0.254	0.623	0.019	0.959	0.277	0.189	2.113	0.273	7.636	sn-glycerol-3-phosphate dehydrogenase (aerobic)
STM3527	STM3527	AAL22388	(3690286..3690831)	0.338	0.165	0.357	0.053	1.056	0.147	0.005	0.384	0.033	2.617	putative inner membrane protein
STM3528	STM3528	AAL22389	(3690841..3692400)	0.965	0.050	0.353	0.027	0.366	0.595	0.078	0.418	0.057	0.702	putative periplasmic phosphate-binding protein
STM3529	STM3529	AAL22390	(3692494..3693603)	0.334	0.152	0.198	0.039	0.592	0.174	0.056	0.265	0.024	1.519	putative glycerol dehydrogenase
STM3530	STM3530	pseudogene; frameshift; putative permease			0.291	0.202	0.227	0.044	0.779	0.180	0.087	0.300	0.080	1.669
STM3531	STM3531	AAL22391	3695271..3696986					N/A					N/A	putative dihydroxyacid dehydratase
STM3532	STM3532	AAL22392	3697030..3697935	0.437	0.153	0.363	0.064	0.832	0.353	0.021	0.360	0.039	1.021	putative dihydrodipicolinate synthetase
STM3533	STM3533	AAL22393	(3697979..3698734)	1.301	0.074	0.971	0.065	0.746	0.525	0.038	0.671	0.044	1.279	putative bacterial transcriptional regulator
glgP	STM3534	AAL22394	(3698912..3701359)	0.989	0.077	2.204	0.466	2.230	0.432	0.063	1.059	0.089	2.449	glycogen phosphorylase
glgA	STM3535	AAL22395	(3701379..3702812)	0.948	0.083	2.759	0.332	2.910	0.789	0.044	1.938	0.027	2.457	glycogen synthase
glgC	STM3536	AAL22396	(3702812..3704107)					N/A					N/A	glucose-1-phosphate adenylyltransferase
glgX	STM3537	AAL22397	(3704122..3706098)	1.331	0.039	2.340	0.123	1.758	0.970	0.033	1.465	0.125	1.510	glycosyl hydrolase
glgB	STM3538	AAL22398	(3706095..3708281)	1.716	0.159	2.755	0.494	1.606	1.448	0.338	2.426	0.210	1.676	1,4-alpha-glucan branching enzyme
asd	STM3539	AAL22399	(3708628..3709734)	4.878	0.553	2.981	0.202	0.611	2.608	0.439	2.653	0.175	1.017	aspartate-semialdehyde dehydrogenase
yhgN	STM3540	AAL22400	3709861..3710241	0.781	0.069	0.652	0.062	0.835	0.478	0.123	0.574	0.078	1.202	putative inner membrane protein
gntU	STM3541	AAL22401	(3710158..3711498)	0.926	0.102	0.429	0.046	0.463	0.298	0.024	0.428	0.047	1.434	low affinity gluconate permease
gntK	STM3542	AAL22402	(3711495..3712028)	0.392	0.152	0.270	0.033	0.688	0.156	0.024	0.252	0.020	1.617	gluconate kinase 2 in GNT I system, thermoresistant
gntR	STM3543	AAL22403	(3712167..3713162)	1.529	0.058	0.966	0.038	0.632	0.673	0.039	0.736	0.060	1.093	transcriptional repressor gnt-I, gntUKR (GalR/LacI familiy)
yhhW	STM3544	AAL22404	(3713292..3713987)	0.655	0.120	0.465	0.077	0.709	0.267	0.015	0.411	0.068	1.539	putative cytoplasmic protein
yhhX	STM3545	AAL22405	(3714111..3715148)	0.301	0.101	0.592	0.055	1.965	0.098	0.020	0.403	0.048	4.130	putative oxidoreductase
yhhY	STM3546	AAL22406	3715617..3716105	0.570	0.143			0.000	0.572	0.031			0.000	putative transferase
STM3547	STM3547	AAL22407	3716370..3717584	0.274	0.148	0.132	0.015	0.483	1.455	0.081	0.801	0.014	0.550	putative transcriptional regulator of sugar metabolism
STM3548	STM3548	AAL22408	3717600..3718361	0.244	0.120	0.164	0.034	0.672	1.200	0.152	1.502	0.058	1.252	putative cytoplasmic protein
STM3549	STM3549	AAL22409	3718415..3719386	0.203	0.166	0.204	0.058	1.004	0.560	0.066	1.319	0.139	2.357	putative inner membrane protein
STM3550	STM3550	AAL22410	3719383..3720417	0.304	0.178	0.189	0.021	0.622	0.582	0.030	1.229	0.068	2.112	putative phosphotriesterase
ggt	STM3551	AAL22411	(3720462..3722204)	0.334	0.146	0.231	0.019	0.690	0.259	0.016	0.546	0.024	2.105	gamma-glutamyltranspeptidase
yhhA	STM3552	AAL22412	3722330..3722746	0.556	0.112	0.648	0.091	1.167	0.278	0.086	0.556	0.028	1.997	putative outer membrane protein
ugpQ	STM3553	AAL22413	(3722759..3723499)	0.820	0.041	0.917	0.057	1.118	0.394	0.023	0.933	0.189	2.368	glycerophosphodiester phosphodiesterase, cytosolic
ugpC	STM3554	AAL22414	(3723496..3724566)	0.558	0.113	0.577	0.038	1.034	0.341	0.021	0.550	0.012	1.614	ABC superfamily (atp_bind), sn-glycerol 3-phosphate transport protein

ugpE	STM3555	AAL22415	(3724568..3725413)	0.407	0.126	0.303	0.051	0.746	0.240	0.015	0.399	0.031	1.660	ABC superfamily (membrane),sn-glycerol 3-phosphate transport protein
ugpA	STM3556	AAL22416	(3725410..3726297)	0.499	0.153			0.000	0.284	0.009			0.000	ABC superfamily (membrane), sn-glycerol 3-phosphate transport protein
ugpB	STM3557	AAL22417	(3726361..3727677)	0.404	0.105	1.661	0.120	4.110	0.215	0.049	1.188	0.088	5.522	ABC superfamily (peri_perm), sn-glycerol 3-phosphate transport protein
STM3558	STM3558	AAL22418	(3727936..3728304)	0.897	0.056	0.471	0.080	0.525	0.402	0.039	0.478	0.022	1.189	homology to death -on-curing protein of phage P1
yhhV	STM3559	AAL22419	(3728301..3728528)	0.855	0.098	0.424	0.012	0.496	0.455	0.068	0.474	0.048	1.042	putative cytoplasmic protein
livF	STM3560	AAL22420	(3728654..3729367)	0.502	0.128	0.370	0.017	0.738	0.431	0.327	0.494	0.041	1.148	ABC superfamily (atp_bind), branched-chain amino acid transporter, high-affinity
livG	STM3561	AAL22421	(3729369..3730136)	0.462	0.157	0.305	0.050	0.661	0.294	0.060	0.525	0.046	1.782	ABC superfamily (atp_bind), branched-chain amino acid transporter, high-affinity
livM	STM3562	AAL22422	(3730133..3731410)	0.453	0.170	0.204	0.037	0.451	0.246	0.023	0.346	0.046	1.409	ABC superfamily (membrane), branched-chain amino acid transporter, high-affinity
livH	STM3563	AAL22423	(3731407..3732333)	0.300	0.148	0.186	0.019	0.621	0.191	0.083	0.291	0.047	1.527	ABC superfamily (membrane), branched-chain amino acid transporter, high-affinity
livK	STM3564	AAL22424	(3732393..3733502)	0.398	0.175	0.359	0.043	0.901	0.184	0.049	0.308	0.036	1.670	ABC superfamily (bind_prot), branched-chain amino acid transporter, high-affinity
yhhK	STM3565	AAL22425	3733924..3734307	2.619	0.226	0.748	0.114	0.285	1.247	0.230	0.888	0.253	0.713	putative acetyltransferase
STM3566	STM3566	AAL22426	3734285..3734419	3.064	0.472	1.149	0.286	0.375	2.993	1.491	1.075	0.505	0.359	putative cytoplasmic protein
livJ	STM3567	AAL22427	(3734502..3735599)	1.662	0.296	0.545	0.133	0.328	0.479	0.058	0.524	0.021	1.096	ABC superfamily (bind_prot), branched-chain amino acid transporter, high-affinity
rpoH	STM3568	AAL22428	(3735927..3736781)	13.257	2.316	10.033	1.385	0.757	8.568	1.343	11.702	0.971	1.366	sigma H (sigma 32) factor of RNA polymerase; transcription of heat shock proteins induced by cytoplasmic stress
ftsX	STM3569	AAL22429	(3737027..3738082)	5.567	0.806	1.943	0.185	0.349	2.970	0.875	2.244	0.108	0.755	putative integral membrane cell division protein
ftsE	STM3570	AAL22430	(3738075..3738743)	5.925	1.005	2.751	0.301	0.464	3.090	0.870	3.934	0.252	1.273	putative ATPase involved in cell division
ftsY	STM3571	AAL22431	(3738746..3740221)	2.531	0.080			0.000	1.479	0.268			0.000	GTPase domain of cell division membrane protein
yhhF	STM3572	AAL22432	3740347..3740943	1.254	0.058	0.688	0.123	0.548	0.514	0.036	0.615	0.046	1.196	putative methyltransferase
yhhL	STM3573	AAL22433	3740930..3741202	1.024	0.069	0.513	0.085	0.501	0.457	0.027	0.488	0.080	1.067	putative inner membrane protein
yhhM	STM3574	AAL22434	(3741224..3741595)	0.761	0.044	0.547	0.056	0.720	0.340	0.022	0.513	0.023	1.510	putative inner membrane protein
yhhN	STM3575	AAL22435	3741737..3742363	3.759	0.407	1.626	0.064	0.432	2.051	0.217	1.576	0.119	0.769	putative inner membrane protein
zntA	STM3576	AAL22436	3742444..3744642	1.348	0.053			0.000	0.699	0.017			0.000	P-type ATPase family, Pb/Cd/Zn/Hg transporting ATPase
t	STM3577	AAL22437	3744842..3746485					N/A					N/A	methyl-accepting transmembrane citrate/phenol chemoreceptor

yhhP	STM3578	AAL22438	(3746509..3746754)	1.537	0.081	1.231	0.170	0.801	1.274	0.200	0.733	0.040	0.575	small ubiquitous protein required for normal growth
yhhQ	STM3579	AAL22439	3746924..3747589	0.510	0.118	0.495	0.135	0.971	0.509	0.027	0.545	0.062	1.070	putative integral membrane protein
STM3580	STM3580	AAL22440	3747662..3748219	2.422	0.131	3.267	0.637	1.349	3.318	0.149	5.844	0.503	1.761	putative inner membrane lipoprotein
yhhS	STM3581	AAL22441	(3748223..3749482)	0.704	0.161	0.529	0.042	0.751	0.349	0.028	0.482	0.035	1.381	putative MFS family transport protein
yhhT	STM3582	AAL22442	3749572..3750621	0.433	0.190			0.000	0.362	0.025			0.000	putative PerM family permease
aT	STM3583	AAL22443	3750673..3751251	3.639	0.274	1.487	0.233	0.409	1.648	0.275	1.767	0.054	1.072	putative Phosphopantetheinyl transferase
nikR	STM3584	AAL22444	3751343..3751744	3.631	0.769	1.020	0.120	0.281	1.181	0.127	0.930	0.072	0.787	nickel-responsive transcriptional regulator
yhhJ	STM3585	AAL22445	(3751834..3752958)	0.695	0.108	0.665	0.064	0.958	0.256	0.084	0.348	0.008	1.361	putative ABC superfamily (atp_bind/membrane) transport protein
yhiH	STM3586	AAL22446	(3752958..3755648)	0.682	0.064	1.151	0.037	1.688	0.421	0.224	0.632	0.148	1.502	putative ABC-type multidrug transport system, ATPase onent; Permease onent of an ABC-transporter
yhiI	STM3587	AAL22447	(3755696..3756763)	1.286	0.032	2.426	0.256	1.886	0.308	0.055	0.822	0.084	2.668	paral putative membrane protein
yhiN	STM3588	AAL22448	(3757069..3758265)	0.535	0.201			0.000	0.349	0.111			0.000	putative periplasmic protein
pitA	STM3589	AAL22449	3758496..3759992	3.887	0.413	2.520	1.309	0.648	4.300	0.724	1.782	0.484	0.414	PiT family, low-affinity phosphate transporter
uspB	STM3590	AAL22450	(3760132..3760467)	4.825	0.808	2.648	0.395	0.549	4.987	1.211	4.447	0.210	0.892	universal stress protein B, involved in stationary-phase resistance to ethanol
uspA	STM3591	AAL22451	3760855..3761289	24.441	8.929	24.211	1.728	0.991	5.388	1.052	11.506	1.028	2.135	universal stress protein A
yhiP	STM3592	AAL22452	3761614..3763083	12.640	1.121	6.712	1.540	0.531	0.385	0.021	0.479	0.004	1.244	putative POT family, peptide transport protein
yhiQ	STM3593	AAL22453	(3763175..3763933)	4.081	0.798	2.262	0.077	0.554	1.671	0.301	1.720	0.060	1.030	putative SAM-dependent methyltransferase
prlC	STM3594	AAL22454	(3763940..3765982)	2.192	0.546	1.780	0.301	0.812	1.480	0.140	3.078	0.199	2.080	oligopeptidase A
STM3595	STM3595	AAL22455	(3766164..3767435)	1.083	0.013	0.702	0.107	0.648	5.480	0.688	17.415	0.654	3.178	putative phosphatase
yhiR	STM3596	AAL22456	3767646..3768488	3.444	0.360	2.111	0.062	0.613	1.851	0.276	1.790	0.329	0.967	putative cytoplasmic protein
gor	STM3597	AAL22457	3768593..3769945	10.905	1.593	3.891	0.363	0.357	4.989	1.339	4.024	0.230	0.806	glutathione oxidoreductase
STM3598	STM3598	AAL22458	(3769992..3771035)	0.835	0.065			0.000	1.917	0.249			0.000	putative L-asparaginase
STM3599	STM3599	AAL22459	(3771094..3772413)	0.370	0.168	0.181	0.021	0.489	0.650	0.091	0.738	0.023	1.135	putative inner membrane protein
STM3600	STM3600	AAL22460	(3772467..3773312)	0.322	0.130	0.245	0.029	0.761	0.732	0.053	1.195	0.103	1.633	putative sugar kinases, ribokinase family
STM3601	STM3601	AAL22461	(3773376..3774353)	0.389	0.113	0.470	0.084	1.209	0.340	0.071	0.797	0.019	2.343	putative phosphosugar isomerase
STM3602	STM3602	AAL22462	(3774529..3775248)	0.518	0.104	0.355	0.061	0.684	0.280	0.031	0.392	0.008	1.398	putative regulatory protein, gntR family
treF	STM3603	AAL22463	3775574..3777223	0.820	0.095	0.637	0.029	0.777	0.534	0.040	0.880	0.044	1.649	cytoplasmic trehalase
STM3604	STM3604	AAL22464	(3777236..3778825)	3.663	0.414	4.757	0.681	1.299	0.340	0.024	0.500	0.094	1.470	putative inner membrane protein
STM3605	STM3605	AAL22465	3779106..3779462	0.551	0.101	0.353	0.034	0.641	0.616	0.081	0.373	0.013	0.605	putative phage endolysin
yhjB	STM3606	AAL22466	(3779468..3780070)	0.365	0.123	0.226	0.039	0.619	2.119	0.258	1.309	0.118	0.618	putative transcriptional regulator (LuxR/UhpA familiy)
yhjC	STM3607	AAL22467	3780701..3781600	0.512	0.167	0.269	0.024	0.525	0.273	0.035	0.274	0.015	1.004	putative transcriptional regulator, LysR family
yhjD	STM3608	AAL22468	3781673..3782701	0.465	0.139	0.303	0.018	0.651	0.279	0.037	0.506	0.020	1.814	putative tRNA-processing ribonuclease
yhjE	STM3609	AAL22469	3783052..3784374	0.485	0.149	0.308	0.065	0.634	0.208	0.002	0.389	0.043	1.870	putative MFS family transport protein
yhjG	STM3610	AAL22470	(3784414..3786474)	0.830	0.135	0.694	0.113	0.836	0.240	0.117	0.444	0.055	1.853	putative inner membrane protein

yhjH	STM3611	AAL22471	(3786584..3787351)	1.941	0.119	2.302	0.420	1.186	0.134	0.015	0.242	0.018	1.812	putative Diguanylate cyclase/phosphodiesterase domain 3
kdgK	STM3612	AAL22472	3787580..3788509	2.182	0.273			0.000	0.445	0.073			0.000	ketodeoxygluconokinase
yhjJ	STM3613	AAL22473	(3788563..3790050)	3.324	0.344	3.330	0.238	1.002	1.508	0.014	1.922	0.113	1.275	putative Zn-dependent peptidase
dctA	STM3614	AAL22474	(3790270..3791556)	27.506	3.693	15.688	1.653	0.570	2.159	0.307	1.421	0.218	0.658	DAACS family, C4-dicarboxylic acids transport protein
yhjK	STM3615	AAL22475	(3791714..3793687)	1.258	0.054	0.841	0.140	0.669	0.688	0.049	0.563	0.027	0.819	putative Diguanylate cyclase/phosphodiesterase
yhjL	STM3616	AAL22476	(3793894..3797436)	1.449	0.081	0.832	0.135	0.574	3.771	0.503	3.610	0.353	0.957	putative TPR-repeat-containing protein
bcsC	STM3617	AAL22477	(3797418..3798527)	1.379	0.129	0.723	0.105	0.524	4.133	1.053	3.898	0.245	0.943	endo-1,4-D-glucanase
yhjN	STM3618	AAL22478	(3798531..3800831)	1.049	0.038	1.056	0.109	1.006	4.647	1.125	5.681	0.401	1.223	putative cellulose synthase
yhjO	STM3619	AAL22479	(3800842..3803466)					N/A					N/A	glycosyltransferase, probably involved in cell wall biogenesis
yhjQ	STM3620	AAL22480	(3803463..3804215)	1.205	0.075	0.790	0.117	0.656	3.421	0.873	5.648	0.257	1.651	putative ATPase involved in chromosome partitioning
yhjR	STM3621	AAL22481	(3804216..3804419)	1.179	0.119	0.586	0.071	0.497	3.173	0.723	2.495	0.084	0.786	putative cytoplasmic protein
yhjS	STM3622	AAL22482	3804664..3806235	0.904	0.097	0.902	0.161	0.998	2.248	0.148	2.603	0.120	1.158	putative cytoplasmic protein
yhjT	STM3623	AAL22483	3806232..3806423	1.065	0.096	0.651	0.027	0.612	3.086	0.314	2.789	0.282	0.904	putative inner membrane protein
yhjU	STM3624	AAL22484	3806420..3808099	1.082	0.032	0.680	0.023	0.628	2.386	0.447	1.978	0.104	0.829	putative inner membrane protein
STM3624A	STM3624A	AAL22485	3808673..3808813					N/A					N/A	cystathionine gamma-synthase
yhjV	STM3625	AAL22486	3808931..3810229	0.377	0.159	0.181	0.032	0.480	1.240	0.376	0.684	0.042	0.552	putative HAAAP family transport protein
dppF	STM3626	AAL22487	(3810330..3811343)					N/A					N/A	ABC superfamily (atp_bind), dipeptide transport protein
dppD	STM3627	AAL22488	(3811340..3812323)	0.550	0.068	0.383	0.051	0.697	0.185	0.005	0.459	0.026	2.476	ABC superfamily (atp_bind), dipeptide transport protein
dppC	STM3628	AAL22489	(3812334..3813236)	0.745	0.034	0.228	0.052	0.305	0.217	0.046	0.336	0.017	1.547	ABC superfamily (membrane), dipeptide transport protein 2
dppB	STM3629	AAL22490	(3813246..3814265)	0.861	0.062	0.216	0.028	0.251	0.211	0.029	0.351	0.016	1.665	ABC superfamily (membrane), dipeptide transport protein 1
dppA	STM3630	AAL22491	(3814422..3816029)	0.965	0.265	0.753	0.138	0.780	0.150	0.008	0.456	0.032	3.051	ABC superfamily (peri_perm), dipeptide transport protein
STM3631	STM3631	AAL22492	(3816585..3817910)	0.431	0.176	0.192	0.054	0.445	0.191	0.007	0.242	0.006	1.270	putative xanthine permease
STM3632	STM3632	AAL22493	(3817968..3819092)	0.615	0.215	0.311	0.027	0.505	0.330	0.023	0.494	0.038	1.494	putative PQQ enzyme repeat
STM3633	STM3633	AAL22494	3819242..3820249	1.004	0.122	0.344	0.038	0.343	0.427	0.031	0.485	0.028	1.137	putative bacterial regulatory proteins, lacI family
proK	STM3634						N/A					N/A		
yhjW	STM3635	AAL22495	(3820576..3822267)	2.835	0.166	1.131	0.180	0.399	1.393	0.257	0.701	0.041	0.503	putative membrane-associated, metal-dependent hydrolase
lpfE	STM3636	AAL22496	(3822485..3823012)	0.516	0.132	0.468	0.047	0.908	0.378	0.127	0.515	0.386	1.364	long polar fimbrial minor protein
lpfD	STM3637	AAL22497	(3823018..3824097)	0.350	0.113	0.263	0.088	0.752	0.243	0.069	0.404	0.039	1.661	long polar fimbrial operon protein

lpfC	STM3638	AAL22498	(3824115..3826643)	0.227	0.157	0.145	0.026	0.637	0.138	0.038	0.270	0.007	1.958	long polar fimbrial outer membrane usher protein
lpfB	STM3639	AAL22499	(3826666..3827364)	0.193	0.112	0.237	0.057	1.231	0.199	0.133	0.350	0.197	1.758	long polar fimbrial chaperone
lpfA	STM3640	AAL22500	(3827449..3827985)	0.339	0.115	0.516	0.114	1.523	0.565	0.095	0.657	0.226	1.163	long polar fimbria
yhjY	STM3641	AAL22501	(3828491..3829195)	0.604	0.085	0.419	0.029	0.694	0.482	0.018	0.542	0.057	1.126	putative lipase
tag	STM3642	AAL22502	3829352..3829933	2.857	0.427	1.983	0.337	0.694	0.562	0.054	0.548	0.026	0.975	3-methyl-adenine DNA glycosylase I, constitutive
yiaC	STM3643	AAL22503	3829911..3830351	1.707	0.157	1.702	0.145	0.997	0.484	0.016	0.387	0.026	0.799	putative acetyltransferase
bisC	STM3644	AAL22504	(3830320..3832653)	1.995	0.146	0.848	0.096	0.425	0.943	0.218	0.993	0.027	1.053	biotin sulfoxide reductase
yiaD	STM3645	AAL22505	3832806..3833468	3.699	0.947	2.291	0.135	0.619	8.432	2.592	10.812	0.949	1.282	putative outer membrane lipoprotein
yiaE	STM3646	AAL22506	3833687..3834661	6.214	1.642	2.572	0.531	0.414	1.498	0.399	1.294	0.151	0.863	2-keto-D-gluconate reductase
yiaF	STM3647	AAL22507	(3834711..3835421)	9.125	1.073	3.288	0.433	0.360	7.198	1.065	4.833	0.203	0.672	putative outer membrane lipoprotein
yiaG	STM3648	AAL22508	3835860..3836150	1.498	0.126	0.477	0.012	0.319	2.108	0.239	0.980	0.025	0.465	putative transcriptional regulator
cspA	STM3649	AAL22509	3836439..3836651					N/A					N/A	major cold shock protein 7.4, transcriptional activator of hns
STM3650	STM3650	AAL22510	3836825..3837364	1.188	0.079	1.600	0.048	1.347	1.034	0.051	0.585	0.049	0.565	putative periplasmic or exported protein
STM3651	STM3651	AAL22511	(3837736..3838221)	1.253	0.136	0.740	0.071	0.590	0.718	0.026	0.896	0.050	1.248	putative acetyltransferase
STM3652	STM3652	AAL22512	(3838209..3838496)	1.011	0.039	0.692	0.084	0.684	0.689	0.058	0.910	0.079	1.321	putative cytoplasmic protein
STM3653	STM3653	AAL22513	(3838674..3839141)	0.325	0.110	0.269	0.038	0.828	0.507	0.191	0.657	0.024	1.296	putative acetyltransferase
STM3654	STM3654	pseudogene; in-frame stop following codon 23			0.505	0.105	0.577	0.021	1.144	0.998	0.176	1.100	0.041	1.103
glyS	STM3655	AAL22514	(3839770..3841839)	2.300	0.080	7.121	1.082	3.097	1.636	0.062	4.077	0.102	2.492	glycine tRNA synthetase, beta subunit
glyQ	STM3656	AAL22515	(3841849..3842760)	1.163	0.126	6.306	0.359	5.420	0.880	0.085	2.422	0.203	2.753	glycine tRNA synthetase, alpha subunit
STM3657	STM3657	AAL22516	(3842899..3843201)	0.688	0.065	0.756	0.101	1.099	0.952	0.165	1.090	0.071	1.144	putative outer membrane lipoprotein
yiaH	STM3658	AAL22517	3843367..3844362	0.592	0.153	0.333	0.035	0.563	0.555	0.019	0.565	0.028	1.018	putative inner membrane protein
yiaB	STM3659	AAL22518	(3844385..3844738)	0.296	0.170	0.199	0.026	0.673	0.322	0.027	0.308	0.034	0.957	putative inner membrane protein
xylB	STM3660	AAL22519	(3844913..3846367)	0.675	0.077	0.513	0.052	0.760	0.394	0.055	0.672	0.059	1.706	xylulokinase
xylA	STM3661	AAL22520	(3846467..3847789)	0.419	0.123	0.451	0.040	1.076	0.302	0.026	0.584	0.048	1.932	D-xylose isomerase
xylR	STM3662	AAL22521	3848152..3849330	1.040	0.060	0.832	0.151	0.800	0.958	0.104	1.086	0.099	1.134	xylose operon regulatory protein (AraC/XylS family)
bax	STM3663	AAL22522	(3849391..3850215)	4.733	0.389	4.357	0.800	0.921	2.617	0.200	3.865	0.081	1.477	gene transcribed divergently from malS
malS	STM3664	AAL22523	3850531..3852558	0.548	0.147	0.201	0.026	0.367	0.218	0.042	0.272	0.012	1.251	alpha-amylase
avtA	STM3665	AAL22524	3852732..3853982	1.629	0.134	0.397	0.050	0.244	0.596	0.032	0.686	0.060	1.152	valine-pyruvate aminotransferase
ysaA	STM3666	AAL22525	(3854019..3854492)	1.310	0.049	1.107	0.134	0.845	0.611	0.041	0.894	0.099	1.462	paral putative oxidoreductase
yiaJ	STM3667	AAL22526	(3854609..3855409)	0.530	0.161	1.044	0.048	1.970	0.380	0.061	1.211	0.055	3.187	transcriptional repressor (IclR family)
yiaK	STM3668	AAL22527	3855639..3856637	0.630	0.132	0.189	0.025	0.300	0.209	0.122	0.275	0.056	1.320	putative malate dehydrogenase
yiaL	STM3669	AAL22528	3856649..3857113	0.405	0.189	0.177	0.025	0.437	0.194	0.004	0.274	0.102	1.412	putative cytoplasmic protein
STM3670	STM3670	AAL22529	3857137..3858069	0.288	0.167	0.132	0.012	0.459	0.185	0.034	0.312	0.032	1.685	putative chemotaxis protein, resembles cheA
yiaM	STM3671	AAL22530	3858208..3858681	0.329	0.162	0.146	0.004	0.445	0.197	0.009	0.382	0.072	1.939	putative transporter

yiaN	STM3672	AAL22531	3858684..3859961	0.198	0.153	0.119	0.023	0.602	0.141	0.007	0.401	0.032	2.838	putative DedA family, membrane protein
yiaO	STM3673	AAL22532	3859973..3860959	0.182	0.158	0.102	0.031	0.561	0.142	0.031	0.312	0.016	2.205	putative dicarboxylate-binding periplasmic protein
lyxK	STM3674	AAL22533	3860963..3862459	0.360	0.174	0.167	0.035	0.465	0.267	0.087	0.672	0.105	2.513	L-xylulose kinase, cryptic
sgbH	STM3675	AAL22534	3862456..3863118					N/A					N/A	putative 3-hexulose-6-phosphate isomerase
sgbU	STM3676	AAL22535	3863111..3863971	0.277	0.199	0.347	0.121	1.253	0.238	0.023	0.696	0.099	2.925	putative 3-hexulose-6-phosphate isomerase
sgbE	STM3677	AAL22536	3863965..3864660					N/A					N/A	L-ribulose-5-phosphate 4-epimerase
STM3678	STM3678	AAL22537	(3864821..3865636)	0.999	0.080	0.675	0.085	0.675	0.272	0.016	0.653	0.047	2.398	putative bacterial regulatory helix-turn-helix proteins, araC family
STM3679	STM3679	AAL22538	3865900..3867855	0.334	0.131	0.515	0.049	1.542	0.149	0.012	0.540	0.038	3.617	putative cytoplasmic protein
aldB	STM3680	AAL22539	(3867973..3869511)	0.859	0.023	0.617	0.107	0.718	0.574	0.067	1.086	0.052	1.894	aldehyde dehydrogenase B (lactaldehyde dehydrogenase)
STM3681	STM3681	AAL22540	3869680..3870561	0.668	0.028	0.304	0.031	0.455	0.623	0.096	1.140	0.067	1.831	putative transcriptional regulator
selB	STM3682	AAL22541	(3870846..3872696)	2.242	0.229	1.549	0.067	0.691	0.961	0.181	1.523	0.083	1.585	selenocysteinyl-tRNA-specific translation factor
selA	STM3683	AAL22542	(3872693..3874084)	1.602	0.120	1.413	0.146	0.882	0.785	0.131	1.352	0.054	1.722	selenocysteine synthase (with SelD)
yibF	STM3684	AAL22543	(3874183..3874791)	3.242	0.318	2.056	0.274	0.634	2.007	0.129	2.806	0.169	1.398	putative glutathione S-transferase
mtlA	STM3685	AAL22544	3875267..3877183	1.254	0.022	2.344	0.186	1.870	0.890	0.119	2.745	0.155	3.084	PTS family, mannitol-specific enzyme IIABC onents
mtlD	STM3686	AAL22545	3877404..3878552	1.751	0.120	1.802	0.211	1.029	1.495	0.115	2.899	0.349	1.939	mannitol-1-phosphate dehydrogenase
mtlR	STM3687	AAL22546	3878549..3879139	1.736	0.229	0.739		0.426	1.335	0.232			0.000	repressor for mtl
STM3688	STM3688	AAL22547	(3879149..3879358)	0.958	0.110	0.535	0.280	0.558	1.590	1.229	0.875	0.185	0.550	putative cytoplasmic protein
yibL	STM3689	AAL22548	3879649..3880011	1.191	0.072	1.013	0.112	0.851	0.655	0.184	0.749	0.030	1.144	putative cytoplasmic protein
STM3690	STM3690	AAL22549	3880501..3881184	0.261	0.131	0.205	0.034	0.786	0.620	0.076	0.459	0.017	0.741	putative inner membrane lipoprotein
STM3691	STM3691	AAL22550	3881228..3885613	0.601	0.182	1.066	0.497	1.773	1.026	1.580	0.896	1.162	0.873	putative inner membrane protein
lldP	STM3692	AAL22551	3885912..3887567	30.142	6.888	19.726	1.322	0.654	1.718	0.229	4.673	0.153	2.720	LctP transporter, L-lactate permease
lldR	STM3693	AAL22552	3887564..3888340	26.238	6.489	17.310	2.351	0.660	1.989	0.403	5.016	0.219	2.523	putative transcriptional regulator for lct operon (GntR family)
lldD	STM3694	AAL22553	3888337..3889527	22.352	11.052	13.850	1.630	0.620	2.363	0.536	7.803	0.589	3.302	L-lactate dehydrogenase
yibK	STM3695	AAL22554	3889591..3890064	4.825	2.294	1.691	0.145	0.351	0.808	0.038	0.751	0.087	0.929	putative tRNA/rRNA methyltransferase
STM3696	STM3696	AAL22555	(3890132..3891136)	0.602	0.132	0.447	0.085	0.742	0.278	0.016	0.348	0.019	1.252	putative transcriptional regulator
STM3697	STM3697	AAL22556	3891455..3892651	0.305	0.169	0.615	0.060	2.021	0.156	0.002	0.257	0.023	1.644	putative mandelate racemase / muconate lactonizing enzyme family
STM3698	STM3698	AAL22557	3892725..3894035	0.710	0.048	0.481	0.039	0.677	0.286	0.029	0.522	0.031	1.825	putative permease
cysE	STM3699	AAL22558	(3894118..3894939)	4.603	0.647	3.443	0.248	0.748	2.734	0.270	3.840	0.141	1.404	serine acetyltransferase
gpsA	STM3700	AAL22559	(3895017..3896036)	7.664	0.957	11.571	1.634	1.510	2.539	0.210	4.289	0.357	1.689	glycerol-3-phosphate dehydrogenase (NAD+)
secB	STM3701	AAL22560	(3896036..3896503)	15.712	2.098	14.500	1.824	0.923	5.676	0.362	5.761	0.346	1.015	molecular chaperone in protein export
grxC	STM3702	AAL22561	(3896547..3896798)	17.224	1.453	11.845	1.113	0.688	7.252	0.333	6.732	0.307	0.928	glutaredoxin 3
yibN	STM3703	AAL22562	(3896885..3897316)	9.286	0.815	5.823	0.719	0.627	4.296	0.365	4.316	0.324	1.005	putative Rhodanese-related sulfurtransferases

pmgI	STM3704	AAL22563	3897564..3899108	0.586	0.136	3.195	0.549	5.454	0.340	0.070	0.687	0.032	2.023	phosphoglyceromutase
yibP	STM3705	AAL22564	3899118..3900401	2.271	0.319	2.207	0.182	0.972	1.633	0.281	1.993	0.147	1.220	paral putative membrane protein
yigQ	STM3706	AAL22565	3900405..3901367	2.790	0.239	1.184	0.102	0.424	2.697	0.651	2.478	0.184	0.919	putative periplasmic protein
yibD	STM3707	AAL22566	(3901354..3902388)	0.634	0.097	0.555	0.036	0.875	8.732	0.554	7.706	0.472	0.883	putative glycosyltransferase
tdh	STM3708	AAL22567	(3902882..3903907)	13.865	3.728	12.007	0.675	0.866	3.745	0.458	4.851	0.480	1.295	threonine 3-dehydrogenase
kbl	STM3709	AAL22568	(3903917..3905113)	20.871	5.193	11.551	1.545	0.553	4.333	0.982	4.753	0.429	1.097	2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)
rfaD	STM3710	AAL22569	3905316..3906248	3.769	0.219	6.934	0.662	1.840	2.125	0.123	2.420	0.300	1.139	ADP-L-glycero-D-mannoheptose-6-epimerase
rfaF	STM3711	AAL22570	3906251..3907297	3.273	0.427	5.679	0.947	1.735	1.964	0.022	2.596	0.396	1.321	ADP-heptose; LPS heptosyltransferase 1
rfaC	STM3712	AAL22571	3907297..3908250	1.261	0.185	2.556	0.399	2.028	0.995	0.239	1.377	0.128	1.383	heptosyl transferase I
rfaL	STM3713	AAL22572	3908290..3909504	3.052	0.102	1.503	0.140	0.493	2.321	0.157	1.395	0.059	0.601	O-antigen ligase
rfaK	STM3714	AAL22573	(3909561..3910706)	2.165	0.029	1.117	0.217	0.516	2.090	0.137	0.976	0.171	0.467	putative hexose transferase, lipopolysaccharide core biosynthesis
rfaZ	STM3715	AAL22574	(3910807..3911616)	4.462	0.362	0.563	0.024	0.126	6.250	1.213	1.429	0.074	0.229	lipopolysaccharide core biosynthesis
rfaY	STM3716	AAL22575	(3911766..3912464)	2.952	0.233	0.675	0.029	0.229	2.981	0.249	1.321	0.200	0.443	lipopolysaccharide core biosynthesis; modification of heptose region of the core
rfaJ	STM3717	AAL22576	(3912487..3913497)	3.321	0.512	0.741	0.045	0.223	4.162	0.548	1.832	0.215	0.440	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaI	STM3718	AAL22577	(3913515..3914528)	3.716	0.426	0.951	0.040	0.256	5.138	0.250	2.612	0.263	0.508	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
rfaB	STM3719	AAL22578	(3914534..3915613)	1.252	0.274	0.553	0.084	0.442	1.763	0.007	1.476	0.047	0.837	UDP-D-galactose:(glucosyl)lipopolysaccharide-1, 6-D-galactosyltransferase
yibR	STM3720	AAL22579	(3915683..3915916)	1.057	0.188	1.089	0.201	1.030	1.346	0.080	1.683	0.390	1.250	putative inner membrane protein
rfaP	STM3721	AAL22580	(3915948..3916745)	0.844	0.191	1.031	0.143	1.222	1.162	0.108	1.791	0.108	1.542	lipopolysaccharide core biosynthesis; phosphorylation of core heptose
rfaG	STM3722	AAL22581	(3916738..3917862)	0.952	0.151	1.548	0.165	1.627	1.766	0.159	2.280	0.139	1.291	glucosyltransferase I
rfaQ	STM3723	AAL22582	(3917859..3918893)	0.878	0.115	1.444	0.128	1.645	0.919	0.013	1.545	0.189	1.681	lipopolysaccharide core biosynthesis; modification of heptose region of core
kdtA	STM3724	AAL22583	3919338..3920615	3.305	0.137	1.338	0.161	0.405	2.120	0.290	1.767	0.178	0.833	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)
kdtB	STM3725	AAL22584	3920624..3921103	5.035	0.298	2.652	0.135	0.527	2.320	0.321	2.450	0.158	1.056	phosphopantetheine adenylyltransferase
mutM	STM3726	AAL22585	(3921131..3921940)	1.332	0.042	0.847	0.184	0.636	0.900	0.061	1.123	0.110	1.247	formamidopyrimidine DNA glycosylase
rpmG	STM3727	AAL22586	(3922038..3922205)	11.582	2.629	7.109	1.082	0.614	6.358	0.600	3.702	0.282	0.582	50S ribosomal subunit protein L33
rpmB	STM3728	AAL22587	(3922226..3922462)	29.140	6.598	14.760	0.349	0.507	17.269	0.205	9.525	1.487	0.552	50S ribosomal subunit protein L28
radC	STM3729	AAL22588	(3922680..3923345)	2.404	0.127	1.654	0.278	0.688	0.887	0.071	0.525	0.057	0.592	putative DNA repair protein, associated with replication forks
dfp	STM3730	AAL22589	3923518..3924741	1.889	0.127	2.777	0.216	1.471	0.928	0.130	1.262	0.080	1.360	flavoprotein affecting synthesis of DNA and pantothenate metabolism

dut	STM3731	AAL22590	3924722..3925177	2.916	0.073	2.880	0.305	0.988	1.031	0.025	1.579	0.165	1.531	deoxyuridinetriphosphatase
ttk	STM3732	AAL22591	3925285..3925881	2.612	0.532	4.543	1.528	1.739	1.653	0.847	1.588	0.510	0.961	putative transcriptional regulator (TetR/ArcR family)
pyrE	STM3733	AAL22592	(3925959..3926600)	3.191	0.206	1.811	0.308	0.568	1.106	0.061	1.178	0.028	1.065	orotate phosphoribosyltransferase
rph	STM3734	AAL22593	(3926679..3927395)	1.054	0.064	1.182	0.144	1.121	0.585	0.032	0.790	0.067	1.350	RNase PH
yicC	STM3735	AAL22594	3927521..3928384	4.791	0.697	1.628	0.084	0.340	1.415	0.113	1.633	0.090	1.153	putative stress-induced protein
STM3736	STM3736	AAL22595	(3928434..3929336)	1.082	0.042	0.401	0.057	0.371	0.428	0.002	0.557	0.012	1.302	putative transcriptional regulator, LysR family
STM3737	STM3737	AAL22596	3929410..3930291	0.415	0.163	0.249	0.031	0.600	0.248	0.027	0.296	0.015	1.194	putative Zn-dependent hydrolase, including glyoxylases
yicF	STM3739	AAL22598	(3931156..3932841)	0.590	0.146	0.408	0.045	0.693	0.299	0.019	0.295	0.022	0.988	putative DNA ligase
gmk	STM3740	AAL22599	3933098..3933721	1.785	0.074	3.902	0.397	2.186	1.041	0.128	1.460	0.140	1.403	guanylate kinase
rpoZ	STM3741	AAL22600	3933776..3934051	2.387	0.180	4.855	0.697	2.034	1.959	0.174	2.454	0.178	1.253	RNA polymerase, omega subunit
spoT	STM3742	AAL22601	3934070..3936181	1.816	0.059	2.819	0.292	1.552	1.469	0.065	1.635	0.072	1.113	bifunctional : (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase
spoU	STM3743	AAL22602	3936186..3936875	2.669	0.106	1.815	0.107	0.680	1.845	0.302	2.000	0.165	1.084	putative tRNA/rRNA methyltransferase
recG	STM3744	AAL22603	3936881..3938962	2.500	0.175	1.182	0.112	0.473	1.598	0.347	1.216	0.108	0.761	DNA helicase, resolution of Holliday junctions, branch migration
STM3745	STM3745	AAL22604	(3938965..3939816)	6.518	1.033	1.185	0.266	0.182	0.906	0.239	0.718	0.049	0.793	putative cytoplasmic protein
gltS	STM3746	AAL22605	(3939819..3941024)	8.494	0.733	1.836	0.192	0.216	1.518	0.302	1.048	0.092	0.690	GltS family, glutamate transport protein
yicE	STM3747	AAL22606	3941252..3942643	0.852	0.227	0.443	0.038	0.520	0.345	0.040	0.380	0.038	1.101	putative NCS2 family, purine/xanthine transport protein
yicH	STM3748	AAL22607	3942764..3944473	2.201	0.215	1.980	0.353	0.900	0.767	0.055	1.221	0.147	1.591	putative inner membrane protein
yicI	STM3749	AAL22608	(3944576..3946894)					N/A					N/A	putative alpha-xylosidase
yicJ	STM3750	AAL22609	(3946906..3948288)	0.227	0.178	0.110	0.031	0.487	0.090	0.016	0.257	0.011	2.863	putative GPH family transport protein
selC	STM3751						N/A					N/A		
STM3752	STM3752	AAL22610	(3948987..3949331)	0.369	0.131	0.158	0.010	0.427	0.751	0.052	0.693	0.068	0.922	putative cytoplasmic protein
sugR	STM3753	AAL22611	3950009..3951199	0.815	0.076	1.242	0.082	1.524	0.481	0.015	0.977	0.121	2.032	ATP binding protein
STM3754	STM3754	AAL22612	3951196..3951546					N/A					N/A	putative cytoplasmic protein
rhuM	STM3755	AAL22613	3951733..3952770	0.533	0.140	0.616	0.109	1.157	0.345	0.028	0.490	0.049	1.421	putative cytoplasmic protein
rmbA	STM3756	AAL22614	3954069..3954686	0.228	0.134	0.169	0.047	0.739	0.419	0.022	0.539	0.080	1.285	putative cytoplasmic protein
misL	STM3757	AAL22615	3954761..3957628	0.355	0.128	0.307	0.055	0.864	0.240	0.076	0.568	0.177	2.365	putative autotransported protein
fidL	STM3758	AAL22616	(3957723..3958187)	0.353	0.119	0.150	0.048	0.426	1.244	0.101	0.905	0.060	0.728	putative inner membrane protein
marT	STM3759	AAL22617	(3958198..3959055)	0.356	0.126	0.147	0.034	0.414	1.265	0.035	1.015	0.106	0.802	putative transcriptional regulatory protein
STM3760	STM3760	AAL22618	(3959108..3959221)					N/A					N/A	putative cytoplasmic protein
slsA	STM3761	AAL22619	3959839..3960519	0.501	0.107	0.533	0.100	1.064	3.886	0.379	6.693	0.094	1.722	putative inner membrane protein
cigR	STM3762	AAL22620	(3960748..3961227)	0.792	0.091	0.857	0.085	1.083	2.909	0.241	2.648	0.260	0.910	putative inner membrane protein
mgtB	STM3763	AAL22621	(3961542..3964268)	0.373	0.132	0.209	0.040	0.562	6.231	0.944	2.008	0.189	0.322	Mg2+ transport protein
mgtC	STM3764	AAL22622	(3964488..3965183)	0.269	0.175	0.136	0.026	0.508	3.692	0.302	0.821	0.093	0.223	Mg2+ transport protein

yicL	STM3765	AAL22623	3965692..3966594	1.489	0.114	0.474	0.011	0.319	3.807	0.503	1.656	0.185	0.435	putative permease, integral membrane protein
STM3766	STM3766	AAL22624	(3966637..3967578)	0.341	0.101	0.336	0.044	0.984	0.294	0.032	0.420	0.035	1.431	putative cytoplasmic protein
STM3767	STM3767	AAL22625	(3967814..3968557)	0.651	0.152	0.592	0.102	0.909	0.263	0.044	0.546	0.098	2.078	putative cytoplasmic protein
STM3768	STM3768	AAL22626	(3968544..3969653)	0.666	0.147	0.474	0.008	0.712	0.231	0.016	0.526	0.046	2.282	putative selenocysteine synthase [L-seryl-tRNA(Ser) selenium transferase
STM3769	STM3769	AAL22627	(3969657..3970517)	0.548	0.140	0.387	0.071	0.706	0.205	0.021	0.268	0.002	1.307	putative phosphotransferase system enzyme II
STM3770	STM3770	AAL22628	(3970514..3971263)	0.548	0.152	0.370	0.047	0.675	0.178	0.025	0.341	0.042	1.918	putative phosphotransferase system enzyme IIC
STM3771	STM3771	AAL22629	(3971409..3971894)	0.745	0.166	0.486	0.026	0.653	0.400	0.083	0.392	0.042	0.980	putative phosphotransferase system enzyme IIB
STM3772	STM3772	AAL22630	(3971905..3972330)	0.877	0.137	0.405	0.096	0.462	0.374	0.112	0.488	0.135	1.303	putative phosphotransferase system enzyme IIA
STM3773	STM3773	AAL22631	(3972549..3975347)	1.487	0.050	0.798	0.062	0.536	0.370	0.011	0.660	0.109	1.783	putative NtrC family transcriptional regulators, ATPase domain
STM3774	STM3774	AAL22632	3975544..3975837	0.639	0.101	0.314	0.047	0.491	0.367	0.272	0.394	0.058	1.074	putative inner membrane protein
STM3775	STM3775	AAL22633	3975943..3977325	0.763	0.067	0.732	0.092	0.960	0.188	0.012	0.407	0.023	2.162	putative glycosyl hydrolase family
yicM	STM3776	AAL22634	(3977385..3978578)	0.691	0.163	0.164	0.023	0.237	0.435	0.019	0.321	0.017	0.739	putative MFS family tranport protein (1st mdule)
STM3777	STM3777	AAL22635	3978794..3979153	0.655	0.066	0.421	0.058	0.643	0.239	0.013	0.448	0.026	1.874	putative cytoplasmic protein
STM3778	STM3778	AAL22636	3979137..3979460	0.600	0.146	0.429	0.023	0.715	0.372	0.068	0.722	0.094	1.942	putative helix-turn-helix protein
STM3779	STM3779	AAL22637	(3979551..3979820)	0.755	0.244	0.316	0.069	0.418	1.057	0.221	1.674	0.029	1.583	putative phosphotransferase system, HPr-related protein
STM3780	STM3780	AAL22638	(3979830..3980690)	0.272	0.136	0.184	0.019	0.677	0.823	0.014	2.957	0.199	3.593	putative fructose-bisphosphate aldolase class-II
STM3781	STM3781	AAL22639	(3980753..3982237)	0.279	0.154	0.308	0.043	1.104	0.557	0.004	1.500	0.301	2.694	putative sugar (pentulose and hexulose) kinase
STM3782	STM3782	AAL22640	(3982230..3983588)	0.376	0.200	0.470	0.024	1.248	1.301	0.041	4.135	0.244	3.178	putative PTS system galactitol-specific enzyme IIC onent
STM3783	STM3783	AAL22641	(3983664..3983951)	1.361	0.192	0.625	0.086	0.459	2.832	0.083	3.284	0.449	1.160	putative periplasmic protein
STM3784	STM3784	AAL22642	(3983948..3984421)	1.756	0.093	0.867	0.038	0.494	1.575	0.154	2.347	0.131	1.490	putative phosphotransferase system mannitol/fructose-specific IIA domain
STM3785	STM3785	AAL22643	(3984439..3985182)	1.602	0.119	1.453	0.290	0.907	0.682	0.029	0.839	0.065	1.231	putative regulatory protein, gntR family
yicN	STM3786	AAL22644	(3985535..3985987)	3.516	0.165	0.572	0.045	0.163	1.163	0.235	0.640	0.053	0.551	putative inner membrane protein
uhpT	STM3787	AAL22645	(3986180..3987571)	0.528	0.157	0.397	0.072	0.752	0.206	0.117	0.331	0.075	1.610	MFS family, hexose phosphate transport protein
uhpC	STM3788	AAL22646	(3987714..3989042)	0.451	0.201	0.226	0.033	0.501	0.302	0.058	0.260	0.036	0.859	membrane protein, regulator of uhpT expression
uhpB	STM3789	AAL22647	(3989052..3990554)	0.862	0.149	0.954	0.148	1.106	0.781	0.125	1.315	0.240	1.685	sensory histidine kinase in two-onent regulatory sytem with UhpA
uhpA	STM3790	AAL22648	(3990554..3991144)	1.004	0.152	0.467	0.062	0.465	0.688	0.032	0.453	0.050	0.658	response regulator (repressor) in two-onent regulatory system wtih UhpB, regulates uhpT operon (LuxR/UhpA family)
STM3791	STM3791	AAL22649	(3991219..3992232)	1.440	0.165	1.012	0.083	0.703	0.478	0.052	0.580	0.107	1.214	putative cytoplasmic protein
STM3792	STM3792	AAL22650	(3992244..3993560)	1.351	0.079	1.016	0.209	0.752	0.451	0.066	0.408	0.100	0.904	putative L-fucose permease
STM3793	STM3793	AAL22651	(3993591..3994511)	0.998	0.047	1.286	0.086	1.288	0.253	0.055	0.360	0.034	1.425	putative sugar kinase, ribokinase family
STM3794	STM3794	AAL22652	3994836..3995621	1.040	0.061	0.576	0.146	0.554	0.335	0.025	0.498	0.085	1.488	putative regulatory protein, deoR family
ilvN	STM3795	AAL22653	(3995623..3995913)	0.998	0.050	0.380	0.065	0.381	0.461	0.030	0.382	0.016	0.830	acetolactate synthase I, small subunit

ilvB	STM3796	AAL22654	(3995917..3997605)	0.847	0.114	0.532	0.100	0.628	0.297	0.019	0.386	0.117	1.298	acetolactate synthase I, large subunit, valine sensitive
ivbL	STM3797	AAL22655	(3997712..3997810)	3.393	0.336			0.000	2.520	2.588			0.000	ilvB operon leader peptide
ysdA	STM3797A; ribosomal slippage							N/A					N/A	
ysdB	STM3796B	AAL22656	3998444..3998533					N/A					N/A	conserved protein in the LexA regulon
STM3796A	STM3796A	AAL22657	3998626..3999486					N/A					N/A	integral membrane protein
emrD	STM3798	AAL22658	3999689..4000873	0.910	0.134	0.662	0.058	0.728	0.989	0.159	0.886	0.067	0.896	MFS family, multidrug tranport protein
STM3799	STM3799	AAL22659	(4000800..4001885)	1.483	0.079			0.000	0.675	0.155			0.000	putative periplasmic protein
dsdC	STM3800	AAL22660	(4001949..4002872)	0.988	0.069	0.359	0.024	0.364	0.312	0.036	0.505	0.042	1.620	transcriptional activator (LysR family)
dsdX	STM3801	AAL22661	4003098..4004435	0.405	0.194			0.000	0.169	0.016	0.430	0.023	2.545	putative Gnt family transport protein
dsdA	STM3802	AAL22662	4004453..4005775	1.295	0.107	0.924	0.162	0.713	0.563	0.069	0.586	0.019	1.041	D-serine deaminase (dehydratase)
yidF	STM3803	AAL22663	(4005857..4006387)	2.104	0.104	1.220	0.156	0.580	1.670	0.134	1.360	0.151	0.815	putative cytoplasmic protein
yidG	STM3804	AAL22664	(4006384..4006746)	0.984	0.188	0.897	0.166	0.911	0.984	0.171	1.131	0.075	1.149	putative inner membrane protein
yidH	STM3805	AAL22665	(4006736..4007083)	0.731	0.147	1.098	0.102	1.502	0.872	0.046	1.798	0.025	2.060	putative inner membrane protein
STM3806	STM3806	pseudogene; frameshift		0.583	0.188	0.542	0.044	0.928	0.432	0.138	0.817	0.027	1.891	
yidE	STM3807	AAL22666	(4007527..4009188)	0.650	0.177	0.509	0.069	0.783	0.337	0.029	0.442	0.043	1.309	paral putative transport protein
ibpB	STM3808	AAL22667	(4009378..4009806)	1.113	0.128	1.055	0.136	0.948	1.047	0.099	3.265	0.104	3.117	small heat shock protein
ibpA	STM3809	AAL22668	(4009916..4010329)	2.173	0.549	0.916	0.099	0.422	2.434	0.072	3.632	0.617	1.492	small heat shock protein
yidQ	STM3810	AAL22669	4010636..4010971	2.892	0.550	1.512	0.149	0.523	1.358	0.052	1.136	0.042	0.836	putative outer membrane lipoprotein
yidR	STM3811	AAL22670	(4010973..4012199)	1.330	0.072	0.710	0.079	0.533	0.656	0.053	0.694	0.057	1.059	putative cytoplasmic protein
ccmH	STM3812	AAL22671	(4012321..4013364)					N/A					N/A	putative heme lyase subunit, cytochrome c-type biogenesis
ccmG	STM3813	AAL22672	(4013361..4013918)					N/A					N/A	heme lyase disulfide oxidoreductase, cytocyhrome c-type biogenesis
ccmF	STM3814	AAL22673	(4013915..4015846)					N/A					N/A	cytochrome c-type biogenesis protein
ccmE	STM3815	AAL22674	(4015843..4016322)					N/A					N/A	periplasmic heme-dependent peroxidase, cytochrome c-type biogenesis protein
ccmD	STM3816	AAL22675	(4016319..4016531)					N/A					N/A	heme exporter protein C, cytochrome c-type biogenesis protein
ccmC	STM3817	AAL22676	(4016528..4017265)					N/A					N/A	ABC superfamily (membrane) heme exporter protein, cytochrome c-type biogenesis protein
ccmB	STM3818	AAL22677	(4017317..4017976)					N/A					N/A	ABC superfamily (membrane) heme exporter protein, cytochrome c-type biogenesis protein
ccmA	STM3819	AAL22678	(4017973..4018590)					N/A					N/A	ABC superfamily (atp_bind), heme exporter protein, cytochrome c-type biogenesis protein
STM3820	STM3820	AAL22679	(4018596..4019996)	0.253	0.162	2.745	0.327	10.851	0.427	0.020	0.527	0.023	1.233	putative cytochrome c peroxidase
torD	STM3821	AAL22680	(4020186..4020818)	0.342	0.196	0.343	0.031	1.003	0.281	0.097	0.343	0.033	1.221	cytoplasmic chaperone which interacts with TorA

torA	STM3822	AAL22681	(4020811..4023363)	0.311	0.212	0.274	0.013	0.881	0.127	0.026	0.235	0.013	1.856	trimethylamine N-oxide reductase subunit
torC	STM3823	AAL22682	(4023353..4024537)	0.361	0.168	0.188	0.040	0.521	0.182	0.020	0.230	0.009	1.263	trimethylamine N-oxide reductase, cytochrome c-type subunit, also has activity as negativer regulator of tor operon
torR	STM3824	AAL22683	4024667..4025359	3.553	0.085	2.863	0.267	0.806	0.944	0.146	1.830	0.054	1.940	response regulator in multi-onent regualtory system wtih TorS (sensory kinase) and TorT (periplasmic sensor), regulates tor operon (TorR family)
torT	STM3825	AAL22684	(4025332..4026372)	0.543	0.148	0.602	0.087	1.108	0.262	0.112	0.512	0.049	1.957	periplasmic sensor in multi-comopnent regulatory system with TorS (sensory kinase) and TorR (regulator), regulates tor operon
torS	STM3826	AAL22685	4026452..4029187	0.485	0.154	0.282	0.037	0.581	0.236	0.046	0.334	0.027	1.414	sensory kinase in multi-onent regulatory system with TorR (regulator) and TorT (periplasmic sensor), regulates tor operon
dgoT	STM3827	AAL22686	(4029213..4030550)	0.355	0.155	0.119	0.022	0.335	0.130	0.011	0.220	0.023	1.694	MFS family, D-galactonate transport protein
dgoA	STM3828	AAL22687	(4030635..4031783)	0.568	0.165	0.248	0.029	0.436	0.243	0.065	0.368	0.005	1.516	galactonate dehydratase in bifunctional: 2-oxo-3-deoxygalactonate 6-phosphate aldolase and galactonate dehydratase
dgoK	STM3829	AAL22688	(4032380..4033258)	0.687	0.111	0.313	0.035	0.456	0.240	0.008	0.336	0.011	1.398	2-oxo-3-deoxygalactonate kinase
dgoR	STM3830	AAL22689	(4033255..4033944)	1.695	0.174	0.656	0.054	0.387	0.488	0.009	0.752	0.009	1.542	galactonate operon transcriptional repressor (GntR family)
yidA	STM3831	AAL22690	(4034205..4035050)	0.913	0.133	0.644	0.062	0.706	0.940	0.115	1.471	0.067	1.565	putative hydrolase of the HAD superfamily
STM3832	STM3832	AAL22691	4035356..4036618	0.300	0.221	0.177	0.040	0.589	0.212	0.066	0.340	0.028	1.605	putative permease
STM3833	STM3833	AAL22692	4036632..4037825	0.347	0.167	0.274	0.027	0.788	0.286	0.059	0.416	0.019	1.453	putative mandelate racemase / muconate lactonizing enzyme family
STM3834	STM3834	AAL22693	4037940..4038836	1.846	0.077	1.544	0.253	0.836	0.490	0.067	0.463	0.028	0.946	putative transcriptional regulator, LysR family
gyrB	STM3835	AAL22694	(4038855..4041269)	4.408	0.227			0.000	3.284	0.022			0.000	DNA gyrase, subunit B (type II topoisomerase)
recF	STM3836	AAL22695	(4041298..4042371)	0.982	0.051	1.163	0.195	1.183	0.611	0.029	0.719	0.013	1.177	gap repair protein
dnaN	STM3837	AAL22696	(4042519..4043619)	2.128	0.058	2.882	0.663	1.354	1.365	0.356	1.516	0.232	1.111	DNA polymerase III, beta-subunit
dnaA	STM3838	AAL22697	(4043624..4045024)	3.750	0.447	2.677	0.288	0.714	2.350	0.209	1.508	0.091	0.642	DNA replication initiator protein
rpmH	STM3839	AAL22698	4045685..4045825	30.249	2.902	5.513	0.146	0.182	13.923	0.965	2.816	0.229	0.202	50S ribosomal subunit protein L34
rnpA	STM3840	AAL22699	4045842..4046201	5.154	0.084	3.293	0.288	0.639	3.392	0.182	1.254	0.014	0.370	RNase P, protein onent (protein C5), processes tRNA, 4.5S RNA
STM3841	STM3841	AAL22700	4046165..4046422	3.125	0.284	2.479	0.273	0.793	2.283	0.105	0.894	0.126	0.392	putative inner membrane protein
yidC	STM3842	AAL22701	4046425..4048071	6.542	0.371	6.579	1.457	1.006	3.493	0.289	2.766	0.231	0.792	putative Preprotein translocase subunit YidC
trmE	STM3843	AAL22702	4048213..4049577	1.882	0.105	0.977	0.042	0.519	0.981	0.086	0.864	0.024	0.881	GTPase for tRNA modification and thiophene and furan oxidation
STM3844	STM3844	pseudogene; in-frame stop; putative integrase			1.093	0.387	0.353	0.096	0.323	0.375	0.071	0.266	0.055	0.708
STM3845	STM3845	AAL22703	4051378..4052340	1.683	0.151	0.562	0.120	0.334	3.312	0.605	1.012	0.045	0.305	putative inner membrane protein
STM3846	STM3846	AAL22704	4052406..4053275	1.165	0.088	0.526	0.057	0.452	2.172	0.300	0.838	0.020	0.386	putative reverse transcriptase (RNA-dependent DNA polymerase)
yidY	STM3847	AAL22705	4054077..4055264	0.339	0.196	0.164	0.028	0.484	0.142	0.020	0.217	0.033	1.532	putative MFS family tranport protein (1st mdule)
yidZ	STM3848	AAL22706	4055233..4056192	0.598	0.221	0.386	0.056	0.645	0.221	0.009	0.335	0.019	1.514	putative transcriptional regulator, LysR family
yieE	STM3849	AAL22707	4056350..4057105	1.276	0.033	0.694	0.109	0.544	0.472	0.072	0.596	0.037	1.261	putative cytoplasmic protein

yieF	STM3850	AAL22708	4057105..4057689	5.356	1.366	1.875	0.299	0.350	1.738	0.333	1.276	0.082	0.734	putative oxidoreductase
yieG	STM3851	AAL22709	(4057734..4059197)	2.035	0.234	0.618	0.073	0.304	0.670	0.093	0.629	0.045	0.939	putative xanthine/uracil permeases family
yieH	STM3852	AAL22710	4059240..4059905	4.020	0.163	0.850	0.186	0.211	0.885	0.092	1.118	0.086	1.263	putative phosphatase/phosphohexomutase
phoU	STM3853	AAL22711	(4060000..4060725)	3.712	0.447	0.914	0.159	0.246	1.268	0.177	1.246	0.065	0.983	regulatory gene for high affinity phosphate uptake
pstB	STM3854	AAL22712	(4060740..4061513)	2.119	0.079	0.694	0.035	0.327	1.317	0.154	1.295	0.028	0.983	ABC superfamily (atp_bind), high-affinity phosphate transporter
pstA	STM3855	AAL22713	(4061600..4062490)	0.623	0.180	0.256	0.052	0.411	0.580	0.073	0.468	0.029	0.807	ABC superfamily (membrane), high-affinity phosphate transporter
pstC	STM3856	AAL22714	(4062490..4063449)	0.613	0.179	0.255	0.085	0.416	0.546	0.071	0.494	0.040	0.906	ABC superfamily (membrane), high-affinity phosphate transporter
pstS	STM3857	AAL22715	(4063585..4064625)	0.422	0.179	0.269	0.050	0.638	0.340	0.021	0.784	0.037	2.309	ABC superfamily (bind_prot), high-affinity phosphate transporter
STM3858	STM3858	AAL22716	(4064792..4066165)	0.751	0.151	0.284	0.022	0.378	0.196	0.020	0.322	0.018	1.644	putative phosphotransferase system fructose-specific onent IIB
STM3859	STM3859	AAL22717	(4066214..4067032)	0.327	0.191	0.169	0.036	0.518	0.117	0.004	0.214	0.011	1.821	putative shikimate / quinate 5-dehydrogenase
STM3860	STM3860	AAL22718	4067127..4068884	0.490	0.130	0.415	0.056	0.846	0.175	0.021	0.312	0.043	1.780	putative dipeptide/oligopeptide/nickel ABC-type transport systems, periplasmic onent
glmS	STM3861	AAL22719	(4069035..4070864)	2.771	0.143	4.923	0.949	1.777	1.353	0.171	1.705	0.130	1.261	L-glutamine:D-fructose-6-phosphate aminotransferase
glmU	STM3862	AAL22720	(4071053..4072423)	3.691	0.295	4.712	0.221	1.276	1.972	0.032	2.040	0.091	1.034	N-acetyl glucosamine-1-phosphate uridyltransferase and glucosamine-1-phosphate acetyl transferase
STM3863	STM3863	AAL22721	(4072743..4073441)	1.000	0.101	0.905	0.173	0.905	0.384	0.040	0.489	0.013	1.273	putative permease
atpC	STM3864	AAL22722	(4073671..4074090)	6.486	1.174	11.344	1.752	1.749	2.396	0.161	5.138	0.556	2.144	membrane-bound ATP synthase, F1 sector, epsilon-subunit
atpD	STM3865	AAL22723	(4074111..4075493)	7.672	1.670	28.871	0.596	3.763	3.871	0.167	12.825	1.497	3.313	membrane-bound ATP synthase, F1 sector, beta-subunit
atpG	STM3866	AAL22724	(4075520..4076383)	8.442	1.337	31.288	2.084	3.706	4.931	0.227	10.919	1.017	2.214	membrane-bound ATP synthase, F1 sector, gamma-subunit
atpA	STM3867	AAL22725	(4076434..4077975)	16.067	2.436	52.096	8.663	3.242	9.236	0.356	21.503	1.368	2.328	membrane-bound ATP synthase, F1 sector, alpha-subunit
atpH	STM3868	AAL22726	(4077988..4078521)	14.342	1.829	51.301	7.875	3.577	7.844	0.975	17.127	1.171	2.183	membrane-bound ATP synthase, F1 sector, delta-subunit
atpF	STM3869	AAL22727	(4078536..4079006)	25.626	3.066	61.127	3.919	2.385	12.978	0.611	26.001	0.762	2.003	membrane-bound ATP synthase, F0 sector, subunit b
atpE	STM3870	AAL22728	(4079066..4079305)	35.128	2.027	35.498	1.676	1.011	15.456	1.130	20.664	1.748	1.337	membrane-bound ATP synthase, F0 sector, subunit c

atpB	STM3871	AAL22729	(4079352..4080167)	22.871	1.601	17.631	1.980	0.771	9.481	0.578	11.167	0.910	1.178	membrane-bound ATP synthase, F0 sector, subunit a, important for FO assembly
atpI	STM3872	AAL22730	(4080176..4080556)	24.399	0.820	6.185	0.809	0.253	9.707	1.315	4.799	0.288	0.494	membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase
gidB	STM3873	AAL22731	(4081172..4081795)	1.290	0.113	1.267	0.166	0.983	0.760	0.029	0.931	0.061	1.225	associate with glucose-inhibited division
gidA	STM3874	AAL22732	(4081898..4083787)	1.391	0.104	1.107	0.167	0.796	1.395	0.138	1.113	0.122	0.798	associate with glucose-inhibited division
mioC	STM3875	AAL22733	(4084166..4084609)	8.465	1.442	1.324	0.083	0.156	3.537	0.329	1.440	0.072	0.407	initiation of chromosome replication
asnC	STM3876	AAL22734	(4084699..4085157)	0.957	0.048	0.565	0.109	0.590	0.418	0.046	0.513	0.025	1.229	transcriptional regulator (AsnC family) for asnA, gidA
asnA	STM3877	AAL22735	4085308..4086300	0.967	0.049	0.603	0.028	0.624	0.495	0.091	0.663	0.051	1.338	asparagine synthetase A
yieM	STM3878	AAL22736	(4086305..4087729)	0.733	0.043	0.498	0.047	0.679	0.358	0.010	0.601	0.073	1.680	putative inner membrane protein
yieN	STM3879	AAL22737	(4087750..4089246)	0.994	0.028	0.986	0.094	0.993	0.476	0.011	0.959	0.033	2.015	paral putative regulator protein
kup	STM3880	AAL22738	4089594..4091462	0.627	0.147	0.425	0.021	0.678	0.399	0.069	0.370	0.059	0.928	KUP family, potassium transport system, low affinity
rbsD	STM3881	AAL22739	4091659..4092078	2.999	0.186	0.373	0.041	0.124	0.238	0.017	0.702	0.075	2.951	D-ribose high-affinity transport system; membrane-associated protein
rbsA	STM3882	AAL22740	4092086..4093591	1.068	0.137	0.297	0.029	0.278	0.171	0.026	0.545	0.061	3.184	ABC superfamily (atp_bind), D-ribose high-affinity transport protein
rbsC	STM3883	AAL22741	4093597..4094562	1.926	0.066	0.875	0.079	0.454	0.395	0.011	0.751	0.055	1.901	ABC superfamily (membrane), D-ribose high-affinity transport protein (1st module, ATP-binding subunit)
rbsB	STM3884	AAL22742	4094587..4095477	4.252	0.611	4.966	0.699	1.168	0.863	0.009	1.999	0.300	2.315	ABC superfamily (peri_perm), D-ribose transport protein
rbsK	STM3885	AAL22743	4095611..4096540	2.914	0.224	4.086	0.750	1.402	0.604	0.024	1.344	0.049	2.224	ribokinase
rbsR	STM3886	AAL22744	4096544..4097542	1.496	0.051	1.764	0.144	1.179	0.374	0.016	0.801	0.062	2.140	transcriptional repressor for rbs operon (GalR/LacI family)
yieO	STM3887	AAL22745	(4097508..4098935)	1.512	0.056	0.566	0.103	0.375	0.541	0.035	0.441	0.050	0.815	putative MFS family tranport protein (1st mdule)
yieP	STM3888	AAL22746	(4098947..4099651)	1.940	0.067	1.651	0.262	0.851	1.746	0.629	1.468	0.394	0.841	putative regulatory protein, gntR family
gltU	STM3890						N/A					N/A		
aspT	STM3895						N/A					N/A		
trpT	STM3896						N/A					N/A		
yifA	STM3897	AAL22747	(4105545..4106393)	5.125	0.734	2.817	0.181	0.550	3.046	0.104	3.266	0.508	1.072	putative transcriptional regulator, LysR family
yifE	STM3898	AAL22748	4106500..4106838	5.485	0.566	3.816	0.465	0.696	4.912	0.457	5.100	0.962	1.038	putative LysR type transcriptional regulator with pssR
yifB	STM3899	AAL22749	(4106863..4108383)	2.846	0.645	0.535	0.140	0.188	3.958	3.360	0.941	0.151	0.238	putative magnesium chelatase, subunit ChlI
ilvL	STM3900	AAL22750	4108735..4108833	5.728	0.792	1.339	0.336	0.234	5.579	0.472	2.700	1.600	0.484	ilvGEDA operon leader peptide
ilvG	STM3901	AAL22751	4108973..4110619	1.591	0.129	0.483	0.047	0.304	1.328	0.299	0.807	0.161	0.608	acetolactate synthase II, large subunit, fragment 1, cryptic
ilvM	STM3902	AAL22752	4110619..4110879	4.137	0.936	1.236	0.221	0.299	4.169	0.919	1.987	0.492	0.477	acetolactate synthase II, small subunit

ilvE	STM3903	AAL22753	4110897..4111826	3.847	0.505	2.121	0.401	0.551	5.551	4.462	2.171	0.223	0.391	branched-chain amino-acid aminotransferase
ilvD	STM3904	AAL22754	4111987..4113837	1.401	0.055	1.432	0.211	1.022	1.147	0.278	1.432	0.206	1.249	dihydroxyacid dehydratase
ilvA	STM3905	AAL22755	4113840..4115384	2.942	0.289	1.643	0.178	0.558	1.873	0.046	1.710	0.379	0.913	threonine deaminase
STM3906	STM3906	AAL22756	4115668..4115985	3.784	1.051	1.253	0.301	0.331	4.365	2.292	2.221	0.708	0.509	putative cytoplasmic protein
STM3907	STM3907	AAL22757	4115982..4116323	7.904	0.993	1.419	0.318	0.179	5.187	2.905	2.885	0.876	0.556	putative cytoplasmic protein
ilvY	STM3908	AAL22758	(4116326..4117213)	1.302	0.097			0.000	0.461	0.019			0.000	positive regulator for ilvC (LysR family)
ilvC	STM3909	AAL22759	4117377..4118852	1.904	0.141	1.548	0.213	0.813	2.342	0.138	3.313	0.550	1.415	ketol-acid reductoisomerase
ppiC	STM3910	AAL22760	(4118944..4119225)	6.689	1.102	1.446	0.091	0.216	3.376	0.197	1.643	0.134	0.487	peptidyl-prolyl cis-trans isomerase C (rotamase C)
STM3911	STM3911	AAL22761	4119514..4119663	0.740	0.130	0.352	0.073	0.476	0.624	0.307	0.484	0.040	0.776	putative inner membrane protein
rep	STM3912	AAL22762	4119763..4121787	1.870	0.255	0.913	0.199	0.488	1.959	0.075	0.953	0.228	0.486	rep helicase, a single-stranded DNA dependent ATPase
gppA	STM3913	AAL22763	(4121827..4123308)					N/A					N/A	guanosine pentaphosphatase and exopolyphosphatase
rhlB	STM3914	AAL22764	(4123427..4124692)					N/A					N/A	putative helicase
trxA	STM3915	AAL22765	4124836..4125165	26.471	4.185	9.463	1.547	0.357	12.327	1.695	8.541	0.275	0.693	thioredoxin 1, redox factor
rhoL	STM3916; pseudogene; no in-frame start								N/A					N/A
rho	STM3917	AAL22766	4125584..4126843	9.233	0.578	7.641	1.524	0.828	5.864	0.825	4.803	0.509	0.819	transcription termination factor Rho; polarity suppressor
rfe	STM3918	AAL22767	4127073..4128176	7.496	0.864	1.458	0.196	0.194	5.530	0.435	2.099	0.173	0.379	undecaprenyl-phosphate N-acetylglucosaminyltransferase
wzzE	STM3919	AAL22768	4128188..4129234	9.710	2.971	2.067	0.337	0.213	6.084	2.041	3.559	0.289	0.585	modulator of enterobacterial common antigen (ECA) polysaccharide chain length
wecB	STM3920	AAL22769	4129290..4130420	8.170	1.446	2.684	0.418	0.328	6.228	1.204	3.303	0.023	0.530	UDP-N-acetyl glucosamine -2-epimerase
wecC	STM3921	AAL22770	4130417..4131679	7.978	1.241	3.785	0.941	0.474	6.135	2.455	5.228	0.498	0.852	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
rffG	STM3922	AAL22771	4131679..4132746	9.491	1.178	3.424	0.328	0.361	7.198	2.890	3.834	0.282	0.533	dTDP-glucose 4,6-dehydratase
rffH	STM3923	AAL22772	4132779..4133003	8.190	0.605	3.018	0.269	0.369	7.345	0.380	3.458	0.243	0.471	glucose-1-phosphate thymidyl transferase
wecD	STM3924	AAL22773	4133110..4133658	6.253	1.177	2.829	0.374	0.452	4.704	1.304	4.032	0.103	0.857	lipopolysaccharide biosynthesis protein
wecE	STM3925	AAL22774	4133663..4134793	7.713	0.968	2.980	1.322	0.386	6.592	3.115	5.103	0.779	0.774	TDP-4-oxo-6-deoxy-D-glucose transaminase
wzxE	STM3926	AAL22775	4134795..4136045	5.982	0.967	1.346	0.188	0.225	5.411	1.664	2.189	0.238	0.405	O-antigen translocase in LPS biosyntesis
STM3927	STM3927	AAL22776	4136042..4137121	4.466	0.527	1.371	0.154	0.307	4.373	0.367	2.467	0.218	0.564	putative inner membrane protein
wecF	STM3928	AAL22777	4137118..4138476	2.850	0.256	0.830	0.130	0.291	2.537	0.332	2.141	0.135	0.844	TDP-Fuc4NAc:lipidII transferase
wecG	STM3929	AAL22778	4138473..4139213	5.548	0.817	0.987	0.215	0.178	4.422	2.311	1.937	0.467	0.438	putative UDP-N-acetyl-D-mannosaminuronic acid transferase
yifK	STM3930	AAL22779	4139420..4140805	4.237	0.577	0.743	0.084	0.175	3.101	0.816	1.039	0.065	0.335	putative APC family, amino-acid transport protein, permease protein
argX	STM3931						N/A					N/A		

hisR	STM3932						N/A					N/A		
leuT	STM3933						N/A					N/A		
proM	STM3934						N/A					N/A		
hemY	STM3935	AAL22780	(4141922..4143121)					N/A					N/A	a late step of protoheme IX synthesis
hemX	STM3936	AAL22781	(4143121..4144290)	8.728	0.624	5.947	0.349	0.681	4.597	0.804	3.980	0.150	0.866	uroporphyrinogen III methylase
hemD	STM3937	AAL22782	(4144312..4145052)	12.245	1.787	4.009	0.628	0.327	7.468	3.180	3.785	0.289	0.507	uroporphyrinogen III synthase
hemC	STM3938	AAL22783	(4145049..4146005)	13.828	1.726	4.433	1.025	0.321	6.299	2.280	4.430	0.606	0.703	porphobilinogen deaminase (hydroxymethylbilane synthase)
cyaA	STM3939	AAL22784	4146367..4148913	3.978	0.377	1.339	0.150	0.337	3.177	0.890	1.672	0.223	0.526	adenylate cyclase
STM3940	STM3940	AAL22785	4149021..4149374	3.493	0.907	0.748	0.134	0.214	3.594	0.520	1.194	0.147	0.332	putative inner membrane protein
STM3941	STM3941	AAL22786	4149560..4150102	3.064	0.533	0.950	0.324	0.310	6.481	4.097	1.966	0.259	0.303	putative inner membrane protein
STM3942	STM3942	AAL22787	4150114..4150476	2.636	0.322	0.972	0.189	0.369	2.977	0.868	1.987	0.442	0.667	putative cytoplasmic protein
cyaY	STM3943	AAL22788	(4150547..4150867)	3.631	0.584	2.000	0.198	0.551	2.636	0.416	1.878	0.505	0.712	putative Frataxin family transport protein
STM3944	STM3944	AAL22789	(4150937..4151326)	3.244	0.894	0.920	0.114	0.284	3.258	0.400	1.422	0.270	0.437	putative inner membrane protein
STM3945	STM3945	pseudogene; 2 frameshifts		0.531	0.113	0.375	0.023	0.705	0.279	0.098	0.247	0.052	0.886	
yifL	STM3946	AAL22790	4152022..4152225	4.978	0.430	2.510	0.370	0.504	8.143	8.051	2.347	0.262	0.288	putative outer membrane lipoprotein
dapF	STM3947	AAL22791	4152259..4153086	4.685	1.020	2.181	0.321	0.465	2.753	0.137	2.162	0.113	0.785	diaminopimelate epimerase
yigA	STM3948	AAL22792	4153083..4153790	11.317	1.252	3.021	0.544	0.267	6.154	1.320	3.346	0.362	0.544	putative cytoplasmic protein
xerC	STM3949	AAL22793	4153787..4154689	5.326	0.543	1.508	0.163	0.283	4.173	1.072	1.684	0.099	0.404	putative integrase/recombinase, site-specific
yigB	STM3950	AAL22794	4154689..4155405	5.204	0.847	1.301	0.113	0.250	4.445	1.787	1.676	0.150	0.377	putative hydrolase of the HAD superfamily
uvrD	STM3951	AAL22795	4155541..4157703	2.465	0.219	0.908	0.113	0.368	2.397	0.825	1.378	0.089	0.575	DNA-dependent ATPase I and helicase II
corA	STM3952	AAL22796	4158175..4159125	4.201	1.418	1.980	0.300	0.471	3.394	1.298	1.713	0.252	0.505	MIT family, Mg2+/Ni2+/Co2+ transport protein (Mg transport system I)
yigF	STM3953	AAL22797	(4159174..4159554)	3.389	1.450	0.727	0.078	0.215	4.643	1.134	1.273	0.174	0.274	putative inner membrane protein
yigG	STM3954	AAL22798	(4159570..4160028)	3.433	1.153	0.944	0.068	0.275	5.838	1.522	1.702	0.392	0.292	putative inner membrane protein
rarD	STM3955	AAL22799	(4160063..4160947)	5.062	1.140	1.038	0.111	0.205	3.240	0.701	1.717	0.137	0.530	chloramphenicol resistance
yigI	STM3956	AAL22800	(4160991..4161476)	11.078	2.983	2.182	0.398	0.197	5.794	6.632	2.376	0.334	0.410	putative protein PaaI, possibly involved in aromatic ounds catabolism
pldA	STM3957	AAL22801	4161623..4162492	4.302	1.061	2.034	0.236	0.473	3.370	1.752	1.081	0.135	0.321	outer membrane phospholipase A
recQ	STM3958	AAL22802	4162558..4164405	2.868	0.305	1.294	0.064	0.451	3.610	0.831	1.442	0.156	0.400	ATP-dependent DNA helicase
rhtC	STM3959	AAL22803	4164469..4165089	3.430	1.107	0.660	0.069	0.192	2.528	1.038	1.053	0.108	0.417	RhtB family, threonine efflux protein
rthB	STM3960	AAL22804	(4165129..4165749)	4.779	2.361	0.602	0.097	0.126	3.170	2.580	0.877	0.130	0.277	homoserine/homoserine lactone efflux protein
pldB	STM3961	AAL22805	4165860..4166876	5.234	0.811	1.348	0.196	0.258	4.443	1.050	1.173	0.061	0.264	lysophospholipase L(2)
yigL	STM3962	AAL22806	4166892..4167692	4.340	0.740	1.075	0.060	0.248	4.171	0.604	1.391	0.156	0.333	putative hydrolase of the HAD superfamily
yigM	STM3963	AAL22807	4167773..4168672	3.303	1.063	0.545	0.063	0.165	2.283	0.333	0.858	0.120	0.376	paral putative transport protein
metR	STM3964	AAL22808	(4168560..4169513)	4.346	2.388	0.742	0.101	0.171	3.265	1.184	1.121	0.139	0.343	regulator for metE and metH (LysR family)
metE	STM3965	AAL22809	4169762..4172026	1.883	0.631	0.451	0.025	0.239	2.218	0.707	0.567	0.073	0.256	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase

STM3966	STM3966	AAL22810	4172370..4173713	2.529	0.535	0.593	0.034	0.235	4.154	2.387	0.925	0.106	0.223	putative arylsulfatase regulator
dlhH	STM3967	AAL22811	(4173793..4174605)	5.350	1.217	1.212	0.180	0.227	3.419	1.257	2.613	0.185	0.764	putative dienelactone hydrolase family
udp	STM3968	AAL22812	4174864..4175625	9.165	3.452	4.178	0.418	0.456	4.365	1.704	5.671	0.277	1.299	uridine phosphorylase
yigN	STM3969	AAL22813	4175765..4177195	3.068	0.765	1.046	0.114	0.341	3.662	1.061	0.896	0.084	0.245	putative inner membrane protein
ubiE	STM3970	AAL22814	4177291..4178046	6.117	0.637	3.590	0.286	0.587	6.068	1.120	2.379	0.158	0.392	S-adenosylmethionine : 2-DMK methyltransferase and 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase
yigP	STM3971	AAL22815	4178056..4178661	4.857	0.360	3.548	0.740	0.731	3.547	1.226	3.609	0.510	1.017	putative inner membrane protein
aarF	STM3972	AAL22816	4178658..4180298	4.291	0.559	2.664	0.267	0.621	3.642	0.701	2.411	0.408	0.662	putative regulator in ubiquinone biosynthesis
tatA	STM3973	AAL22817	4180504..4180758	11.001	1.457	6.813	1.241	0.619	7.253	0.789	6.987	1.781	0.963	onent of Sec-independent protein secretion pathway
tatB	STM3974	AAL22818	4180762..4181310	4.510	0.405	6.417	0.505	1.423	2.977	0.268	4.153	0.206	1.395	onent of Sec-independent protein secretion pathway
tatC	STM3975	AAL22819	4181313..4182092	5.873	0.322	3.331	0.181	0.567	5.629	1.421	2.879	0.441	0.512	part of sec-independent protein export, integral membrane protein
yigW	STM3976	AAL22820	4182134..4182916	2.197	0.313	1.161	0.230	0.528	1.715	0.829	1.206	0.290	0.703	putative hydrolase of PHP superfamily
rfaH	STM3977	AAL22821	(4182924..4183412)	4.350	0.551	2.094	0.267	0.481	2.991	0.041	2.517	0.846	0.842	transcriptional activator affecting biosynthesis of lipopolysaccharide core, F pilin, and haemolysin
yigC	STM3978	AAL22822	4183598..4185076	10.141	1.132	5.893	1.237	0.581	5.383	1.068	3.221	1.235	0.598	putative oxidoreductase
ubiB	STM3979	AAL22823	4185162..4185863	11.245	0.817	5.436	0.257	0.483	6.683	1.078	4.351	0.576	0.651	FMN reductase
STM3980	STM3980	AAL22824	4186117..4186830	2.794	0.231	1.040	0.208	0.372	3.250	0.777	2.422	0.846	0.745	putative outer membrane protein
STM3981	STM3981	AAL22825	4186882..4187940	1.866	0.335	0.642	0.092	0.344	2.548	0.034	2.138	0.698	0.839	putative cytoplasmic protein
fadA	STM3982	AAL22826	(4188137..4189300)	3.751	0.661	3.287	0.655	0.876	2.442	0.632	2.178	0.918	0.892	3-ketoacyl-CoA thiolase; (thiolase I, acetyl-CoA transferase), in lex with FadB catalyzes EC 2.3.1.16 reaction
fadB	STM3983	AAL22827	(4189310..4191499)	5.324	0.865	8.912	0.468	1.674	2.263	1.090	2.286	0.411	1.010	3-hydroxyacyl-coA dehydrogenase (EC 1.1.1.35) of 4-enzyme FadB protein
pepQ	STM3984	AAL22828	4191689..4193020	3.767	0.209	3.367	0.681	0.894	2.821	1.152	2.376	0.311	0.842	proline dipeptidase
yigZ	STM3985	AAL22829	4193020..4193634	4.622	0.438	1.875	0.212	0.406	3.614	1.392	2.111	0.532	0.584	putative cytoplasmic protein
trkH	STM3986	AAL22830	4193673..4195124	3.639	0.366	1.444	0.389	0.397	3.095	0.343	1.433	0.313	0.463	Trk family, potassium transport protein, requires TrkE
hemG	STM3987	AAL22831	4195136..4195681	6.883	0.481	4.574	0.459	0.665	23.112	7.077	4.051	0.120	0.175	protoporphyrin oxidase
ileT	STM3989		14.977	0.780	12.156	2.628	0.812	58.051	15.356	28.452	3.940	0.490		
alaT	STM3990						N/A					N/A		
mobB	STM3993	AAL22832	(4201684..4202199)	1.166	0.093	1.653	0.241	1.417	1.256	0.428	1.536	0.221	1.223	molybdopterin-guanine dinucleotide biosynthesis protein B, GTP-binding
mobA	STM3994	AAL22833	(4202196..4202780)	1.046	0.049	1.194	0.120	1.142	0.667	0.145	1.209	0.230	1.814	putative molybdopterin-guanine dinucleotide biosynthesis protein
yihD	STM3995	AAL22834	4202850..4203119	1.776	0.134	2.946	0.333	1.659	0.974	0.117	1.599	0.121	1.642	putative cytoplasmic protein

yihE	STM3996	AAL22835	4203196..4204182	2.805	0.093	1.524	0.226	0.543	2.746	0.236	1.406	0.104	0.512	putative homoserine kinase type II, protein kinase
dsbA	STM3997	AAL22836	4204199..4204822	5.620	0.435	4.237	0.155	0.754	4.636	0.133	3.657	0.182	0.789	periplasmic protein disulfide isomerase I
yihG	STM3998	AAL22837	(4204835..4205743)	1.262	0.154	0.666	0.113	0.528	0.883	0.129	0.796	0.176	0.902	putative endonuclease
polA	STM3999	AAL22838	4206131..4208917	1.703	0.031	2.758	0.122	1.620	0.602	0.105	0.972	0.052	1.616	DNA polymerase I, 3' --> 5' polymerase, 5' --> 3' and 3' --> 5' exonuclease
spf	STM4000	AAL22839	4209084..4209131	3.446	0.523	2.803	0.303	0.813	3.042	0.680	2.427	0.603	0.798	spot 42 RNA, inhibition of DNA synthesis
yihA	STM4001	AAL22840	(4209252..4209884)	2.298	0.051	1.236	0.145	0.538	0.997	0.028	0.938	0.053	0.940	putative GTPase, involved in coordination of cell cycle
STM4002	STM4002	AAL22841	4210124..4210348	7.560	3.739	6.771	0.541	0.896	17.876	6.158	5.835	1.213	0.326	putative cytoplasmic protein
yihI	STM4003	AAL22842	4210467..4210982	1.719	0.042	1.854	0.203	1.079	1.809	0.260	1.782	0.080	0.985	putative cytoplasmic protein
hemN	STM4004	AAL22843	4211171..4212544	2.261	0.148	1.643	0.318	0.726	1.879	0.058	1.109	0.014	0.590	O2-independent coproporphyrinogen III oxidase
glnG	STM4005	AAL22844	(4212857..4214266)	0.514	0.163	0.703	0.091	1.367	0.280	0.007	0.640	0.254	2.284	response regulator in two-onent regulatory system with GlnL (EBP family)
glnL	STM4006	AAL22845	(4214275..4215324)	0.717	0.159	0.766	0.195	1.068	0.458	0.102	0.568	0.177	1.241	sensory kinase (phosphatase) in two-onent regulatory system with GlnG (nitrogen regulator II, NRII)
glnA	STM4007	AAL22846	(4215599..4217008)	1.403	0.201	3.076	0.504	2.192	1.130	0.061	1.192	0.067	1.055	glutamine synthetase
STM4008	STM4008	AAL22847	(4216987..4217415)	2.096	0.241	1.856	0.248	0.886	1.912	0.498	0.921	0.066	0.482	putative cytoplasmic protein
typA	STM4009	AAL22848	4217384..4219207	3.585	0.145	3.858	0.275	1.076	3.846	0.096	2.620	0.146	0.681	GTP-binding elongation factor family protein
STM4010	STM4010	AAL22849	(4219262..4219996)	0.475	0.151	0.316	0.074	0.665	0.351	0.049	0.358	0.019	1.019	putative hydrolase
STM4011	STM4011	AAL22850	(4219981..4220859)	0.304	0.153	0.190	0.034	0.624	0.287	0.075	0.343	0.031	1.194	putative inner membrane protein
STM4012	STM4012	AAL22851	(4220856..4222097)	0.289	0.195	0.130	0.035	0.448	0.422	0.054	0.428	0.007	1.016	putative coproporphyrinogen III oxidase and related FeS oxidoreductases
STM4013	STM4013	AAL22852	(4222099..4222974)	0.256	0.178	0.164	0.003	0.640	0.635	0.100	0.540	0.103	0.851	putative membrane-associated, metal-dependent hydrolase
STM4014	STM4014	AAL22853	(4222967..4223992)	0.272	0.142	0.121	0.007	0.444	0.289	0.006	0.306	0.028	1.057	putative periplasmic protein
STM4015	STM4015	AAL22854	(4224005..4224853)	0.217	0.175	0.169	0.015	0.780	0.194	0.047	0.336	0.022	1.730	putative cytoplasmic protein
yshA	STM4016	AAL22855	(4225010..4225702)	0.241	0.181	0.145	0.046	0.601	0.390	0.070	0.461	0.066	1.182	putative outer membrane protein
yihO	STM4017	AAL22856	(4225770..4227191)	0.245	0.180	0.120	0.026	0.490	0.264	0.028	0.253	0.003	0.958	putative GPH family transport protein
yihP	STM4018	AAL22857	(4227237..4228619)	0.333	0.153	0.211	0.028	0.636	0.181	0.029	0.281	0.016	1.550	putative GPH family transport protein
yihQ	STM4019	AAL22858	(4228665..4230701)	0.328	0.182			0.000	0.919	0.158			0.000	putative alpha-xylosidase
yihR	STM4020	AAL22859	(4230745..4231602)	0.744	0.137	0.343	0.040	0.461	0.489	0.069	0.497	0.042	1.016	putative aldose-1-epimerase
yihS	STM4021	AAL22860	(4231606..4232847)	0.466	0.162	0.285	0.040	0.611	0.209	0.087	0.332	0.079	1.586	putative isomerase
yihT	STM4022	AAL22861	(4232863..4233741)	0.255	0.196	0.166	0.036	0.651	0.413	0.341	0.363	0.037	0.879	putative aldolase
yihU	STM4023	AAL22862	(4233764..4234660)	0.302	0.205	0.135	0.028	0.447	0.207	0.015	0.256	0.015	1.237	putative oxidoreductase
yihV	STM4024	AAL22863	4234825..4235721	0.783	0.176	0.341	0.048	0.436	0.291	0.031	0.419	0.017	1.442	putative sugar kinase
yihW	STM4025	AAL22864	4235755..4236558	3.249	0.229	1.621	0.075	0.499	1.111	0.209	1.259	0.170	1.132	putative glycerol-3-phosphate regulon repressor (DeoR family)

yihX	STM4026	AAL22865	4236749..4237348	2.867	0.189	2.626	0.114	0.916	5.184	0.621	10.790	0.265	2.081	paral putative enzyme
rbn	STM4027	AAL22866	4237342..4238214	1.106	0.040	1.509	0.287	1.364	1.835	0.146	4.637	0.073	2.527	tRNA processing exoribonuclease BN
yihZ	STM4028	AAL22867	4238211..4238648	2.074	0.279	1.885	0.256	0.909	2.269	0.258	4.573	0.396	2.016	D-Tyr-tRNA(Tyr) deacylase
yiiD	STM4029	AAL22868	4238645..4239634	1.702	0.201	1.558	0.153	0.916	1.994	0.409	2.678	0.075	1.343	putative acetyltransferase
STM4030	STM4030	AAL22869	(4239649..4240095)	1.007	0.027	0.823	0.085	0.818	0.952	0.048	1.156	0.049	1.214	putative cytoplasmic protein
STM4031	STM4031	AAL22870	(4240092..4240403)	0.865	0.067	0.794	0.185	0.918	0.584	0.045	0.823	0.115	1.410	putative cytoplasmic protein
STM4032	STM4032	AAL22871	(4240489..4241418)	1.007	0.117	0.603	0.074	0.599	0.675	0.095	0.746	0.052	1.106	putative acetyl esterase
STM4033	STM4033	AAL22872	4241984..4242238	1.029	0.094	1.161	0.237	1.128	0.593	0.186	0.907	0.077	1.530	putative bacterial regulatory protein, merR family
fdhE	STM4034	AAL22873	(4242285..4243214)	3.630	0.572	4.031	0.315	1.110	1.623	0.168	2.523	0.147	1.554	putative formate dehydrogenase formation protein ? Mn_fn
fdoI	STM4035	AAL22874	(4243211..4243846)	8.880	1.890	6.405	1.227	0.721	3.541	0.878	3.508	0.443	0.991	formate dehydrogenase, cytochrome B556 (FDO) subunit
fdoH	STM4036	AAL22875	(4243843..4244745)	9.268	1.767	15.480	0.432	1.670	3.973	0.780	7.239	0.664	1.822	formate dehydrogenase-O, Fe-S subunit
fdoG	STM4037	AAL22876	(4244758..4247808)	6.936	2.099	19.705	4.049	2.841	2.233	0.568	5.717	1.580	2.560	formate dehydrogenase
fdhD	STM4038	AAL22877	4248003..4248839	1.238	0.086	1.710	0.292	1.381	0.816	0.012	0.944	0.072	1.157	putative formate dehydrogenase formation protein
STM4039	STM4039	AAL22878	(4249107..4250138)	0.362	0.122	0.490	0.079	1.354	0.654	0.036	0.573	0.084	0.877	putative inner membrane lipoprotein
yiiG	STM4040	AAL22879	4250363..4251421	0.953	0.133	0.125	0.018	0.131	0.574	0.238	0.288	0.022	0.501	putative cytoplasmic protein
STM4041	STM4041	AAL22880	(4251776..4252099)	1.058	0.039	0.171	0.014	0.161	0.428	0.017	0.538	0.050	1.255	putative inner membrane protein
STM4042	STM4042	AAL22881	(4252099..4252758)	2.362	0.086	0.467	0.034	0.198	0.788	0.138	0.836	0.125	1.061	putative branched-chain amino acid permease
STM4042A	STM4042A	AAL22882	4252841..4253407					N/A					N/A	hypothetical protein
yiiL	STM4043	AAL22883	(4253496..4253810)	1.272	0.059	1.048	0.179	0.824	0.398	0.046	0.467	0.071	1.173	putative cytoplasmic protein
STM4044	STM4044	AAL22884	(4253807..4254955)	0.669	0.136	1.241	0.118	1.855	0.208	0.047	0.384	0.024	1.846	putative iron-containing alcohol dehydrogenase
rhaD	STM4045	AAL22885	(4255082..4255909)	0.567	0.120	0.283	0.041	0.498	0.165	0.043	0.241	0.028	1.457	rhamnulose-1-phosphate aldolase
rhaA	STM4046	AAL22886	(4256052..4257311)	0.346	0.197	0.182	0.031	0.528	0.164	0.030	0.356	0.084	2.170	L-rhamnose isomerase
rhaB	STM4047	AAL22887	(4257308..4258777)	0.245	0.169	0.149	0.039	0.609	0.107	0.026	0.231	0.018	2.162	rhamnulokinase
rhaS	STM4048	AAL22888	4259065..4259901	0.404	0.137	0.448	0.089	1.108	0.207	0.063	0.390	0.022	1.887	positive regulator for rhaBAD operon (AraC/XylS family)
rhaR	STM4049	AAL22889	4260054..4260902	0.434	0.148	0.682	0.091	1.572	0.130	0.033	0.332	0.015	2.557	positive regulator for rhaRS operon (AraC/XylS familiy)
rhaT	STM4050	AAL22890	(4260899..4261933)	0.385	0.218	0.418	0.105	1.084	0.249	0.025	0.309	0.041	1.240	DMT Superfamily, L-rhamnose:H+ symporter protein
STM4051	STM4051	AAL22891	4262552..4263235	0.242	0.176	0.135	0.011	0.560	0.412	0.067	0.385	0.015	0.937	putative outer membrane protein
STM4052	STM4052	AAL22892	(4263393..4264700)	0.352	0.222	0.211	0.065	0.599	0.170	0.022	0.233	0.028	1.371	putative C4-dicarboxylate transport system
STM4053	STM4053	AAL22893	(4264693..4265208)	0.368	0.199	0.268	0.010	0.730	0.239	0.036	0.224	0.025	0.935	putative C4-dicarboxylate transport system
STM4054	STM4054	AAL22894	(4265227..4266210)	0.481	0.126	0.145	0.016	0.302	0.210	0.036	0.321	0.061	1.525	putative dicarboxylate-binding periplasmic protein
sodA	STM4055	AAL22895	4266539..4267159	23.912	2.422	1.394	0.057	0.058	7.190	1.123	6.619	0.345	0.921	superoxide dismutase, manganese

yiiM	STM4056	AAL22896	4267166..4267918	1.563	0.032	1.618	0.168	1.035	0.787	0.002	1.115	0.053	1.417	putative cytoplasmic protein
STM4057	STM4057	AAL22897	4267930..4268325	1.668	0.207	1.822	0.223	1.092	0.760	0.136	0.808	0.075	1.063	putative inner membrane protein
xA	STM4058	AAL22898	(4268376..4269749)	3.170	0.309	2.280	0.439	0.719	2.963	1.602	1.891	0.165	0.638	sensory kinase in two-onent regulatory system with xR, senses misfolded proteins in bacterial envelope
xR	STM4059	AAL22899	(4269746..4270444)	6.179	1.346	3.379	0.436	0.547	10.048	0.213	4.380	0.510	0.436	response reguator in two-onent regulatory system with xA, regulates expression of protein folding and degrading factors (OmpR family)
xP	STM4060	AAL22900	4270595..4271095	2.307	0.491	1.592	0.091	0.690	6.472	0.856	1.751	0.098	0.271	periplasmic repressor of x regulon by interaction with xA, rescue from transitory stresses
yiiP	STM4061	AAL22901	4271243..4272145	1.433	0.141	0.927	0.225	0.647	2.047	0.174	1.795	0.127	0.877	putative CDF family transport protein
pfkA	STM4062	AAL22902	4272330..4273292	0.956	0.081	2.782	0.287	2.911	0.994	0.077	3.189	0.161	3.209	6-phosphofructokinase I
sbp	STM4063	AAL22903	4273496..4274485	0.378	0.194	0.320	0.062	0.846	0.667	0.178	0.569	0.032	0.853	ABC superfamily (bind_prot), sulfate transport protein
ushB	STM4064	AAL22904	4274586..4275341	1.234	0.263	1.695	0.179	1.373	5.523	0.166	7.187	0.472	1.301	CDP-diacylglycerol phosphotidylhydrolase
STM4065	STM4065	AAL22905	4275604..4276938	0.528	0.152	0.185	0.029	0.349	1.172	0.248	0.742	0.060	0.633	putative permease of the Na+:galactoside symporter family
STM4066	STM4066	AAL22906	4276949..4277908	0.851	0.115	0.309	0.053	0.364	1.329	0.322	0.906	0.027	0.682	putative sugar kinase, ribokinase family
STM4067	STM4067	AAL22907	4277918..4278958	1.969	0.132	1.014	0.080	0.515	3.416	0.742	2.893	0.165	0.847	putative ADP-ribosylglycohydrolase
STM4068	STM4068	AAL22908	4279021..4279743	2.115	0.177	0.905	0.027	0.428	1.089	0.195	0.986	0.040	0.906	putative regulatory protein, gntR family
STM4069	STM4069	AAL22909	4279841..4280005	0.778	0.156	0.381	0.085	0.489	0.806	0.696	0.430	0.037	0.533	putative periplasmic protein
STM4070	STM4070	AAL22910	4280021..4280152	0.625	0.115	0.577	0.128	0.923	1.296	1.369	1.235	0.056	0.953	putative cytoplasmic protein
STM4071	STM4071	AAL22911	(4280242..4280508)	0.623	0.018	0.682	0.156	1.096	0.423	0.074	0.550	0.054	1.300	putative Mannose-6-phosphate isomerase
ydeV	STM4072	AAL22912	(4280606..4282198)	0.775	0.040	1.329	0.140	1.714	0.445	0.033	0.869	0.024	1.953	putative sugar kinase
ydeW	STM4073	AAL22913	(4282286..4283245)	2.001	0.090	1.487	0.068	0.743	0.792	0.059	0.720		0.909	putative transcriptional repressor
ego	STM4074	AAL22914	4283501..4285036	0.664	0.063	1.648	0.119	2.483	0.150	0.036	0.329	0.018	2.188	putative ABC-type sugar, aldose transport system, ATPase onent
ydeY	STM4075	AAL22915	4285030..4286073	1.044	0.058	0.939	0.159	0.899	0.235	0.023	0.301	0.057	1.282	putative ABC superfamily (membrane), sugar transport protein
ydeZ	STM4076	AAL22916	4286070..4287071	1.242	0.298	0.562	0.086	0.452	0.284	0.032	0.436	0.013	1.535	putative ABC superfamily (membrane), sugar transport protein
yneA	STM4077	AAL22917	4287100..4288122	0.572	0.052	1.037	0.062	1.812	0.308	0.149	0.657	0.017	2.132	putative ABC superfamily (peri_perm), sugar transport protein
yneB	STM4078	AAL22918	4288151..4289026	0.370	0.065	0.884	0.047	2.393	0.963	0.019	1.106	0.068	1.148	putative fructose-1,6-bisphosphate aldolase
yneC	STM4079	AAL22919	4289070..4289399	0.650	0.039	0.776	0.099	1.194	4.049	0.324	4.306	0.182	1.064	putative inner membrane protein
STM4080	STM4080	AAL22920	4289409..4290173	1.352	0.138	1.436	0.195	1.062	4.542	0.227	5.784	0.147	1.273	putative ribulose-5-phosphate 3-epimerase
tpiA	STM4081	AAL22921	(4290265..4291032)	15.832	3.978	15.015	4.007	0.948	5.571	0.973			0.000	triosephosphate isomerase
yiiQ	STM4082	AAL22922	(4291145..4291741)	2.702	0.307	1.623	0.274	0.601	1.017	0.013	1.064	0.126	1.045	putative periplasmic protein
yiiR	STM4083	AAL22923	4291842..4292270	1.339	0.165	0.629	0.087	0.470	0.711	0.071	0.513	0.048	0.722	putative inner membrane protein
fpr	STM4084	AAL22924	(4292377..4293123)	2.865	1.028	1.764	0.164	0.616	0.993	0.091	0.937	0.081	0.944	ferredoxin-NADP reductase

glpX	STM4085	AAL22925	(4293220..4294230)	4.077	0.610	2.875	0.396	0.705	1.286	0.124	0.981	0.070	0.763	unknown function in glycerol metabolism
glpK	STM4086	AAL22926	(4294342..4295850)	1.163	0.483	0.974	0.110	0.838	1.072	0.025	0.871	0.091	0.812	glycerol kinase
glpF	STM4087	AAL22927	(4295871..4296716)	1.906	0.399	6.378	0.821	3.345	0.265	0.022	3.684	0.171	13.890	MIP channel, glycerol diffusion
yiiU	STM4088	AAL22928	4297115..4297354	7.061	0.996	8.285	1.734	1.173	3.016	0.157	5.887	1.160	1.952	putative cytoplasmic protein
menG	STM4089	AAL22929	(4297576..4298061)	12.622	1.462	4.987	1.066	0.395	6.123	1.874	4.054	0.589	0.662	putative methyltransferase in menaquinone biosynthesis protein
menA	STM4090	AAL22930	(4298154..4299083)	1.367	0.125	0.848	0.115	0.620	1.056	0.038	0.943	0.031	0.893	1,4-dihydroxy-2-naphthoate octaprenyltransferase
hslU	STM4091	AAL22931	(4299150..4300481)	1.004	0.114	2.349	0.232	2.339	1.575	0.085	4.926	0.575	3.127	ATPase onent of the HslUV protease
hslV	STM4092	AAL22932	(4300491..4301021)	1.426	0.257	2.889	0.528	2.026	1.914	0.044	5.418	0.162	2.831	peptidase onent of the HslUV protease
ftsN	STM4093	AAL22933	(4301113..4302087)	1.502	0.124	2.642	0.212	1.759	0.858	0.050	1.986	0.171	2.315	essential cell division protein
cytR	STM4094	AAL22934	(4302181..4303206)	1.350	0.081	1.807	0.157	1.339	0.561	0.019	1.203	0.066	2.143	transcriptional repressor (GalR/LacI family)
priA	STM4095	AAL22935	(4303361..4305559)	1.692	0.066	1.274	0.138	0.753	1.212	0.124	1.339	0.131	1.105	primosomal protein N' (= factor Y) directs replication fork assembly at D-loops
rpmE	STM4096	AAL22936	4305763..4305975	9.666	0.750	7.039	1.254	0.728	7.036	1.709	5.894	0.490	0.838	50S ribosomal subunit protein L31
STM4097	STM4097	AAL22937	(4306021..4306683)	0.960	0.047	0.701	0.087	0.731	0.572	0.071	0.458	0.102	0.802	putative outer membrane lipoprotein
STM4098	STM4098	AAL22938	(4306884..4308674)	0.404	0.080	0.180	0.014	0.445	0.428	0.129	0.322	0.048	0.751	putative arylsulfate sulfotransferase
metJ	STM4099	AAL22939	(4309131..4309448)	3.136	0.691	2.491	0.380	0.795	1.396	0.057	1.432	0.120	1.025	transcriptional repressor of all met genes but metF (MetJ family)
metB	STM4100	AAL22940	4309713..4310873	3.286	0.405	0.862	0.108	0.262	1.197	0.240	0.762	0.034	0.637	cystathionine gamma-synthase
metL	STM4101	AAL22941	4310876..4313308					N/A					N/A	aspartokinase II in bifunctional enxyme: aspartokinase II; homoserine dehydrogenase II
STM4102	STM4102	AAL22942	(4313424..4314281)	0.404	0.154	0.165	0.035	0.408	0.538	0.019	0.373	0.028	0.694	putative inner membrane protein
STM4103	STM4103	AAL22943	(4315517..4316641)	0.804	0.104	0.330	0.034	0.410	0.371	0.000	0.620	0.061	1.673	putative cytoplasmic protein
STM4104	STM4104	AAL22944	4316777..4318333	0.453	0.107	0.223	0.027	0.491	0.380	0.030	0.576	0.063	1.514	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase or related esterase
metF	STM4105	AAL22945	4318528..4319418	0.579	0.143	0.583	0.084	1.008	0.279	0.027	0.477	0.096	1.710	5,10-methylenetetrahydrofolate reductase
katG	STM4106	AAL22946	4319583..4321763	0.653	0.106	4.253	0.538	6.512	0.323	0.191	0.579	0.049	1.791	catalase; hydroperoxidase HPI(I)
yijF	STM4107	AAL22947	(4321821..4322444)	0.590	0.256	0.553	0.092	0.937	0.494	0.102	0.202	0.039	0.410	putative periplasmic protein
gldA	STM4108	AAL22948	(4322703..4323806)	1.432	0.106	4.376	0.925	3.055	0.769	0.231	1.173	0.191	1.526	glycerol dehydrogenase, NAD
talC	STM4109	AAL22949	(4323818..4324480)	0.613	0.085	1.720	0.266	2.806	0.286	0.053	0.817	0.040	2.856	putative transaldolase
ptsA	STM4110	AAL22950	(4324491..4326992)	0.382	0.133	0.612	0.065	1.603	0.141	0.013	0.326	0.030	2.314	General PTS family, enzyme I
STM4111	STM4111	pseudogene; frameshift						N/A					N/A	
frwC	STM4112	AAL22951	4327301..4328380	0.344	0.135	0.359	0.029	1.044	0.140	0.031	0.366	0.099	2.617	PTS system fructose-like IIC onent
frwB	STM4113	AAL22952	4328395..4328715	0.601	0.035	0.616	0.008	1.024	0.768	0.057	1.117	0.093	1.455	PTS system fructose-like IIB onent 1
pflD	STM4114	AAL22953	4328814..4331111	0.634	0.112	0.577	0.014	0.910	0.637	0.031	1.146	0.075	1.797	putative pyruvate formate lyase II
pflC	STM4115	AAL22954	4331077..4331955	0.787	0.051	0.534	0.055	0.679	0.669	0.074	0.953	0.083	1.424	putative pyruvate formate lyase activating enzyme 2

frwD	STM4116	AAL22955	4331957..4332310	0.468	0.071	0.415	0.010	0.886	0.301	0.039	0.602	0.067	2.001	PTS system fructose-like IIB onent 2
yijO	STM4117	AAL22956	(4332297..4333148)	0.510	0.103	0.576	0.072	1.128	0.378	0.012	0.598	0.029	1.582	paral putative regulator (AraC/XylS family)
yijP	STM4118	AAL22957	(4333309..4335042)	1.261	0.182	1.338	0.242	1.061	3.872	0.140	3.035	0.162	0.784	putative Integral membrane protein
ppc	STM4119	AAL22958	(4335253..4337904)	0.949	0.030	1.944	0.195	2.048	0.899	0.088	2.444	0.062	2.720	phosphoenolpyruvate carboxylase
argE	STM4120	AAL22959	(4338273..4339424)	1.426	0.149	2.126	0.057	1.490	0.640	0.034	1.688	0.019	2.638	acetylornithine deacetylase
argC	STM4121	AAL22960	4339513..4340517	0.882	0.032	0.647	0.081	0.734	0.582	0.017	1.017	0.033	1.746	N-acetyl-gamma-glutamylphosphate reductase
argB	STM4122	AAL22961	4340525..4341301	1.088	0.051	0.916	0.057	0.842	0.591	0.058	1.546	0.091	2.617	acetylglutamate kinase
argH	STM4123	AAL22962	4341419..4342795					N/A					N/A	argininosuccinate lyase
oxyR	STM4125	AAL22963	4343080..4343997	10.006	1.700	8.141	0.883	0.814	4.954	1.057	4.423	0.148	0.893	regulatory protein sensor for oxidative stress, regulates intracellular hydrogen peroxide (LysR family)
udhA	STM4126	AAL22964	(4343980..4345380)	14.979	0.865	13.345	2.116	0.891	3.600	0.233	4.382	0.361	1.217	soluble pyridine nucleotide transhydrogenase
yijC	STM4127	AAL22965	4345579..4346214	15.433	2.920	4.468	0.638	0.289	3.740	0.652	2.605	0.149	0.697	putative transcriptional repressor (TetR/AcrR family)
yijD	STM4128	AAL22966	4346230..4346589	9.423	0.763	3.260	0.341	0.346	3.452	0.820	2.858	0.218	0.828	putative inner membrane protein
trmA	STM4129	AAL22967	(4346636..4347736)	1.862	0.195	0.962	0.034	0.516	0.948	0.006	0.707	0.063	0.746	tRNA (uracil-5-)-methyltransferase
btuB	STM4130	AAL22968	4348110..4349954	2.579	0.143	3.486	0.213	1.352	0.814	0.076	1.009	0.263	1.239	outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23
murI	STM4131	AAL22969	4349899..4350750	2.911	0.111	3.451	0.883	1.185	3.197	0.852	2.937	0.444	0.919	glutamate racemase
ileU	STM4133						N/A					N/A		
STM4134	STM4134						N/A					N/A		
murB	STM4137	AAL22970	4356672..4357700	2.400	0.177	2.044	0.242	0.852	3.060	0.011	2.232	0.130	0.729	UDP-N-acetylenolpyruvoylglucosamine reductase
birA	STM4138	AAL22971	4357697..4358659	2.818	0.594	1.372	0.170	0.487	2.450	0.062	1.694	0.387	0.691	bifunctional: biotin-[acetylCoA carboxylase] holoenzyme synthetase; biotin operon transcriptional repressor (BirA family)
coaA	STM4139	AAL22972	(4358694..4359644)	2.349	0.152	1.765	0.260	0.751	0.863	0.091	1.084	0.065	1.257	pantothenate kinase
STM4140	STM4140	pseudogene; no in-frame start		2.288	0.325	2.285	0.292	0.999	1.557	0.991	1.338	0.104	0.859	
STM4141	STM4141	AAL22973	(4359853..4360026)	3.886	0.757	4.977	0.281	1.281	2.148	0.433	3.490	0.497	1.624	putative cytoplasmic protein
thrU	STM4142						N/A					N/A		
tyrU	STM4143						N/A					N/A		
glyT	STM4144						N/A					N/A		
thrT	STM4145						N/A					N/A		
tufB	STM4146	AAL22974	4360603..4361787	32.446	1.743	106.579	15.348	3.285	16.331	0.563	39.574	0.784	2.423	protein chain elongation factor EF-Tu (duplicate of tufA)
secE	STM4147	AAL22975	4362017..4362400	7.530	0.707	9.669	1.759	1.284	9.871	0.683	7.763	0.406	0.786	preprotein translocase IISP family, membrane subunit
nusG	STM4148	AAL22976	4362402..4362947	6.472	0.268	8.586	1.032	1.327	6.395	0.073	6.781	0.218	1.060	onent in transcription antitermination
rplK	STM4149	AAL22977	4363105..4363533	18.022	2.729	30.354	1.761	1.684	12.953	0.484	14.250	1.248	1.100	50 S ribosomal subunit protein L11

rplA	STM4150	AAL22978	4363537..4364241	14.190	2.422	22.752	3.143	1.603	10.896	1.516	11.344	0.277	1.041	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11
rplJ	STM4151	AAL22979	4364661..4365158	45.283	3.809	64.726	2.314	1.429	29.955	1.587	21.718	0.942	0.725	50S ribosomal subunit protein L10
rplL	STM4152	AAL22980	4365225..4365590	28.968	1.932	29.041	5.760	1.003	22.378	0.428	14.147	1.358	0.632	50S ribosomal subunit protein L7/L12
rpoB	STM4153	AAL22981	4365908..4369936					N/A					N/A	RNA polymerase, beta subunit
rpoC	STM4154	AAL22982	4370013..4374236					N/A					N/A	RNA polymerase, beta prime subunit
STM4155	STM4155	AAL22983	4374278..4374601	0.510	0.136	0.793	0.294	1.555	0.848	0.056	0.534	0.084	0.629	putative inner membrane protein
STM4156	STM4156	AAL22984	(4374607..4374951)	0.480	0.089	0.661	0.038	1.377	0.920	0.171	0.553	0.077	0.601	putative cytoplasmic protein
STM4157	STM4157	AAL22985	4375350..4376360	0.487	0.153	0.305	0.063	0.627	1.179	0.070	0.958	0.021	0.813	putative cytoplasmic protein
STM4158	STM4158	AAL22986	4376683..4376871	0.470	0.231	0.579	0.091	1.232	0.908	0.011	0.778	0.198	0.856	putative cytoplasmic protein
thiH	STM4159	AAL22987	(4377022..4378155)	0.427	0.123	0.327	0.051	0.765	0.214	0.004	0.306	0.034	1.428	deoxyxylulose-5-P + thi-S-COSH + tyrosine = 4-methyl-5-(beta-hydroxyethyl)thiazole-P + 4-hydroxy-benzyl-alcohol + C1 of tyrosine
thiG	STM4160	AAL22988	(4378152..4378922)	0.558	0.174	0.469	0.029	0.841	0.220	0.014	0.416	0.018	1.895	deoxyxylulose-5-P + thi-S-COSH + tyrosine = 4-methyl-5-(beta-hydroxyethyl)thiazole-P + 4-hydroxy-benzyl-alcohol + C1 of tyrosine
STM4161	STM4161	AAL22989	(4378924..4379124)	0.522	0.186	0.413	0.019	0.791	0.842	0.107	0.423	0.097	0.503	putative involved in thiamine biosynthesis
thiF	STM4162	AAL22990	(4379105..4379863)	0.550	0.079	0.562	0.095	1.023	0.217	0.021	0.703	0.092	3.237	catalyzes the adenylation of thisS as part of thiazole synthesis, also with ThiI it catalyses the transfer of sulfur from cysteine to the ThiS enzyme
thiE	STM4163	AAL22991	(4379856..4380491)	0.511	0.102	0.360	0.054	0.705	0.208	0.078	0.266	0.014	1.276	thiamin phosphate synthase (thiamine phosphate pyrophosphorylase)
thiC	STM4164	AAL22992	(4380491..4382386)	0.675	0.017	0.528	0.108	0.781	0.254	0.154	0.300	0.038	1.183	5'-phosphoryl-5-aminoimidazole = 4-amino-5-hydroxymethyl-2-methylpyrimidine-P
rsd	STM4165	AAL22993	(4382750..4383238)	2.481	0.374	3.017	0.358	1.216	0.486	0.052	0.814	0.081	1.674	regulator of sigma D, has binding activity to the major sigma subunit of RNAP
yjaD	STM4166	AAL22994	4383331..4384104	4.683	0.509	1.414	0.120	0.302	3.212	1.461	1.890	0.282	0.588	putative NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding
hemE	STM4167	AAL22995	4384145..4385209	2.398	0.313	2.519	0.250	1.051	1.064	0.144	1.452	0.049	1.365	uroporphyrinogen decarboxylase
nfi	STM4168	AAL22996	4385219..4385890	2.126	0.174	1.798	0.181	0.845	1.555	0.178	1.561	0.063	1.004	endonuclease V (deoxyinosine 3'endoduclease)
yjaG	STM4169	AAL22997	4385932..4386522	2.667	0.323	3.454	0.444	1.295	1.539	0.196	1.637	0.118	1.063	putative cytoplasmic protein
hupA	STM4170	AAL22998	4386709..4386981	70.130	18.968	41.193	4.100	0.587	34.722	1.932	22.595	1.315	0.651	DNA-binding protein HU-alpha (HU-2)
yjaH	STM4171	AAL22999	4386993..4387685	4.722	0.733	2.706	0.646	0.573	1.950	0.018	1.289	0.049	0.661	putative inner membrane protein
zraP	STM4172	AAL23000	(4387727..4388182)	0.824	0.116	0.629	0.074	0.763	0.367	0.032	0.466	0.016	1.272	zinc-resistance associated protein
hydH	STM4173	AAL23001	4388436..4389833	1.305	0.071	1.209	0.126	0.926	0.309	0.009	0.463	0.060	1.500	sensory kinase in two onent regulatory system with HydG
hydG	STM4174	AAL23002	4389839..4391164	1.844	0.171	1.399	0.238	0.759	0.498	0.055	0.745	0.103	1.495	response regulator in two-onent reguatory system with HydH, regulates hydrogenase 3 activity (EBP family)
purD	STM4175	AAL23003	(4391161..4392450)	1.700	0.232	1.251	0.258	0.736	0.415	0.047	0.939	0.070	2.264	phosphoribosylglycinamide synthetase (GAR synthetase)

purH	STM4176	AAL23004	(4392462..4394051)	1.192	0.208	1.597	0.096	1.340	0.949	0.224	1.338	0.129	1.411	bifunctional: phosphoribosylaminoimidazolecarboxamide formyltransferase; IMP cyclohydrolase
gltV	STM4178						N/A					N/A		
yjaB	STM4181	AAL23005	(4400247..4400684)	2.305	0.257	1.845	0.220	0.800	1.811	0.359	2.178	0.156	1.203	putative acetyltransferase
metA	STM4182	AAL23006	4400841..4401770	0.870	0.041	0.558	0.052	0.641	0.522	0.014	0.669	0.094	1.280	homoserine transsuccinylase
aceB	STM4183	AAL23007	4402039..4403640	0.306	0.139	0.322	0.036	1.052	0.171	0.018	0.484	0.028	2.840	malate synthase A
aceA	STM4184	AAL23008	4403672..4404976	0.652	0.173	0.365	0.065	0.560	0.408	0.019	0.789	0.020	1.930	isocitrate lyase
aceK	STM4185	AAL23009	4405078..4406829	0.351	0.100	0.218	0.015	0.621	0.171	0.018	0.299	0.032	1.747	isocitrate dehydrogenase kinase/phosphatase, also has ATPase activity
STM4186	STM4186	AAL23010	(4406793..4407200)	1.033	0.061	0.757	0.061	0.733	0.356	0.228	0.440	0.083	1.236	putative cytoplasmic protein
iclR	STM4187	AAL23011	(4407211..4408035)	1.677	0.144	0.947	0.151	0.565	0.418	0.039	0.511	0.055	1.221	acetate operon transcriptional repressor (IclR family)
metH	STM4188	AAL23012	4408252..4412022	1.945	0.359	0.904	0.031	0.465	1.076	0.221	1.053	0.053	0.979	B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of metE and metF
yjbB	STM4189	AAL23013	4412289..4413920	1.337	0.167	0.708	0.066	0.530	1.520	0.195	0.837	0.054	0.551	putative PNaS family transport protein
pepE	STM4190	AAL23014	(4413996..4414685)	1.733	0.194	4.128	0.361	2.382	0.488	0.165	1.003	0.067	2.056	(alpha)-aspartyl dipeptidase
STM4191	STM4191	AAL23015	4414757..4414858	0.877	0.346	1.559	0.284	1.778	0.925	0.397	0.791	0.108	0.855	putative cytoplasmic protein
STM4192	STM4192	AAL23016	4414893..4415432	0.827	0.115	2.106	0.208	2.546	0.433	0.055	1.065	0.050	2.458	putative cytoplasmic protein
yjbC	STM4193	AAL23017	4415479..4416348	1.073	0.076	1.638	0.260	1.526	0.481	0.059	0.926	0.079	1.924	putative pseudouridine synthase
yjbD	STM4194	AAL23018	(4416345..4416617)	1.378	0.041	0.944	0.110	0.684	0.550	0.090	0.653	0.035	1.187	putative cytoplasmic protein
STM4195	STM4195	AAL23019	(4416715..4417656)	0.696	0.096	0.345	0.063	0.496	0.583	0.381	0.465	0.060	0.797	putative Na+-dependent transporter
STM4196	STM4196	AAL23020	(4417918..4418646)	0.226	0.124	0.202	0.024	0.896	0.505	0.047	0.296	0.026	0.586	putative cytoplasmic protein
STM4197	STM4197	AAL23021	(4418843..4419133)	0.391	0.067			0.000	0.555	0.111			0.000	putative inner membrane protein
STM4198	STM4198	AAL23022	(4419382..4419837)	0.283	0.174	0.202	0.045	0.713	0.531	0.076	0.813	0.105	1.533	putative cytoplasmic protein
STM4199	STM4199	AAL23023	(4419834..4420439)	0.337	0.191	0.238	0.053	0.706	0.666	0.019	1.432	0.085	2.151	putative cytoplasmic protein
STM4200	STM4200	AAL23024	(4420444..4422189)	0.237	0.207	0.104	0.018	0.440	0.304	0.030	0.620	0.048	2.041	putative phage tail fiber protein H
STM4201	STM4201	AAL23025	(4422192..4422824)	0.218	0.160	0.122	0.018	0.560	0.254	0.046	0.343	0.024	1.353	putative phage tail protein
STM4202	STM4202	AAL23026	(4422817..4423932)	0.270	0.174	0.160	0.009	0.594	0.392	0.139	0.323	0.051	0.823	putative phage baseplate protein
STM4203	STM4203	AAL23027	(4423923..4424282)	0.369	0.214	0.151	0.024	0.410	0.698	0.017	0.318	0.025	0.456	putative phage baseplate protein
STM4204	STM4204	AAL23028	(4424446..4425993)	0.670	0.139	0.164	0.037	0.244	4.270	0.574	1.474	0.137	0.345	putative inner membrane protein
STM4205	STM4205	AAL23029	(4425993..4426922)	0.549	0.136	0.158	0.039	0.288	2.999	0.448	1.142	0.067	0.381	putative phage glycosyltransferase
STM4206	STM4206	AAL23030	(4426919..4427281)	0.555	0.120	0.211	0.050	0.379	3.387	0.752	1.116	0.096	0.329	putative phage glucose translocase
STM4207	STM4207	AAL23031	(4427609..4428331)	0.576	0.096	0.533	0.092	0.926	0.626	0.054	0.627	0.029	1.002	putative phage baseplate onent
STM4208	STM4208	AAL23032	(4428341..4429384)	0.361	0.176	0.250	0.025	0.693	0.268	0.033	0.488	0.042	1.818	putative cytoplasmic protein
STM4209	STM4209	AAL23033	(4429372..4429581)	0.432	0.107	0.330	0.012	0.763	0.343	0.215	0.582	0.044	1.697	putative inner membrane protein
STM4210	STM4210	AAL23034	(4429581..4430534)	0.324	0.211	0.255	0.019	0.787	0.237	0.024	0.472	0.021	1.990	putative methyl-accepting chemotaxis protein
STM4211	STM4211	AAL23035	(4430534..4432888)	0.368	0.205	0.214	0.053	0.582	0.347	0.112	0.440	0.028	1.268	putative phage tail protein
STM4212	STM4212	AAL23036	(4433440..4433964)	0.230	0.144	0.210	0.095	0.914	0.639	0.032	0.829	0.096	1.298	putative phage tail core protein

STM4213	STM4213	AAL23037	(4433964..4435391)	0.326	0.177	0.231	0.039	0.709	0.517	0.082	0.651	0.042	1.257	putative phage tail sheath protein
STM4214	STM4214	AAL23038	(4435381..4435578)	0.417	0.154	0.180	0.047	0.431	0.555	0.207	0.439	0.045	0.791	putative cytoplasmic protein
STM4215	STM4215	AAL23039	(4435575..4436030)	0.274	0.218	0.118	0.023	0.431	0.387	0.023	0.363	0.008	0.937	putative cytoplasmic protein
STM4216	STM4216	AAL23040	(4436190..4436504)	0.227	0.159	0.151	0.076	0.667	0.278	0.048	0.246	0.029	0.887	putative inner membrane protein
STM4217	STM4217	AAL23041	(4436517..4437122)	0.247	0.170	0.132	0.052	0.533	0.250	0.026	0.335	0.067	1.339	putative soluble lytic murein transglycosylase
STM4218	STM4218	AAL23042	(4437125..4437412)	0.404	0.135	0.175	0.004	0.433	0.466	0.035	0.315	0.019	0.676	putative inner membrane protein
STM4219	STM4219	AAL23043	4438132..4438335	0.526	0.093	0.290	0.026	0.552	1.478	0.041	0.837	0.043	0.566	putative cytoplasmic protein
lysC	STM4220	AAL23044	(4438468..4439817)	1.566	0.058	1.104	0.121	0.705	0.790	0.061	1.199	0.059	1.519	aspartokinase III, lysine sensitive
pgi	STM4221	AAL23045	4440162..4441811	3.289	0.075	4.539	0.488	1.380	2.752	0.059	2.988	0.136	1.086	glucosephosphate isomerase
yjbE	STM4222	AAL23046	4442252..4442497	0.544	0.114	0.478	0.038	0.878	17.939	2.412	3.680	0.173	0.205	putative outer membrane protein
yjbF	STM4223	AAL23047	4442531..4443199	0.387	0.175	0.274	0.042	0.707	3.551	0.680	1.397	0.080	0.393	putative outer membrane lipoprotein
yjbG	STM4224	AAL23048	4443196..4443933	0.401	0.221	0.189	0.014	0.472	3.708	0.710	1.068	0.034	0.288	putative periplasmic protein
yjbH	STM4225	AAL23049	4443933..4446029	0.386	0.142	0.202	0.016	0.522	1.863	0.438	0.580	0.022	0.311	putative outer membrane lipoprotein
yjbA	STM4226	AAL23050	4446172..4446582	0.450	0.152	0.169	0.021	0.375	2.234	0.068	1.051	0.066	0.471	putative inner membrane protein
malG	STM4227	AAL23051	(4446748..4447638)	1.856	0.298	0.271	0.037	0.146	0.761	0.423	0.525	0.043	0.689	ABC superfamily (membrane), maltose transport protein
malF	STM4228	AAL23052	(4447653..4449197)	0.372	0.084	0.381	0.030	1.024	0.292	0.059	0.287	0.104	0.983	ABC superfamily (membrane), maltose transport protein
malE	STM4229	AAL23053	(4449329..4450528)	0.751	0.105	1.348	0.211	1.795	0.473	0.027	0.361	0.038	0.764	ABC superfamily (bind_prot) maltose transport protein, substrate recognition for transport and chemotaxis
malK	STM4230	AAL23054	4450881..4451990	0.583	0.061	0.536	0.043	0.919	0.286	0.102	0.274	0.017	0.957	bifunctional: ABC superfamily (atp_bind), maltose transportprotein; phenotypic repressor of mal operon
lamB	STM4231	AAL23055	4452079..4453437	4.451				0.000	1.062				0.000	phage lambda receptor protein; maltose high-affinity receptor, facilitates diffusion of maltose and maltoseoligosaccharides
malM	STM4232	AAL23056	4453601..4454518	1.033	0.053	0.679	0.026	0.657	0.576	0.000	0.570	0.077	0.990	periplasmic protein of mal regulon
ubiC	STM4233	AAL23057	4454699..4455196	3.312	0.272	1.892	0.269	0.571	0.976	0.163	0.787	0.014	0.807	chorismate pyruvate lyase
ubiA	STM4234	AAL23058	4455210..4456082	2.864	0.137	1.768	0.113	0.617	1.056	0.073	0.698	0.035	0.661	p-hydroxybenzoate: octaprenyltransferase
plsB	STM4235	AAL23059	(4456181..4458601)	3.866	0.286	3.781	0.616	0.978	2.442	0.403	1.831	0.091	0.750	glycerolphosphate acyltransferase activity
dgkA	STM4236	AAL23060	4458772..4459140	2.098	0.048	1.208	0.107	0.576	6.330	0.742	2.491	0.201	0.394	diacylglycerol kinase
lexA	STM4237	AAL23061	4459249..4459857	4.224	0.353	2.029	0.335	0.480	4.726	0.160	1.984	0.081	0.420	SOS response regulator, transcriptional repressor (LexA family)
dinF	STM4238	AAL23062	4460035..4461360	1.250	0.088	0.479	0.077	0.383	1.132	0.004	0.496	0.045	0.438	DNA-damage-inducible protein F, induced by UV and mitomycin C; SOS, lexA regulon
STM4239	STM4239	AAL23063	4461357..4461470	2.531	0.966	1.257	0.414	0.496	1.943	0.200	1.120	0.131	0.576	putative cytoplasmic protein
yjbJ	STM4240	AAL23064	4461489..4461701	1.209	0.218	0.736	0.070	0.609	3.266	0.372	1.601	0.133	0.490	putative cytoplasmic protein
zur	STM4241	AAL23065	(4461800..4462315)	1.559	0.053	0.696	0.138	0.446	0.883	0.016	0.867	0.040	0.982	transcriptional repressor of znuABC operon (Fur family)
STM4242	STM4242	AAL23066	4462562..4463872	0.429	0.143	0.275	0.020	0.640	0.274	0.071	0.311	0.035	1.139	putative outer membrane or exported

yjbN	STM4243	AAL23067	4463960..4464958	1.456	0.200	0.731	0.098	0.502	1.141	0.080	0.596	0.036	0.522	putative TIM-barrel enzymes, possibly dehydrogenases, nifR3 family
yjbO	STM4244	AAL23068	4465126..4465368	0.624	0.168	0.442	0.030	0.707	0.662	0.151	0.570	0.016	0.861	putative inner membrane protein
qor	STM4245	AAL23069	(4465543..4466526)	1.044	0.113	1.017	0.094	0.974	0.604	0.105	0.770	0.025	1.275	quinone oxidoreductase, NADPH dependent
dnaB	STM4246	AAL23070	4466591..4468006	2.329	0.190	1.478	0.145	0.635	1.051	0.096	0.857	0.041	0.815	putative replicative DNA helicase;chromosome replication; chain elongation
alr	STM4247	AAL23071	4468038..4469117	3.784	0.695	1.333	0.274	0.352	1.834	0.384	0.802	0.081	0.437	alanine racemase 1, biosynthetic
tyrB	STM4248	AAL23072	4469303..4470496	8.289	1.620	1.303	0.142	0.157	2.143	0.464	1.187	0.120	0.554	tyrosine aminotransferase, tyrosine repressible
aphA	STM4249	AAL23073	4470683..4471396	2.686	0.088	4.263	0.819	1.587	0.784	0.106	1.091	0.051	1.391	non-specific acid phosphatase/phosphotransferase, class B
yjbQ	STM4250	AAL23074	4471525..4471941	0.646	0.062	1.503	0.129	2.326	0.260	0.028	0.678	0.053	2.607	putative cytoplasmic protein
yjbR	STM4251	AAL23075	4471944..4472300	0.475	0.045	1.648	0.061	3.473	0.204	0.030	0.824	0.013	4.048	putative cytoplasmic protein
STM4252	STM4252	AAL23076	(4472301..4472639)	0.424	0.142	0.652	0.090	1.535	0.231	0.126	0.398	0.038	1.721	putative inner membrane protein
STM4253	STM4253	AAL23077	(4472626..4473081)	0.342	0.116	0.326	0.098	0.954	0.237	0.077	0.335	0.053	1.416	putative outer membrane lipoprotein
uvrA	STM4254	AAL23078	(4473213..4476038)	0.832	0.081	1.336	0.203	1.605	0.844	0.018	0.994	0.011	1.178	UvrA with UvrBC is a DNA excision repalr enzyme
STM4255	STM4255	AAL23079	4476003..4476119	0.634	0.065	1.119	0.068	1.765	0.694	0.180	1.066	0.082	1.536	putative cytoplasmic protein
ssb	STM4256	AAL23080	4476286..4476816					N/A					N/A	ssDNA-binding protein controls activity of RecBCD nuclease
STM4257	STM4257	AAL23081	4477857..4478489	0.668	0.170	0.635	0.035	0.951	0.499	0.020	0.397	0.005	0.795	putative inner membrane or exported
STM4258	STM4258	AAL23082	4478486..4479874	0.484	0.129	0.902	0.136	1.861	0.359	0.054	0.568	0.031	1.583	putative methyl-accepting chemotaxis protein
STM4259	STM4259	AAL23083	4479864..4481183	0.365	0.125	0.691	0.086	1.891	0.391	0.069	0.567	0.019	1.451	putative ABC exporter outer membrane onent homolog
STM4260	STM4260	AAL23084	4481180..4482457	0.490	0.068	0.737	0.111	1.504	0.479	0.038	0.722	0.016	1.508	membrane permease, predicted cation efflux pump
STM4261	STM4261	AAL23085	4482474..4499153	0.406	0.138	0.852	0.087	2.101	0.478	0.054	1.355	0.063	2.834	putative inner membrane protein
STM4262	STM4262	AAL23086	4499193..4501259	0.424	0.144	0.192	0.026	0.454	1.213	0.066	0.798	0.058	0.658	putative ABC-type bacteriocin/lantibiotic exporter, contain an N-terminal double-glycine peptidase domain
yjcB	STM4263	AAL23087	(4501537..4501818)	0.402	0.195	0.276	0.035	0.686	0.546	0.109	0.712	0.013	1.305	putative inner membrane protein
yjcC	STM4264	AAL23088	4502381..4503982	0.451	0.123	0.159	0.031	0.353	1.233	0.062	0.624	0.060	0.506	putative diguanylate cyclase/phosphodiesterase
soxS	STM4265	AAL23089	(4503970..4504293)	2.951	0.116	1.152	0.079	0.390	2.052	0.823	0.562	0.093	0.274	transcriptional activator of superoxide response regulon (AraC/XylS family)
soxR	STM4266	AAL23090	4504380..4504838	0.645	0.142	0.408	0.057	0.633	0.730	0.524	0.440	0.051	0.602	redox-sensing transcriptional activator SoxR, contains iron-sulfur center for redox-sensing (MerR family)
STM4267	STM4267	AAL23091	4505131..4505799	1.008	0.046	0.359	0.048	0.356	0.844	0.064	1.252	0.103	1.483	putative glutathione S-transferase
yjcD	STM4268	AAL23092	4506146..4507495	1.818	0.603	0.384	0.123	0.212	1.002	0.235	0.499	0.031	0.498	putative xanthine/uracil permease family
yjcE	STM4269	AAL23093	4507645..4509291	1.647	0.027	0.988	0.100	0.600	2.297	0.433	3.604	0.271	1.569	putative A1 family, Na:H transport protein
STM4270	STM4270	AAL23094	(4509386..4510273)	0.737	0.118	0.422	0.078	0.573	0.468	0.008	0.533	0.021	1.139	putative transcriptional regulator, LysR family

STM4271	STM4271	AAL23095	4510377..4510787	0.406	0.111	0.160	0.020	0.395	0.215	0.018	0.259	0.017	1.207	putative inner membrane protein
STM4272	STM4272	AAL23096	4510780..4511469	0.774	0.122	0.203	0.031	0.263	0.324	0.010	0.369	0.021	1.137	putative inner membrane protein
yjcG	STM4273	AAL23097	(4511508..4513157)	1.616	0.958	0.389	0.032	0.241	0.351	0.064	0.521	0.022	1.484	putative SSS family transport protein
yjcH	STM4274	AAL23098	(4513154..4513468)	1.734	1.093	0.712	0.062	0.411	0.291	0.024	0.509	0.030	1.749	putative inner membrane protein
acs	STM4275	AAL23099	(4513714..4515672)	1.358	0.142	1.130	0.161	0.832	2.115	4.002	1.546	0.490	0.731	acetyl-CoA synthetase
STM4276	STM4276	AAL23100	4515859..4516005	1.727	0.567	1.845	0.041	1.068	1.565	0.528	0.525	0.153	0.336	putative cytoplasmic protein
nrfA	STM4277	AAL23101	4516104..4517540	0.423	0.119	4.413	0.676	10.428	0.128	0.052	0.244	0.022	1.914	nitrite reductase periplasmic cytochrome c(552)
nrfB	STM4278	AAL23102	4517565..4518218	0.308	0.096	3.126	0.417	10.157	0.099	0.026	0.219	0.038	2.209	formate-dependent nitrite reductase; a penta-haeme cytochrome c
nrfC	STM4279	AAL23103	4518215..4518886	0.385	0.124	3.146	0.436	8.176	0.167	0.007	0.299	0.055	1.794	putative nitrite reductase; formate-dependent, Fe-S centers
nrfD	STM4280	AAL23104	4518883..4519839	0.466	0.209	2.920	0.294	6.267	0.170	0.012	0.342	0.037	2.016	putative nitrate reductase, formate dependent
nrfE	STM4281	AAL23105	4519832..4522054	0.281	0.151	1.311	0.245	4.658	0.140	0.030	0.217	0.007	1.551	formate-dependent nitrite reductase; involved in attachment of haem c to cytochrome c552
nrfG	STM4282	AAL23106	4522051..4522671	0.486	0.082	1.151	0.113	2.367	0.212	0.082	0.281	0.049	1.322	part of formate-dependent nitrite reductase lex; involved in attachment of haem c to cytochrome c552
gltP	STM4283	AAL23107	4523016..4524326	6.390	1.511	1.772	0.089	0.277	1.395	0.126	1.738	0.101	1.246	DAACS family, glutamate:aspartate symport protein
yjcO	STM4284	AAL23108	(4524484..4525173)	0.807	0.035	0.452	0.027	0.560	0.366	0.030	0.634	0.022	1.735	putative TPR repeat protein
fdhF	STM4285	AAL23109	(4525350..4527497)	0.350	0.109	0.751	0.121	2.143	0.267	0.088	0.482	0.065	1.803	formate dehydrogenase
lpxO	STM4286	AAL23110	(4527852..4528760)	0.711	0.053	0.711	0.093	1.000	0.634	0.060	2.950	0.249	4.656	putative dioxygenase for synthesis of lipid
phnO	STM4287	AAL23111	(4529018..4529482)	0.379	0.096	0.298	0.040	0.785	0.716	0.049	1.210	0.067	1.689	putative regulator in phn operon
phnB	STM4288	AAL23112	(4529604..4530047)	0.775	0.092	0.444	0.075	0.573	0.523	0.082	0.863	0.019	1.650	putative cytoplasmic protein
phnA	STM4289	AAL23113	(4530167..4530502)	3.279	0.241	2.182	0.244	0.665	1.044	0.266	0.792	0.019	0.758	putative alkylphosphonate uptake protein in phosphonate metabolism
proP	STM4290	AAL23114	4530970..4532472	2.106	0.274	0.606	0.050	0.288	2.024	0.341	1.812	0.132	0.895	MFS family, low-affinity proline transporter (proline permease II)
basS	STM4291	AAL23115	(4532639..4533709)	1.135	0.075	1.938	0.181	1.708	1.887	0.105	3.030	0.343	1.605	sensory kinase in two-onent regulatory system with BasR
basR	STM4292	AAL23116	(4533719..4534387)	0.771	0.031	2.616	0.175	3.393	1.413	0.092	3.460	0.250	2.449	response regulator in two-onent regulatory system with BasS (OmpR family)
yjdB	STM4293	AAL23117	(4534384..4536027)	1.464	0.077	0.959	0.146	0.656	2.664	0.253	1.854	0.105	0.696	putative integral membrane protein
yjdE	STM4294	AAL23118	(4536161..4537498)	0.480	0.171			0.000	0.529	0.121			0.000	putative APC family, putrescine/ornithine transport protein, cryptic
adiY	STM4295	AAL23119	(4537638..4538399)	0.322	0.097	0.529	0.104	1.641	0.749	0.033	1.357	0.071	1.812	transcriptional activator of adiA (AraC/XylS family)
adi	STM4296	AAL23120	(4538697..4540967)	0.294	0.137	0.240	0.022	0.814	0.172	0.050	0.432	0.043	2.507	arginine decarboxylase, catabolic; inducible by acid

melR	STM4297	AAL23121	(4541197..4542129)	0.378	0.162	0.734	0.154	1.940	0.154	0.042	0.321	0.021	2.076	regulator of melibiose operon (AraC/XylS family)
melA	STM4298	AAL23122	4542398..4543753	0.575	0.117	0.552	0.058	0.961	0.207	0.044	0.242	0.005	1.167	alpha-galactosidase
melB	STM4299	AAL23123	4543837..4545267	0.488	0.097	0.680	0.155	1.393	0.180	0.013	0.280	0.018	1.553	GPH family, melibiose permease II
fumB	STM4300	AAL23124	(4545365..4547011)	1.595	0.072	9.006	1.329	5.646	1.014	0.067	1.306	0.014	1.288	fumarase B (fumarate hydratase class I), anaerobic isozyme
dcuB	STM4301	AAL23125	(4547107..4548447)	0.965	0.124	5.049	0.278	5.232	2.180	0.464	1.237	0.041	0.567	Dcu family, anaerobic C4-dicarboxylate transporter
STM4302	STM4302	AAL23126	(4548594..4548860)	0.613	0.054	1.033	0.129	1.684	1.423	0.457	0.541	0.061	0.380	putative cytoplasmic protein
dcuR	STM4303	AAL23127	(4549177..4549896)	1.142	0.086	1.447	0.092	1.267	1.412	0.054	1.528	0.207	1.082	response regulator in two-onent regulatory system with DcuS, regulates anaerobic fumarate respiration
dcuS	STM4304	AAL23128	(4549893..4551524)	0.859	0.073			0.000	0.591	0.081			0.000	sensory histidine kinase in two-onent retgulatory system with DcuR, senses fumarate/C4-dicarboxylate
STM4305	STM4305	AAL23129	4551958..4554309	0.195	0.123	0.865	0.089	4.429	0.189	0.031	0.399	0.070	2.115	putative anaerobic dimethyl sulfoxide reductase, subunit A
STM4306	STM4306	AAL23130	4554323..4554949	0.224	0.133	0.957	0.055	4.270	0.162	0.050	0.378	0.040	2.329	putative anaerobic dimethyl sulfoxide reductase, subunit B
STM4307	STM4307	AAL23131	4554942..4555715	0.375	0.178			0.000	0.397	0.074			0.000	putative anaerobic dimethyl sulfoxide reductase, subunit C
STM4308	STM4308	AAL23132	4555731..4556384	0.275	0.127	0.452	0.050	1.643	0.198	0.056	0.302	0.017	1.525	putative onent of anaerobic dehydrogenases
STM4309	STM4309	AAL23133	(4556468..4557868)	0.207	0.149	0.109	0.007	0.525	0.106	0.011	0.214	0.029	2.007	putative periplasmic or exported protein
STM4310	STM4310	AAL23134	4558172..4559077	0.293	0.137	0.463	0.046	1.580	0.274	0.035	0.255	0.034	0.930	putative inner membrane protein
tnpA_6	STM4311	AAL23135	4559416..4559874					N/A					N/A	transposase for IS200
STM4312	STM4312	AAL23136	(4560083..4560352)	0.483	0.035	1.755	0.093	3.636	1.287	0.158	0.505	0.077	0.392	putative phage protein
STM4313	STM4313	AAL23137	(4560360..4560575)	0.502	0.022	2.390	0.220	4.764	1.002	0.645	0.530	0.058	0.530	putative cytoplasmic protein
rtsB	STM4314	AAL23138	(4560598..4560885)	0.698	0.125	4.220	0.891	6.046	0.900	0.471	0.937		1.040	putative bacterial regulatory proteins, luxR family
rtsA	STM4315	AAL23139	(4560882..4561757)	0.747	0.010	7.320	0.554	9.798	0.779	0.066	1.274	0.065	1.635	putative AraC-type DNA-binding domain-containing protein
STM4316	STM4316	AAL23140	(4562022..4562243)	1.502	0.273	1.056	0.084	0.703	4.143	6.901	0.957	0.024	0.231	putative cytoplasmic protein
STM4317	STM4317	AAL23141	4562560..4562853	0.616	0.072	1.342	0.186	2.179	0.763	0.106	1.541	0.067	2.020	putative helix-turn-helix protein, copG family
STM4318	STM4318	AAL23142	4562850..4563341	0.649	0.158	0.851	0.146	1.311	1.286	0.212	1.341	0.065	1.043	putative acetyltransferase
phoN	STM4319	AAL23143	(4563589..4564341)	0.594	0.151	1.214	0.220	2.043	28.097	1.483	43.099	2.770	1.534	non-specific acid phosphatase
STM4320	STM4320	AAL23144	4565999..4566331	0.912	0.040	0.374	0.037	0.410	0.603	0.027	0.588	0.090	0.976	putative bacterial regulatory protein, merR family
pheR	STM4321						N/A					N/A		
yjdC	STM4322	AAL23145	(4566770..4567345)	4.941	1.054	1.422	0.266	0.288	3.133	0.592	1.906	0.167	0.608	putative bacterial regulatory protein, merR family
dsbD	STM4323	AAL23146	(4567382..4569085)	1.842	0.145	1.001	0.068	0.543	0.922	0.123	0.705	0.012	0.764	thiol:disulfide interchange protein, cytochrome c-type biogenesis
cutA	STM4324	AAL23147	(4569061..4569408)	1.105	0.078			0.000	0.509	0.039	0.692		1.360	putative periplasmic divalent cation tolerance protein; cytochrome c biogenesis

dcuA	STM4325	AAL23148	(4569529..4570830)	0.905	0.057	3.113	0.627	3.440	0.352	0.011	0.611	0.043	1.735	Dcu family, anaerobic dicarboxylate transport protein
aspA	STM4326	AAL23149	(4570945..4572381)	13.780	1.179	106.382	8.070	7.720	1.952	0.057	3.907	0.189	2.001	aspartate ammonia-lyase (aspartase)
fxsA	STM4327	AAL23150	4572683..4573198	3.389	0.596	2.727	0.650	0.805	2.957	0.604	1.762	0.127	0.596	suppresses F exclusion of bacteriophage T7
yjeH	STM4328	AAL23151	(4573257..4574498)	1.188	0.079	1.739	0.187	1.465	3.044	0.452	2.023	0.352	0.665	putative transporter, cytoplasmic membrane protein
mopB	STM4329	AAL23152	4574774..4575067	6.043	1.462	20.619	2.161	3.412	9.033	0.352	28.901	1.686	3.199	chaperone Hsp10, affects cell division
mopA	STM4330	AAL23153	4575111..4576757	8.817	2.616	42.131	6.298	4.779	13.775	0.569	75.297	4.973	5.466	chaperone Hsp60 with peptide-dependent ATPase activity, affects cell division
yjeI	STM4331	AAL23154	4576983..4577354	19.911	7.381	11.985	0.648	0.602	5.092	1.060	6.928	1.427	1.361	putative outer membrane lipoprotein
yjeJ	STM4332	AAL23155	(4577402..4578259)	1.499	0.160			0.000	1.266	0.079			0.000	putative inner membrane protein
yjeK	STM4333	AAL23156	(4578541..4579569)	2.662	0.180	1.458	0.423	0.548	1.555	0.150			0.000	putative aminomutase
efp	STM4334	AAL23157	4579610..4580176	21.146	1.554	10.783	0.806	0.510	9.204	0.876	6.822	0.345	0.741	elongation factor P (EF-P)
ecnA	STM4335	AAL23158	4580195..4580371	2.448	0.252	1.857	0.433	0.759	1.386	0.102	0.843	0.128	0.608	putative entericidin A precursor
ecnB	STM4336	AAL23159	4580479..4580625	3.299	0.761	1.928	0.240	0.584	2.956	0.426	1.758	0.083	0.595	putative entericidin B precursor
ecnR	STM4337	AAL23160	(4580656..4581243)	1.200	0.081			0.000	1.016	0.142			0.000	putative bacterial regulatory protein, luxR family
sugE	STM4338	AAL23161	4581500..4581817	1.651	0.118	1.177	0.096	0.713	0.845	0.101	0.692	0.038	0.819	putative DMT superfamily transport protein
blc	STM4339	AAL23162	(4581834..4582367)	0.865	0.052	1.474	0.102	1.705	0.563	0.044	0.781	0.070	1.387	outer membrane lipoprotein (lipocalin)
frdD	STM4340	AAL23163	(4582479..4582838)	4.890	1.203	22.769	1.111	4.656	2.633	0.536	1.920	0.082	0.729	fumarate reductase, anaerobic, membrane anchor polypeptide
frdC	STM4341	AAL23164	(4582849..4583244)	3.737	0.708	25.871	4.498	6.923	1.788	0.227	1.588	0.226	0.888	fumarate reductase, anaerobic, membrane anchor polypeptide
frdB	STM4342	AAL23165	(4583255..4583989)	2.669	0.387	39.053	7.549	14.630	1.143	0.072	1.847	0.145	1.615	fumarate reductase, anaerobic, Fe-S protein subunit
frdA	STM4343	AAL23166	(4583982..4585772)	3.484	0.455	44.011	1.489	12.632	1.419	0.093	2.319	0.154	1.634	fumarate reductase, anaerobic, flavoprotein subunit
yjeA	STM4344	AAL23167	4586095..4587072	1.106	0.094	1.273	0.092	1.151	0.925	0.036	0.580	0.092	0.627	putative pyruvate oxidase (lysyl-tRNA synthetase)
yjeM	STM4345	AAL23168	4587298..4588800	0.755	0.094	0.282	0.038	0.374	3.569	1.050	1.519	0.064	0.426	putative APC family, amino-acid transport protein
yjeO	STM4346	AAL23169	4588852..4589166	1.710	0.075	0.442	0.083	0.259	3.650	1.200	0.931	0.059	0.255	putative inner membrane protein
yjeP	STM4347	AAL23170	(4589233..4592559)	1.039	0.054	0.696	0.063	0.669	0.881	0.084	0.639	0.041	0.725	putative periplasmic binding protein
psd	STM4348	AAL23171	(4592578..4593546)	2.223	0.167	3.514	0.146	1.581	1.739	0.176	1.655	0.199	0.952	phosphatidylserine decarboxylase
yjeQ	STM4349	AAL23172	(4593638..4594714)	3.165	0.234	1.720	0.115	0.544	1.906	0.329	1.646	0.091	0.863	putative GTPase
orn	STM4350	AAL23173	4594797..4595342	2.098	0.151	1.347	0.252	0.642	0.704	0.146	0.802	0.052	1.139	oligoribonuclease
STM4351	STM4351	AAL23174	(4595404..4596144)	0.820	0.056	1.033	0.027	1.260	0.414	0.035	0.484	0.028	1.168	putative arginine-binding periplasmic protein
glyV	STM4352						N/A					N/A		
glyX	STM4353						N/A					N/A		

glyY	STM4354						N/A					N/A		
yjeS	STM4355	AAL23175	(4597229..4598383)	1.884	0.100	0.821	0.145	0.436	0.894	0.147	0.678	0.128	0.759	putative Fe-S protein
yjeF	STM4356	AAL23176	4598367..4599914	2.340	0.303	1.105	0.060	0.472	1.249	0.333	1.285	0.075	1.029	putative sugar kinase
yjeE	STM4357	AAL23177	4599886..4600347	2.398	0.200	1.238	0.169	0.516	1.396	0.312	1.325	0.089	0.949	putative nucleotide-binding protein
amiB	STM4358	AAL23178	4600364..4601683	3.507	0.691	1.971	0.277	0.562	1.312	0.231	1.619	0.064	1.235	N-acetylmuramoyl-l-alanine amidase II, a murein hydrolase
mutL	STM4359	AAL23179	4601693..4603549					N/A					N/A	enzyme in methyl-directed mismatch repair, stimulates binding of Vsr and MutS to heteroduplex DNA
miaA	STM4360	AAL23180	4603542..4604492	14.524	2.736	5.315	0.257	0.366	14.136	2.482	6.372	0.461	0.451	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase
hfq	STM4361	AAL23181	4604575..4604883	22.439	4.114	8.122	0.882	0.362	15.746	2.318	8.866	0.360	0.563	host factor I for bacteriophage Q beta replication, a growth-related protein
hflX	STM4362	AAL23182	4604955..4606235	4.415	0.428	4.552	0.485	1.031	4.851	0.193	3.800	0.142	0.783	putative GTP-ase, together with HflCK possibly involved in phage lambda cII repressor stability
hflK	STM4363	AAL23183	4606451..4607710	2.550	0.244	5.724	0.776	2.245	5.280	0.393	7.965	0.905	1.509	with HflC, part of modulator for protease specific for FtsH phage lambda cII repressor
hflC	STM4364	AAL23184	4607713..4608717	6.815	0.967	7.336	1.348	1.076	9.769	1.198	14.351	0.479	1.469	with HflK, part of modulator for protease specific for FtsH phage lambda cII repressor
yjeT	STM4365	AAL23185	4608796..4608993	1.124	0.086	2.054	0.153	1.827	1.165	0.112	1.856	0.116	1.594	putative inner membrane protein
purA	STM4366	AAL23186	4609096..4610394	3.658	0.190	8.424	0.668	2.303	1.577	0.058	3.248	0.184	2.060	adenylosuccinate synthetase
yjeB	STM4367	AAL23187	4610601..4611026	2.014	0.142	1.982	0.372	0.984	1.199	0.029	1.193	0.188	0.995	putative negative regulator
vacB	STM4368	AAL23188	4611064..4613502	1.401	0.075	3.923	0.838	2.800	0.770	0.107	1.991	0.098	2.587	putative exoribonuclease
yjfH	STM4369	AAL23189	4613593..4614324	1.956	0.248	2.599	0.418	1.329	1.793	0.225	2.108	0.201	1.176	putative tRNA/rRNA methyltransferase
yjfI	STM4370	AAL23190	4614456..4614860	0.348	0.117	0.468	0.035	1.347	1.772	0.058	1.043	0.076	0.588	putative cytoplasmic protein
yjfJ	STM4371	AAL23191	4614875..4615573	0.373	0.163	0.407	0.042	1.093	1.558	0.064	1.821	0.165	1.168	putative Phage shock protein A, IM30, suppresses sigma54-dependent transcription
STM4372	STM4372	AAL23192	4615573..4616643					N/A					N/A	resembles eukaryotic-type potassium channels
yjfK	STM4373	AAL23193	4616616..4617299	0.283	0.137	0.172	0.028	0.607	0.716	0.015	0.736	0.055	1.029	putative cytoplasmic protein
yjfL	STM4374	AAL23194	4617317..4617715			0.193	0.018	N/A	0.646	0.063	0.760	0.389	1.176	putative inner membrane protein
yjfM	STM4375	AAL23195	4617725..4618363	0.309	0.210	0.252	0.038	0.815	0.566	0.051	0.730	0.075	1.291	putative inner membrane protein
yjfC	STM4376	AAL23196	4618366..4619529	0.583	0.216	0.272	0.029	0.466	0.964	0.133	0.499	0.016	0.517	putative glutathionylspermidine synthase
aidB	STM4377	AAL23197	4619614..4621236					N/A					N/A	putative acyl-CoA dehydrogenase; adaptive response (transcription activated by Ada)
yjfN	STM4378	AAL23198	(4621281..4621601)	4.650	0.413	10.341	1.952	2.224	0.527	0.086	0.588	0.122	1.116	putative inner membrane protein
yjfO	STM4379	AAL23199	(4621687..4622016)	5.872	0.359	10.321	1.864	1.758	0.420	0.024	0.573	0.134	1.364	putative lipoprotein
yjfP	STM4380	AAL23200	4622200..4622949	0.777	0.071	1.373	0.126	1.767	0.229	0.046	0.496	0.051	2.166	putative hydrolase of the alpha/beta superfamily
yjfQ	STM4381	AAL23201	(4622946..4623701)	1.000	0.055	1.102	0.111	1.101	0.303	0.033	0.678	0.043	2.239	putative transcriptional repressor (DeoR family)

yjfR	STM4382	AAL23202	(4623806..4624870)	0.424	0.125	0.340	0.112	0.802	0.258	0.057	0.529	0.165	2.048	putative Zn-dependent hydrolases of the beta-lactamase fold
sgaT	STM4383	AAL23203	4625200..4626630	0.317	0.174	0.304	0.051	0.957	0.107	0.011	0.188	0.012	1.761	putative PTS enzyme IIsga subunit
sgaB	STM4384	AAL23204	4626646..4626951	0.409	0.159	0.606	0.043	1.482	0.437	0.231	0.345	0.039	0.790	putative PTS enzyme IIsga subunit
ptxA	STM4385	AAL23205	4626961..4627425	0.296	0.120	0.527	0.054	1.780	0.158	0.020	0.252	0.034	1.596	putative PTS enzyme IIsga subunit
sgaH	STM4386	AAL23206	4627439..4628089	0.675	0.388	0.808	0.087	1.197	0.225	0.013	0.379	0.028	1.684	putative hexulose phosphate synthase (arabino hexulose phosphate formaldehyde lyase)
sgaU	STM4387	AAL23207	4628099..4628953	0.322	0.128	0.793	0.141	2.463	0.201	0.094	0.369	0.036	1.834	putative hexulose-6-phosphate isomerase
sgaE	STM4388	AAL23208	4628953..4629639	0.367	0.126	0.650	0.061	1.774	0.201	0.034	0.337	0.019	1.675	putative L-ribulose 5-phosphate 4-epimerase
yjfY	STM4389	AAL23209	(4629768..4630043)	0.813	0.070	1.266	0.186	1.558	0.714	0.226	0.722	0.054	1.012	putative outer membrane protein
STM4390	STM4390	AAL23210	4630237..4630443	1.520	0.118	2.863	0.121	1.884	1.373	0.223	1.014	0.072	0.738	putative cytoplasmic protein
rpsF	STM4391	AAL23211	4630514..4630909	8.602	0.662	21.319	1.457	2.478	6.963	0.450	7.685	0.209	1.104	30S ribosomal subunit protein S6
priB	STM4392	AAL23212	4630916..4631230	9.641	0.221	22.792	3.147	2.364	6.449	0.694	6.525	0.339	1.012	primosomal replication protein N
rpsR	STM4393	AAL23213	4631235..4631462	5.835	0.167	17.789	1.884	3.049	4.180	0.525	4.970	0.270	1.189	30S ribosomal subunit protein S18
rplI	STM4394	AAL23214	4631504..4631953	5.920	0.371	18.553	1.371	3.134	4.160	0.122	4.715	0.374	1.133	50S ribosomal subunit protein L9
yifZ	STM4395	AAL23215	4632101..4633027	0.437	0.135	0.515	0.119	1.177	0.261	0.053	0.321	0.054	1.229	putative permease
ytfB	STM4396	AAL23216	(4633077..4633712)	2.281	0.226	1.436	0.275	0.629	1.062	0.212	1.220	0.081	1.149	putative cell envelope opacity-associated protein A
fklB	STM4397	AAL23217	4633890..4634552	10.043	1.013	3.554	0.443	0.354	4.337	0.413	2.479	0.139	0.572	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase)
cycA	STM4398	AAL23218	4634848..4636257	9.366	2.694	3.576	0.303	0.382	2.178	0.503	1.192	0.084	0.547	APC family, D-alanine/D-serine/glycine transport protein
ytfE	STM4399	AAL23219	(4636369..4637031)	1.076	0.131	0.721	0.039	0.670	0.287	0.060	0.338	0.079	1.178	putative cell morphogenesis
ytfF	STM4400	AAL23220	(4637134..4638099)	1.676	0.327			0.000	0.338	0.034			0.000	putative cationic amino acid transporter
ytfG	STM4401	AAL23221	(4638180..4639028)	0.490	0.205	0.300	0.035	0.611	0.208	0.059	0.258	0.015	1.240	paral putative reductase
ytfH	STM4402	AAL23222	4639116..4639502	1.142	0.043	0.631	0.073	0.553	0.345	0.077	0.465	0.046	1.346	putative transcriptional regulator
dB	STM4403	AAL23223	(4639560..4641503)	2.527	0.243	3.876	0.351	1.534	0.473	0.029	1.006	0.023	2.128	2':3'-cyclic-nucleotide 2'-phosphodiesterase
cysQ	STM4404	AAL23224	4641771..4642511	2.695	0.510	1.493	0.048	0.554	0.709	0.080	1.440	0.097	2.031	affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis
ytfJ	STM4405	AAL23225	(4642501..4643058)	1.569	0.262	1.197	0.206	0.763	0.781	0.044	1.453	0.079	1.861	putative transcriptional regulator
ytfK	STM4406	AAL23226	4643319..4643591	3.907	1.278	3.599	0.434	0.921	5.926	1.141	3.173	0.110	0.535	putative cytoplasmic protein
ytfL	STM4407	AAL23227	(4643676..4645019)	1.308	0.043	1.098	0.102	0.840	1.269	0.120	1.327	0.090	1.046	putative hemolysin-related protein
msrA	STM4408	AAL23228	(4645202..4645840)	1.317	0.084	1.618	0.351	1.229	1.789	0.221	5.327	1.061	2.978	peptide methionine sulfoxide reductase
ytfM	STM4409	AAL23229	4646053..4647786	0.718	0.083	1.169	0.072	1.629	0.744	0.025	2.267	0.088	3.048	putative outer membrane protein
ytfN	STM4410	AAL23230	4647783..4651562					N/A					N/A	putative periplasmic protein
ytfP	STM4411	AAL23231	4651565..4651909	5.125	0.489	2.740	0.231	0.535	3.293	0.190	3.210	0.200	0.975	putative cytoplasmic protein
STM4412	STM4412	AAL23232	(4651963..4653171)	0.598	0.123	0.576	0.089	0.964	0.802	0.020	0.948	0.105	1.182	putative pemease

STM4413	STM4413	AAL23233	(4653168..4654331)	0.585	0.112	0.522	0.125	0.893	0.707	0.334	0.661	0.067	0.934	putative imidazolonepropionase and related amidohydrolases
ppa	STM4414	AAL23234	(4654741..4655271)	27.576	5.762	11.632	0.678	0.422	10.940	2.396	9.268	0.594	0.847	inorganic pyrophosphatase
fbp	STM4415	AAL23235	(4655498..4656496)	9.051	0.266	8.248	1.282	0.911	2.345	0.127	2.575	0.168	1.098	fructose-bisphosphatase
mpl	STM4416	AAL23236	4656671..4658050	3.110	0.240	2.949	0.520	0.948	1.912	0.296	1.898	0.143	0.993	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl- meso-diaminopimelate ligase
STM4417	STM4417	AAL23237	4658541..4659374	0.499	0.089	0.618	0.082	1.237	0.554	0.123	0.803	0.083	1.448	putative transcriptional regulator
STM4418	STM4418	AAL23238	(4659425..4660858)	0.329	0.151	0.217	0.017	0.660	0.206	0.018	0.220	0.015	1.067	sugar (and other) transporter
STM4419	STM4419	AAL23239	4661317..4662753	0.442	0.182	0.279	0.032	0.632	0.228	0.016	0.196	0.017	0.861	sugar (and other) transporter
STM4420	STM4420	AAL23240	(4663106..4663915)	0.800	0.100	1.281	0.203	1.602	0.236	0.025	0.490	0.040	2.078	putative inner membrane protein
STM4421	STM4421	AAL23241	(4663940..4665445)	0.361	0.140	0.691	0.058	1.915	0.143	0.007	0.268	0.024	1.873	putative NAD-dependent aldehyde dehydrogenase
STM4422	STM4422	AAL23242	(4665461..4665763)	0.388	0.103	0.408	0.059	1.053	0.253	0.115	0.254	0.014	1.004	putative cytoplasmic protein
STM4423	STM4423	AAL23243	4665886..4666710	0.426	0.166	0.445	0.040	1.044	0.165	0.078	0.160	0.015	0.967	putative AraC-type DNA-binding domain-containing protein
STM4424	STM4424	AAL23244	4666970..4667890	0.362	0.172	0.199	0.035	0.549	0.574	0.011	0.457	0.056	0.796	putative endonuclease
STM4425	STM4425	AAL23245	4667909..4668919	0.315	0.125	0.201	0.022	0.638	0.653	0.030	0.939	0.037	1.438	putative dehydrogenase
srfJ	STM4426	AAL23246	4669016..4670359	0.372	0.151	0.137	0.003	0.369	0.405	0.084	0.710	0.050	1.753	activated by transcription factor SsrB, similar to Homo sapiens lysosomal glucosyl ceramidase
STM4427	STM4427	AAL23247	4670360..4671193	0.786	0.170	0.260	0.021	0.331	0.537	0.017	0.712	0.028	1.326	putative endonuclease
STM4428	STM4428	AAL23248	(4671190..4672356)	0.548	0.202	0.295	0.029	0.538	0.283	0.245	0.381	0.027	1.347	putative permease
STM4429	STM4429	AAL23249	(4672417..4673217)	0.466	0.137	0.356	0.063	0.765	0.146	0.040	0.250	0.011	1.714	putative cytoplasmic protein
STM4430	STM4430	AAL23250	(4673403..4674353)	0.399	0.113	0.329	0.044	0.824	0.132	0.023	0.266	0.021	2.019	putative sugar kinase, ribokinase family
STM4431	STM4431	AAL23251	4674770..4675819	0.431	0.136	0.391	0.066	0.906	0.130	0.042	0.271	0.026	2.093	puttive thiamine pyrophosphate-requiring enzyme
STM4432	STM4432	AAL23252	4675900..4676709	0.496	0.165	0.459	0.045	0.926	0.211	0.054	0.399	0.023	1.893	putative thiamine pyrophosphate-requiring enzyme
STM4433	STM4433	AAL23253	4676890..4677912	0.275	0.132	0.321	0.020	1.169	0.286	0.026	0.482	0.029	1.687	putative thiamine pyrophosphate-requiring enzyme, oxidoreductase family
STM4434	STM4434	AAL23254	4677985..4679211	0.265	0.175	0.176	0.035	0.662	0.500	0.079	0.336	0.055	0.671	putative permease
STM4435	STM4435	AAL23255	4679372..4680187	0.374	0.151	0.206	0.037	0.552	0.343	0.037	0.620	0.036	1.808	putative cytoplasmic protein
STM4436	STM4436	AAL23256	4680240..4681124	0.473	0.082	0.414	0.084	0.875	0.575	0.095	0.869	0.037	1.513	putative endonuclease
yjgA	STM4437	AAL23257	(4681180..4681731)	5.465	0.932	2.139	0.173	0.391	2.434	0.378	1.909	0.091	0.784	putative cytoplasmic protein
pmbA	STM4438	AAL23258	4681827..4683179	1.363	0.044	1.824	0.181	1.338	0.743	0.036	1.390	0.051	1.871	putative peptide maturation protein, maturation of antibiotic MccB17, see tld genes
cybC	STM4439	AAL23259	4683278..4683664	6.759	0.833	1.546	0.241	0.229	5.899	0.527	4.244	0.275	0.719	cytochrome b(562)
STM4440	STM4440	AAL23260	4683942..4684280	0.809	0.090	0.553	0.053	0.684	0.330	0.023	0.613	0.048	1.856	putative cytoplasmic protein
STM4441	STM4441	AAL23261	4684291..4684653	0.745	0.065	0.565	0.064	0.759	0.245	0.017	0.446	0.047	1.825	putative cytoplasmic protein

STM4442	STM4442	AAL23262	4684653..4684955	0.758	0.090	0.409	0.083	0.539	0.311	0.097	0.342	0.072	1.099	putative cytoplasmic protein
STM4443	STM4443	AAL23263	4684978..4685754	0.870	0.192	0.336	0.010	0.386	1.536	4.954	0.443	0.014	0.289	putative inner membrane protein
STM4444	STM4444	AAL23264	4685766..4686410	0.478	0.084	0.508	1.721	1.061	0.168	0.002	0.232	0.020	1.377	putative inner membrane protein
STM4445	STM4445	AAL23265	4686469..4687602	0.646	0.156	0.404	0.038	0.625	0.280	0.045	0.454	0.089	1.622	putative dihydroorotase
STM4446	STM4446	AAL23266	4687586..4688704	0.482	0.017	0.381	0.029	0.791	0.205	0.049	0.533	0.065	2.604	putative selenocysteine synthase [L-seryl-tRNA(Ser) selenium transferase
STM4447	STM4447	AAL23267	4688701..4689330	0.668	0.032	0.524	0.111	0.784	0.299	0.031	0.580	0.083	1.941	putative periplasmic protein
STM4448	STM4448	AAL23268	4689457..4691370	0.835	0.072	0.365	0.059	0.437	0.272	0.023	0.396	0.024	1.452	putative phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
STM4449	STM4449	AAL23269	4691448..4691690					N/A					N/A	putative helix-turn-helix protein, copG family
STM4450	STM4450	AAL23270	4691680..4691964	1.069	0.023	0.975	0.326	0.912	0.349	0.090	0.377	0.025	1.082	putative inner membrane protein
nrdG	STM4451	AAL23271	(4691968..4692432)	0.670	0.106	0.847	0.064	1.265	0.338	0.125	0.271	0.035	0.802	anaerobic ribonucleotide reductase activating protein
nrdD	STM4452	AAL23272	(4692553..4694691)	0.284	0.154	2.460	0.469	8.655	0.175	0.057	0.232	0.015	1.323	anaerobic ribonucleoside-triphosphate reductase
treC	STM4453	AAL23273	(4695100..4696752)	0.899	0.009	3.271	0.536	3.637	0.222	0.010	0.383	0.056	1.724	trehalose- 6-P hydrolase, alternative inducer of maltose system, cytoplasmic
treB	STM4454; pseudogene; frameshift				5.452	0.250	6.098	0.323	1.119	1.241	0.216	0.903	0.077	0.728
treR	STM4455	AAL23274	(4698357..4699304)	0.643	0.091	0.462	0.109	0.718	0.297	0.185	0.340	0.186	1.144	transcriptional repressor of treABC (GalR/LacI family)
mgtA	STM4456	AAL23275	4699688..4702396					N/A					N/A	P-type ATPase, Mg2+ ATPase transporter
STM4457	STM4457	AAL23276	(4702512..4702958)	5.641	0.994	1.756	0.223	0.311	1.627	0.323	0.780	0.028	0.480	putative transposase
yjgF	STM4458	AAL23277	(4703033..4703419)	19.351	3.846	20.546	1.523	1.062	4.874	0.565	5.397	0.268	1.107	putative translation initiation inhibitor
pyrI	STM4459	AAL23278	(4703496..4703957)	1.427	0.070	1.939	0.085	1.359	0.453	0.019	0.739	0.050	1.632	aspartate carbamoyltransferase, regulatory subunit (allosteric regulation)
pyrB	STM4460	AAL23279	(4703970..4704905)	0.871	0.071	1.122	0.069	1.288	0.279	0.052	0.541	0.072	1.941	aspartate carbamoyltransferase, catalytic subunit
pyrL	STM4461	AAL23280	(4704941..4705042)	0.977	0.258	0.792	0.251	0.811	0.828	0.352	0.890	0.410	1.074	pyrBI operon leader peptide
yjgG	STM4462	AAL23281	4705022..4705162	0.717	0.191	0.374	0.070	0.521	0.873	0.455	0.273	0.084	0.312	putative cytoplasmic protein
STM4463	STM4463	AAL23282	(4705132..4705620)	0.286	0.156	0.274	0.054	0.959	0.176	0.057	0.244	0.016	1.383	putative arginine repressor
STM4464	STM4464	AAL23283	(4705807..4707210)	0.874	0.136	0.338	0.069	0.386	0.792	0.411	0.332	0.053	0.419	putative arginine repressor
STM4465	STM4465	AAL23284	(4707266..4708270)	0.362	0.184	0.312	0.055	0.864	0.324	0.011	0.466	0.040	1.436	putative ornithine carbamoyltransferase
STM4466	STM4466	AAL23285	(4708382..4709314)	0.684	0.101	0.503	0.139	0.735	0.695	0.149	0.545	0.103	0.785	putative carbamate kinase
STM4467	STM4467	AAL23286	(4709325..4710545)	0.784	0.175	0.687	0.032	0.876	0.926	0.316	0.520	0.096	0.562	putative arginine deiminase
yjgK	STM4468	AAL23287	4711221..4711673	0.301	0.079	0.476	0.058	1.582	0.169	0.013	0.523	0.061	3.100	putative cytoplasmic protein
argI	STM4469	AAL23288	(4711747..4712751)	0.398	0.074	0.393	0.086	0.988	0.336	0.054	0.690	0.020	2.051	ornithine carbamoyltransferase 1
yjgD	STM4470	AAL23289	4712917..4713333	3.812	0.785	1.761	0.158	0.462	1.253	0.060	0.905	0.067	0.722	putative cytoplasmic protein

miaE	STM4471	AAL23290	4713345..4714157	0.562	0.096	0.617	0.034	1.100	0.485	0.032	0.615	0.046	1.266	hydroxylase for synthesis of 2-methylthio-cis-ribozeatin in tRNA
ytgA	STM4472	AAL23291	(4714391..4714879)	0.360	0.064	0.252	0.010	0.700	2.467	0.015	0.806	0.041	0.327	putative inner membrane protein
yjgM	STM4473	AAL23292	(4714986..4715489)	1.528	0.060	0.484	0.112	0.317	7.870	1.422	2.754	0.174	0.350	putative acetyltransferase
yjgN	STM4474	AAL23293	4715684..4716871	0.376	0.096	0.257	0.042	0.684	1.077	0.147	0.455	0.078	0.422	putative inner membrane protein
valS	STM4475	AAL23294	(4717013..4719868)	4.014	1.142	3.325	0.158	0.828	4.093	4.693	2.644	0.497	0.646	valine tRNA synthetase
holC	STM4476	AAL23295	(4719868..4720350)	3.699	0.587	4.362	0.444	1.179	1.709	0.400	3.362	0.185	1.967	DNA polymerase III, chi subunit
pepA	STM4477	AAL23296	(4720448..4721959)	9.786	1.108	8.065	0.332	0.824	4.530	0.091	7.650	0.599	1.689	aminopeptidase A
STM4478	STM4478	AAL23297	(4722003..4722122)	10.207	2.227	4.986	0.554	0.488	4.239	0.686	3.625	0.519	0.855	putative cytoplasmic protein
yjgP	STM4479	AAL23298	4722354..4723454	1.830	0.080	1.515	0.135	0.828	1.235	0.211	1.155	0.079	0.935	putative permease
yjgQ	STM4480	AAL23299	4723454..4724536	1.984	0.199	0.983	0.063	0.495	1.150	0.076	0.909	0.077	0.790	putative permease
idnR	STM4481	AAL23300	(4724731..4725729)	0.456	0.124	0.352	0.071	0.773	0.263	0.002	0.579	0.037	2.202	L-idonate regulator (GalR/LacI family)
idnT	STM4482	AAL23301	(4725793..4727112)	0.466	0.172	0.267	0.028	0.573	0.538	0.027	1.007	0.104	1.870	GntP family, L-idonate transport protein
idnO	STM4483	AAL23302	(4727174..4727938)	0.715	0.232	0.317	0.040	0.443	1.282	0.481	1.625	0.116	1.267	5-keto-D-gluconate-5-reductase
idnD	STM4484	AAL23303	(4727963..4728994)	0.247	0.115	0.255	0.041	1.032	0.427	0.022	1.287	0.062	3.014	L-idonate 5-dehydrogenase
idnK	STM4485	AAL23304	4729211..4729741			0.387	0.072	N/A	0.808	0.006	1.120	0.025	1.387	D-gluconate kinase, thermosensitive
yjgB	STM4486	AAL23305	(4729769..4730788)	0.632	0.138	0.550	0.075	0.870	0.821	0.006	1.233	0.120	1.502	putative alcohol dehydrogenase
leuX	STM4487						N/A					N/A		
STM4488	STM4488	AAL23306	4731314..4731601	0.410	0.151	0.341	0.047	0.833	0.221	0.052	0.389	0.024	1.756	putative integrase
STM4489	STM4489	AAL23307	4731963..4735478					N/A					N/A	putative superfamily I DNA helicases
STM4490	STM4490	AAL23308	4735575..4736564	1.185	0.037	1.413	0.202	1.192	0.670	0.042	1.759	0.212	2.624	putative Mrr restriction endonuclease
STM4491	STM4491	AAL23309	(4736677..4738761)	0.525	0.092	1.185	0.203	2.257	0.412	0.034	0.725	0.059	1.762	putative ATP-dependent Lon protease
STM4492	STM4492	AAL23310	(4738772..4741369)	0.592	0.049	1.794	0.180	3.029	0.424	0.058	0.987	0.055	2.326	putative cytoplasmic protein
STM4493	STM4493	AAL23311	(4741372..4742193)	0.914	0.054	1.591	0.114	1.740	0.791	0.040	1.565	0.221	1.978	putative cytoplasmic protein
STM4494	STM4494	AAL23312	(4742171..4743262)	1.069	0.028	1.951	0.318	1.825	0.812	0.044	2.013	0.135	2.479	putative ABC-type sugar/spermidine/putrescine transport systems, ATPase onent
STM4495	STM4495	AAL23313	(4743262..4746939)					N/A					N/A	putative type II restriction enzyme, methylase subunit
STM4496	STM4496	AAL23314	(4746985..4750626)	0.500	0.090	1.674	0.347	3.346	0.406	0.027	0.804	0.065	1.981	putative ATPase involved in DNA repair
STM4497	STM4497	AAL23315	(4750638..4751240)	1.371	0.046	1.299	0.096	0.947	0.730	0.006	1.055	0.136	1.445	putative cytoplasmic protein
STM4498	STM4498	AAL23316	(4751237..4751839)	2.522	0.158	1.350	0.132	0.535	1.198	0.080	1.227	0.150	1.024	putative inner membrane protein
yeeN	STM4499	AAL23317	(4752665..4753390)	4.503	0.857	1.650	0.162	0.366	4.023	0.216	1.827	0.169	0.454	putative cytoplasmic protein
yjhP	STM4500	AAL23318	(4753941..4755572)	0.388	0.127	0.898	0.126	2.316	0.212	0.035	0.394	0.044	1.860	putative SAM-dependent methyltransferase
STM4501	STM4501	AAL23319	(4755577..4755834)	0.400	0.099	0.500	0.063	1.252	0.207	0.060	0.395	0.045	1.905	putative cytoplasmic protein
STM4502	STM4502	AAL23320	4756323..4756931	0.374	0.108	0.285	0.028	0.760	0.205	0.035	0.485	0.085	2.365	putative cytoplasmic protein
STM4503	STM4503	AAL23321	4757441..4758178	4.757	0.216	2.397	0.414	0.504	3.218	0.056	2.034	0.164	0.632	putative inner membrane protein
STM4504	STM4504	AAL23322	4758454..4759365	0.478	0.056	0.349	0.042	0.729	6.208	0.757	3.836	0.230	0.618	putative cytoplasmic protein
STM4505	STM4505	AAL23323	4759570..4760031	0.652	0.086	0.378	0.039	0.579	18.209	2.973	11.690	0.834	0.642	putative inner membrane or exported

STM4506	STM4506	AAL23324	(4760028..4760702)	0.551	0.114	0.686	0.201	1.244	5.667	0.309	3.808	0.317	0.672	putative dienelactone hydrolase
uxuR	STM4507	AAL23325	4761052..4761825	0.900	0.032	1.447	0.202	1.608	0.773	0.023	1.407	0.061	1.820	transcriptional repressor for uxu operon
trpS2	STM4508	AAL23326	(4761826..4762839)	0.263	0.109	0.263	0.027	0.999	0.240	0.013	0.388	0.068	1.617	putative tryptophanyl-tRNA synthetase
STM4509	STM4509	AAL23327	4763557..4764087	0.498	0.084	0.412	0.034	0.827	4.993	0.872	2.651	0.421	0.531	putative cytoplasmic protein
STM4510	STM4510	AAL23328	4764326..4765060	0.273	0.138	0.302	0.061	1.106	0.789	0.078	0.641	0.041	0.812	putative aspartate racemase
yjiE	STM4511	AAL23329	(4765066..4765974)	0.502	0.111	0.315	0.035	0.627	0.352	0.088	0.302	0.014	0.859	putative transcriptional regulator, LysR family
iadA	STM4512	AAL23330	(4766093..4767265)	0.428	0.172	0.909	0.078	2.122	0.340	0.036	0.685	0.079	2.013	isoaspartyl dipeptidase
yjiG	STM4513	AAL23331	(4767278..4767739)	0.465	0.133	0.538	0.088	1.157	0.271	0.055	0.415	0.062	1.532	putative permease
yjiH	STM4514	AAL23332	(4767736..4768620)	0.352	0.125	0.267	0.029	0.758	0.222	0.079	0.296	0.015	1.337	putative inner membrane protein
yjiJ	STM4515	AAL23333	(4769280..4770464)	3.271	1.005	0.681	0.033	0.208	0.376	0.005	0.742	0.137	1.975	putative sugar transporter
yjiN	STM4516	AAL23334	(4770684..4771955)	0.437	0.074	0.271	0.071	0.620	0.209	0.028	0.531	0.104	2.536	putative inner membrane protein
yjiO	STM4517	AAL23335	(4772042..4773283)	0.293	0.145	0.187	0.032	0.639	0.220	0.039	0.255	0.015	1.163	putative MFS family transport protein
STM4518	STM4518	AAL23336	4773762..4774277	0.450	0.095	0.229	0.022	0.508	0.242	0.064	0.300	0.032	1.238	putative inner membrane protein
STM4519	STM4519	AAL23337	4774458..4775828	0.655	0.041	0.620	0.090	0.946	1.798	0.113	2.335	0.179	1.299	putative NAD-dependent aldehyde dehydrogenase
STM4520	STM4520	AAL23338	(4775923..4776066)	0.497	0.097	0.284	0.092	0.573	1.179	0.107	0.610	0.029	0.517	putative cytoplasmic protein
yjiS	STM4521	AAL23339	4776033..4776197	0.420	0.120	0.201	0.037	0.479	1.999	0.140	1.359	0.200	0.680	putative cytoplasmic protein
STM4522	STM4522	AAL23340	(4776272..4776973)	0.394	0.030	0.187	0.030	0.473	1.582	0.124	1.046	0.103	0.661	putative inner membrane protein
yjiW	STM4523	AAL23341	(4777047..4777379)	0.864	0.228	0.330	0.050	0.382	1.482	0.130	0.819	0.048	0.552	LexA regulated, putative SOS response
hsdS	STM4524	AAL23342	(4777606..4779015)	0.901	0.059	0.881	0.128	0.978	0.664	0.038	0.384	0.027	0.579	specificity determinant for hsdM and hsdR
hsdM	STM4525	AAL23343	(4779012..4780601)	0.833	0.064	1.120	0.157	1.345	0.570	0.049	0.853	0.078	1.496	DNA methylase M, host modification
hsdR	STM4526	AAL23344	(4780759..4784268)					N/A					N/A	endonuclease R, host restriction
mrr	STM4527	AAL23345	4784466..4785380	0.487	0.083	0.697	0.049	1.432	0.216	0.022	0.468	0.025	2.166	restriction of methylated adenine
STM4528	STM4528	AAL23346	4785649..4785936	0.575	0.111	1.484	0.052	2.582	0.276	0.098	0.773	0.076	2.806	putative inner membrane protein
STM4529	STM4529	AAL23347	4785923..4786225	0.655	0.112	1.163	0.075	1.775	0.454	0.362	0.451	0.074	0.994	putative cytoplasmic protein
yjiA	STM4530	AAL23348	(4786300..4787256)	1.407	0.156	1.649	0.104	1.172	0.560	0.028	0.814	0.018	1.453	putative cobalamin synthesis protein
yjiX	STM4531	AAL23349	(4787267..4787470)	1.430	0.312	1.353	0.108	0.947	0.620	0.042	0.831	0.069	1.340	putative cytoplasmic protein
yjiY	STM4532	AAL23350	(4787565..4789715)	0.729	0.042	0.716	0.073	0.982	0.223	0.056	0.429	0.022	1.924	putative carbon starvation protein
tsr	STM4533	AAL23351	4790082..4791743	5.815	0.622	9.805	1.544	1.686	0.274	0.010	0.450	0.056	1.645	methyl-accepting chemotaxis protein I, serine sensor receptor
STM4534	STM4534	AAL23352	4792067..4794832	0.759	0.071	0.739	0.072	0.974	0.236	0.038	0.361	0.025	1.530	putative NtrC family transcriptional regulators, ATPase domain
STM4535	STM4535	AAL23353	4794934..4795356	0.443	0.123	0.743	0.072	1.677	0.290	0.147	0.825	0.040	2.847	putative PTS permease
STM4536	STM4536	AAL23354	4795371..4795832	0.283	0.128	0.776	0.060	2.741	0.137	0.012	0.779	0.118	5.671	putative PTS permease
STM4537	STM4537	AAL23355	4795858..4796637	0.228	0.109	0.463	0.029	2.031	0.172	0.021	0.591	0.004	3.446	putative PTS permease
STM4538	STM4538	AAL23356	4796627..4797463	0.255	0.153	0.586	0.072	2.298	0.288	0.031	0.862	0.064	2.996	putative PTS permease
STM4539	STM4539	AAL23357	4797476..4798537	0.341	0.165	0.769	0.032	2.256	0.448	0.012	0.954	0.032	2.132	putative glucosamine-fructose-6-phosphate aminotransferase

STM4540	STM4540	AAL23358	4798534..4799565	0.555	0.094	0.681	0.078	1.227	1.152	0.045	1.721	0.177	1.495	putative glucosamine-fructose-6-phosphate aminotransferase
mdoB	STM4541	AAL23359	(4799699..4801951)	1.133	0.019	1.941	0.537	1.713	3.691	0.223	3.766	0.545	1.021	phosphoglycerol transferase I
yjjA	STM4542	AAL23360	(4802273..4802734)	0.940	0.087	1.128	0.069	1.199	0.741	0.075	1.210	0.080	1.634	putative outer membrane protein
dnaC	STM4543	AAL23361	(4802792..4803529)	1.358	0.098	1.611	0.127	1.187	0.925	0.065	1.216	0.067	1.315	chromosome replication; initiation and chain elongation
dnaT	STM4544	AAL23362	(4803532..4804071)	1.767	0.137	0.958	0.133	0.542	1.042	0.086	1.218	0.087	1.169	primosomal protein I
STM4545	STM4545	AAL23363	(4804164..4804637)	0.449	0.126	0.530	0.043	1.180	0.332	0.010	0.666	0.031	2.008	putative inner membrane protein
yjjP	STM4546	AAL23364	(4804628..4805539)	0.443	0.143	0.629	0.036	1.421	0.491	0.004	1.016	0.065	2.070	paral putative membrane protein
yjjQ	STM4547	AAL23365	4806117..4806842	0.338	0.147	0.187	0.038	0.552	0.385	0.019	0.351	0.112	0.913	putative transcriptional regulator (LuxR/UhpA family)
bglJ	STM4548	AAL23366	4806803..4807477	0.249	0.095	0.339	0.042	1.362	0.187	0.032	0.511	0.106	2.736	transcriptional regulator (activator) of bgl operon (LuxR/UhpA family)
STM4549	STM4549	AAL23367	(4807528..4807986)	1.484	0.093	1.769	0.094	1.192	0.807	0.061	1.807	0.086	2.240	putative cytoplasmic protein
fhuF	STM4550	AAL23368	(4808137..4808925)	0.599	0.087	0.283	0.040	0.472	0.203	0.037	0.497	0.028	2.450	ferric hydrozamate transport, involved in reduction of ferric iron in cytoplasmic ferrioxamine B
STM4551	STM4551	AAL23369	(4809046..4810110)	0.354	0.135	0.200	0.028	0.564	0.211	0.003	0.287	0.018	1.364	putative diguanylate cyclase/phosphodiesterase domain 1
STM4552	STM4552	AAL23370	4810361..4810597	0.991	0.112	0.401	0.072	0.405	0.511	0.027	0.350	0.049	0.686	putative inner membrane protein
leuV	STM4553						N/A					N/A		
leuP	STM4554						N/A					N/A		
leuQ	STM4555						N/A					N/A		
rsmC	STM4556	AAL23371	(4811138..4812166)	2.488	0.212	1.217	0.174	0.489	3.035	0.544	1.143	0.068	0.377	16S rRNA m2G 1207 methylse
holD	STM4557	AAL23372	4812269..4812706	1.449	0.098	1.243	0.142	0.858	0.983	0.062	0.698	0.081	0.710	DNA polymerase III, psi subunit
rimI	STM4558	AAL23373	4812651..4813097	0.801	0.119	1.059	0.111	1.322	0.567	0.169	0.597	0.074	1.054	modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine
yjjG	STM4559	AAL23374	4813116..4813796	0.862	0.132	1.202	0.014	1.394	0.509	0.026	0.759	0.108	1.491	putative haloacid dehalogenase-like hydrolase
prfC	STM4560	AAL23375	4813888..4815477	1.396	0.093	1.095	0.088	0.785	1.230	0.082	1.165	0.154	0.948	peptide chain release factor RF-3
osmY	STM4561	AAL23376	4815879..4816496	4.889	1.103	2.306	0.393	0.472	11.887	0.203	16.113	0.668	1.356	hyperosmotically inducible periplasmic protein, RpoS-dependent stationary phase gene
STM4562	STM4562	AAL23377	4816607..4816786	3.215	1.005	0.674	0.098	0.210	9.499	0.419	3.557	0.293	0.374	putative inner membrane protein
yjjU	STM4563	AAL23378	4816910..4817983	3.426	0.913	1.020	0.204	0.298	2.091	0.532	1.384	0.153	0.662	putative phosphoesterase
yjjV	STM4564	AAL23379	4817980..4818753	1.548	0.022	1.193	0.231	0.770	0.808	0.018	1.174	0.136	1.452	putative hydrolase
yjjW	STM4565	AAL23380	(4818786..4819649)	0.683	0.128	1.306	0.194	1.911	0.369	0.109	0.409	0.023	1.106	pyruvate formate lyase activating enzyme
yjjI	STM4566	AAL23381	(4819621..4821171)	0.322	0.148	2.067	0.365	6.430	0.165	0.029	0.453	0.017	2.737	putative cytoplasmic protein
deoC	STM4567	AAL23382	4821413..4822210	1.192	0.076	1.518	0.154	1.273	1.362	0.138	2.673	0.261	1.962	2-deoxyribose-5-phosphate aldolase
deoA	STM4568	AAL23383	4822334..4823656	1.026	0.015	1.138	0.209	1.109	1.169	0.311	1.452	0.122	1.242	thymidine phosphorylase
deoB	STM4569	AAL23384	4823708..4824931	1.468	0.062	5.418	0.523	3.692	1.831	0.051	4.187	0.336	2.286	phosphopentomutase

deoD	STM4570	AAL23385	4825141..4825860	1.391	0.055	4.531	0.330	3.258	0.975	0.031	2.824	0.344	2.897	purine-nucleoside phosphorylase
STM4571	STM4571	AAL23386	(4825898..4826470)	0.462	0.098	0.644	0.023	1.393	0.305	0.004	0.429	0.056	1.408	putative outer membrane protein
stjB	STM4572	AAL23387	(4826467..4828875)	0.266	0.111	0.218	0.045	0.821	0.225	0.036	0.291	0.028	1.295	putative fimbrial usher protein
stjC	STM4573	AAL23388	(4828889..4829596)	0.579	0.059	0.291	0.042	0.503	1.044	0.064	0.877	0.160	0.840	putative fimbrial chaparone protein
STM4574	STM4574	AAL23389	(4829674..4830363)	0.228	0.082	0.196	0.012	0.860	0.961	0.115	1.129	0.027	1.175	putative outer membrane protein
STM4575	STM4575	AAL23390	(4830411..4831100)	0.237	0.131	0.182	0.017	0.771	1.090	0.109	1.227	0.086	1.125	putative outer membrane protein
lplA	STM4576	AAL23391	(4831413..4832429)	0.669	0.044	0.718	0.111	1.073	0.511	0.020	0.888	0.107	1.736	lipoate-protein ligase A
smp	STM4577	AAL23392	(4832463..4833107)	1.095	0.056	0.719	0.070	0.656	0.648	0.077	0.853	0.038	1.316	membrane protein, transcribed divergently from serB
serB	STM4578	AAL23393	4833224..4834192	3.342	0.275	1.948	0.068	0.583	2.017	0.199	1.318	0.039	0.653	3-phosphoserine phosphatase
radA	STM4579	AAL23394	4834276..4835658	2.284	0.200	1.310	0.205	0.574	1.579	0.202	1.380	0.045	0.874	putative ATP-dependent protease, DNA repair protein
nadR	STM4580	AAL23395	4835809..4837041	2.421	0.132	1.311	0.257	0.542	1.360	0.032	1.043	0.075	0.767	three acitivities: regulator of nadAB transcription, regulator of PnuC activity, also contains NMN adenylyltransferase activity
yjjK	STM4581	AAL23396	(4837159..4838826)	2.927	0.161	6.572	0.844	2.245	1.989	0.088	4.619	0.408	2.323	putative ABC superfamily (atp_bind) transport protein
slt	STM4582	AAL23397	4838999..4840972	2.277	0.427	1.906	0.137	0.837	1.371	0.141	1.592	0.032	1.161	lytic murein transglycosylase, soluble
trpR	STM4583	AAL23398	4841030..4841356	4.494	1.169	1.436	0.359	0.320	1.618	0.218	1.339	0.253	0.828	transcriptional repressor for trp operon and aroH (TrpR family)
yjjX	STM4584	AAL23399	(4841458..4841973)	1.474	0.064	1.007	0.179	0.683	0.571	0.070	0.665	0.092	1.165	putative cytoplasmic protein
gpmB	STM4585	AAL23400	4842022..4842669	3.036	0.212	2.813	0.221	0.926	1.291	0.185	2.404	0.229	1.863	putative phosphoglyceromutase 2
rob	STM4586	AAL23401	(4842666..4843535)	6.295	0.627	2.750	0.537	0.437	2.657	0.415	2.755	0.313	1.037	transcriptional regulator (AraC/XylS family)
creA	STM4587	AAL23402	4843747..4844220	2.257	0.470	1.688	0.127	0.748	1.227	0.157	1.723	0.037	1.405	putative periplasmic protein
creB	STM4588	AAL23403	4844233..4844922	3.148	0.428	2.261	0.088	0.718	1.665	0.308	2.186	0.080	1.313	response regulator in two-onent regulatory system with CreC (OmpR family)
creC	STM4589	AAL23404	4844922..4846346	1.610	0.253	0.703	0.131	0.437	0.703	0.152	0.681	0.129	0.969	sensory kinase (alternative) in two-onent regulatory system with CreB (or alternatively PhoB), senses catabolite repression,
creD	STM4590	AAL23405	4846404..4847753	0.552	0.059	0.221	0.031	0.400	0.221	0.008	0.318	0.012	1.440	tolerance to colicin E2
sthE	STM4591	AAL23406	(4847811..4848896)	0.434	0.087	0.164	0.015	0.378	0.379	0.072	0.364	0.049	0.961	putative major fimbrial subunit
sthD	STM4592	AAL23407	(4848937..4849494)	0.274	0.133	0.161	0.036	0.587	0.258	0.055	0.265	0.065	1.028	putative fimbrial subunit
sthB	STM4593	AAL23408	(4849512..4852049)					N/A					N/A	putative fimbrial usher protein
sthA	STM4594	AAL23409	(4852095..4852778)	0.284	0.133	0.158	0.030	0.558	0.457	0.019	0.535	0.060	1.171	putative fimbrial chaparone protein
STM4595	STM4595	AAL23410	(4852849..4853394)	0.276	0.119	0.262	0.045	0.948	1.043	0.099	1.085	0.142	1.040	putative fimbrial chaparone protein
STM4596	STM4596	AAL23411	(4853733..4854404)	0.570	0.056	0.415	0.057	0.729	2.050	0.189	1.373	0.103	0.670	putative inner membrane protein
STM4597	STM4597	AAL23412	(4854789..4855103)	2.084	0.325	1.056	0.211	0.507	1.802	0.168	1.135	0.084	0.630	putative periplasmic protein
arcA	STM4598	AAL23413	(4855370..4856086)	26.400	4.983	14.805	1.414	0.561	15.436	1.334	15.681	0.854	1.016	response regulator (OmpR family) in two-onent regulatory system with ArcB (or xA), regulates genes in aerobic pathways
yjjY	STM4599	AAL23414	4856182..4856322	29.804	5.980	8.916	0.615	0.299	16.484	2.605	11.194	0.253	0.679	putative inner membrane protein

STM2252	STM2252			0.704	0.100	7.641	0.931	10.849	1.090	0.197	0.915	0.072	0.839
STM2250	STM2250			0.708	0.114	10.256	1.426	14.486	1.093	0.365	1.171	0.069	1.071
STM2248	STM2248			0.437	0.165	5.490	0.158	12.561	0.736	0.027	0.682	0.070	0.926
STM3246	STM3246			57.864	18.434	26.950	2.600	0.466	59.465	11.573	61.645	8.729	1.037
STM1044	STM1044			1.130	0.179	2.263	0.266	2.003	9.652	0.494	14.538	1.204	1.506
STM3894	STM3894			49.690	21.787	63.495	9.306	1.278	22.012	1.162	64.183	5.253	2.916
STM0559	STM0559			0.872	0.174	0.138	0.011	0.159	0.685	0.075	0.242	0.020	0.353
STM2693	STM2693			66.909	22.218	35.531	3.010	0.531	41.098	7.204	29.252	6.770	0.712
STM3738	STM3738			0.727	0.115	0.409	0.063	0.562	1.883	0.523	0.611	0.032	0.324
STM0467	STM0467			7.558	8.375	0.930	0.298	0.123	2.453	0.909	2.681	0.487	1.093
STM4124	STM4124			2.004	0.264	1.543	0.131	0.770	2.536	5.798	1.429	0.612	0.564
STM1398	STM1398			0.258	0.060	0.215	0.026	0.833	6.613	0.174	10.481	0.971	1.585
STM1397	STM1397			0.394	0.098	0.369	0.041	0.938	8.505	0.283	17.103	1.040	2.011
STM4600	STM4600			1.016	0.045	0.835	0.102	0.822	0.845	0.205	0.774	0.028	0.916
STM1985	STM1985			3.022	0.601	2.435	0.128	0.806	2.810	0.383	2.750	0.753	0.979
STM1983	STM1983			0.948	0.052	1.296	0.246	1.368	1.458	0.091	0.797	0.050	0.547
STM2966	STM2966			16.287	5.134	13.391	5.146	0.822	7.874	2.193	3.678	0.997	0.467
PSLT001	PSLT001	NP_490493		0.699	0.139	0.979	0.023	1.399	0.388	0.037	1.101	0.060	2.836
PSLT002	PSLT002	NP_490494						N/A					N/A
PSLT003	repC	NP_490495		3.203	0.686	0.923	0.056	0.288	2.128	0.022	1.039	0.118	0.488
PSLT004	repA3	NP_490496		3.997	0.577	2.293	0.214	0.574	2.377	0.355			0.000
PSLT005	tap	NP_490497		4.656	0.380			0.000	4.187				0.000
PSLT006	repA	NP_490498		2.158	0.011	0.787	0.046	0.365	1.513	0.058	1.199	0.163	0.792
PSLT007	PSLT007	NP_490499						N/A					N/A
PSLT008	srgC	NP_490500		0.575	0.256	0.287	0.067	0.499	0.850	0.069	1.126	0.042	1.324
PSLT009	rcK	NP_490501		0.419	0.309	0.362	0.067	0.865	2.750	0.511	5.947	0.225	2.163
PSLT010	srgB	NP_490502						N/A					N/A
PSLT011	srgA	NP_490503		0.465	0.379	0.221	0.050	0.474	2.920	0.719	3.079	0.530	1.055
PSLT012	orf7	NP_490504		0.548	0.323	0.320	0.037	0.583	6.339	0.951	8.748	0.697	1.380
PSLT013	pefI	NP_490505		0.565	0.236	0.410	0.022	0.726	7.812	0.578	8.537	0.583	1.093
PSLT014	orf6	NP_490506		1.371	0.072	0.823	0.071	0.600	5.935	0.146	6.316	0.373	1.064
PSLT015	orf5	NP_490507		0.785	0.308	0.262	0.044	0.333	0.612	0.172	1.062	0.042	1.736
PSLT016	pefD	NP_490508		0.446	0.381	0.229	0.051	0.513	0.314	0.008	0.887	0.085	2.827
PSLT017	pefC	NP_490509		0.276	0.371	0.159	0.038	0.579	0.260	0.028	0.709	0.012	2.726
PSLT018	pefA	NP_490510		0.387	0.289	0.483	0.075	1.247	3.365	0.728	6.701	0.709	1.992
PSLT019	pefB	NP_490511		0.318	0.274	0.206	0.028	0.648	0.962	0.047	0.999	0.082	1.038
PSLT020	PSLT020	NP_490512						N/A					N/A
PSLT021	PSLT021			0.581	0.335	0.414	0.127	0.713	0.441	0.096	0.662	0.070	1.502

PSLT022	repA2			0.508	0.302	0.174	0.025	0.343	0.342	0.038	0.517	0.077	1.508
PSLT023	repA2	NP_490513		3.727	0.169	2.344	0.143	0.629	2.615	0.189	2.590	0.238	0.991
PSLT024	PSLT024	NP_490514		2.688	0.079	1.476	0.235	0.549	1.874	0.301	1.912	0.088	1.020
PSLT025	PSLT025	NP_490515		0.499	0.164	0.293	0.038	0.587	0.581	0.219	0.577	0.045	0.993
PSLT026	PSLT026	NP_490516		1.049	0.073	0.459	0.119	0.438	0.748	0.051	0.869	0.029	1.162
PSLT027	ccdA	NP_490517		2.189	0.359	3.273	0.148	1.495	1.209	0.107	1.937	0.060	1.603
PSLT028	ccdB	NP_490518		2.695	0.425	3.591	0.128	1.333	1.649	0.277	2.586	0.098	1.568
PSLT029	PSLT029	NP_490519		2.158	0.096	2.662	0.622	1.234	1.455	0.144	2.448	0.018	1.682
PSLT030	PSLT030	NP_490520		2.510	0.067	4.470	0.164	1.781	1.441	0.213	2.476	0.163	1.718
PSLT031	rsdB	NP_490521		2.311	0.142	2.490	0.146	1.077	1.503	0.289	2.416	0.080	1.607
PSLT032	PSLT032	NP_490522		7.035	0.750	6.259	1.166	0.890	7.151	0.778	11.174	5.408	1.562
PSLT033	PSLT033	NP_490523						N/A					N/A
PSLT034	PSLT034	NP_490524		0.877	0.211	0.976	0.101	1.113	0.323	0.047	0.676	0.062	2.093
pSLT035	PSLT035	NP_490525		2.352	0.480	5.539	0.634	2.355	0.710	0.088	1.151	0.068	1.622
PSLT036	PSLT036	NP_490526		0.722	0.184	0.429	0.083	0.593	0.717	0.097	0.858	0.081	1.197
PSLT037	spvD	NP_490527		0.300	0.211	0.259	0.037	0.865	1.923	0.245	4.957	0.433	2.578
PSLT038	spvC	NP_490528		0.286	0.290	0.144	0.012	0.505	3.048	0.030	10.665	1.141	3.499
PSLT039	spvB	NP_490529		0.330	0.261	0.154	0.023	0.468	1.318	0.105	9.698	1.058	7.358
PSLT040	spvA	NP_490530		0.628	0.233	0.375	0.078	0.598	5.079	1.143	27.041	2.007	5.324
PSLT041	spvR	NP_490531		0.320	0.266	0.150	0.017	0.470	1.577	0.294	1.120	0.173	0.710
PSLT042	PSLT042	NP_490532		0.422	0.255	0.316	0.034	0.749	0.771	0.084	1.110	0.153	1.439
PSLT043	PSLT043	NP_490533		1.646	0.078	2.477	0.136	1.504	2.212	0.294	3.886	0.380	1.757
PSLT044	rlgA	NP_490534		3.106	0.389	3.230	0.171	1.040	4.545	1.109	6.466	1.031	1.423
PSLT045	PSLT045	NP_490535		5.760	0.623	5.606	0.488	0.973	10.185	2.842	18.412	1.249	1.808
PSLT046	PSLT046	NP_490536		6.097	0.214	4.395	0.448	0.721	29.836	3.296	38.783	2.250	1.300
PSLT047	PSLT047	NP_490537		0.903	0.202	0.700	0.165	0.775	0.724	0.050	1.049	0.177	1.450
PSLT048	tlpA	NP_490538		0.668	0.182	1.397	0.110	2.091	0.511	0.186	1.799	0.419	3.523
PSLT049	PSLT049	NP_490539		0.794	0.247	0.821	0.038	1.034	0.591	0.090	1.121	0.032	1.898
PSLT050	PSLT050	NP_490540		1.039	0.307	0.970	0.106	0.933	0.657	0.039	0.981	0.094	1.492
PSLT051	samB	NP_490541		1.698	0.153	3.194	0.204	1.881	1.104	0.079	2.724	0.251	2.468
PSLT052	parA	NP_490542		1.170	0.025	1.622	0.097	1.386	0.479	0.033	1.245	0.118	2.601
PSLT053	parB	NP_490543		1.628	0.080	2.241	0.358	1.377	0.792	0.035	2.121	0.101	2.678
PSLT054	samB	NP_490544		0.702	0.276	0.432	0.035	0.615	0.464	0.056	0.749	0.119	1.617
PSLT055	samA	NP_490545		0.635	0.252	0.454	0.036	0.714	0.690	0.107	0.686	0.054	0.995
PSLT056	PSLT056	NP_490546		0.310	0.368	0.171		0.550	0.182	0.051	0.487		2.671
PSLT057	PSLT057	NP_490547		0.353	0.337	0.142	0.020	0.403	0.185	0.024	0.361	0.087	1.957
PSLT058	PSLT058			0.436	0.419	0.193	0.056	0.443	0.201	0.017	0.440	0.041	2.187
PSLT059	PSLT059	NP_490548		0.441	0.392	0.216	0.019	0.490	0.295	0.132	0.583	0.070	1.972

PSLT060	PSLT060	NP_490549		0.625	0.395	0.699	0.030	1.117	0.394	0.109	0.991	0.495	2.517
PSLT061	PSLT061	NP_490550		0.392	0.360	0.298	0.043	0.760	0.351	0.114	0.731	0.033	2.086
PSLT062	PSLT062	NP_490551		0.334	0.255	0.121	0.013	0.362	0.225	0.075	0.308	0.039	1.370
PSLT063	PSLT063	NP_490552						N/A					N/A
PSLT064	PSLT064	NP_490553		0.680	0.258	0.175	0.037	0.257	0.687	0.508	0.517	0.030	0.753
PSLT065	PSLT065			0.691	0.404	0.684	0.075	0.991	0.643	0.560	0.999	0.360	1.553
PSLT066	ssbB	NP_490554		0.352	0.436	0.198	0.024	0.563	0.175	0.020	0.388	0.021	2.216
PSLT067	PSLT067	NP_490555		0.605	0.247	0.250	0.009	0.412	0.332	0.010	0.495	0.124	1.488
PSLT068	PSLT068	NP_490556		0.368	0.400	0.158	0.016	0.429	0.182	0.010	0.493	0.058	2.701
PSLT069	psiB	NP_490557		0.527	0.428	0.278	0.065	0.527	0.356	0.036	0.753	0.108	2.114
PSLT070	psiA	NP_490558		0.585	0.258	0.383	0.056	0.654	0.416	0.071	0.844	0.183	2.031
PSLT071	PSLT071			0.307	0.271	0.138	0.008	0.448	0.508	0.041	0.475	0.102	0.934
PSLT072	finP	NP_490559		0.611	0.316	0.196	0.070	0.320	4.447	0.488	2.418	0.069	0.544
PSLT073	traM	NP_490560		0.638	0.163	0.171	0.068	0.268	5.497	0.017	2.568	0.262	0.467
PSLT074	finP			0.564	0.281	0.523	0.369	0.927	2.328	0.578	0.891	0.311	0.383
PSLT075	traJ	NP_490561						N/A					N/A
PSLT076	traY	NP_490562		0.279	0.183	0.193	0.022	0.692	1.339	0.063	1.023	0.179	0.764
PSLT077	traA	NP_490563		0.357	0.326	0.209	0.069	0.586	2.122	0.594	2.115	0.124	0.996
PSLT078	traL	NP_490564		0.292	0.359	0.164	0.045	0.561	0.812	0.101	0.980	0.135	1.208
PSLT079	traE	NP_490565		0.286	0.360	0.131	0.023	0.458	0.534	0.064	0.701	0.092	1.313
PSLT080	traK	NP_490566		0.428	0.361	0.189	0.011	0.440	0.776	0.030	1.647	0.112	2.122
PSLT081	traB	NP_490567		0.327	0.366	0.129	0.019	0.395	0.451	0.108	0.961	0.103	2.131
PSLT082	traP	NP_490568		0.272	0.332	0.131	0.037	0.480	0.386	0.046	0.831	0.043	2.151
PSLT083	trbD	NP_490569		0.350	0.283	0.309	0.089	0.882	0.744	0.303	1.688	0.027	2.269
PSLT084	traV	NP_490570		0.274	0.377			0.000	0.807	0.014			0.000
PSLT085	traR	NP_490571		0.411	0.314	0.252	0.015	0.614	0.708	0.058	0.996	0.033	1.406
PSLT087	PSLT087	NP_490572		0.296	0.323	0.149	0.051	0.504	0.609	0.067	0.957	0.105	1.572
PSLT088	traC	NP_490573		0.348	0.450	0.129	0.024	0.370	0.411	0.052	0.937	0.048	2.280
PSLT089	trbI	NP_490574		0.404	0.397	0.216	0.035	0.533	0.663	0.049	1.332	0.105	2.009
PSLT091	traW	NP_490575		0.506	0.458	0.192	0.017	0.379	0.718	0.164	1.363	0.115	1.898
PSLT092	traU	NP_490576		0.338	0.333	0.118	0.013	0.348	0.458	0.084	0.950	0.065	2.073
PSLT093	PSLT093	NP_490577		0.367	0.286	0.172	0.013	0.469	0.419	0.059	0.754	0.054	1.799
PSLT094	trbC	NP_490578		0.351	0.368			0.000	0.376	0.050			0.000
PSLT095	traN	NP_490579		0.412	0.410	0.262	0.043	0.635	0.296	0.043	0.967	0.048	3.266
PSLT096	trbE	NP_490580		0.347	0.248	0.219	0.015	0.630	0.485	0.067	0.773	0.097	1.593
PSLT097	traF	NP_490581		0.343	0.312	0.159	0.011	0.465	0.428	0.010	0.993	0.042	2.319
PSLT098	traQ	NP_490582		0.336	0.318	0.240		0.716	0.926	0.079			0.000
PSLT099	trbB	NP_490583		0.424	0.427	0.213	0.067	0.502	0.895	0.121	2.269	0.125	2.535

PSLT100	traH	NP_490584		0.358	0.296	0.218	0.016	0.608	0.578	0.087	2.290	0.214	3.962
PSLT101	traG	NP_490585		0.537	0.190	0.500	0.055	0.931	0.586	0.095	1.946	0.196	3.321
PSLT102	traS	NP_490586		1.127	0.105			0.000	4.110	0.142			0.000
PSLT103	traT	NP_490587		0.997	0.075	10.890	1.590	10.925	3.054	1.099	11.075	1.874	3.627
PSLT104	traD	NP_490588		0.383	0.387	0.402	0.045	1.049	0.663	0.089	1.647	0.121	2.484
PSLT105	trbH	NP_490589		0.499	0.265	0.691	0.062	1.385	0.638	0.082	1.391	0.092	2.181
PSLT106	PSLT106	NP_490590		0.550	0.307	0.762	0.080	1.386	0.911	0.459	1.467	0.111	1.610
PSLT107	PSLT107	NP_490591		0.545	0.299	1.000	0.109	1.836	0.794	0.110	1.564	0.110	1.970
PSLT108	traI	NP_490592						N/A					N/A
PSLT109	PSLT109			1.333	0.262	0.577	0.060	0.433	1.738	0.559	2.967	0.259	1.707
PSLT110	traX	NP_490593		0.960	0.200	0.449	0.068	0.467	0.987	0.322	1.447	0.095	1.465
PSLT111	PSLT111			1.231	0.109	1.257	0.178	1.021	0.708	0.179	1.588	0.058	2.242