Supplementary Table S1A. Summary of sequencing and annotation statistics from metagenomic libraries (2 biological replicates; both with 3 technical replicates) assembled from methanogenic rice paddy soil microcosms.

	Mean	SEM	Max	Min	Units
Raw (unfiltered) forward reads	3,827,003	172,996.79	4,000,000	1,578,045	# reads/metagenome
Raw (unfiltered) reverse reads	3,999,392	413.16	4,000,000	3,995,743	# reads/metagenome
QC-filtered forward reads	3,318,562	175,385.23	3,889,962	996,047	# reads/metagenome
QC-filtered reverse reads	3,318,562	175,385.23	3,889,962	996,047	# reads/metagenome
QC-filtered merged paired end reads	306,024	42,851.74	357,639	135,028	# reads/metagenome
QC-filtered merged paired end read size	154.37	1.05	190	100	Bases/read
GC content	54.65%	0.21%	55%	51%	Percent/metagenome
Predicted protein-coding reads	303,743	42,537.09	354,987	134,005	Protein-coding genes/metagenome
Relative abundance of rRNA	0.75%	0.01%	0.78%	0.70%	Percent/metagenome
Bacterial fraction of protein-coding genes	64.64%	4.78%	72.91%	46.33%	Percent annotatable/metagenome
Archaeal fraction of protein-coding genes	35.35%	6.13%	43.67%	17.09%	Percent annotatable/metagenome
Eukaryotic fraction of protein-coding genes	1.14%	0.19%	1.14%	0.70%	Percent annotatable/metagenome
Viral fraction of protein-coding genes	0.05%	0.007%	0.07%	0.03%	Percent annotatable/metagenome

Supplementary Table S1B. Summary of sequencing and annotation statistics from the metatranscriptomic libraries (6 biological replicates; each with 2 technical replicates) assembled from methanogenic rice paddy soil microcosms.

	Mean	SEM	Max	Min	Units
Raw (unfiltered) forward reads	3,813,285	186,715.50	4,000,000	2,132,845	Bases/metatranscriptome
Raw (unfiltered) reverse reads	2,791,739	204,487.62	4,000,000	2,020,792	# reads/metatranscriptome
QC-filtered forward reads	2,222,209	258,033.28	2,776,927	1,454,663	# reads/metatranscriptome
QC-filtered reverse reads	2,222,209	258,033.28	2,776,927	1,454,663	# reads/metatranscriptome
QC-filtered merged paired end reads	1,115,233	244,024.87	1,850,452	15,515	QC-filtered reads/metatranscriptome
QC-filtered merged paired end read size	154.40	1.14	190	100	Bases/read
GC content	54.73%	0.44%	57%	51%	Percent/metatranscriptome
Predicted protein-coding reads	158,039	37,234.75	230,399	8667	Proteins/metatranscriptome
Relative abundance of rRNA	83.95%	1.54%	96%	66%	Percent/metatranscriptome
Bacterial fraction of protein-coding genes	52.45%	3.29%	69.9%	39.38%	Percent annotatable/metatranscriptome
Archaeal fraction of protein-coding genes	33.17%	3.43%	55.34%	11.92%	Percent annotatable/metatranscriptome
Eukaryotic fraction of protein-coding genes	13.61%	1.35%	15.4%	11.58%	Percent annotatable/metatranscriptome
Viral fraction of protein-coding genes	0.06%	0.02%	0.34%	0%	Percent annotatable/metatranscriptome

Supplementary Table S2. Statistics from assembly of QC-filtered non-merged metagenomic and QC-filtered merged metatranscriptomic reads from libraries constructed from methanogenic rice paddy sediment microcosms. The values represent the averages and standard errors of the mean (SEM) from metagenomic (2 biological replicates; both with 3 technical replicates) and metatranscriptomic (6 biological replicates; each with 2 technical replicates) assemblies.

	Number of reads assembled to larger contigs	Percentage of reads assembled	Total number of assembled contigs	Mean contig size (bp)	Maximum contig size (bp)	Minimum contig size (bp)	Read Coverage	# ORFs identified in contigs
Metagenomic libraries	645018 +/- 11656	21.75% +/- 3.15%	17191 +/- 3798	455 +/- 95.30	6419 +/- 1293	150	4.31 +/- 1.73	12473 +/- 730.12
Metatranscriptomic libraries	26378 +/- 10248	17.04% +/- 2.33%	7432 +/- 1640	217 +/- 17.14	941 +/- 169.56	150	5.91 +/- 0.78	4070 +/- 1858.10

Supplementary Table S3A. Taxonomic classification of archaeal QC-filtered merged metatranscriptomic reads (~150 bp in size) determined by Genomepeek, MG-RAST, BLASTx, and Kraken software programs. Values represent the mean and standard error of all biological and technical replicates.

Software program	**Percent methanogens**	**Methanobacteriaceae**	**Methanocalculaceae**	**Methanocellaceae**	**Methanomicrobiaceae**	**Methanoregulaceae**	***Methanothrix***	**other Methanosarcinaceae genera**	**Methanospirillaceae**	***Methanosarcina***
Genomepeek	91.54% +/- 10.01%	13.86% +/- 12.16%	1.14% +/- 0.81%	2.83% +/- 2.61%	13.29% +/- 10.99%	9.78% +/- 7.82%	13.20 +/- 9.78%	6.39% +/- 5.02%	1.75% +/- 0.98%	23.61% +/- 13.50%
MG-RAST	82.19% +/- 10.39%	12.85% +/- 9.68%	0.67% +/- 0.12%	0.51% +/- 0.38%	4.45% +/- 3.91%	6.96% +/- 4.02%	22.14% +/- 6.16%	5.35% +/- 3.81%	5.65% +/- 3.56%	35.12% +/- 14.94%
BLASTx	97.65% +/- 2.59%	13.91% +/- 7.77%	0.86% +/- 0.23%	1.35% +/- 1.08%	28.79% +/- 6.39%	1.62% +/- 0.80%	19.59% +/- 7.22%	7.35% +/- 4.29%	0.20% +/- 0.12%	23.89% +/- 6.78%
Kraken	97.10% +/- 1.07%	14.37% +/- 3.99%	0.15% +/- 0.01%	1.01% +/- 0.20%	5.32% +/- 1.10%	4.74% +/- 1.65%	37.59% +/- 8.56%	4.52% +/- 2.32%	0.50% +/- 0.23%	25.61% +/- 3.68%

Supplementary Table S3B. Taxonomic classification of archaeal QC-filtered merged metagenomic reads (~150 bp in size) determined by Genomepeek, MG-RAST, BLASTx, and Kraken software programs. Values represent the mean and standard error of all biological and technical replicates.

Software program	**Percent methanogens**	**Methanobacteriaceae**	**Methanocalculaceae**	**Methanocellaceae**	**Methanomicrobiaceae**	**Methanoregulaceae**	***Methanothrix***	**other Methanosarcinaceae genera**	**Methanospirillaceae**	***Methanosarcina***
Genomepeek	74.10% +/- 18.09%	10.61 +/- 6.89%	2.61% +/- 2.28%	13.75% +/- 6.67%	0.92% +/- 0.51%	17.31% +/- 6.18%	14.73% +/- 9.46%	9.53% +/- 6.55%	6.85% +/- 3.43%	15.31% +/- 12.94%
MG-RAST	66.31% +/- 7.54%	9.49% +/- 2.39%	4.79% +/- 1.18%	2.49% +/- 1.14%	5.82% +/- 3.28%	18.09% +/- 3.79%	9.81% +/- 4.72%	10.58% +/- 3.19%	4.28% +/- 3.38%	17.36% +/- 2.37%
BLASTx	71.59% +/- 24.18%	12.07+/- 3.64%	4.32% +/- 1.51%	4.37% +/- 1.22%	2.68% +/- 0.59%	9.63% +/- 2.13%	14.98% +/- 0.63%	12.44% +/- 11.79%	10.22% +/- 1.67%	25.58% +/- 1.67%
Kraken	66.27% +/- 9.62%	4.64% +/- 4.48%	13.49% +/- 7.58%	15.15% +/- 4.10%	7.82% +/- 6.66%	8.21% +/- 1.12%	17.49% +/- 7.58%	4.23% +/- 1.83%	1.70% +/- 1.22%	22.81% +/- 6.20%

Supplementary Table S3C. Taxonomic classification of bacterial QC-filtered merged metatranscriptomic reads (~150 bp in size) determined by Genomepeek, MG-RAST, BLASTx, and Kraken software programs. Values represent the mean and standard deviation of all biological and technical replicates.

Software program	**Actinobacteria**	**alphaproteobacteria**	**Bacteroidetes**	**betaproteobacteria**	**Other deltaproteobacteria**	**Firmicutes**	**gammaproteobacteria**	**Other Desulfuromondales**	**Geobacteraceae**
Genomepeek	6.32% +/- 1.27%	8.61% +/- 1.73%	5.93% +/- 3.15%	12.98% +/- 5.67%	11.74% +/- 9.21%	9.11% +/- 6.97%	11.62% +/- 5.27%	3.11% +/- 2.66%	24.73% +/- 14.73%
MG-RAST	3.80% +/- 1.13%	5.25% +/- 2.26%	2.35% +/- 1.17%	15.27% +/- 3.39%	6.36% +/- 2.16%	15.90% +/- 4.04%	14.01% +/- 3.02%	3.14% +/- 2.42%	12.14% +/- 1.36%
BLASTx	5.77% +/- 1.06%	4.08% +/- 1.61%	1.75% +/- 0.35%	9.16% +/- 0.52%	8.53% +/- 7.10%	13.26% +/- 8.39%	25.29+/- 13.27%	5.75% +/- 2.03%	23.97% +/- 10.01%
Kraken	8.85% +/- 1.91%	17.13% +/- 6.14%	2.89% +/- 0.72%	15.45% +/- 3.59%	7.13% +/- 4.82%	8.91% +/- 2.39%	14.40% +/- 6.97%	1.64% +/- 0.62%	13.79% +/- 8.65%

Supplementary Table S3D. Taxonomic classification of bacterial QC-filtered merged metagenomic reads (~150 bp in size) determined by Genomepeek, MG-RAST, BLASTx, and Kraken software programs. Values represent the mean and standard error of all biological and technical replicates.

Software program	**Actinobacteria**	**alphaproteobacteria**	**Bacteroidetes**	**betaproteobacteria**	**Other deltaproteobacteria**	**Firmicutes**	**gammaproteobacteria**	**Other Desulfuromondales**	**Geobacteraceae**
Genomepeek	7.93% +/- 3.52%	12.26% +/- 4.61%	6.28% +/- 2.49%	7.07% +/- 2.21%	9.76 +/- 5.78%	18.48% +/- 8.23%	8.16% +/- 2.11%	6.88% +/- 6.17%	14.10% +/- 5.29%
MG-RAST	6.49% +/- 3.00%	6.50% +/- 1.93%	3.27% +/- 2.27%	10.05% +/- 5.61%	6.60% +/- 2.46%	12.05% +/- 3.44%	6.25% +/- 1.45%	5.92% +/- 2.32%	13.46% +/- 4.04%
BLASTx	5.87% +/- 3.01%	6.88% +/- 2.26%	3.71% +/- 1.78%	8.59% +/- 4.07%	8.15% +/- 4.63%	17.14% +/- 4.75%	4.28% +/- 1.73%	4.86% +/- 5.63%	15.16% +/- 8.01%
Kraken	4.84% +/ 0.55	10.31% +/- 1.27%	4.25% +/- 1.39%	22.07% +/- 7.35%	7.37% +/- 2.06%	15.83% +/- 3.53%	10.84% +/- 2.50%	7.63% +/- 2.43%	11.33% +/- 2.45%

Supplementary Table S4A. Phylogenetic distribution of archaeal open reading frames translated from contigs assembled from QC-filtered merged metatranscriptomic and nonmerged metagenomic reads determined by the BLASTp algorithm. Contigs were assembled with MegaHit software and ORFs were identified with Prodigal software. Values represent the mean and standard error of the mean for all biological and technical replicates.

Library	**Percent methanogens**	**Methanobacteriaceae**	**Methanocalculaceae**	**Methanocellaceae**	**Methanomicrobiaceae**	**Methanoregulaceae**	***Methanothrix***	**other Methanosarcinaceae genera**	**Methanospirillaceae**	***Methanosarcina***
ORFs from metatranscriptomic contigs	86.32% +/- 3.65	14.55% +/- 8.63	2.25 +/- 1.29	8.41% +/- 2.78	2.64% +/- 1.99	5.62% +/- 3.15	24.33% +/- 2.77	6.21% +/- 1.42	2.15% +/- 1.31	26.16% +/- 2.94
ORFs from metagenomic contigs	71.42% +/- 3.83	13.26% +/- 3.22	2.39% +/- 0.75	6.54% +/- 1.97	5.70% +/- 2.16	7.33% +/- 1.73	14.55% +/- 1.19	11.75% +/- 1.36	6.06% +/- 3.60	23.75% +/- 4.52

Supplementary Table S4B. Phylogenetic distribution of bacterial open reading frames translated from contigs assembled from QC-filtered merged metatranscriptomic and nonmerged metagenomic reads determined by the BLASTp algorithm. Contigs were assembled with MegaHit software and ORFs were identified with Prodigal software. Values represent the mean and standard error of the mean for all biological and technical replicates.

Library	**Actinobacteria**	**alphaproteobacteria**	**Bacteroidetes**	**betaproteobacteria**	**Other deltaproteobacteria**	**Firmicutes**	**gammaproteobacteria**	**Other Desulfuromondales**	**Geobacteraceae**
ORFs from metatranscriptomic contigs	12.12% +/- 1.43	14.26% +/- 0.88	7.65% +/- 1.52	9.88% +/- 1.36	6.74% +/- 1.47	15.22% +/- 2.15	16.09% +/- 3.21	1.32% +/- 0.41	10.35% +/- 1.70
ORFs from metagenomic contigs	8.53% +/- 2.23	5.30% +/- 1.72	6.18% +/- 1.01	11.63% +/- 3.28	5.86% +/- 1.35	11.67% +/- 1.24	23.15% +/- 7.44	6.22% +/- 1.36	14.59 +/- 3.62

Suplementary Table S5. List of Type IV *pilA* genes used to build the hidden Markov model database, the blastn and blastx databases, and the database used to map metatranscriptomic and metagenomic reads to e-pilin and long *pilA* nucleotide sequences with ArrayStar and Bowtie2.

Organism	**Pilin class**	**Locus ID**
Geobacter bemidjiensis	e-pilin	Gbem_2590
Geobacter bremensis	e-pilin	K419DRAFT_00801
Pelobacter seleniigenes	e-pilin	N909DRAFT_0006
Geobacter sp. OR-1	e-pilin	WP_041974243
Geobacter sp. M18	e-pilin	GM18_2492
Geobacter sp. M21	e-pilin	GM21_1636
Desulfuromonas sp. TF	e-pilin	DTFDRAFT_03630
Geoalkalibacter ferrihydriticus	e-pilin	Ga0056053_00657
Geoalkalibacter subterraneus	e-pilin	WP_040199521
Desulfuromonas thiophila	e-pilin	Ga0056074_12312
Geobacter metallireducens	e-pilin	Gmet_1399
Geobacter lovleyi	e-pilin	Glov_2096
Geobacter sulfurreducens	e-pilin	GSU1496
Geobacter pickeringii	e-pilin	Ga0069007_111762
Desulfuromusa kysingii	e-pilin	Ga0056096_02700
Geobacter argillaceus	e-pilin	Ga0052872_01800, Ga0052872_01802
Geobacter soli	e-pilin	WP_039645155
Geopsychrobacter electrodiphilus	e-pilin	D888DRAFT_2042
Pelobacter propionicus	e-pilin	Ppro_1656
Desulfuromonas subbituminosa	long type IVa pilA	Ga0064601_106193
Geobacter uraniireducens	long type IVa pilA	Gura_2677
Geobacter daltonii	long type IVa pilA	Geob_3369
Desulfuromonas soudanensis WTL	long type IVa pilA	Ga0069009_112157
Pelobacter carbinolicus	long type IVa pilA	Pcar_2154, Pcar_2144
Desulfobacter postgatei	long type IVa pilA	DespoDRAFT_1114
Desulfobacterium autotrophicum	e-pilin	HRM2_27700
Thermincola ferriacetica	long type IVa pilA	TferDRAFT_00608
Carboxydothermus ferrireducens	long type IVa pilA	CarfeDRAFT_00001450
Deferrisoma camini	long type IVa pilA	DefcaDRAFT_3089, DefcaDRAFT_3087
Fervidicella metallireducens	long type IVa pilA	Q428_01340
Desulfovibrio vulgaris	long type IVa pilA	Ga0076800_111227
Thermincola potens	long type IVa pilA	WP_049771692
Carboxydothermus hydrogenoformans	long type IVa pilA	CHY_0635
Shewanella oneidensis	long type IVa pilA	SO0417
Anaeromyxobacter dehalogenans	long type IVa pilA	A2cp1_0669
Thermoanaerobacter ethanolicus	long type IVa pilA	TeCCSD1DRAFT_1919
Thermoanaerobacter cellulolyticus	long type IVa pilA	N907DRAFT_0879
Caloramator australicus	long type IVa pilA	WP_008908368
Desulfotomaculum reducens	long type IVa pilA	Dred_1042
Anaeromyxobacter sp. strain FW109-5	long type IVa pilA	Anae109_0680
Desulfosporosinus orientis	long type IVa pilA	Desor_0988
Acidithiobacillus ferrooxidans	long type IVa pilA	AFE_0416
Acidithiobacillus ferrivorans	long type IVa pilA	Ga0058672_17875
Desulfosporosinus meridei	long type IVa pilA	Desmer_0976, Desmer_0977
Aeromonas hydrophila	long type IVa pilA	AHA_0692
Shewanella algae	long type IVa pilA	BryDRAFT_00594
Rhodoferax ferrireducens	long type IVa pilA	Rfer_1265

Acidithrix ferrooxidans	long type IVa pilA	AFO_01365
Alkaliphilus metalliredigens	long type IVa pilA	Amet_3479
Clostridium beijerinckii	long type IVa pilA	Cbei_4216
Desulfitobacterium hafniese	long type IVa pilA	Dhaf_3553
Desulfitobacterium metallireducens	long type IVa pilA	Desme_2113
Ferrimonas baelerica	long type IVa pilA	Fbal_0401
Geovibrio thiophilus	long type IVa pilA	K300DRAFT_1049, K300DRAFT_1050
Pantoea agglomerans	long type IVa pilA	Ga0004745_2907
Thermus scotoductus	long type IVa pilA	WP_038068616
Tepidimicrobium xylanilyticum	long type IVa pilA	Ga0056071_02505
Shewanella amazonensis	long type IVa pilA	Sama_0370
Shewanella putrefaciens	long type IVa pilA	Sput200_3560
Shewanella baltica	long type IVa pilA	Sbal175DRAFT_2072
Shewanella peizotolerans	long type IVa pilA	swp_4760
Shewanella decolorationis	long type IVa pilA	SdecDRAFT01_04314
Shewanella frigidimarina	long type IVa pilA	Sfri_3782
Shewanella loihica	long type IVa pilA	Ga0069557_1249
Shewanella pealeana	long type IVa pilA	Spea_3315
Desulfobacterium autotrophicum	epilin	HRM2_27700
Hippea maritima	epilin	Hipma_0737
Hippea alviniae	epilin	G415DRAFT_0872
Deferribacter desulfuricans	epilin	DEFDS_1270
Flexistipes sinusarabici	epilin	Flexsi_2291, Flexsi_2288
Desulfobacula toluolica	epilin	TOL2_21350
Desulfobacula phenolica	epilin	Ga0066824_11648
Desulfobacula sp. TS	epilin	Ga0097800_108051
Desulfobotulus alkaliphilus	epilin	LZ24DRAFT_00006
Desulfobotulus sapovorans	epilin	BR04DRAFT_00394
Thauera linaloolentis	epilin and long type 4a pilin	C666_06285, C666_05425, C666_15290
Thauera terpenica	epilin and long type 4a pilin	M622_11345, M622_01585
Thauera humireducens	epilin and long type 4a pilin	WP_048709378, WP_048706629

Supplementary Table S6. QC-filtered merged metatranscriptomic protein coding reads that mapped to genes from the *Geobacter sulfurreducens* genome that were significantly transcribed in RNAseq libraries assembled with mRNA extracted from methanogenic rice paddy soils. Transcript reads with expression levels ≥ median $\log_2$ RPKM values (5.7) were considered significant. All $\log_2$ RPKM values represent average expression values from six metatranscriptomic libraries; SEM is the standard error of the mean.

Locus ID	**Annotation**	**Gene abbr**	**Average $\log_2$ RPKM**	**SEM**	**Functional category**
GSU1994	hypothetical protein		11.59	0.13	Hypothetical protein
GSU2870	50S ribosomal protein L33	*rpmG*	11.59	0.42	Protein synthesis
GSU2906	hypothetical protein		11.54	0.12	Hypothetical protein
GSU1278	hypothetical protein		11.40	0.07	Hypothetical protein
GSU2315	hypothetical protein		11.38	0.14	Hypothetical protein
GSU2929	hemerythrin		11.37	0.10	Unknown function
GSU3209	iojap-related protein	*rsfS*	11.31	0.12	Unknown function
GSU1814	septum formation initiator family protein		11.30	0.42	Cell division
GSU0216	hypothetical protein		11.30	0.07	Hypothetical protein
GSU3629	hypothetical protein		11.29	0.25	Hypothetical protein
GSU2438	prevent-host-death family protein		11.20	0.52	Mobilome: prophages and transposons
GSU0847	rubredoxin		11.19	0.40	Energy metabolism
GSU2398	hypothetical protein		11.18	0.10	Hypothetical protein
GSU1836	nitrogen regulatory protein P-II	*glnB*	11.09	0.40	Central intermediary metabolism
GSU0228	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative		11.09	0.38	Protein fate
GSU2205	hypothetical protein		11.03	0.25	Hypothetical protein
GSU3449	ferredoxin	*frx-4*	11.02	0.11	Energy metabolism
GSU0381	lipoprotein, putative		11.00	0.42	Unknown function
GSU1286	response receiver CheY associated with MCPs of class 34H	*cheY34H*	10.99	0.10	Chemotaxis
GSU3507	hypothetical protein		10.99	0.25	Hypothetical protein
GSU2956	redox-active disulfide protein 2		10.93	0.51	Unknown function
GSU3235	50S ribosomal protein L27	*rpmA*	10.92	0.13	Protein synthesis
GSU0836	RNA polymerase-binding protein Rnk	*rnk-2*	10.91	0.11	Transcription
GSU2343	sodium/proton antiporter complex Mrp, protein B	*mrpB*	10.91	0.11	Transport and binding proteins
GSU2747	hypothetical protein		10.90	0.07	Hypothetical protein
GSU0831	nitrogen regulatory protein P-II family		10.89	0.09	Central intermediary metabolism
GSU0612	cytochrome c	*ppcA*	10.88	0.08	Energy metabolism
GSU2120	integration host factor subunit alpha	*ihfA-2*	10.87	0.19	Mobilome:prophages, transposons
GSU1565	hypothetical protein		10.86	0.07	Hypothetical protein
GSU2470	hypothetical protein		10.86	0.07	Hypothetical protein

GSU0589	thiamin biosynthesis sulfur carrier protein	*thiS*	10.84	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0077	hypothetical protein		10.84	0.07	Hypothetical protein
GSU3107	50S ribosomal protein L31	*rpmE*	10.84	0.07	Protein synthesis
GSU1795	ribonuclease PH	*rph*	10.78	0.36	Degradation of RNA
GSU1118	universal stress protein Usp	*usp-2*	10.76	0.11	Signal transduction mechanisms
GSU1353	prevent-host-death family protein		10.75	0.12	Mobilome: prophages, transposons
GSU1396	hypothetical protein		10.74	0.10	Hypothetical protein
GSU2173	lipoprotein, putative		10.74	0.28	Unknown function
GSU3543	acyltransferase		10.72	0.19	Fatty acid and phospholipid metabolism
GSU3305	hypothetical protein		10.72	0.25	Hypothetical protein
GSU1604	acyl carrier protein	*acpP-2*	10.71	0.11	Fatty acid and phospholipid metabolism
GSU0848	ferredoxin	*frx-5*	10.67	0.07	Energy metabolism
GSU3189	hypothetical protein		10.67	0.10	Hypothetical protein
GSU3310	hypothetical protein		10.67	0.10	Hypothetical protein
GSU0644	RNA-binding protein (KH domain)		10.65	0.40	Unknown function
GSU2153	hypothetical protein		10.63	0.53	Hypothetical protein
GSU2970	hypothetical protein		10.63	0.42	Hypothetical protein
GSU1450	endonuclease III, putative		10.59	0.15	Purines, pyrimidines, nucleosides, and nucleotides
GSU3566	hypothetical protein		10.58	0.34	Hypothetical protein
GSU0455	rare lipoprotein A domain protein		10.58	0.42	Unknown function
GSU0468	hypothetical protein		10.57	0.11	Hypothetical protein
GSU0904	HD domain protein		10.57	0.09	Unknown function
GSU2924	hypothetical protein		10.56	0.43	Hypothetical protein
GSU1357	hypothetical protein		10.56	0.30	Hypothetical protein
GSU0539	hypothetical protein		10.55	0.08	Hypothetical protein
GSU1589	ribosome-binding factor A	*rbfA*	10.53	0.14	Protein synthesis
GSU1087	hypothetical protein		10.49	0.10	Hypothetical protein
GSU1196	hypothetical protein		10.47	0.07	Hypothetical protein
GSU3289	hypothetical protein		10.46	0.14	Hypothetical protein
GSU1727	transcriptional regulator, TraR/DksA family		10.46	0.23	Transcriptional regulator
GSU1670	lipoprotein, putative		10.46	0.33	Unknown function
GSU3111	hypothetical protein		10.45	0.20	Hypothetical protein
GSU1181	hypothetical protein		10.45	0.42	Hypothetical protein
GSU3505	AzlD family membrane protein		10.45	0.30	Transport and binding proteins
GSU0576	hypothetical protein		10.44	0.19	Hypothetical protein
GSU1026	hypothetical protein		10.42	0.27	Hypothetical protein

GSU0661	ribose-phosphate pyrophosphokinase	*prsA*	10.41	0.10	Purines, pyrimidines, nucleosides, and nucleotides
GSU3560	hypothetical protein		10.40	0.42	Hypothetical protein
GSU0208	hypothetical protein		10.38	0.07	Hypothetical protein
GSU0807	apo-citrate lyase 2'-(5''-triphosphoribosyl)-3'-dephospho-coenzyme A transferase	*citX*	10.37	0.16	Energy metabolism
GSU1094	hypothetical protein		10.36	0.40	Hypothetical protein
GSU1522	transcriptional regulator, MerR family		10.36	0.15	Transcriptional regulator
GSU2109	hypothetical protein		10.35	0.11	Hypothetical protein
GSU0038	lipoprotein, putative		10.35	0.12	Unknown function
GSU3174	type VI secretion system needle tube protein TssD	*tssD*	10.34	0.28	Bacterial secretion
GSU0813	phospholipid transport system substrate-binding protein		10.34	0.11	Lipid transport and metabolism
GSU3339	co-chaperonin GroES	*groES*	10.33	0.40	Protein fate
GSU2865	50S ribosomal protein L10	*rplJ*	10.32	0.28	Protein synthesis
GSU0178	helix-turn-helix transcriptional regulator HxlR	*hxlR*	10.30	0.34	Transcriptional regulation
GSU2834	30S ribosomal protein S13	*rpsM*	10.29	0.42	Protein synthesis
GSU2846	50S ribosomal protein L24	*rplX*	10.29	0.23	Protein synthesis
GSU0722	hypothetical protein		10.28	0.10	Hypothetical protein
GSU3527	hypothetical protein		10.27	0.40	Hypothetical protein
GSU3576	lipoprotein		10.26	0.19	Unknown function
GSU1075	Holliday junction resolvase	*ruvC*	10.25	0.10	DNA recombination, replication, and repair
GSU2936	hypothetical protein		10.25	0.31	Hypothetical protein
GSU1270	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase	*pyrR*	10.25	0.09	Purines, pyrimidines, nucleosides, and nucleotides
GSU0151	acetylornithine aminotransferase	*argD*	10.24	0.07	Amino acid biosynthesis
GSU3092	hypothetical protein	*yqeY*	10.24	0.08	Hypothetical protein
GSU1709	SsrA-binding protein	*smpB*	10.24	0.41	Protein synthesis
GSU1805	phosphoglucosamine mutase	*glmM*	10.23	0.25	Cell envelope
GSU2353	hypothetical protein		10.23	0.40	Hypothetical protein
GSU0041	LexA family transcriptional repressor	*lexA-1*	10.22	0.07	DNA replication, recombination, and repair
GSU3571	hypothetical protein		10.21	0.56	Hypothetical protein
GSU3402	hypothetical protein		10.21	0.15	Hypothetical protein
GSU2591	ISGsu5, transposase		10.18	0.21	Mobilome:prophages, transposons
GSU2845	50S ribosomal protein L5	*rplE*	10.18	0.24	Protein synthesis
GSU1631	metallo-beta-lactamase family protein		10.17	0.10	Unknown function
GSU3581	hypothetical protein		10.15	0.05	Hypothetical protein
GSU0834	hypothetical protein		10.15	0.10	Hypothetical protein
GSU1054	tRNA (5-carboxymethylaminomethyl-2-thio-U34) synthesis sulfur	*tusA-2*	10.15	0.70	Protein synthesis

	carrier protein				
GSU2208	lipopolysaccharide biogenesis outer membrane chaperone lipoprotein LptE	*lptE*	10.15	0.10	Transport and binding protein
GSU2973	lipoprotein, putative		10.15	0.10	Unknown function
GSU0058	CRISPR-associated endoribonuclease Cas2	*cas2-1*	10.14	0.09	Mobilome:prophages, transposons
GSU1501	ABC transporter ATP-binding protein	*xapD*	10.14	0.04	Transport and binding protein
GSU0398	phage shock protein E, putative		10.12	0.19	Mobilome: prophages, transposons
GSU2847	50S ribosomal protein L14	*rplN*	10.12	0.17	Protein synthesis
GSU3519	cold shock DNA/RNA-binding protein		10.10	0.28	Defense mechanisms
GSU0384	hypothetical protein		10.10	0.20	Hypothetical protein
GSU1241	hypothetical protein		10.10	0.64	Hypothetical protein
GSU2193	hypothetical protein		10.10	0.08	Hypothetical protein
GSU3298	transcriptional regulator, XRE family with cupin sensor		10.10	0.09	Transcriptional regulator
GSU2987	transcriptional regulator, Fur family		10.10	0.42	Transcriptional regulator
GSU2322	hypothetical protein		10.09	0.26	Hypothetical protein
GSU3489	hypothetical protein		10.09	0.17	Hypothetical protein
GSU2176	hypothetical protein		10.09	0.27	Hypothetical protein
GSU3593	hypothetical protein		10.09	0.11	Hypothetical protein
GSU1220	response regulator		10.09	0.10	Signal transduction
GSU1712	hypothetical protein		10.08	0.27	Hypothetical protein
GSU0498	hypothetical protein		10.08	0.40	Hypothetical protein
GSU1851	glycosyl transferase, group 1 family protein		10.06	0.17	Cell envelope
GSU3332	cytochrome c family protein, putative		10.06	0.40	Energy metabolism
GSU1680	hypothetical protein		10.06	0.42	Hypothetical protein
GSU2197	hypothetical protein		10.05	0.08	Hypothetical protein
GSU1116	hypothetical protein		10.05	0.25	Hypothetical protein
GSU1134	cell division protein ZapA	*zapA*	10.04	0.10	Cell division
GSU1711	integrative genetic element Gsu5, resolvase		10.04	0.19	Mobilome:prophages, transposons
GSU1114	TPR domain protein		10.04	0.11	Unknown function
GSU1855	capsule polysaccharide export protein, putative		10.03	0.14	Cell envelope
GSU0068	cytochrome c family protein		10.03	0.14	Energy metabolism
GSU0114	F0F1 ATP synthase subunit epsilon	*atpC*	10.03	0.24	Energy metabolism
GSU1354	plasmid stabilization system family protein		10.02	0.09	Bacterial conjugation
GSU2805	nitrogenase molybdenum-iron cofactor biosynthesis protein NifX	*nifX*	10.02	0.33	Central intermediary metabolism
GSU0110	F0F1 ATP synthase subunit delta	*atpH*	10.02	0.17	Energy metabolism
GSU2304	hypothetical protein		10.02	0.15	Hypothetical protein
GSU0019	pentapeptide repeat domain protein		10.02	0.25	Unknown function
GSU0845	Rieske 2Fe-2S family protein		10.02	0.25	Unknown function
GSU1507	ADP-heptose--lipopolysaccharide heptosyltransferase	*xapJ*	10.01	0.18	Cell wall/membrane/envelope biogenesis

GSU0098	cell polarity determinant GTPase-activating protein MglB	*mglB*	10.01	0.15	Signal transduction mechanisms
GSU2009	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.-)		10.00	0.07	Amino acid transporter
GSU0418	hypothetical protein		10.00	0.25	Hypothetical protein
GSU0188	hypothetical protein		10.00	0.32	Hypothetical protein
GSU1652	hypothetical protein		10.00	0.17	Hypothetical protein
GSU0164	hypothetical protein		10.00	0.40	Hypothetical protein
GSU0708	small multidrug resistance family transporter EmrE	*emrE*	10.00	0.09	Transport and binding proteins
GSU0815	mce-related protein		10.00	0.42	Unknown function
GSU2284	conserved hypothetical protein TIGR00043		9.99	0.42	Hypothetical protein
GSU0142	phosphatidylglycerophosphatase A	*pgpA*	9.99	0.42	Lipid transport and metabolism
GSU1301	scaffold protein CheW associated with MCPs of class 34H	*cheW34H*	9.97	0.28	Chemotaxis
GSU2725	cytochrome c family protein		9.97	0.12	Energy metabolism
GSU3539	hypothetical protein		9.97	0.07	Hypothetical protein
GSU2151	ssDNA-binding protein	*ssb-1*	9.96	0.21	DNA replication, recombination, and repair
GSU2112	hypothetical protein		9.96	0.24	Hypothetical protein
GSU0705	cytochrome c biogenesis protein, CcmF/CcyK/CcsA family		9.95	0.35	Energy metabolism
GSU1381	hypothetical protein		9.95	0.07	Hypothetical protein
GSU0155	hypothetical protein		9.95	0.38	Hypothetical protein
GSU3597	hypothetical protein		9.94	0.41	Hypothetical protein
GSU3604	hypothetical protein		9.94	0.25	Hypothetical protein
GSU0172	hypothetical protein		9.94	0.40	Hypothetical protein
GSU1595	deoxyuridine 5'-triphosphate nucleotidohydrolase	*dut*	9.94	0.70	Purines, pyrimidines, nucleosides, and nucleotides
GSU1990	sensor histidine kinase		9.94	0.29	Signal transduction
GSU3334	cytochrome c family protein, putative		9.93	0.10	Energy metabolism
GSU3175	hypothetical protein		9.93	0.10	Hypothetical protein
GSU1425	prolipoprotein diacylglyceryl transferase	*lgt*	9.92	0.04	Protein modification and repair
GSU0081	hypothetical protein		9.91	0.11	Hypothetical protein
GSU2234	50S ribosomal protein L28	*rpmB*	9.91	0.40	Protein synthesis
GSU1854	UDP-glucose/GDP-mannose dehydrogenase family protein		9.90	0.44	Cell envelope
GSU0538	ATP-independent chaperone	*hspA-1*	9.90	0.31	Protein fate
GSU1475	tRNA (2'O-methyl-C32/U32)-methyltransferase	*trmJ*	9.90	0.24	Protein synthesis
GSU3176	LysM domain protein		9.90	0.34	Unknown function
GSU1667	hypothetical protein		9.89	0.70	Hypothetical protein
GSU2129	hypothetical protein		9.89	0.70	Hypothetical protein
GSU1152	hypothetical protein		9.89	0.07	Hypothetical protein
GSU1669	hypothetical protein		9.88	0.07	Hypothetical protein
GSU1185	hypothetical protein		9.88	0.42	Hypothetical protein

GSU3282	siroheme synthase, N-terminal domain	*cysG*	9.87	0.49	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2979	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	*folK*	9.87	0.42	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0999	UDP-N-acetylglucosamine acyltransferase	*lpxA-2*	9.87	0.10	Cell envelope
GSU0347	NADH dehydrogenase I subunit J	*nuoJ-1*	9.87	0.28	Energy metabolism
GSU2832	30S ribosomal protein S4	*rpsD*	9.87	0.25	Protein synthesis
GSU2954	arsenite efflux pump protein	*acr3*	9.86	0.10	Detoxification
GSU1308	hypothetical protein		9.86	0.34	Hypothetical protein
GSU3004	cobalt ABC transporter membrane protein CbiMN	*cbiMN*	9.86	0.25	Transport and binding proteins
GSU0425	flagellar biogenesis protein FliR	*fliR*	9.85	0.12	Cell motility
GSU0364	cytochrome c	*ppcB*	9.85	0.17	Energy metabolism
GSU2841	50S ribosomal protein L18	*rplR*	9.85	0.28	Protein synthesis
GSU0514	transcriptional regulator, IclR family		9.85	0.07	Transcriptional regulator
GSU2803	nitrogenase molybdenum-iron cofactor biosynthesis protein NifB	*nifB*	9.84	0.10	Central intermediary metabolism
GSU1379	ferric uptake regulation protein Fur	*fur*	9.84	0.18	Inorganic ion transport and metabolism
GSU1155	glutaredoxin family protein		9.84	0.28	Protein fate
GSU2838	50S ribosomal protein L15	*rplO*	9.84	0.43	Protein synthesis
GSU0353	membrane protein YqaA	*yqaA*	9.84	0.16	Unknown function
GSU1777	type II secretion system pseudopilin PulG	*pulG*	9.82	0.43	Bacterial secretion
GSU0348	NADH dehydrogenase I subunit K	*nuoK-1*	9.82	0.31	Energy metabolism
GSU3472	hypothetical protein		9.82	0.26	Hypothetical protein
GSU1787	cytochrome c family protein		9.81	0.20	Energy metabolism
GSU0593	hypothetical protein		9.81	0.09	Hypothetical protein
GSU1218	hypothetical protein		9.81	0.25	Hypothetical protein
GSU0704	hypothetical protein		9.81	0.09	Hypothetical protein
GSU2417	hypothetical protein		9.81	0.42	Hypothetical protein
GSU3491	hypothetical protein		9.81	0.40	Hypothetical protein
GSU2537	arginine decarboxylase	*speA*	9.80	0.22	Central intermediary metabolism
GSU0652	NAD synthetase	*nadE*	9.79	0.38	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3159	mutT/nudix family protein		9.79	0.53	DNA replication, recombination and repair
GSU0220	cytochrome c oxidase, coo3-type, subunit III	*coxC*	9.78	0.08	Energy metabolism
GSU1497	hypothetical protein	*pilA-C*	9.78	0.28	Hypothetical protein
GSU1965	hypothetical protein		9.78	0.08	Hypothetical protein
GSU1988	hypothetical protein		9.78	0.28	Hypothetical protein
GSU1277	transcription elongation factor GreA	*greA*	9.78	0.21	Transcription
GSU3469	50S ribosomal protein L34	*rpmH*	9.77	0.53	Protein synthesis

GSU2206	30S ribosomal protein S20	*rpsT*	9.77	0.42	Protein synthesis
GSU1291	response regulator		9.77	0.09	Signal transduction
GSU2377	hypothetical protein		9.76	0.22	Hypothetical protein
GSU1449	hypothetical protein		9.75	0.48	Hypothetical protein
GSU3478	hypothetical protein		9.75	0.07	Hypothetical protein
GSU2775	hypothetical protein		9.75	0.30	Hypothetical protein
GSU2635	hemerythrin		9.75	0.07	Unknown function
GSU3616	hypothetical protein		9.74	0.10	Hypothetical protein
GSU0710	hypothetical protein		9.74	0.28	Hypothetical protein
GSU0331	periplasmic trypsin-like serine protease DegP	*degP*	9.74	0.34	Protein fate
GSU0336	ATP synthase-associated magnesium import membrane protein AtpZ	*atpZ*	9.73	0.21	Inorganic ion transport proteins
GSU2861	30S ribosomal protein S7	*rpsG*	9.73	0.59	Protein synthesis
GSU1540	lipoprotein, putative		9.73	0.09	Unknown function
GSU1898	putative membrane protein		9.73	0.34	Unknown function
GSU1849	hypothetical protein		9.72	0.30	Hypothetical protein
GSU2571	helix-turn-helix iron-sulfur cluster-binding transcriptional regulator IscR	*iscR-2*	9.72	0.40	Transcriptional regulation
GSU3594	hypothetical protein		9.71	0.10	Hypothetical protein
GSU2773	hypothetical protein		9.70	0.14	Hypothetical protein
GSU0269	hypothetical protein		9.70	0.53	Hypothetical protein
GSU0362	hypothetical protein		9.70	0.04	Hypothetical protein
GSU2964	molybdate transport regulatory protein ModE	*modE*	9.70	0.09	Transport and binding proteins
GSU3078	cell division protein MraZ	*mraZ*	9.69	0.27	Cell division
GSU1391	Fic family protein		9.69	0.18	Cell division
GSU3551	hypothetical protein		9.69	0.28	Hypothetical protein
GSU2618	preprotein translocase subunit YajC	*yajC*	9.69	0.08	Protein and peptide secretion and trafficking
GSU1743	lipoprotein, putative		9.69	0.08	Unknown function
GSU1774	cell division ABC transporter membrane protein FtsX	*ftsX*	9.68	0.11	Cell division
GSU1096	phosphate ABC transporter ATP-binding protein	*pstB*	9.68	0.25	Inorganic ion transporter protein
GSU0202	xanthine dehydrogenase accessory factor		9.68	0.12	Posttranslation modification, protein turnover, chaperones
GSU1420	hemolysin A	*rfaQ*	9.68	0.09	Unknown function
GSU0647	hypothetical protein		9.67	0.36	Hypothetical protein
GSU2335	universal stress protein Usp	*usp-4*	9.67	0.07	Signal transduction mechanisms
GSU2007	amino acid/amide ABC transporter membrane protein 2, HAAT family (TC 3.A.1.4.-)		9.66	0.20	Amino acid transporter
GSU0720	desulfoferrodoxin ferrous iron-binding domain		9.66	0.11	Energy metabolism
GSU2925	hypothetical protein		9.66	0.10	Hypothetical protein
GSU2792	hypothetical protein		9.65	0.10	Hypothetical protein
GSU1672	hydroxypyruvate reductase	*hprA*	9.64	0.11	Energy metabolism

GSU1991	CAAX amino terminal protease family protein		9.64	0.07	Protein fate
GSU1837	peptidase, family M23/M37 domain protein		9.64	0.28	Protein fate
GSU1641	cytochrome bd menaquinol oxidase, subunit II	*cydB*	9.63	0.34	Energy metabolism
GSU3503	hypothetical protein		9.63	0.35	Hypothetical protein
GSU3182	hypothetical protein		9.63	0.21	Hypothetical protein
GSU0659	polysaccharide deacetylase domain protein		9.62	0.30	Carbohydrate transport and metabolism
GSU3068	UDP-N-acetylmuramate--L-alanine ligase	*murC*	9.62	0.03	Cell envelope
GSU1179	hypothetical protein		9.62	0.35	Hypothetical protein
GSU1477	LemA family protein		9.62	0.21	Unknown function
GSU0067	carbonic anhydrase	*can-1*	9.61	0.15	Central intermediary metabolism
GSU1568	hypothetical protein		9.61	0.42	Hypothetical protein
GSU2116	hypothetical protein		9.61	0.09	Hypothetical protein
GSU1902	isopropylmalate/citramalate isomerase, small subunit	*leuD*	9.60	0.34	Amino acid biosynthesis
GSU2003	hypothetical protein		9.60	0.07	Hypothetical protein
GSU2440	hypothetical protein		9.60	0.25	Hypothetical protein
GSU0827	hypothetical protein		9.60	0.10	Hypothetical protein
GSU2467	hypothetical protein/integrase, fusion		9.60	0.08	Mobilome:prophages, transposons
GSU1888	lipopolysaccharide ABC transporter ATP-binding protein	*lptB*	9.60	0.29	Transport and binding protein
GSU3398	metal ion efflux outer membrane protein family protein, putative		9.60	0.15	Transport and binding proteins
GSU0023	TPR domain protein		9.60	0.09	Unknown function
GSU3028	flagellar basal body stator protein MotB	*motB*	9.59	0.19	Cell motility
GSU1818	phosphoglycerate mutase (EC 5.4.2.1)	*apgM*	9.59	0.42	Energy metabolism
GSU1120	response regulator		9.59	0.14	Signal transduction
GSU0800	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)		9.58	0.10	Amino acid transporter
GSU0712	hypothetical protein		9.58	0.28	Hypothetical protein
GSU3520	hypothetical protein		9.58	0.07	Hypothetical protein
GSU1478	uncharacterized protein		9.58	0.48	Unknown function
GSU2168	DNA repair protein RadC		9.57	0.03	DNA repair
GSU3280	thioredoxin-related protein		9.57	0.11	Energy metabolism
GSU0879	response receiver scaffold protein CheV	*cheV*	9.56	0.57	Chemotaxis
GSU2455	hypothetical protein		9.56	0.10	Hypothetical protein
GSU2332	hypothetical protein		9.56	0.17	Hypothetical protein
GSU0256	hemerythrin		9.56	0.30	Unknown function
GSU1694	hydrolase, haloacid dehalogenase-like family		9.56	0.17	Unknown function
GSU1956	acetyltransferase, GNAT family		9.56	0.28	Unknown function
GSU3526	STAS domain-containing protein		9.56	0.27	Unknown function
GSU0026	Cell division and transport-associated protein TolA (TC 2.C.1.2.1)		9.55	0.32	Cell division
GSU0420	flagellar basal body-associated protein FliL	*fliL*	9.55	0.53	Cell motility

GSU3559	hypothetical protein		9.55	0.53	Hypothetical protein
GSU3382	hypothetical protein		9.55	0.47	Hypothetical protein
GSU0402	hemerythrin family protein		9.55	0.48	Unknown function
GSU2104	lipoprotein, putative		9.55	0.28	Unknown function
GSU0597	hypothetical protein		9.54	0.07	Hypothetical protein
GSU3521	hypothetical protein		9.54	0.09	Hypothetical protein
GSU0303	sensory box protein		9.54	0.10	Signal transduction
GSU2287	response regulator		9.54	0.38	Signal transduction
GSU2010	CBS domain protein		9.54	0.35	Unknown function
GSU2371	tryptophan synthase subunit alpha	*trpA*	9.53	0.70	Amino acid biosynthesis
GSU1295	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)		9.53	0.08	Amino acid transporter
GSU1722	creatinine amidohydrolase		9.53	0.08	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2515	cytochrome c family protein, putative		9.53	0.23	Energy metabolism
GSU0954	hypothetical protein		9.53	0.07	Hypothetical protein
GSU1852	hypothetical protein		9.52	0.26	Hypothetical protein
GSU0934	hypothetical protein		9.52	0.42	Hypothetical protein
GSU3238	Rieske 2Fe-2S family protein		9.52	0.28	Unknown function
GSU3333	3-deoxy-7-phosphoheptulonate synthase	*aroG-1*	9.51	0.70	Amino acid biosynthesis
GSU2707	acetate kinase A/propionate kinase 2	*ackA-1*	9.51	0.42	Energy metabolism
GSU2233	hypothetical protein		9.51	0.10	Hypothetical protein
GSU1995	hypothetical protein		9.51	0.25	Hypothetical protein
GSU0294	HD domain protein		9.51	0.09	Unknown function
GSU0552	hypothetical protein		9.50	0.07	Hypothetical protein
GSU1665	rhomboid family protein		9.50	0.40	Unknown function
GSU1528	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)		9.49	0.10	Amino acid transporter
GSU0277	ABC transporter, ATP-binding/permease protein		9.49	0.11	Transport and binding protein
GSU0767	tia invasion determinant-related protein		9.49	0.26	Unknown function
GSU2472	virulence associated protein C	*vapC*	9.49	0.46	Unknown function
GSU1069	hypothetical protein		9.48	0.28	Hypothetical protein
GSU1637	orotate phosphoribosyltransferase	*pyrE*	9.48	0.53	Purines, pyrimidines, nucleosides, and nucleotides
GSU1146	NitT/TauT family transport system substrate-binding protein		9.48	0.35	Transport and binding proteins
GSU3548	type IV pilus minor pilin PilE	*pilE*	9.47	0.17	Cell motility
GSU1300	methyl-accepting chemotaxis sensory transducer class 34H	*mcp34H-4*	9.47	0.25	Chemotaxis
GSU0614	cytochrome c biogenesis protein, CcmF/CcyK/CcsA family		9.47	0.10	Energy metabolism
GSU3473	hypothetical protein		9.46	0.16	Hypothetical protein
GSU2572	serine O-acetyltransferase	*cysE-1*	9.45	0.36	Amino acid biosynthesis

GSU1910	acetolactate synthase 3 regulatory subunit	*ilvN*	9.45	0.29	Amino acid biosynthesis
GSU1176	succinate dehydrogenase/fumarate reductase, cytochrome b558 subunit	*frdC*	9.45	0.27	Energy metabolism
GSU1967	hypothetical protein		9.45	0.13	Hypothetical protein
GSU3549	hypothetical protein		9.45	0.42	Hypothetical protein
GSU0685	diploptene adenosyltransferase and reductase	*hpnH*	9.45	0.36	Unknown function
GSU3155	cytochrome c nitrite and sulfite reductase, menaquinol-oxidizing subunit	*nrfH*	9.44	0.09	Energy metabolism
GSU2076	cytochrome c	*omcZ*	9.44	0.28	Energy metabolism
GSU3502	hypothetical protein		9.44	0.18	Hypothetical protein
GSU3584	hypothetical protein		9.43	0.32	Hypothetical protein
GSU0896	zinc protease TldD modulator of DNA gyrase	*tldD*	9.43	0.12	Protein degradation
GSU2743	cytochrome c family protein		9.42	0.42	Energy metabolism
GSU0035	2',5' RNA ligase, putative		9.42	0.40	Protein synthesis
GSU1954	hypothetical protein		9.41	0.12	Hypothetical protein
GSU0272	hypothetical protein		9.41	0.40	Hypothetical protein
GSU1592	30S ribosomal protein S15	*rpsO*	9.41	0.07	Protein synthesis
GSU1779	type II secretion system protein PulP	*pulP*	9.40	0.21	Bacterial secretion
GSU0230	twitching motility pilus retraction protein	*pilT-2*	9.40	0.07	Cell motility
GSU0849	iron-sulfur cluster repair protein ScdA	*scdA*	9.40	0.28	Energy metabolism
GSU2298	hypothetical protein		9.40	0.30	Hypothetical protein
GSU2562	protein phosphohistidine phosphatase SixA	*sixA*	9.40	0.18	Regulatory functions
GSU0676	lipoprotein, putative		9.40	0.47	Unknown function
GSU1958	polysaccharide deacetylase domain protein		9.39	0.27	Carbohydrate transport and metabolism
GSU2246	bifunctional UDP-N-acetylglucosamine 4,6-dehydratase/UDP-2-acetamido-2,6-dideoxy-alpha-D-xylo-4-hexulose 5-epimerase	*wbjB*	9.39	0.26	Cell envelope
GSU1521	integration host factor subunit alpha	*ihfA-1*	9.39	0.40	Mobilome:prophages, transposons
GSU1151	hydrolase	*hpnK*	9.39	0.01	Unknown function
GSU2663	lipoprotein, putative		9.38	0.28	Unknown function
GSU0160	dihydrodipicolinate reductase	*dapB*	9.37	0.08	Amino acid biosynthesis
GSU1892	3-deoxy-D-manno-octulosonate-8-phosphate phosphatase	*kdsC*	9.37	0.42	Cell envelope
GSU0358	periplasmic nitrate reductase maturation protein NapF		9.37	0.17	Energy metabolism
GSU2660	hypothetical protein		9.37	0.10	Hypothetical protein
GSU1662	hypothetical protein		9.37	0.29	Hypothetical protein
GSU0516	hypothetical protein		9.37	0.53	Hypothetical protein
GSU0224	hypothetical protein		9.37	0.28	Hypothetical protein
GSU2965	hypothetical protein		9.37	0.07	Hypothetical protein
GSU1752	elongation factor P	*efp-2*	9.37	0.09	Protein synthesis
GSU0171	YaiI/YqxD family protein		9.37	0.10	Unknown function
GSU3304	outer membrane channel OmpJ	*ompJ*	9.36	0.20	Cell envelope
GSU2305	peptidoglycan-associated lipoprotein		9.36	0.40	Cell envelope

GSU0553	hypothetical protein		9.36	0.50	Hypothetical protein
GSU2306	5-carboxyamino-1-(5-phosphoribosyl)imidazole carboxymutase	*purE-2*	9.36	0.07	Purines, pyrimidines, nucleosides and nucleotides
GSU0866	YGGT family protein		9.36	0.18	Unknown function
GSU1666	iron-sulfur cluster-binding protein		9.35	0.10	Energy metabolism
GSU2730	hypothetical protein		9.35	0.10	Hypothetical protein
GSU3621	hypothetical protein		9.35	0.10	Hypothetical protein
GSU2868	transcription elongation factor NusG	*nusG*	9.35	0.18	Transcription
GSU2202	transcriptional regulator, LysR family		9.35	0.10	Transcriptional regulator
GSU1495	sigma-54-dependent transcriptional response regulator PilR	*pilR*	9.35	0.29	Transcriptional regulator
GSU0869	LysM domain/NLP/P60 family protein		9.35	0.09	Unknown function
GSU0480	NifU-like domain protein		9.35	0.70	Unknown function
GSU3340	chaperonin GroEL	*groEL*	9.34	0.31	Protein fate
GSU2850	50S ribosomal protein L16	*rplP*	9.34	0.41	Protein synthesis
GSU3294	rubredoxin:oxygen/nitric oxide oxidoreductase	*roo*	9.33	0.11	Energy metabolism
GSU0748	hypothetical protein		9.33	0.10	Hypothetical protein
GSU0315	hypothetical protein		9.33	0.17	Hypothetical protein
GSU2720	bidirectional hydrogenase complex protein HoxU	*hoxU*	9.32	0.16	Energy metabolism
GSU2282	CBS domain protein		9.32	0.27	Unknown function
GSU3020	hexapeptide transferase family protein		9.31	0.41	Cell envelope
GSU0421	flagellar motor switch protein FliM	*fliM*	9.31	0.30	Cell motility
GSU0000.1	chromosomal replication initiation protein	*dnaA*	9.31	0.17	DNA replication
GSU1178	succinate dehydrogenase/fumarate reductase iron-sulfur subunit	*frdB*	9.31	0.58	Energy metabolism
GSU1309	hypothetical protein		9.31	0.11	Hypothetical protein
GSU0053	CRISPR-associated protein Csb1	*csb1*	9.31	0.60	Mobilome:prophages, transposons
GSU2625	transcriptional regulator, ArsR family		9.31	0.07	Transcriptional regulator
GSU2751	anaerobic C4-dicarboxylate transporter	*dcuB*	9.31	0.29	Transport and binding proteins
GSU2303	sodium/proton antiporter, NhaA family (TC 2.A.33.1.1)		9.31	0.36	Transport and binding proteins
GSU3040	flagellar assembly protein FliW	*fliW*	9.30	0.10	Cell motility
GSU1876	methyl-accepting chemotaxis protein		9.30	0.52	Chemotaxis
GSU2071	ribonuclease H	*rnhA*	9.30	0.25	Degradation of RNA
GSU1227	ABC transporter, ATP-binding protein		9.30	0.46	Transport and binding protein
GSU1646	lipoprotein, putative		9.30	0.09	Unknown function
GSU2037	type IV pilus minor pilin FimU	*fimU*	9.28	0.10	Cell motility
GSU2578	scaffold protein CheW associated with MCPs of classes 40H and 40+24H	*cheW64H-2*	9.28	0.39	Chemotaxis
GSU3375	mutT/nudix family protein		9.28	0.07	DNA replication, recombination and repair
GSU1283	hypothetical protein		9.28	0.53	Hypothetical protein
GSU1949	hypothetical protein		9.28	0.21	Hypothetical protein

GSU0289	hypothetical protein		9.28	0.22	Hypothetical protein
GSU3206	transcriptional regulator, TraR/DksA family		9.28	0.53	Transcriptional regulator
GSU0798	amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.1.3.-)		9.27	0.09	Amino acid transporter
GSU2082	dTDP-4-dehydrorhamnose 3,5-epimerase		9.27	0.10	Cell envelope
GSU0806	2'-(5''-triphosphoribosyl)-3'-dephospho-coenzyme A synthase	*citG*	9.27	0.27	Coenzyme transport and metabolism
GSU0741	Ech-hydrogenase-related complex, HyfE-like integral membrane subunit	*ehrC*	9.27	0.18	Energy metabolism
GSU0338	NADH dehydrogenase I subunit A	*nuoA-1*	9.27	0.28	Energy metabolism
GSU2780	hypothetical protein		9.27	0.07	Hypothetical protein
GSU1879	two component transcriptional regulator, winged helix family		9.27	0.15	Transcriptional regulation
GSU1883	PTS system, IIA component, putative		9.27	0.19	Transport and binding proteins
GSU1510	glycosyl transferase, group 2 family protein		9.26	0.23	Cell envelope
GSU0376	glycine cleavage system lipoyl carrier protein	*gcvH-1*	9.26	0.42	Energy metabolism
GSU3362	hypothetical protein		9.26	0.53	Hypothetical protein
GSU0141	hypothetical protein		9.26	0.23	Hypothetical protein
GSU1451	3-hydroxyisobutyrate dehydrogenase family protein		9.26	0.08	Lipid transport and metabolism
GSU1516	translation initiation factor IF-3	*infC*	9.26	0.30	Protein synthesis
GSU2860	elongation factor G	*fusA-3*	9.26	0.11	Protein synthesis
GSU2094	response regulator		9.26	0.28	Signal transduction
GSU0679	tellurite resistance protein-related protein		9.26	0.07	Unknown function
GSU3394	amino acid/amide ABC transporter membrane protein 1, HAAT family (TC 3.A.1.4.-)		9.25	0.33	Amino acid transporter
GSU0131	hypothetical protein		9.25	0.42	Hypothetical protein
GSU1715	hypothetical protein		9.25	0.10	Hypothetical protein
GSU2840	30S ribosomal protein S5	*rpsE*	9.25	0.37	Protein synthesis
GSU1878	histidine kinase (EC 2.7.13.3)		9.25	0.42	Signal transduction mechanisms
GSU3229	two component transcriptional regulator, LuxR family		9.25	0.21	Transcriptional regulation
GSU1399	magnesium transport protein CorA	*corA-1*	9.25	0.09	Transport and binding protein
GSU1432	TPR domain protein		9.25	0.10	Unknown function
GSU0542	GGDEF domain protein		9.25	0.14	Unknown function
GSU1817	outer membrane lipoprotein, Slp family, putative		9.24	0.32	Cell envelope
GSU1011	hypothetical protein		9.24	0.28	Hypothetical protein
GSU0149	sensor histidine kinase/response regulator		9.24	0.53	Signal transduction
GSU2543	polysaccharide deacetylase domain protein		9.23	0.21	Carbohydrate transport and metabolism
GSU0073	outer membrane protein, putative		9.23	0.07	Cell envelope
GSU3511	hypothetical protein		9.23	0.08	Hypothetical protein
GSU0129	polypeptide formylmethionine deformylase	*def-1*	9.23	0.10	Protein fate
GSU0837	response regulator		9.23	0.25	Signal transduction

GSU1474	DedA family protein		9.23	0.40	Unknown function
GSU2769	metallo-beta-lactamase family protein		9.23	0.15	Unknown function
GSU1616	ImpB/MucB/SamB family protein		9.22	0.26	DNA repair
GSU3283	cytochrome c biogenesis protein, CcmF/CcyK/CcsA family		9.22	0.25	Energy metabolism
GSU0118	hypothetical protein		9.22	0.07	Hypothetical protein
GSU2091	phosphoribosylaminoimidazolesuccinocarboxamide synthase	*purC*	9.22	0.08	Purines, pyrimidines, nucleosides, and nucleotides
GSU1019	hypoxanthine/guanine transport membrane protein	*pbuG*	9.22	0.30	Purines, pyrimidines, nucleosides, and nucleotides
GSU0799	amino acid ABC transporter membrane protein, PAAT family (TC 3.A.1.3.-)		9.21	0.10	Amino acid transporter
GSU0115	4-hydroxythreonine-4-phosphate dehydrogenase	*pdxA*	9.21	0.10	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0408	flagellar basal body rod protein FlgC	*flgC*	9.21	0.53	Cell motility
GSU0126	iron-sulfur cluster-binding oxidoreductase	*yccM-1*	9.21	0.23	Energy metabolism
GSU1193	fructose-bisphosphate aldolase (EC 4.1.2.13)		9.21	0.33	Energy metabolism
GSU0165	hypothetical protein		9.21	0.31	Hypothetical protein
GSU0233	hypothetical protein		9.21	0.28	Hypothetical protein
GSU2546	hypothetical protein		9.21	0.17	Hypothetical protein
GSU3488	hypothetical protein		9.21	0.70	Hypothetical protein
GSU0666	30S ribosomal protein S18	*rpsR*	9.21	0.40	Protein synthesis
GSU3379	S-methyl-5-thio-alpha-D-ribose-1-phosphate isomerase	*mtnA*	9.20	0.47	Amino acid biosynthesis
GSU0222	cytochrome c oxidase, coo3-type, cytochrome c subunit II, one heme-binding site	*coxB*	9.20	0.14	Energy metabolism
GSU0265	hypothetical protein		9.20	0.08	Hypothetical protein
GSU3592	hypothetical protein		9.20	0.47	Hypothetical protein
GSU1882	phosphocarrier protein HPr	*ptsH*	9.20	0.31	Signal transduction mechanisms
GSU0902	Signal transduction response regulator, receiver domain		9.20	0.42	Signal transduction mechanisms
GSU2355	hypothetical protein		9.19	0.07	Hypothetical protein
GSU1585	ribosome maturation factor RimP		9.19	0.40	Protein synthesis
GSU2596	lipoprotein, putative		9.19	0.38	Unknown function
GSU3097	imidazole glycerol phosphate synthase subunit HisH	*hisH*	9.18	0.33	Amino acid biosynthesis
GSU1828	chorismate mutase (EC 5.4.99.5)	*pheA1*	9.18	0.07	Amino acid biosynthesis
GSU0145	recombinase A	*recA*	9.18	0.29	DNA repair
GSU2968	hypothetical protein		9.18	0.10	Hypothetical protein
GSU2817	transcriptional regulator, LysR family		9.18	0.14	Transcriptional regulator
GSU1982	general secretion pathway protein-related protein		9.17	0.21	Bacterial secretion
GSU2683	2-dehydropantoate 2-reductase	*panE*	9.17	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2308	malate oxidoreductase, NAD-dependent	*mleA*	9.17	0.10	Energy metabolism

GSU1177	succinate dehydrogenase flavoprotein subunit	*frdA*	9.17	0.26	Energy metabolism
GSU2148	hypothetical protein		9.17	0.18	Hypothetical protein
GSU2519	(R)-2-hydroxyacyl-CoA dehydratase YjiM	*yjiM*	9.17	0.09	Secondary metabolites biosynthesis
GSU1479	putative membrane protein		9.17	0.07	Unknown function
GSU0324	type II secretion system minor pseudopilin GspI	*gspI*	9.16	0.17	Bacterial secretion
GSU3035	hypothetical protein		9.16	0.28	Hypothetical protein
GSU0534	helix-turn-helix iron-sulfur cluster-binding transcriptional regulator IscR	*iscR-1*	9.16	0.08	Transcriptional regulation
GSU3609	ABC transporter ATP-binding protein	*ybhF-C*	9.16	0.40	Transport and binding protein
GSU2021	xaa-pro dipeptidase	*pepQ-2*	9.15	0.10	Amino acid metabolism
GSU2818	hypothetical protein		9.15	0.08	Hypothetical protein
GSU2427	hypothetical protein		9.15	0.28	Hypothetical protein
GSU0355	hypothetical protein		9.15	0.42	Hypothetical protein
GSU2648	hypothetical protein		9.15	0.08	Hypothetical protein
GSU2727	hypothetical protein		9.15	0.22	Hypothetical protein
GSU3380	aspartyl/glutamyl-tRNA amidotransferase subunit B	*gatB*	9.15	0.10	Protein synthesis
GSU3060	transcriptional regulator, TetR family		9.15	0.29	Transcriptional regulator
GSU2981	outer membrane transport energization protein TonB (TC 2.C.1.1.1)		9.15	0.42	Transport and binding proteins
GSU0872	lipoprotein, putative		9.15	0.08	Unknown function
GSU0627	GDP-L-fucose synthase	*fcl*	9.14	0.08	Cell envelope
GSU1786	cytochrome c family protein		9.14	0.16	Energy metabolism
GSU3454	radical SAM domain protein		9.14	0.10	Unknown function
GSU0424	flagellar biogenesis protein FliQ	*fliQ*	9.13	0.10	Cell motility
GSU1679	hypothetical protein		9.12	0.09	Hypothetical protein
GSU0061	hypothetical protein		9.12	0.17	Hypothetical protein
GSU0257	hypothetical protein		9.12	0.25	Hypothetical protein
GSU1360	hypothetical protein		9.12	0.33	Hypothetical protein
GSU0663	peptidyl-tRNA hydrolase	*pth*	9.12	0.25	Protein synthesis
GSU0234	bidirectional formate transporter	*fdhC*	9.12	0.10	Transport and binding proteins
GSU0310	NTE family protein		9.12	0.12	Unknown function
GSU1506	SAM-dependent methyltransferase, FkbM family	*xapI*	9.12	0.19	Unknown function
GSU2311	YeeE/YedE family protein		9.12	0.27	Unknown function
GSU3244	hypothetical protein		9.11	0.42	Hypothetical protein
GSU0390	hypothetical protein		9.11	0.30	Hypothetical protein
GSU2105	ATP-dependent Lon protease		9.11	0.13	Protein fate
GSU1885	HPr kinase/phosphorylase	*hprK*	9.11	0.33	Regulatory functions
GSU2429	PPIC-type PPIASE domain protein		9.11	0.18	Unknown function
GSU1496	Type IV pilA protein	*e-pilin*	9.10	0.26	Cell motility
GSU1704	GAF sensor methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-1*	9.10	0.43	Chemotaxis
GSU2913	cytochrome c	*omcP*	9.10	0.42	Energy metabolism

GSU3504	hypothetical protein		9.10	0.25	Hypothetical protein
GSU2959	hypothetical protein		9.10	0.07	Hypothetical protein
GSU3290	hypothetical protein		9.10	0.28	Hypothetical protein
GSU0667	hypothetical protein		9.10	0.47	Hypothetical protein
GSU2814	rubrerythrin		9.09	0.27	Energy metabolism
GSU0076	hypothetical protein		9.09	0.53	Hypothetical protein
GSU2469	hypothetical protein		9.09	0.22	Hypothetical protein
GSU0599	sensor histidine kinase		9.09	0.23	Signal transduction
GSU1929	MgtC family protein		9.09	0.40	Unknown function
GSU3185	hypothetical protein		9.08	0.28	Hypothetical protein
GSU3349	Kynurenine formamidase (EC 3.5.1.9)		9.07	0.14	Amino acid transport and metabolism
GSU0779	periplasmically oriented, membrane-bound formate dehydrogenase, b-type cytochrome subunit	*fdnI*	9.07	0.28	Energy metabolism
GSU0092	heterodisulfide oxidoreductase, iron-sulfur cluster-binding subunit C	*hdrC*	9.07	0.09	Energy metabolism
GSU1850	hypothetical protein		9.07	0.39	Hypothetical protein
GSU2853	30S ribosomal protein S19	*rpsS*	9.07	0.10	Protein synthesis
GSU2770	hypothetical protein		9.06	0.07	Hypothetical protein
GSU2808	cytochrome c family protein		9.05	0.10	Energy metabolism
GSU0618	cytochrome c	*omcE*	9.05	0.40	Energy metabolism
GSU3474	hypothetical protein		9.05	0.53	Hypothetical protein
GSU1221	ammonium transporter (TC 1.A.11)		9.05	0.09	Inorganic ion transporter protein
GSU2855	50S ribosomal protein L23	*rplW*	9.05	0.10	Protein synthesis
GSU1577	cob(I)yrinate a,c-diamide adenosyltransferase	*cobA*	9.05	0.21	Transport and binding proteins
GSU3369	selenocysteine synthase	*selA*	9.04	0.43	Amino acid biosynthesis
GSU1955	capK related-protein		9.04	0.31	Coenzyme transport and metabolism
GSU0096	recombination protein RecR	*recR*	9.04	0.17	DNA repair
GSU1907	CDP-diacylglycerol--serine O-phosphatidyltransferase	*pssA*	9.04	0.17	Fatty acid and phospholipid metabolism
GSU0163	hypothetical protein		9.04	0.10	Hypothetical protein
GSU2442	RelA/SpoT domain protein		9.04	0.27	Unknown function
GSU0664	GTP-binding protein YchF	*ychF*	9.04	0.27	Unknown function
GSU0153	argininosuccinate synthase	*argG*	9.03	0.28	Amino acid biosynthesis
GSU2083	glucose-1-phosphate thymidylyltransferase	*rmlA*	9.03	0.20	Cell envelope
GSU0407	flagellar basal body rod protein FlgB	*flgB*	9.03	0.28	Cell motility
GSU0179	NADPH-dependent FMN reductase domain protein		9.03	0.36	Energy metabolism
GSU2013	phosphoglucomutase/phosphomannomutase family protein		9.03	0.40	Energy metabolism
GSU0790	hypothetical protein		9.03	0.18	Hypothetical protein
GSU2889	hypothetical protein		9.03	0.40	Hypothetical protein

GSU0519	hypothetical protein		9.03	0.42	Hypothetical protein
GSU1021	hypothetical protein		9.03	0.09	Hypothetical protein
GSU1908	phosphatidylserine decarboxylase		9.03	0.42	Lipid transport and metabolism
GSU1363	RNA-directed DNA polymerase (EC 2.7.7.49)		9.03	0.41	Mobilome:prophages, transposons
GSU1234	signal peptide peptidase A. Serine peptidase. MEROPS family S49		9.03	0.42	Protein fate
GSU0168	Fic family protein		9.02	0.10	Cell division
GSU1470	2-oxoglutarate:ferredoxin oxidoreductase subunit gamma	*korC*	9.02	0.25	Energy metabolism
GSU0316	hypothetical protein		9.02	0.07	Hypothetical protein
GSU0137	hypothetical protein		9.02	0.07	Hypothetical protein
GSU0214	hypothetical protein		9.02	0.42	Hypothetical protein
GSU1935	biotin operon repressor and biotin--acetyl-CoA carboxylase ligase	*birA*	9.02	0.26	Regulatory functions
GSU0451	two component transcriptional regulator, winged helix family		9.02	0.28	Transcriptional regulation
GSU2188	ABC transporter, ATP-binding protein		9.02	0.15	Transport and binding protein
GSU0108	ATP synthase F0, B' subunit	*atpX*	9.01	0.28	Energy metabolism
GSU2204	outer membrane channel cytochrome c, 1 heme-binding site	*omcL*	9.01	0.13	Energy metabolism
GSU3223	cytochrome c family protein		9.01	0.10	Energy metabolism
GSU1642	hypothetical protein		9.01	0.28	Hypothetical protein
GSU3553	hypothetical protein		9.01	0.29	Hypothetical protein
GSU1788	NHL repeat domain protein		9.01	0.15	Unknown function
GSU1239	glutamate synthase (NADPH) GltB2 subunit (EC 1.4.1.13)		9.00	0.11	Amino acid biosynthesis
GSU0305	hydrogenase nickel incorporation protein HypB	*hypB*	9.00	0.11	Energy metabolism
GSU1008	enoyl-ACP reductase	*fabI*	9.00	0.21	Fatty acid and phospholipid metabolism
GSU0095	conserved hypothetical protein TIGR00103		9.00	0.25	Hypothetical protein
GSU1556	hypothetical protein		9.00	0.36	Hypothetical protein
GSU0370	hypothetical protein		9.00	0.29	Hypothetical protein
GSU0943	hypothetical protein		9.00	0.31	Hypothetical protein
GSU1200	SSU ribosomal protein S1P		9.00	0.36	Protein synthesis
GSU1292	sensory box histidine kinase		9.00	0.15	Signal transduction
GSU0629	lipopolysaccharide/O-antigen transporter, putative		9.00	0.34	Transport and binding protein
GSU0325	type II secretion system minor pseudopilin GspH	*gspH*	8.99	0.14	Bacterial secretion
GSU2087	phosphoheptose isomerase	*gmhA*	8.99	0.42	Cell envelope
GSU3203	outer membrane lipoprotein carrier protein LolA, putative		8.99	0.40	Cell envelope
GSU2661	hypothetical protein		8.99	0.23	Hypothetical protein
GSU2496	hypothetical protein		8.99	0.27	Hypothetical protein
GSU1914	membrane-associated zinc metalloprotease RseP	*rseP*	8.99	0.12	Protein fate
GSU2622	HAMP domain/GAF domain/HD domain protein		8.99	0.08	Unknown function
GSU1242	L-aspartate aminotransferase apoenzyme (EC 2.6.1.1)		8.98	0.12	Amino acid transport and metabolism
GSU3147	molybdopterin nucleotidyltransferase and molybdopterin-guanine	*mobA-1*	8.98	0.25	Biosynthesis of cofactors,

	dinucleotide biosynthesis protein MobB				prosthetic groups, and carriers
GSU0028	Cell division and transport-associated protein TolQ (TC 2.C.1.2.1)		8.98	0.39	Cell division
GSU3036	flagellin export facilitator protein FliS	*fliS*	8.98	0.28	Cell motility
GSU0783	hydrogenase 2 protein HybA	*hybA*	8.98	0.36	Energy metabolism
GSU1322	cytochrome c biogenesis protein CcdA	*ccdA*	8.98	0.49	Energy metabolism
GSU1948	hypothetical protein		8.98	0.27	Hypothetical protein
GSU0485	hypothetical protein		8.98	0.41	Hypothetical protein
GSU1498	hypothetical protein	*xapA*	8.98	0.12	Hypothetical protein
GSU1525	RNA polymerase sigma-38 factor, stationary phase	*rpoS*	8.98	0.11	Transcription
GSU1409	NifU-like domain protein		8.98	0.59	Unknown function
GSU1084	hypothetical protein		8.97	0.15	Hypothetical protein
GSU0630	hypothetical protein		8.97	0.07	Hypothetical protein
GSU1476	MtN3 and saliva related transmembrane protein		8.97	0.70	Unknown function
GSU0349	NADH dehydrogenase I subunit L	*nuoL-1*	8.96	0.09	Energy metabolism
GSU2682	hypothetical protein		8.96	0.34	Hypothetical protein
GSU2075	subtilisin		8.96	0.07	Protein fate
GSU1773	M23/M37 peptidase domain protein		8.96	0.45	Protein fate
GSU0655	RNA polymerase sigma-32 factor RpoH	*rpoH*	8.96	0.26	Transcription
GSU1626	transcriptional regulator, GntR family		8.96	0.07	Transcriptional regulator
GSU0828	metal ion efflux outer membrane protein family protein, putative		8.96	0.35	Transport and binding proteins
GSU1745	OmpA domain protein		8.96	0.11	Transport and binding proteins
GSU3438	phosphonoacetate hydrolase	*phnA*	8.96	0.28	Unknown function
GSU1393	CRISPR-associated protein, Cas2 family	*cas2-2*	8.95	0.10	Mobile and extrachromosomal element functions
GSU3053	RNA polymerase sigma-28 factor for flagellar operon	*fliA*	8.94	0.29	Chemotaxis
GSU1765	farnesyl-diphosphate synthase (EC 2.5.1.10)		8.94	0.30	Coenzyme transport and metabolism
GSU0804	NAD(P)H:quinone oxidoreductase	*wrbA*	8.94	0.16	Energy metabolism
GSU3302	methylmalonyl-CoA mutase (EC 5.4.99.2)		8.94	0.16	Lipid transport and metabolism
GSU2000	tRNA delta(2)-isopentenylpyrophosphate transferase	*miaA*	8.94	0.42	Protein synthesis
GSU1273	carbamoyl phosphate synthase small subunit	*carA*	8.94	0.31	Purines, pyrimidines, nucleosides, and nucleotides
GSU1976	glycosyl transferase, group 1 family protein		8.93	0.27	Cell envelope
GSU1033	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-7*	8.93	0.11	Chemotaxis
GSU1071	hypothetical protein		8.93	0.10	Hypothetical protein
GSU0570	hypothetical protein		8.93	0.36	Hypothetical protein
GSU2983	hypothetical protein		8.93	0.28	Hypothetical protein
GSU1541	hypothetical protein		8.93	0.53	Hypothetical protein
GSU1676	hypothetical protein		8.93	0.50	Hypothetical protein
GSU1352	tRNA (5-carboxymethylaminomethyl-2-thio-U34) synthesis sulfur	*tusA-1*	8.93	0.28	Protein synthesis

	carrier protein				
GSU3208	23S rRNA (3-N-methyl-pseudoU1915)-methyltransferase	*rlmH*	8.93	0.30	Protein synthesis
GSU0858	TonB-dependent receptor, putative		8.93	0.50	Transport and binding proteins
GSU2505	NHL repeat domain protein		8.93	0.42	Unknown function
GSU0121	periplasmically oriented, membrane-bound [NiFe]-hydrogenase b-type cytochrome subunit	*hyaB*	8.92	0.25	Energy metabolism
GSU3628	phosphoglycerate kinase	*pgk*	8.92	0.21	Energy metabolism
GSU2200	hypothetical protein		8.92	0.10	Hypothetical protein
GSU0436	twitching motility pilus retraction protein	*pilT-3*	8.91	0.20	Cell motility
GSU1013	chemotaxis MotB protein, putative		8.91	0.21	Chemotaxis
GSU2890	cytochrome c biogenesis protein, CcmF/CcyK/CcsA family		8.91	0.58	Energy metabolism
GSU1089	iron-sulfur cluster-binding protein		8.91	0.08	Energy metabolism
GSU3590	hypothetical protein		8.91	0.28	Hypothetical protein
GSU0821	hypothetical protein		8.91	0.43	Hypothetical protein
GSU2152	hypothetical protein		8.91	0.42	Hypothetical protein
GSU1111	ribosomal RNA large subunit methyltransferase N	*rlmN*	8.91	0.30	Protein synthesis
GSU1730	branched-chain amino acid ABC transporter ATP-binding protein	*livF*	8.90	0.27	Transport and binding proteins
GSU0116	transglycosylase		8.90	0.17	Unknown function
GSU3432	NADH dehydrogenase I subunit K	*nuoK-2*	8.89	0.70	Energy metabolism
GSU3259	cytochrome c family protein		8.89	0.07	Energy metabolism
GSU2057	hypothetical protein		8.89	0.09	Hypothetical protein
GSU3557	hypothetical protein		8.89	0.39	Hypothetical protein
GSU0389	phosphate transporter, putative		8.89	0.36	Inorganic ion transporter protein
GSU2857	50S ribosomal protein L3	*rplC*	8.89	0.16	Protein synthesis
GSU1698	TPR domain protein		8.89	0.28	Unknown function
GSU2213	GAF domain protein		8.89	0.11	Unknown function
GSU0972	ATPase, AAA family		8.89	0.33	Unknown function
GSU0701	cytochrome c	*omcJ*	8.88	0.10	Energy metabolism
GSU1947	hypothetical protein		8.88	0.46	Hypothetical protein
GSU2891	hypothetical protein		8.88	0.15	Hypothetical protein
GSU2915	two component, sigma54 specific, transcriptional regulator, Fis family		8.88	0.27	Transcriptional regulation
GSU2698	transcriptional regulator, TetR family		8.88	0.46	Transcriptional regulator
GSU3287	hydrolase, TatD family		8.88	0.07	Unknown function
GSU0357	cytochrome c family protein		8.87	0.06	Energy metabolism
GSU1188	rhomboid family protein		8.87	0.53	Unknown function
GSU2006	amino acid/amide ABC transporter membrane protein 1, HAAT family (TC 3.A.1.4.-)		8.86	0.13	Amino acid transporter
GSU1975	NAD-dependent epimerase/dehydratase family protein		8.86	0.14	Cell envelope
GSU1317	octaprenyl diphosphate synthase	*ispB*	8.86	0.21	Coenzyme transport and metabolism

GSU0109	ATP synthase F0 subunit B	*atpF*	8.86	0.52	Energy metabolism
GSU3308	adenylosuccinate synthetase	*purA*	8.86	0.10	Purines, pyrimidines, nucleosides, and nucleotides
GSU1162	ABC transporter, ATP-binding protein		8.86	0.25	Transport and binding protein
GSU2036	type IV pilus minor pilin PilV	*pilV-2*	8.85	0.41	Cell motility
GSU1613	A/G-specific DNA-adenine glycosylase (EC 3.2.2.-)		8.85	0.25	DNA repair
GSU1368	hypothetical protein		8.85	0.08	Hypothetical protein
GSU3018	hypothetical protein		8.85	0.41	Hypothetical protein
GSU0064	integrative genetic element Gsu32, integrase		8.85	0.29	Mobilome:prophages, transposons
GSU1590	DHH family/DHHA1 domain protein		8.85	0.21	Unknown function
GSU3073	UDP-N-acetylmuramylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase	*murF*	8.84	0.09	Cell envelope
GSU2933	cytochrome b/b6 complex, iron-sulfur subunit		8.84	0.07	Energy metabolism
GSU0681	sensory box histidine kinase		8.84	0.29	Signal transduction
GSU1163	ABC transporter, permease protein		8.84	0.08	Transport and binding protein
GSU1723	mechanosensitive ion channel family protein		8.84	0.27	Transport and binding proteins
GSU1578	B12-binding protein		8.84	0.40	Transport and binding proteins
GSU3132	histone-like protein	*hup*	8.84	0.53	Unknown function
GSU2476	TPR domain protein		8.84	0.12	Unknown function
GSU1490	shikimate 5-dehydrogenase	*aroE*	8.83	0.11	Amino acid biosynthesis
GSU1510.1	glycosyltransferase		8.83	0.07	Cell envelope
GSU3050	flagellar basal body P-ring formation protein FlgA	*flgA*	8.83	0.09	Cell motility
GSU0111	F0F1 ATP synthase subunit alpha	*atpA*	8.83	0.15	Energy metabolism
GSU1629	glyceraldehyde-3-phosphate dehydrogenase, type I	*gapA*	8.83	0.27	Energy metabolism
GSU3221	cytochrome c family protein		8.83	0.07	Energy metabolism
GSU3218	cytochrome c family protein		8.83	0.29	Energy metabolism
GSU2928	hypothetical protein		8.83	0.08	Hypothetical protein
GSU2147	cadmium-translocating P-type ATPase		8.83	0.17	Inorganic ion transport proteins
GSU2781	efflux transporter, RND family, MFP subunit		8.83	0.17	Transport and binding proteins
GSU2403	hypothetical protein		8.82	0.29	Hypothetical protein
GSU0483	7-cyano-7-deazaguanine synthase	*queC*	8.82	0.25	Protein synthesis
GSU1203	potassium/proton antiporter, CPA1 family (TC 2.A.36)		8.82	0.28	Transport and binding protein
GSU1840	PAP2 family protein		8.82	0.40	Unknown function
GSU3146	pyranopterin triphosphate synthase	*moaA*	8.81	0.30	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0435	MSHA biogenesis protein MshE, putative	*pilB*	8.81	0.40	Cell motility
GSU0378	glycine dehydrogenase subunit 2	*gcvP2*	8.81	0.09	Energy metabolism
GSU0290	3-oxoacyl-ACP synthase	*fabH-1*	8.81	0.28	Fatty acid and phospholipid metabolism
GSU2072	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative		8.81	0.70	Fatty acid and phospholipid

					metabolism
GSU1548	hypothetical protein		8.81	0.10	Hypothetical protein
GSU3509	hypothetical protein		8.81	0.25	Hypothetical protein
GSU3522	hypothetical protein		8.81	0.43	Hypothetical protein
GSU3598	hypothetical protein		8.81	0.43	Hypothetical protein
GSU0391	Outer membrane efflux family protein		8.81	0.10	Transport and binding proteins
GSU1782	type II secretion system ATPase PulM	*pulM*	8.80	0.28	Bacterial secretion
GSU0728	polyphosphate-dependent AMP kinase	*ppk-2*	8.80	0.09	Central intermediary metabolism
GSU2820	nitrogenase molybdenum-iron protein subunit alpha	*nifD*	8.80	0.17	Central intermediary metabolism
GSU1062	cytochrome c, putative		8.80	0.25	Energy metabolism
GSU3385	phosphoenolpyruvate carboxykinase	*pckA*	8.80	0.39	Energy metabolism
GSU0865	cell division protein DivIVA, putative		8.79	0.24	Cell division
GSU0087	heterodisulfide oxidoreductase, iron-sulfur cluster-binding subunit E	*hdrE*	8.79	0.45	Energy metabolism
GSU1733	branched-chain amino acid ABC transporter membrane protein	*livH*	8.79	0.11	Transport and binding proteins
GSU1981	hypothetical protein		8.78	0.24	Hypothetical protein
GSU1735	branched-chain amino acid ABC transporter substrate-binding protein	*livK-2*	8.78	0.26	Transport and binding proteins
GSU3580	lipoprotein		8.78	0.33	Unknown function
GSU1936	quinolinate phosphoribosyltransferase, decarboxylating	*nadC*	8.77	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2032	type IV pilus biogenesis ATPase PilM	*pilM*	8.77	0.42	Cell motility
GSU3019	dehydrogenase, E1 component, alpha and beta subunits		8.77	0.31	Energy metabolism
GSU1931	hypothetical protein		8.77	0.28	Hypothetical protein
GSU1913	nucleoid maintenance protease YeaZ	*yeaZ*	8.77	0.10	Protein fate
GSU3148	GAF sensor signal transduction histidine kinase (EC 2.7.13.3)		8.77	0.28	Signal transduction mechanisms
GSU3210	nicotinate/nicotinamide mononucleotide adenylyltransferase	*nadD*	8.76	0.26	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1066	type IV pilus assembly protein PilY	*pilY1-1*	8.76	0.09	Cell motility
GSU2119	integrative genetic element Gsu56, integrase		8.76	0.22	Mobilome:prophages, transposons
GSU1265	sensor histidine kinase/response regulator		8.76	0.16	Signal transduction
GSU1610	efflux transporter, RND family, MFP subunit		8.76	0.18	Transport and binding proteins
GSU1979	exopolysaccharide synthesis membrane protein H (exosortase)	*epsH*	8.75	0.20	Cell envelope
GSU1985	outer membrane protein, putative		8.75	0.22	Cell envelope
GSU1741	pppGpp 5'-phosphohydrolase and exopolyphosphatase	*gppA-1*	8.75	0.25	Central intermediary metabolism
GSU0755	hypothetical protein		8.75	0.40	Hypothetical protein
GSU3251	hypothetical protein		8.75	0.17	Hypothetical protein
GSU0318	peptidase, M48 family		8.75	0.05	Protein fate
GSU1909	ketol-acid reductoisomerase	*ilvC*	8.74	0.23	Amino acid biosynthesis
GSU2608	chorismate mutase and prephenate dehydratase	*pheA*	8.74	0.42	Amino acid biosynthesis
GSU0032	heat shock protein GrpE	*grpE*	8.74	0.14	Defense mechanisms
GSU3266	DNA helicase II, putative		8.74	0.42	DNA replication

GSU0339	NADH dehydrogenase I subunit B	*nuoB*	8.74	0.28	Energy metabolism
GSU0696	glucose 1-dehydrogenase		8.74	0.25	Energy metabolism
GSU0517	hypothetical protein		8.74	0.30	Hypothetical protein
GSU2662	hypothetical protein		8.74	0.34	Hypothetical protein
GSU3139	hypothetical protein		8.74	0.07	Hypothetical protein
GSU0280	DNA-binding protein Fis		8.74	0.42	Signal transduction mechanisms
GSU1797	ComEA-related protein		8.73	0.28	Bacterial conjugation
GSU3021	DegT/DnrJ/EryC1/StrS family protein		8.73	0.31	Cell envelope
GSU2252	heptosyltransferase family protein		8.73	0.25	Cell envelope
GSU2947	heavy metal sensor signal transduction histidine kinase (EC 2.7.13.3)		8.73	0.28	Defense mechanisms
GSU0506	methylamine utilization protein MauE, putative		8.73	0.14	Energy metabolism
GSU2644	hypothetical protein		8.73	0.49	Hypothetical protein
GSU2043	type IV prepilin-like proteins leader peptide processing enzyme	*pilD*	8.72	0.29	Cell motility
GSU0809	carbonic anhydrase, putative		8.72	0.42	Central intermediary metabolism
GSU1603	3-oxoacyl-ACP reductase	*fabG-2*	8.72	0.13	Fatty acid and phospholipid metabolism
GSU1358	hypothetical protein		8.72	0.14	Hypothetical protein
GSU3407	hypothetical protein		8.72	0.40	Hypothetical protein
GSU2835	methionine aminopeptidase	*map*	8.72	0.29	Protein fate
GSU0255	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		8.72	0.45	Signal transduction
GSU0991	glycosyl transferase, group 1 family protein		8.71	0.15	Cell envelope
GSU2048	hypothetical protein		8.71	0.41	Hypothetical protein
GSU1085	hypothetical protein		8.71	0.43	Hypothetical protein
GSU3170	hypothetical protein		8.71	0.17	Hypothetical protein
GSU2002	hypothetical protein		8.71	0.42	Hypothetical protein
GSU3009	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	*cobT*	8.70	0.70	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0583	methyl-accepting chemotaxis sensory transducer, class 40+24H	*mcp64H-1*	8.70	0.07	Chemotaxis
GSU1861	2-ketoisovalerate ferredoxin reductase	*vorA*	8.70	0.28	Energy metabolism
GSU0275	hypothetical protein		8.70	0.70	Hypothetical protein
GSU2830	50S ribosomal protein L17	*rplQ*	8.70	0.28	Protein synthesis
GSU1138	Ser/Thr protein phosphatase family protein		8.70	0.53	Unknown function
GSU1351	iron-sulfur cluster-binding protein		8.69	0.24	Energy metabolism
GSU3022	hypothetical protein		8.69	0.46	Hypothetical protein
GSU1438	hypothetical protein		8.69	0.15	Hypothetical protein
GSU1126	phage SPO1 DNA polymerase-related protein		8.69	0.10	Mobilome: prophages, transposons
GSU2410	ATP-independent chaperone	*hspA-2*	8.69	0.40	Protein fate
GSU3314	lipoprotein, putative		8.69	0.21	Unknown function
GSU3453	uroporphyrinogen decarboxylase	*hemE*	8.68	0.26	Biosynthesis of cofactors, prosthetic groups, and carriers

GSU1702	glucokinase (EC 2.7.1.2)		8.68	0.53	Carbohydrate transport and metabolism
GSU2718	bidirectional NAD-reducing hydrogenase, large subunit	*hoxL*	8.68	0.70	Energy metabolism
GSU0619	hypothetical protein		8.68	0.42	Hypothetical protein
GSU3387	transcriptional regulator, AraC family		8.68	0.08	Transcriptional regulator
GSU1881	phosphoenolpyruvate--protein phosphotransferase	*ptsI*	8.67	0.10	Carbohydrate transport and metabolism
GSU1612	phosphoglyceromutase	*gpmA*	8.67	0.10	Carbohydrate transport and metabolism
GSU1511	glycosyl transferase, group 1 family protein		8.67	0.47	Cell envelope
GSU2212	response receiver CheY associated with MCPs of class 40H	*cheY40H-4*	8.67	0.53	Chemotaxis
GSU2370	acetyl-CoA carboxylase, carboxyl transferase subunit beta	*accD*	8.67	0.37	Fatty acid and phospholipid metabolism
GSU2713	hypothetical protein		8.67	0.50	Hypothetical protein
GSU0117	hypothetical protein		8.67	0.08	Hypothetical protein
GSU1911	acetolactate synthase large subunit	*ilvB*	8.66	0.29	Amino acid biosynthesis
GSU1003	nitrogen fixation master sigma-54-dependent transcriptional response regulator	*gnfM*	8.66	0.31	Central intermediary metabolism
GSU1535	exodeoxyribonuclease V subunit alpha	*recD*	8.66	0.07	DNA metabolism
GSU1466	malate dehydrogenase	*mdh*	8.66	0.32	Energy metabolism
GSU3224	hypothetical protein		8.66	0.40	Hypothetical protein
GSU2854	50S ribosomal protein L2	*rplB*	8.66	0.28	Protein synthesis
GSU1148	sensor histidine kinase		8.66	0.15	Signal transduction
GSU3554	hypothetical protein		8.65	0.39	Hypothetical protein
GSU1830	hypothetical protein		8.65	0.25	Hypothetical protein
GSU3426	hypothetical protein		8.65	0.07	Hypothetical protein
GSU0938	hypothetical protein		8.65	0.10	Hypothetical protein
GSU0948	ABC transporter, permease protein, putative		8.65	0.18	Transport and binding protein
GSU1435	peptide ABC transporter, permease protein		8.65	0.38	Transport and binding proteins
GSU2220	scaffold protein CheW associated with MCPs of class 40H	*cheW40H-1*	8.64	0.10	Chemotaxis
GSU2124	thioredoxin-related domain protein		8.64	0.15	Energy metabolism
GSU1649	cytochrome b/b6		8.64	0.70	Energy metabolism
GSU1738	indolepyruvate oxidoreductase subunit beta	*iorB-1*	8.64	0.42	Energy metabolism
GSU2935	cytochrome c family protein		8.64	0.15	Energy metabolism
GSU2510	hypothetical protein		8.64	0.40	Hypothetical protein
GSU1125	hypothetical protein		8.64	0.07	Hypothetical protein
GSU3578	hypothetical protein		8.64	0.26	Hypothetical protein
GSU3030	hypothetical protein		8.64	0.11	Hypothetical protein

GSU3390	hypothetical protein		8.64	0.07	Hypothetical protein
GSU0007	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		8.64	0.34	Signal transduction
GSU1502	phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase	*xapE*	8.64	0.09	Unknown function
GSU2317	trkA domain protein		8.64	0.16	Unknown function
GSU0853	CBS domain protein		8.64	0.08	Unknown function
GSU3408	L-threonine aldolase	*ltaE*	8.63	0.34	Amino acid biosynthesis
GSU2247	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)		8.63	0.07	Cell envelope
GSU0354	hypothetical protein		8.63	0.25	Hypothetical protein
GSU2520	(R)-2-hydroxyacyl-CoA dehydratase-radicalizing ATPase YjiL	*yjiL*	8.63	0.10	Secondary metabolites biosynthesis
GSU2823	RND family efflux pump membrane fusion protein	*ybhG*	8.63	0.37	Transport and binding proteins
GSU2896	ankyrin-related protein		8.63	0.22	Unknown function
GSU0227	type II DNA modification methyltransferase, putative		8.62	0.07	Bacterial secretion
GSU1303	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-11*	8.62	0.31	Chemotaxis
GSU3239	ribonuclease G	*cafA*	8.62	0.28	Degradation of RNA
GSU0564	hypothetical protein		8.62	0.08	Hypothetical protein
GSU2249	hypothetical protein		8.62	0.42	Hypothetical protein
GSU1336	membrane protein, TerC family		8.62	0.44	Inorganic ion transport and metabolism
GSU0169	ABC transporter, ATP-binding protein		8.62	0.40	Transport and binding protein
GSU2074	PPIC-type PPIASE domain protein		8.62	0.37	Unknown function
GSU3273	hypothetical protein		8.61	0.27	Hypothetical protein
GSU3258	hypothetical protein		8.61	0.53	Hypothetical protein
GSU2825	ABC transporter membrane protein	*ybhS*	8.61	0.43	Transport and binding protein
GSU1445	TonB-dependent receptor, putative		8.61	0.30	Transport and binding proteins
GSU3365	cysteinyl-tRNA ligase	*cysS*	8.60	0.40	Amino acid biosynthesis
GSU2005	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1.4.-)		8.60	0.18	Amino acid transporter
GSU1442	carbonic anhydrase family protein		8.60	0.30	Central intermediary metabolism
GSU2643	cytochrome c family protein		8.60	0.07	Energy metabolism
GSU1339	hypothetical protein		8.60	0.40	Hypothetical protein
GSU1499	hypothetical protein	*xapB*	8.60	0.17	Hypothetical protein
GSU0690	hypothetical protein		8.60	0.70	Hypothetical protein
GSU2842	50S ribosomal protein L6	*rplF*	8.60	0.21	Protein synthesis
GSU3138	sensor histidine kinase/response regulator		8.60	0.17	Signal transduction
GSU0700	sensory box/response regulator		8.60	0.40	Signal transduction
GSU0029	hydrolase, carbon-nitrogen family		8.60	0.10	Unknown function
GSU1493	type IV pilus inner membrane protein PilC	*pilC*	8.59	0.36	Cell motility

GSU1615	hypothetical protein		8.59	0.31	Hypothetical protein
GSU0992	hypothetical protein		8.59	0.19	Hypothetical protein
GSU3001	cobalt ABC transporter ATP-binding protein	*cbiO*	8.59	0.25	Transport and binding proteins
GSU1696	MoxR family protein		8.59	0.07	Unknown function
GSU3461	thioesterase family protein		8.59	0.10	Unknown function
GSU1622	L-lactate permease		8.58	0.18	Carbohydrate transport and metabolism
GSU1789	glycosyl transferase, group 2 family protein		8.58	0.46	Cell envelope
GSU1229	lipoprotein, putative		8.58	0.20	Unknown function
GSU0327	type II secretion system inner membrane protein GspF	*gspF*	8.57	0.42	Bacterial secretion
GSU2190	class II Aldolase and Adducin N-terminal domain protein		8.57	0.15	Carbohydrate transport and metabolism
GSU2078	cell shape-determining protein RodA	*rodA*	8.57	0.11	Cell division
GSU0623	glycosyl transferase, group 2 family protein		8.57	0.07	Cell envelope
GSU1063	type IV pilus minor pilin PilV	*pilV-1*	8.57	0.10	Cell motility
GSU1030	methyl-accepting chemotaxis sensory transducer, class 40H, Cache_2 domain-containing	*mcp40H-5*	8.57	0.31	Chemotaxis
GSU2409	heat shock protein, Hsp20 family		8.57	0.10	Defense mechanisms
GSU0085	heterodisulfide oxidoreductase, NAD(P)H oxidoreductase subunit F	*hdrF*	8.57	0.09	Energy metabolism
GSU1093	hypothetical protein		8.57	0.16	Hypothetical protein
GSU1749	hypothetical protein		8.57	0.10	Hypothetical protein
GSU0578	glycyl-tRNA ligase subunit alpha	*glyQ*	8.57	0.35	Protein synthesis
GSU2046	response regulator		8.57	0.42	Signal transduction
GSU2354	transcriptional regulator, IclR family		8.57	0.20	Transcriptional regulator
GSU2480	potassium-transporting ATPase subunit A	*kdpA*	8.57	0.29	Transport and binding protein
GSU2960	molybdate ABC transporter ATP-binding protein	*modC*	8.57	0.35	Transport and binding proteins
GSU2172	OmpA domain protein, putative		8.56	0.50	Cell envelope
GSU2613	iron/zinc/nickel/cobalt/cadmium efflux protein	*fieF*	8.56	0.31	Defense mechanisms
GSU2796	electron transfer flavoprotein subunit alpha	*etfA*	8.56	0.13	Energy metabolism
GSU0632	hypothetical protein		8.56	0.10	Hypothetical protein
GSU0986	tail lysozyme, putative		8.56	0.10	Mobilome:prophages, transposons
GSU3348	Hsp33-like chaperonin	*hslO*	8.56	0.39	Protein fate
GSU1419	transcriptional regulator, Cro/CI family		8.56	0.25	Transcriptional regulator
GSU1832	chromosome segregation and condensation protein ScpA	*scpA*	8.55	0.10	Cell division
GSU0036	capsule biosynthesis protein, putative		8.55	0.25	Cell envelope
GSU3596	hypothetical protein		8.55	0.07	Hypothetical protein
GSU0052	CRISPR-associated protein	*csx14*	8.55	0.17	Mobilome:prophages, transposons
GSU1754	translation elongation factor P-lysyl-lysine 2,3-aminomutase	*yjeK*	8.55	0.27	Protein synthesis
GSU0671	ribosomal large subunit pseudouridine synthase C		8.55	0.43	Protein synthesis
GSU1053	sensory box protein		8.55	0.25	Signal transduction

GSU0079	transcriptional regulator, XRE family with cupin sensor		8.55	0.28	Transcriptional regulator
GSU1433	peptide ABC transporter, periplasmic peptide-binding protein		8.55	0.10	Transport and binding proteins
GSU1404	radical SAM domain protein		8.55	0.07	Unknown function
GSU0406	TPR domain protein		8.55	0.11	Unknown function
GSU2382	anthranilate synthase component II	*trpG*	8.54	0.23	Amino acid biosynthesis
GSU1815	UDP-glucuronate decarboxylase	*uxs*	8.54	0.20	Cell envelope
GSU3184	hypothetical protein		8.54	0.25	Hypothetical protein
GSU1566	hypothetical protein		8.54	0.28	Hypothetical protein
GSU3547	hypothetical protein		8.54	0.53	Hypothetical protein
GSU3089	RNA polymerase sigma-70 factor RpoD	*rpoD*	8.54	0.19	Transcription
GSU1869	lipoprotein, putative		8.54	0.15	Unknown function
GSU0274	cytochrome c family protein		8.53	0.31	Energy metabolism
GSU2201	cytochrome c family protein		8.53	0.46	Energy metabolism
GSU1825	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	*pgsA*	8.53	0.28	Fatty acid and phospholipid metabolism
GSU0672	hypothetical protein		8.53	0.33	Hypothetical protein
GSU2395	hypothetical protein		8.53	0.36	Hypothetical protein
GSU1887	RNA polymerase sigma-54 factor RpoN	*rpoN*	8.53	0.23	Transcription
GSU0018	transcriptional regulator, GntR family		8.53	0.08	Transcriptional regulator
GSU1930	GTP-binding domain protein		8.53	0.25	Unknown function
GSU0124	competence protein F, putative		8.52	0.33	Bacterial conjugation
GSU0045	hypothetical protein		8.52	0.49	Hypothetical protein
GSU1853	hypothetical protein		8.52	0.19	Hypothetical protein
GSU1661	hypothetical protein		8.52	0.42	Hypothetical protein
GSU1897	MTA/SAH nucleosidase, putative		8.52	0.10	Nucleotide transport and metabolism
GSU2430	SPFH domain, Band 7 family protein		8.52	0.52	Unknown function
GSU1912	dihydroxy-acid dehydratase	*ilvD*	8.51	0.10	Amino acid biosynthesis
GSU1961	glycosyl transferase, group 2 family protein		8.51	0.25	Cell envelope
GSU1619	response receiver CheY	*cheY-4*	8.51	0.53	Chemotaxis
GSU2051	phenylacetate--coenzyme A ligase	*paaK-3*	8.51	0.36	Coenzyme transport and metabolism
GSU2466	hypothetical protein		8.51	0.17	Hypothetical protein
GSU1025	hypothetical protein		8.51	0.37	Hypothetical protein
GSU0797	conserved hypothetical protein TIGR00427		8.51	0.28	Hypothetical protein
GSU0057	CRISPR-associated exonuclease Cas4 and endodeoxyribonuclease Cas1	*cas1-1*	8.51	0.34	Mobilome:prophages, transposons
GSU1197	RNA methyltransferase, TrmH family, group 2, putative		8.51	0.07	Protein synthesis
GSU0518	sodium/solute symporter family protein	*aplD*	8.51	0.08	Transport and binding proteins
GSU0426	flagellar biosynthesis protein FlhB	*flhB*	8.50	0.15	Cell motility
GSU1095	phosphate transport system regulatory protein PhoU	*phoU*	8.50	0.41	Inorganic ion transporter protein

GSU1246	deoxyguanosinetriphosphate triphosphohydrolase-like protein		8.50	0.34	Purines, pyrimidines, nucleosides, and nucleotides
GSU2061	acetyltransferase	*argA*	8.49	0.25	Amino acid biosynthesis
GSU2065	inorganic polyphosphate/ATP-NAD kinase	*ppnK*	8.49	0.17	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0413	flagellum-specific ATPase FliI	*fliI*	8.49	0.12	Cell motility
GSU0215	5,10-methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	*folD-1*	8.49	0.12	Coenzyme transport and metabolism
GSU2108	hypothetical protein		8.49	0.25	Hypothetical protein
GSU1268	transcriptional regulator, LysR family		8.49	0.07	Transcriptional regulator
GSU1889	lipopolysaccharide ABC transporter periplasmic protein LptA	*lptA*	8.49	0.07	Transport and binding protein
GSU2373	lipoprotein, putative		8.49	0.07	Unknown function
GSU3194	thiamin monophosphate kinase	*thiL*	8.48	0.44	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2874	N-acetyl-gamma-glutamyl-phosphate reductase	*argC*	8.48	0.23	Energy metabolism
GSU1307	nonheme ferritin	*ftn*	8.48	0.33	Energy metabolism
GSU0887	hypothetical protein		8.48	0.28	Hypothetical protein
GSU0961	ISGsu4, transposase		8.48	0.34	Mobilome:prophages, transposons
GSU2599	ISGsu4, transposase		8.48	0.34	Mobilome:prophages, transposons
GSU3276	LysM domain protein		8.48	0.14	Unknown function
GSU3404	amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.1.3.-)		8.47	0.20	Amino acid transporter
GSU1060	hypothetical protein		8.47	0.10	Hypothetical protein
GSU3359	hypothetical protein		8.47	0.14	Hypothetical protein
GSU0025	tolB protein		8.47	0.42	Transport and binding proteins
GSU1210	metallo-beta-lactamase family protein		8.47	0.25	Unknown function
GSU1471	HD domain protein		8.47	0.13	Unknown function
GSU1778	type II secretion system secretin lipoprotein PulQ	*pulQ*	8.46	0.31	Bacterial secretion
GSU1957	glycosyl transferase, group 1 family protein		8.46	0.30	Cell envelope
GSU0594	cytochrome c family protein		8.46	0.40	Energy metabolism
GSU2024	hypothetical protein		8.46	0.25	Hypothetical protein
GSU3612	30S ribosomal protein S12	*rpsL*	8.46	0.53	Protein synthesis
GSU2222	sensor histidine kinase CheA associated with MCPs of class 40H	*cheA40H*	8.46	0.05	Signal transduction
GSU1997	PDZ domain protein		8.46	0.17	Unknown function
GSU0502	lipoprotein, putative		8.46	0.53	Unknown function
GSU3405	amino acid ABC transporter membrane protein, PAAT family (TC 3.A.1.3.-)		8.45	0.19	Amino acid transporter
GSU2942	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-19*	8.45	0.31	Chemotaxis
GSU3436	NADH:ubiquinone oxidoreductase subunit H	*nuoH-2*	8.45	0.29	Energy metabolism

GSU0240	malonyl-CoA--acyl carrier protein transacylase	*fabD-1*	8.45	0.70	Fatty acid biosynthesis
GSU1328	hypothetical protein		8.45	0.28	Hypothetical protein
GSU2901	hypothetical protein		8.45	0.40	Hypothetical protein
GSU1337	hypothetical protein		8.45	0.10	Hypothetical protein
GSU1870	diguanylate cyclase with GAF sensor		8.45	0.40	Regulatory functions
GSU2113	transcriptional regulator, putative		8.45	0.28	Transcriptional regulator
GSU3268	ferrous iron transport protein B	*feoB-2*	8.45	0.11	Transport and binding protein
GSU2123	HD domain protein		8.45	0.51	Unknown function
GSU3406	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)		8.44	0.53	Amino acid transporter
GSU0329	type II secretion system lipoprotein GspD	*gspD*	8.44	0.09	Bacterial secretion
GSU1488	hypothetical protein		8.44	0.07	Hypothetical protein
GSU1969	hypothetical protein		8.44	0.26	Hypothetical protein
GSU0789	response regulator		8.44	0.53	Signal transduction
GSU2396	putative transposase		8.44	0.42	Unknown function
GSU0150	acetylglutamate kinase	*argB*	8.43	0.10	Amino acid biosynthesis
GSU1970	N-acetylneuraminate synthase	*neuB*	8.43	0.07	Cell envelope
GSU0684	scaffold protein CheW associated with MCPs of class 34H	*cheW34H-4*	8.43	0.28	Chemotaxis
GSU0490	succinyl:acetate coenzyme A transferase	*ato-3*	8.43	0.35	Energy metabolism
GSU0591	cytochrome c family protein		8.43	0.70	Energy metabolism
GSU1103	acyl-CoA synthase		8.43	0.32	Fatty acid and phospholipid metabolism
GSU3388	hypothetical protein		8.43	0.17	Hypothetical protein
GSU1758	phosphoribosylaminoimidazole synthetase	*purM*	8.43	0.07	Purines, pyrimidines, nucleosides, and nucleotides
GSU2744	major facilitator family transporter		8.43	0.27	Transport and binding protein
GSU3125	mannitol dehydrogenase	*mtd*	8.42	0.07	Carbohydrate transport and metabolism
GSU0268	hypothetical protein		8.42	0.25	Hypothetical protein
GSU1463	aspartyl-tRNA ligase	*aspS*	8.42	0.25	Protein synthesis
GSU3230	sensory box histidine kinase		8.42	0.15	Signal transduction
GSU0768	AzlC family protein		8.42	0.18	Transport and binding proteins
GSU3614	ResB-like family cytochrome c biogenesis protein		8.42	0.17	Unknown function
GSU3066	D-alanine--D-alanine ligase	*ddl*	8.41	0.25	Cell envelope
GSU2418	methyl viologen-reducing hydrogenase, small subunit	*mvhS*	8.41	0.25	Energy metabolism
GSU2681	iron-sulfur cluster-binding protein		8.41	0.45	Energy metabolism
GSU0308	hydrogenase expression/formation protein HypD	*hypD*	8.41	0.40	Energy metabolism
GSU1367	hypothetical protein		8.41	0.48	Hypothetical protein
GSU3299	carboxyl transferase domain protein		8.41	0.17	Lipid transport and metabolism

GSU1365	Mrr restriction system protein, putative		8.41	0.12	Nucleotide transport and metabolism
GSU3377	endonuclease III-like protein	*nth*	8.41	0.28	Purines, pyrimidines, nucleosides, and nucleotides
GSU1530	ATP phosphoribosyltransferase	*hisGL*	8.40	0.36	Amino acid biosynthesis
GSU0439	4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.39)		8.40	0.10	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1106	type I citrate synthase	*gltA*	8.40	0.43	Energy metabolism
GSU2146	hypothetical protein		8.40	0.53	Hypothetical protein
GSU1387	CRISPR processing complex protein CasC	*cse4*	8.40	0.40	Mobilome:prophages, transposons
GSU0776	two component, sigma54 specific, transcriptional regulator, Fis family		8.40	0.20	Transcriptional regulation
GSU2481	potassium-transporting ATPase, B subunit	*kdpB*	8.40	0.26	Transport and binding protein
GSU1598	uncharacterized protein		8.40	0.40	Unknown function
GSU2755	amino acid-binding domain sensor histidine kinase (EC 2.7.13.3)		8.39	0.13	Amino acid transporter
GSU2207	DNA polymerase III subunit delta	*holA*	8.39	0.09	DNA replication
GSU2592	hypothetical protein		8.39	0.37	Hypothetical protein
GSU0855	membrane protein, TerC family		8.39	0.12	Inorganic ion transport and metabolism
GSU1400	diguanylate cyclase (GGDEF) domain		8.39	0.10	Lipid transport and metabolism
GSU0447	50S ribosomal protein L11 methyltransferase	*prmA*	8.39	0.10	Protein synthesis
GSU2685	membrane protein YhhJ	*yhhJ*	8.39	0.45	Transport and binding proteins
GSU2949	PAP2 family protein		8.39	0.51	Unknown function
GSU3225	NHL repeat domain protein		8.39	0.70	Unknown function
GSU0654	thiamin biosynthesis thiocarboxylate synthase	*thiF-1*	8.38	0.23	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3056	flagellar biosynthesis protein FlhA	*flhA*	8.38	0.42	Cell motility
GSU0334	ATP synthase F0 subunit A	*atpB*	8.38	0.29	Energy metabolism
GSU2837	preprotein translocase subunit SecY	*secY*	8.38	0.59	Protein and peptide secretion and trafficking
GSU2511	periplasmic sensor diguanylate cyclase/phosphodiesterase		8.38	0.27	Signal transduction mechanisms
GSU2903	phosphonate transport system substrate-binding protein		8.38	0.10	Transport and binding proteins
GSU1742	Na/Pi-cotransporter family protein		8.38	0.07	Transport and binding proteins
GSU0617	NHL repeat domain protein		8.38	0.07	Unknown function
GSU0851	rhomboid family protein		8.38	0.26	Unknown function
GSU0885	cobyrinic acid a,c-diamide synthase family protein		8.37	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2253	glycosyl transferase, group 1 family protein		8.37	0.40	Cell envelope
GSU1942	UDP-N-acetyl-D-galactosamine 6-dehydrogenase	*capL*	8.37	0.39	Cell envelope
GSU1921	30S ribosomal protein S2	*rpsB*	8.37	0.36	Protein synthesis
GSU2099	transcriptional regulator, LytTR family		8.37	0.42	Transcriptional regulator

GSU1644	ABC transporter, ATP-binding protein		8.37	0.29	Transport and binding protein
GSU2878	aspartate-semialdehyde dehydrogenase	*asd*	8.36	0.07	Amino acid biosynthesis
GSU1468	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	*korA*	8.36	0.23	Energy metabolism
GSU0782	periplasmically oriented, membrane-bound [NiFe]-hydrogenase small subunit	*hybS*	8.36	0.15	Energy metabolism
GSU1225	hypothetical protein		8.36	0.70	Hypothetical protein
GSU2162	hypothetical protein		8.36	0.40	Hypothetical protein
GSU2863	DNA-directed RNA polymerase subunit beta	*rpoB*	8.36	0.41	Transcription
GSU0210	putative ABC transport system substrate-binding protein		8.36	0.22	Transport and binding protein
GSU1799	aspartate kinase (EC 2.7.2.4)		8.35	0.25	Amino acid biosynthesis
GSU1153	outer membrane protein, OMP85 family		8.35	0.27	Cell envelope
GSU0883	ferric enterobactin receptor, putative		8.35	0.04	Inorganic ion transport and metabolism
GSU0895	diguanylate cyclase with GAF sensor		8.35	0.27	Lipid transport and metabolism
GSU1753	translation elongation factor P-lysine lysyltransferase	*genX*	8.35	0.10	Protein synthesis
GSU0392	efflux transporter, RND family, MFP subunit		8.35	0.07	Transport and binding proteins
GSU0674	hybrid cluster protein	*hcp*	8.35	0.19	Unknown function
GSU0998	replicative DNA helicase	*dnaB*	8.33	0.28	DNA replication
GSU1465	isocitrate dehydrogenase	*icd*	8.33	0.18	Energy metabolism
GSU1651	fructose-1,6-bisphosphatase	*fbp*	8.33	0.10	Energy metabolism
GSU0959	hypothetical protein		8.33	0.31	Hypothetical protein
GSU1216	thiol reductant ABC exporter, ATP-binding protein CydC	*cydC*	8.33	0.08	Transport and binding proteins
GSU1659	histidyl-tRNA ligase	*hisS*	8.32	0.34	Amino acid biosynthesis
GSU1343	isochorismatase family protein		8.32	0.21	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2621	stage II sporulation-related protein		8.32	0.07	Cell division
GSU2441	hypothetical protein		8.32	0.35	Hypothetical protein
GSU1489	hypothetical protein		8.32	0.25	Hypothetical protein
GSU1960	serine O-acetyltransferase	*cysE-2*	8.31	0.39	Amino acid biosynthesis
GSU3027	flagellar basal body stator protein MotA	*motA*	8.31	0.19	Cell motility
GSU0772	NADPH-dependent FMN reductase domain protein		8.31	0.40	Energy metabolism
GSU1469	2-oxoglutarate ferredoxin oxidoreductase subunit beta	*korB*	8.31	0.53	Energy metabolism
GSU1546	hypothetical protein		8.31	0.17	Hypothetical protein
GSU1012	hypothetical protein		8.31	0.37	Hypothetical protein
GSU2180	transposase, IS4 family		8.31	0.30	Mobilome: prophages and transposons
GSU0252	ISGsu1, transposase		8.31	0.30	Mobilome:prophages, transposons
GSU0299	ISGsu1, transposase		8.31	0.30	Mobilome:prophages, transposons
GSU0957	ISGsu1, transposase		8.31	0.30	Mobilome:prophages, transposons
GSU0065	tRNA (adenosine-34) deaminase	*tadA*	8.31	0.32	Protein synthesis

GSU1345	transcriptional regulator, BadM/Rrf2 family		8.31	0.70	Transcriptional regulator
GSU2031	type IV pilus biogenesis protein PilN	*pilN*	8.30	0.07	Cell motility
GSU2821	nitrogenase iron protein	*nifH*	8.30	0.40	Central intermediary metabolism
GSU1284	cytochrome c, putative		8.30	0.70	Energy metabolism
GSU0450	hypothetical protein		8.30	0.22	Hypothetical protein
GSU2321	hypothetical protein		8.30	0.28	Hypothetical protein
GSU3372	cardiolipin synthase	*cls-2*	8.30	0.50	Lipid transport and metabolism
GSU1793	trigger factor	*tig*	8.30	0.34	Protein fate
GSU1437	peptidase, M48 family		8.30	0.33	Protein fate
GSU0015	periplasmic chaperone for outer membrane proteins SurA		8.30	0.35	Protein fate
GSU2787	transcriptional regulator, LysR family		8.30	0.23	Transcriptional regulator
GSU0586	radical SAM domain-containing iron-sulfur cluster-binding oxidoreductase	*yhcC-2*	8.30	0.10	Unknown function
GSU0572	HAD-superfamily hydrolase, subfamily IA, variant 3		8.30	0.07	Unknown function
GSU1768	ParA family protein		8.29	0.05	Cell division
GSU0571	dihydrofolate reductase	*folA*	8.29	0.10	Coenzyme transport and metabolism
GSU0786	periplasmically oriented, membrane-bound [NiFe]-hydrogenase maturation protease	*hybP*	8.29	0.10	Energy metabolism
GSU1098	phosphate ABC transporter membrane protein PstC	*pstC*	8.29	0.29	Inorganic ion transporter protein
GSU0048	integrase		8.29	0.53	Mobilome:prophages, transposons
GSU1728	pyruvate formate lyase activating enzyme		8.29	0.55	Protein fate
GSU0820	signal peptide peptidase SppA	*sppA*	8.29	0.10	Protein fate
GSU0923	ATP-dependent Lon protease (La)	*lon-1*	8.29	0.40	Protein fate
GSU2209	leucyl-tRNA ligase	*leuS*	8.29	0.22	Protein synthesis
GSU0496	efflux transporter, RND family, MFP subunit		8.29	0.37	Transport and binding proteins
GSU3172	type VI secretion system needle sheath protein TssB	*tssB*	8.28	0.10	Bacterial secretion
GSU0193	L-sorbosone dehydrogenase, putative		8.28	0.14	Carbohydrate transport and metabolism
GSU0107	chromosome segregation DNA-binding protein		8.28	0.53	Cell division
GSU1716	adenosine-5'-phosphosulfate reductase, glutathione-dependent	*apr*	8.28	0.28	Central intermediary metabolism
GSU1785	cytochrome c family protein, putative		8.28	0.17	Energy metabolism
GSU1926	hypothetical protein		8.28	0.40	Hypothetical protein
GSU1845	hypothetical protein		8.28	0.26	Hypothetical protein
GSU1932	hypothetical protein		8.28	0.24	Hypothetical protein
GSU1074	hypothetical protein		8.28	0.42	Hypothetical protein
GSU2189	sensor histidine kinase		8.28	0.07	Signal transduction
GSU3361	transglutaminase domain protein		8.28	0.42	Unknown function
GSU0321	type II secretion system protein GspL	*gspL*	8.27	0.28	Bacterial secretion
GSU1416	iron-sulfur cluster-binding protein		8.27	0.28	Energy metabolism

GSU0463	hypothetical protein		8.27	0.28	Hypothetical protein
GSU2790	hypothetical protein		8.27	0.53	Hypothetical protein
GSU1189	peptidase, M48 family		8.27	0.70	Protein fate
GSU1933	elongation factor G	*fusA-1*	8.27	0.16	Protein synthesis
GSU2856	50S ribosomal protein L4	*rplD*	8.27	0.48	Protein synthesis
GSU2296	metal dependent phosphohydrolase		8.27	0.50	Signal transduction mechanisms
GSU2133	lipoprotein, putative		8.27	0.07	Unknown function
GSU0687	NAD-dependent nucleoside diphosphate-sugar epimerase/dehydratase	*hpnA*	8.26	0.10	Cell envelope
GSU3226	cytochrome c family protein		8.26	0.40	Energy metabolism
GSU0075	hypothetical protein		8.26	0.21	Hypothetical protein
GSU0499	M23/M37 peptidase domain protein		8.26	0.40	Protein fate
GSU0596	response regulator		8.26	0.28	Signal transduction
GSU0951	transcriptional regulator, TetR family		8.26	0.07	Transcriptional regulator
GSU3435	ankyrin repeat protein		8.26	0.53	Unknown function
GSU0486	L-threonine ammonia-lyase (EC 4.3.1.19)	*ilvA*	8.25	0.27	Amino acid biosynthesis
GSU1487	riboflavin kinase and FAD synthetase	*ribF*	8.25	0.70	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2939	short chain amide porin (TC 1.B.16)		8.25	0.40	Cell envelope
GSU2295	hypothetical protein		8.25	0.10	Hypothetical protein
GSU2908	hypothetical protein		8.25	0.46	Hypothetical protein
GSU3306	hypothetical protein		8.25	0.42	Hypothetical protein
GSU2399	serine/threonine-protein kinase HipA		8.25	0.11	Signal transduction mechanisms
GSU0946	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)		8.25	0.28	Signal transduction mechanisms
GSU2826	ABC transporter membrane protein	*ybhR*	8.25	0.54	Transport and binding protein
GSU1124	phosphopantothenylcysteine decarboxylase and phosphopantothenate--cysteine ligase	*coaBC*	8.24	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1180	cell division ATP-dependent zinc protease FtsH	*ftsH-1*	8.24	0.34	Cell division
GSU1214	tetracenomycin polyketide synthesis 8-o-methyltransferase, putative		8.24	0.10	Transcriptional regulation
GSU1009	GTP-binding protein		8.24	0.31	Unknown function
GSU2462	homoserine O-acetyltransferase	*metX*	8.23	0.17	Amino acid biosynthesis
GSU1688	2,5-diamino-6-(5'-phosphoribosylamino)-4-(3H)-pyrimidinone deaminase and 5-amino-6-(5'-phosphoribosylamino)uracil reductase	*ribD*	8.23	0.17	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3037	flagellar filament cap protein FliD	*fliD*	8.23	0.19	Cell motility
GSU1004	nitrogen fixation master sensor histidine kinase, PAS domain-containing	*gnfL*	8.23	0.23	Central intermediary metabolism
GSU2100	catalase/hydroperoxidase HPI(I)	*katG*	8.23	0.37	Defense mechanisms
GSU1049	ribonuclease Z		8.23	0.10	Degradation of RNA
GSU3443	NADH dehydrogenase subunit E	*nuoE-2*	8.23	0.70	Energy metabolism
GSU1726	hypothetical protein		8.23	0.40	Hypothetical protein
GSU1819	integrase/recombinase XerD	*xerD*	8.23	0.15	Mobilome:prophages, transposons
GSU2090	peptidyl-prolyl cis-trans isomerase D		8.23	0.31	Protein fate

GSU0646	tRNA (guanine-N(1)-)-methyltransferase	*trmD*	8.23	0.28	Protein synthesis
GSU1460	prolyl-tRNA ligase	*proS*	8.23	0.12	Protein synthesis
GSU3300	biotin-requiring enzyme subunit		8.23	0.19	Unknown function
GSU3173	type VI secretion system needle sheath protein TssC	*tssC*	8.22	0.15	Bacterial secretion
GSU2996	cobalt-precorrin-6B C5,C15-methyltransferase and C12-decarboxylase	*cobL*	8.22	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3156	methyl-accepting chemotaxis sensory transducer, class 30H	*mcp30H*	8.22	0.17	Chemotaxis
GSU2101	formate acetyltransferase		8.22	0.21	Energy metabolism
GSU0636	hypothetical protein		8.22	0.48	Hypothetical protein
GSU1708	chlorohydrolase, Atz/Trz family		8.22	0.20	Nucleotide transport and metabolism
GSU1139	tyrosyl-tRNA ligase	*tyrS*	8.22	0.07	Protein synthesis
GSU2916	sensor histidine kinase		8.22	0.43	Signal transduction
GSU1296	sensory box histidine kinase/response regulator		8.22	0.09	Signal transduction
GSU2700	tungstate ABC transporter periplasmic tungstate-binding protein	*tupA*	8.22	0.39	Transport and binding proteins
GSU2545	Maf-like protein	*maf*	8.22	0.42	Unknown function
GSU1681	cobyrinic acid a,c-diamide synthase family protein		8.21	0.18	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0733	rod shape-determining protein MreB	*mreB-2*	8.21	0.47	Cell division
GSU0414	flagellar export protein FliJ	*fliJ*	8.21	0.53	Cell motility
GSU1112	methylthioadenosine phosphorylase	*mtaP*	8.21	0.17	Central intermediary metabolism
GSU3279	excinuclease ABC subunit C	*uvrC*	8.21	0.27	DNA metabolism
GSU3296	D-lactate/glycolate dehydrogenase, FAD-binding protein	*glcD-1*	8.21	0.26	Energy metabolism
GSU0794	pyridine nucleotide-disulfide oxidoreductase/rhodanese domain protein		8.21	0.20	Inorganic ion transport and metabolism
GSU2050	preprotein translocase subunit SecA	*secA*	8.21	0.38	Protein and peptide secretion and trafficking
GSU2702	tungstate ABC transporter ATP-binding protein	*tupC*	8.21	0.28	Transport and binding proteins
GSU1570	membrane protein, TerC family		8.20	0.38	Inorganic ion transport and metabolism
GSU0261	Kef-type potassium/proton antiporter, CPA2 family (TC 2.A.37.1)		8.20	0.41	Inorganic ion transporter proteins
GSU2859	elongation factor Tu	*tuf-1*	8.20	0.43	Protein synthesis
GSU2871	elongation factor Tu	*tuf-2*	8.20	0.43	Protein synthesis
GSU1260	ABC transporter, permease protein		8.20	0.42	Transport and binding protein
GSU1903	3-isopropylmalate dehydratase large subunit	*leuC*	8.19	0.18	Amino acid biosynthesis
GSU2974	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase	*metF-2*	8.19	0.22	Amino acid biosynthesis
GSU1915	1-deoxy-D-xylulose 5-phosphate reductoisomerase	*dxr*	8.19	0.19	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3133	peptidoglycan transglycosylase and transpeptidase MrcA	*mrcA*	8.19	0.20	Cell envelope

GSU0043	ImpB/MucB/SamB family protein		8.19	0.07	DNA repair
GSU2932	cytochrome b/b6		8.19	0.07	Energy metabolism
GSU1964	hypothetical protein		8.19	0.47	Hypothetical protein
GSU0264	drug resistance transporter, Bcr/CflA family		8.19	0.07	Transport and binding proteins
GSU2266	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	*lpxD*	8.18	0.10	Cell envelope
GSU3169	hypothetical protein		8.18	0.30	Hypothetical protein
GSU1067	hypothetical protein		8.18	0.21	Hypothetical protein
GSU0793	hypothetical protein		8.18	0.35	Hypothetical protein
GSU3105	hypothetical protein		8.18	0.17	Hypothetical protein
GSU1918	ribosome recycling factor	*frr*	8.18	0.25	Protein synthesis
GSU1272	dihydroorotase	*pyrC*	8.18	0.40	Purines, pyrimidines, nucleosides, and nucleotides
GSU1483	transcriptional regulator, MarR family		8.18	0.53	Transcriptional regulator
GSU2454	putative permease		8.18	0.10	Unknown function
GSU2121	transglycosylase SLT domain protein		8.18	0.70	Unknown function
GSU3100	bifunctional histidinal dehydrogenase/ histidinol dehydrogenase	*hisD*	8.17	0.40	Amino acid biosynthesis
GSU0626	GDP-mannose 4,6-dehydratase and GDP-6-deoxy-D-lyxo-4-hexulose reductase	*gmd*	8.17	0.10	Cell envelope
GSU0419	flagellar hook protein FlgE	*flgE*	8.17	0.22	Cell motility
GSU0522	ATP-dependent RNA helicase RhlB	*rhlB*	8.17	0.48	DNA replication, recombination and repair
GSU1640	cytochrome bd menaquinol oxidase, subunit I	*cydA*	8.17	0.25	Energy metabolism
GSU1553	hypothetical protein		8.17	0.28	Hypothetical protein
GSU0511	hypothetical protein		8.17	0.25	Hypothetical protein
GSU2260	phospholipid/lipopolysaccharide-flipping ABC transporter MsbA	*msbA*	8.17	0.34	Lipid transport and metabolism
GSU2341	monovalent cation/H+ antiporter subunit D	*mrpD*	8.17	0.05	Transport and binding proteins
GSU0548	radical SAM domain protein		8.17	0.46	Unknown function
GSU0505	rhodanese-like domain protein		8.17	0.70	Unknown function
GSU1166	TPR domain protein		8.17	0.42	Unknown function
GSU1718	sulfate adenylyltransferase, subunit 1	*cysN*	8.16	0.28	Central intermediary metabolism
GSU0217	nitroreductase family protein		8.16	0.25	Central intermediary metabolism
GSU2329	cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	*cfa*	8.16	0.07	Fatty acid and phospholipid metabolism
GSU2114	hypothetical protein		8.16	0.28	Hypothetical protein
GSU3317	hypothetical protein		8.16	0.12	Hypothetical protein
GSU3193	ATP-dependent Lon protease (La)	*lon-3*	8.16	0.57	Protein fate
GSU0850	thiol:disulfide interchange protein DsbC		8.16	0.42	Protein fate
GSU2568	tRNA (2-methylthio-N6-threonylcarbamyl-A37) methylthiotransferase	*mtaB*	8.16	0.60	Protein synthesis
GSU0962	Cache sensor signal transduction histidine kinase (EC 2.7.13.3)		8.16	0.20	Signal transduction mechanisms
GSU2809	transcriptional regulator, Fur family		8.16	0.53	Transcriptional regulator

GSU3322	magnesium transport protein CorA	*corA-2*	8.16	0.27	Transport and binding protein
GSU2473	virulence associated protein B	*vapB*	8.16	0.53	Unknown function
GSU1906	2-isopropylmalate synthase	*leuA*	8.15	0.14	Amino acid biosynthesis
GSU0829	heavy metal efflux pump, CzcB family		8.15	0.07	Defense mechanisms
GSU3441	NADH dehydrogenase I subunit F	*nuoF-2*	8.15	0.07	Energy metabolism
GSU0740	Ech-hydrogenase-related complex, NuoH-like integral membrane subunit	*ehrB*	8.15	0.42	Energy metabolism
GSU0219	cytochrome c oxidase, coo3-type, cytochrome o subunit I	*coxA*	8.15	0.42	Energy metabolism
GSU2195	inosine-5'-monophosphate dehydrogenase	*guaB*	8.15	0.27	Purines, pyrimidines, nucleosides, and nucleotides
GSU3324	transcriptional regulator, Cro/CI family		8.15	0.07	Transcriptional regulator
GSU0266	transcriptional regulator, LysR family		8.15	0.53	Transcriptional regulator
GSU0769	RarD protein, DMT superfamily transporter	*rarD*	8.15	0.43	Transport and binding proteins
GSU0156	argininosuccinate lyase	*argH*	8.14	0.14	Amino acid biosynthesis
GSU3307	ATP phosphoribosyltransferase regulatory subunit	*hisZ*	8.14	0.23	Amino acid biosynthesis
GSU2183	Fic family protein		8.14	0.37	Cell division
GSU0670	lipoprotein cytochrome c	*omcX*	8.14	0.18	Energy metabolism
GSU1951	hypothetical protein		8.14	0.10	Hypothetical protein
GSU3583	hypothetical protein		8.14	0.28	Hypothetical protein
GSU0054	CRISPR-associated protein Csb2	*csb2*	8.14	0.26	Mobilome:prophages, transposons
GSU1446	radical SAM domain protein		8.14	0.20	Unknown function
GSU3344	putative serine protein kinase, PrkA		8.14	0.09	Unknown function
GSU3177	type VI secretion system needle syringe protein TssI	*tssI*	8.13	0.18	Bacterial secretion
GSU1691	6,7-dimethyl-8-ribityllumazine synthase	*ribH*	8.13	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3063	cell division protein FtsZ	*ftsZ*	8.13	0.25	Cell division
GSU0360	OmpA domain protein		8.13	0.07	Cell envelope
GSU2657	multicopper oxidase, manganese oxidase family	*ompC*	8.13	0.08	Energy metabolism
GSU2110	hypothetical protein		8.13	0.26	Hypothetical protein
GSU3403	hypothetical protein		8.13	0.30	Hypothetical protein
GSU0711	endonuclease/exonuclease/phosphatase family protein		8.13	0.30	Purines, pyrimidines, nucleosides, and nucleotides
GSU0682	two component transcriptional regulator, LuxR family		8.13	0.07	Transcriptional regulation
GSU2270	lipoprotein release ABC transporter membrane protein	*lolE*	8.13	0.12	Transport and binding protein
GSU0212	ABC transporter, ATP-binding protein		8.13	0.64	Transport and binding protein
GSU0241	BchE/P-methylase family protein		8.13	0.07	Unknown function
GSU0113	F0F1 ATP synthase subunit beta	*atpD*	8.12	0.19	Energy metabolism
GSU2231	hypothetical protein		8.12	0.42	Hypothetical protein
GSU0680	hypothetical protein		8.12	0.24	Hypothetical protein
GSU1519	phenylalanyl-tRNA ligase subunit alpha	*pheS*	8.12	0.14	Protein synthesis

GSU2665	efflux transporter, RND family, MFP subunit		8.12	0.25	Transport and binding proteins
GSU2029	type IV pilus assembly lipoprotein PilP	*pilP*	8.11	0.10	Cell motility
GSU3262	excinuclease ABC subunit B	*uvrB*	8.11	0.23	DNA metabolism
GSU3151	hypothetical protein		8.11	0.07	Hypothetical protein
GSU1333	hypothetical protein		8.11	0.53	Hypothetical protein
GSU2843	30S ribosomal protein S8	*rpsH*	8.11	0.28	Protein synthesis
GSU2735	transcriptional regulator, TetR family		8.11	0.15	Transcriptional regulator
GSU3291	membrane-bound proton-translocating pyrophosphatase	*hppA*	8.11	0.19	Transport and binding proteins
GSU3386	lipoprotein, putative		8.11	0.10	Unknown function
GSU1607	serine hydroxymethyltransferase	*glyA*	8.10	0.39	Amino acid biosynthesis
GSU2027	chorismate synthase	*aroC*	8.10	0.25	Amino acid biosynthesis
GSU1459	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	*ispG*	8.10	0.18	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3024	spore maturation protein CgeB		8.10	0.07	Cell division
GSU1986	glycosyl transferase domain protein		8.10	0.09	Cell envelope
GSU1032	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-6*	8.10	0.08	Chemotaxis
GSU0198	hypothetical protein		8.10	0.25	Hypothetical protein
GSU2225	GTP-binding protein Der	*engA*	8.10	0.07	Protein synthesis
GSU3108	transcription termination factor Rho	*rho*	8.10	0.38	Transcription
GSU1923	lipopolysaccharide ABC transporter membrane protein LptG	*lptG*	8.10	0.66	Transport and binding protein
GSU2269	ABC transporter ATP-binding protein	*lolD*	8.10	0.21	Transport and binding protein
GSU2372	methyl-accepting chemotaxis sensory transducer, class 40+24H	*mcp64H-2*	8.09	0.36	Chemotaxis
GSU1421	DNA repair exonuclease SbcCD, D subunit	*sbcD-1*	8.09	0.51	DNA repair
GSU1384	helicase Cas3	*cas3-2*	8.09	0.07	DNA replication, recombination and repair
GSU2539	carboxynorspermidine dehydrogenase		8.09	0.20	Energy metabolism
GSU1605	3-oxoacyl-(acyl carrier protein) synthase II	*fabF-2*	8.09	0.45	Fatty acid and phospholipid metabolism
GSU0638	hypothetical protein		8.09	0.53	Hypothetical protein
GSU2638	hypothetical protein		8.09	0.53	Hypothetical protein
GSU1050	sensory box histidine kinase		8.09	0.40	Signal transduction
GSU1586	transcription elongation factor NusA	*nusA*	8.09	0.31	Transcription
GSU1091	lipoprotein, putative		8.09	0.43	Unknown function
GSU1061	aspartate aminotransferase		8.08	0.25	Amino acid biosynthesis
GSU2122	TraG family protein		8.08	0.24	Bacterial conjugation
GSU2704	pyranopterin monophosphate cyclase	*moaC*	8.08	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1706	pantoate--beta-alanine ligase	*panC*	8.08	0.42	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1707	group II decarboxylase		8.08	0.20	Biosynthesis of cofactors,

					prosthetic groups, and carriers
GSU1374	methyl-accepting chemotaxis sensory transducer,	*mcp40H-26*	8.08	0.28	Chemotaxis
GSU1950	capK related-protein		8.08	0.07	Coenzyme transport and metabolism
GSU2435	branched-chain alpha-keto acid dehydrogenase E2 subunit	*aceF*	8.08	0.09	Energy metabolism
GSU0843	NADH oxidase, putative		8.08	0.07	Energy metabolism
GSU0170	GreA/GreB family elongation factor		8.08	0.53	Transcription
GSU2490	oxalate/formate antiporter, putative		8.08	0.40	Transport and binding proteins
GSU0159	dihydrodipicolinate synthase	*dapA*	8.07	0.47	Amino acid biosynthesis
GSU0604	phosphomethylpyrimidine synthase ThiC	*thiC-1*	8.07	0.44	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2360	maltooligosyl trehalose synthase (EC 5.4.99.15)		8.07	0.21	Carbohydrate transport and metabolism
GSU3069	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	*murG*	8.07	0.70	Cell envelope
GSU2428	pyruvate carboxylase	*pyc*	8.07	0.08	Energy metabolism
GSU1500	hypothetical protein		8.07	0.42	Hypothetical protein
GSU1282	hypothetical protein		8.07	0.42	Hypothetical protein
GSU2346	hypothetical protein		8.07	0.21	Hypothetical protein
GSU0471	sensor histidine kinase		8.07	0.17	Signal transduction
GSU1236	glutamate synthase (NADPH) GltB1 subunit (EC 1.4.1.13)		8.06	0.49	Amino acid biosynthesis
GSU0945	cystathionine gamma-synthase/beta-lyase	*metC-2*	8.06	0.10	Amino acid biosynthesis
GSU1503	glycosyltransferase	*xapF*	8.06	0.18	Cell envelope
GSU2038	type IV pilus assembly protein PilY	*pilY1-2*	8.06	0.40	Cell motility
GSU0510	NADPH oxidoreductase subunit beta	*sfrB*	8.06	0.26	Energy metabolism
GSU1394	laccase family multicopper oxidase	*ompB*	8.06	0.20	Energy metabolism
GSU1713	conserved hyothetical protein, truncation		8.06	0.28	Hypothetical protein
GSU2199	hypothetical protein		8.06	0.23	Hypothetical protein
GSU1776	type II secretion system pseudopilin OxpG	*oxpG*	8.05	0.28	Bacterial secretion
GSU2703	molybdopterin--molybdenum ligase	*moeA*	8.05	0.25	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1512	UDP-galactopyranose mutase (EC 5.4.99.9)		8.05	0.07	Cell envelope
GSU1816	UDP-glucose 6-dehydrogenase	*ugd*	8.05	0.42	Cell envelope
GSU3433	NADH dehydrogenase I subunit J	*nuoJ-2*	8.05	0.53	Energy metabolism
GSU0343	NADH dehydrogenase I subunit F	*nuoF-1*	8.05	0.45	Energy metabolism
GSU1212	hypothetical protein		8.05	0.47	Hypothetical protein
GSU1791	ATP-dependent protease ATP-binding subunit ClpX	*clpX*	8.05	0.17	Protein fate
GSU1798	(R)-citramalate synthase	*cimA*	8.04	0.34	Amino acid biosynthesis
GSU1350	thiamin biosynthesis thiocarboxylate synthase	*thiF-2*	8.04	0.21	Biosynthesis of cofactors,

					prosthetic groups, and carriers
GSU1484	soluble lytic murein transglycosylase, putative		8.04	0.15	Cell envelope
GSU3564	hypothetical protein		8.04	0.70	Hypothetical protein
GSU0723	hypothetical protein		8.04	0.70	Hypothetical protein
GSU1204	Kef-type potassium/proton antiporter, CPA2 family (TC 2.A.37.1)		8.04	0.19	Inorganic ion transporter proteins
GSU3466	preprotein translocase subunit YidC	*yidC*	8.04	0.49	Protein and peptide secretion and trafficking
GSU1494	sensor histidine kinase PilS, PAS domain-containing	*pilS*	8.04	0.26	Signal transduction
GSU1443	sensor histidine kinase/response regulator		8.04	0.28	Signal transduction
GSU0008	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)		8.04	0.28	Signal transduction
GSU1866	phoH family protein		8.04	0.36	Unknown function
GSU2919	transketolase, A protein	*tklA*	8.04	0.28	Unknown function
GSU3122	metallo-beta-lactamase family protein		8.04	0.70	Unknown function
GSU1796	DHH family protein		8.04	0.29	Unknown function
GSU1868	aminotransferase, class V		8.04	0.24	Unknown function
GSU1695	threonine synthase	*thrC*	8.03	0.07	Amino acid biosynthesis
GSU0983	hypothetical protein		8.03	0.39	Hypothetical protein
GSU3384	cardiolipin synthetase, putative		8.03	0.34	Lipid transport and metabolism
GSU2601	TPR domain/SEC-C motif domain protein		8.03	0.42	Unknown function
GSU1361	Piwi domain protein		8.03	0.40	Unknown function
GSU0441	dehypoxanthinylfutalosine cyclase	*mqnC-2*	8.02	0.50	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2652	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-18*	8.02	0.48	Chemotaxis
GSU3331	pyruvate kinase	*pyk*	8.02	0.32	Energy metabolism
GSU0777	periplasmically oriented, membrane-bound formate dehydrogenase, major subunit, selenocysteine-containing	*fdnG*	8.02	0.15	Energy metabolism
GSU0613	ResB-like family protein		8.02	0.14	Unknown function
GSU2434	octanoyl-(acyl carrier protein)--protein octanoyltransferase	*lipB*	8.01	0.61	Protein fate
GSU0034	chaperone protein DnaJ	*dnaJ*	8.01	0.52	Protein fate
GSU1380	ferrous iron transport protein B	*feoB-1*	8.01	0.22	Transport and binding protein
GSU2650	amino acid ABC transporter membrane protein, PAAT family (TC 3.A.1.3.-)		8.00	0.41	Amino acid transporter
GSU2250	glycosyl transferase, group 1 family protein		8.00	0.38	Cell envelope
GSU2084	D-glycero-D-mannoheptose-1,7-bisphosphate phosphatase	*gmhB*	8.00	0.70	Cell envelope
GSU0090	heterodisulfide oxidoreductase, FAD-binding and iron-sulfur cluster-binding subunit A	*hdrA*	8.00	0.18	Energy metabolism
GSU1772	periplasmic carboxy-terminal processing protease lipoprotein	*ctpA-2*	8.00	0.28	Protein fate
GSU1219	glutamyl-tRNA ligase	*gltX*	8.00	0.41	Protein synthesis
GSU0598	two component, sigma54 specific, transcriptional regulator, Fis family		8.00	0.07	Transcriptional regulation

GSU0013	transcriptional regulator, MarR family		8.00	0.28	Transcriptional regulator
GSU2008	amino acid/amide ABC transporter ATP-binding protein 1, HAAT family (TC 3.A.1.4.-)		7.99	0.40	Amino acid transporter
GSU1430	hypothetical protein		7.99	0.53	Hypothetical protein
GSU1099	phosphate ABC transporter substrate-binding protein	*pstS*	7.99	0.53	Inorganic ion transporter protein
GSU0856	membrane-bound zinc-dependent protease HtpX	*htpX-1*	7.99	0.28	Protein fate
GSU0894	peptidyl-prolyl cis-trans isomerase, cyclophilin-type		7.99	0.53	Protein fate
GSU2876	50S ribosomal protein L13	*rplM*	7.99	0.28	Protein synthesis
GSU0881	sensor histidine kinase		7.99	0.07	Signal transduction
GSU1809	cell division ATP-dependent zinc protease FtsH	*ftsH-2*	7.98	0.31	Cell division
GSU1794	nucleoside-triphosphatase	*rdgB*	7.98	0.10	DNA replication, recombination, and repair
GSU0476	hypothetical protein		7.98	0.70	Hypothetical protein
GSU1472	hypothetical protein		7.98	0.19	Hypothetical protein
GSU1792	ATP-dependent Clp protease proteolytic subunit	*clpP*	7.98	0.10	Protein fate
GSU2815	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.98	0.47	Signal transduction
GSU1010	transglycosylase, Slt family		7.98	0.48	Unknown function
GSU1183	O-acetyl-L-homoserine sulfhydrylase	*metY-1*	7.97	0.25	Amino acid biosynthesis
GSU3098	imidazoleglycerol-phosphate dehydratase	*hisB*	7.97	0.70	Amino acid biosynthesis
GSU1917	undecaprenyl pyrophosphate synthase	*uppS*	7.97	0.40	Cell envelope
GSU2299	cytochrome c family protein		7.97	0.07	Energy metabolism
GSU3358	hypothetical protein		7.97	0.28	Hypothetical protein
GSU1344	hypothetical protein		7.97	0.10	Hypothetical protein
GSU2062	response regulator receiver modulated diguanylate cyclase		7.97	0.42	Signal transduction
GSU0841	sigma-54 dependent DNA-binding response regulator		7.97	0.44	Transcriptional regulator
GSU3062	radical SAM domain protein		7.97	0.34	Unknown function
GSU2089	rod shape-determining protein MreB	*mreB-1*	7.96	0.08	Cell division
GSU2822	nitrogen fixation transcript antitermination response regulator, ANTAR domain-containing	*gnfR*	7.96	0.50	Central intermediary metabolism
GSU0094	DNA polymerase III subunits gamma and tau	*dnaX*	7.96	0.34	DNA replication
GSU0763	helicase, putative		7.96	0.33	DNA replication, recombination and repair
GSU0231	hypothetical protein		7.96	0.10	Hypothetical protein
GSU1385	Cascade antiviral complex protein	*cse1*	7.96	0.37	Mobile and extrachromosomal element functions
GSU2741	transcriptional regulator, TetR family		7.96	0.25	Transcriptional regulator
GSU2272	lipoprotein, putative		7.96	0.10	Unknown function
GSU0651	hydrolase, carbon-nitrogen family		7.96	0.21	Unknown function
GSU0016	PPIC-type PPIASE domain protein		7.96	0.29	Unknown function
GSU2236	GTP/GDP 3'-pyrophosphokinase and (p)ppGpp 3'-	*relA*	7.95	0.33	Adaptations to atypical conditions

	pyrophosphohydrolase				
GSU2731	lipoprotein cytochrome c	*omcC*	7.95	0.44	Energy metabolism
GSU2161	hypothetical protein		7.95	0.21	Hypothetical protein
GSU2414	putative ABC transport system permease protein		7.95	0.19	Transport and binding protein
GSU0244	radical SAM domain protein		7.95	0.41	Unknown function
GSU1904	decarboxylase family protein		7.95	0.45	Unknown function
GSU1833	tryptophanyl-tRNA ligase	*trpS*	7.94	0.28	Amino acid biosynthesis
GSU1725	DNA repair exonuclease SbcCD, C subunit	*sbcC-2*	7.94	0.07	DNA repair
GSU0590	hypothetical protein		7.94	0.53	Hypothetical protein
GSU3360	peptidase, M16 family		7.94	0.25	Protein fate
GSU2313	response regulator receiver modulated diguanylate cyclase		7.94	0.48	Signal transduction
GSU0844	potassium uptake protein, Trk family		7.94	0.28	Transport and binding protein
GSU3329	radical SAM domain protein		7.94	0.19	Unknown function
GSU1224	TPR domain protein		7.94	0.32	Unknown function
GSU3401	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1.4.-)		7.93	0.31	Amino acid transporter
GSU2811	cytochrome c Hsc		7.93	0.28	Energy metabolism
GSU3311	hypothetical protein		7.93	0.28	Hypothetical protein
GSU0520	tRNA pseudouridine 13 synthase	*truD*	7.93	0.20	Protein synthesis
GSU0825	pirin family protein		7.93	0.28	Unknown function
GSU0213	radical SAM domain protein		7.93	0.29	Unknown function
GSU1801	CBS domain protein		7.93	0.28	Unknown function
GSU2086	hypothetical protein		7.92	0.42	Hypothetical protein
GSU2118	integrative genetic element Gsu21, integrase		7.92	0.40	Mobilome:prophages, transposons
GSU1485	exoribonuclease R	*rnr*	7.92	0.26	Transcription
GSU1052	hydrolase, alpha/beta fold family		7.92	0.28	Unknown function
GSU1984	polysaccharide chain length determinant protein, putative		7.91	0.24	Carbohydrate transport and metabolism
GSU1983	polysaccharide biosynthesis protein, putative		7.91	0.64	Carbohydrate transport and metabolism
GSU1620	iron-sulfur cluster binding protein, putative		7.91	0.36	Energy metabolism
GSU3180	hypothetical protein		7.91	0.10	Hypothetical protein
GSU2907	hypothetical protein		7.91	0.42	Hypothetical protein
GSU1634	phosphoribosylformylglycinamidine synthase, PurS and PurL domains	*purSL*	7.91	0.36	Purines, pyrimidines, nucleosides, and nucleotides
GSU2610	LysM domain protein		7.91	0.40	Unknown function
GSU2026	shikimate kinase	*aroK*	7.90	0.53	Amino acid biosynthesis
GSU0069	oxidoreductase, iron-sulfur cluster-binding subunit		7.90	0.40	Energy metabolism
GSU1857	hypothetical protein		7.90	0.42	Hypothetical protein
GSU0304	aminopeptidase N	*pepN*	7.90	0.06	Peptide degradation

GSU0721	RNA polymerase factor sigma-70	*rpoE*	7.90	0.53	Transcription
GSU3074	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	*murE*	7.89	0.15	Cell envelope
GSU2495	cytochrome c family protein		7.89	0.42	Energy metabolism
GSU3181	3-oxoacyl-(acyl carrier protein) synthase		7.89	0.26	Fatty acid and phospholipid metabolism
GSU2333	hypothetical protein		7.89	0.25	Hypothetical protein
GSU2961	molybdate ABC transporter permease	*modB*	7.89	0.25	Transport and binding proteins
GSU1149	EAL domain protein		7.89	0.70	Unknown function
GSU3222	NHL repeat domain protein		7.89	0.61	Unknown function
GSU0477	hydrolase, haloacid dehalogenase-like family		7.89	0.10	Unknown function
GSU1963	polysaccharide biosynthesis domain protein		7.88	0.24	Carbohydrate transport and metabolism
GSU1491	type IV pilus biogenesis ATPase PilB	*pilB*	7.88	0.61	Cell motility
GSU1822	DNA mismatch repair protein MutS	*mutS-1*	7.88	0.20	DNA repair
GSU0778	periplasmically oriented, membrane-bound formate dehydrogenase, iron-sulfur cluster-binding subunit	*fdnH*	7.88	0.53	Energy metabolism
GSU1222	histone deacetylase/AcuC/AphA family protein		7.88	0.34	Unknown function
GSU0070	oxidoreductase, membrane subunit		7.87	0.70	Energy metabolism
GSU1996	cytochrome c family protein		7.87	0.26	Energy metabolism
GSU0817	phospholipid/cholesterol/gamma-HCH transport system permease protein		7.87	0.07	Lipid transport and metabolism
GSU1017	hypoxanthine-guanine phosphoribosyltransferase		7.87	0.53	Purines, pyrimidines, nucleosides, and nucleotides
GSU0093	ABC transporter, ATP-binding/permease protein		7.87	0.28	Transport and binding protein
GSU2759	potassium/proton antiporter	*kefB*	7.87	0.28	Transport and binding protein
GSU1734	branched-chain amino acid ABC transporter substrate-binding protein	*livK-1*	7.87	0.20	Transport and binding proteins
GSU0157	fibronectin type III domain protein		7.87	0.07	Unknown function
GSU1141	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-10*	7.86	0.40	Chemotaxis
GSU1041	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-25*	7.86	0.20	Chemotaxis
GSU2641	hypothetical protein		7.86	0.41	Hypothetical protein
GSU3337	hypothetical protein		7.86	0.53	Hypothetical protein
GSU1429	serine phosphatase		7.85	0.30	Amino acid transport and metabolism
GSU0582	methyl-accepting chemotaxis sensory transducer, class 40H dimer with helix-swapped heme-binding site-containing PAS domain	*mcp40H-2*	7.85	0.18	Chemotaxis
GSU1611	AcrB/AcrD/AcrF family protein		7.85	0.27	Defense mechanisms
GSU0375	glycine cleavage system T protein	*gcvT*	7.85	0.41	Energy metabolism
GSU2445	aconitase (EC 4.2.1.3)		7.85	0.48	Energy metabolism

GSU2312	sulfate transporter family protein		7.85	0.34	Transport and binding proteins
GSU2135	heavy metal efflux pump, CzcA family		7.84	0.31	Defense mechanisms
GSU2230	DNA polymerase III subunit delta	*holB*	7.84	0.48	DNA replication
GSU2448	2-oxoglutarate dehydrogenase, E2 protein, dihydrolipoamide succinyltransferase	*sucB*	7.84	0.17	Energy metabolism
GSU1602	malonyl-CoA--acyl carrier protein transacylase	*fabD-2*	7.84	0.21	Fatty acid biosynthesis
GSU2597	transposase, IS4 family		7.84	0.32	Mobilome: prophages, transposons
GSU0559	ISGsu2, transposase		7.84	0.32	Mobilome:prophages, transposons
GSU1297	ISGsu2, transposase		7.84	0.32	Mobilome:prophages, transposons
GSU3357	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.84	0.27	Signal transduction
GSU3252	GAF sensor signal transduction histidine kinase (EC 2.7.13.3)		7.84	0.20	Signal transduction mechanisms
GSU0631	glycosyl transferase, group 2 family protein		7.83	0.28	Cell envelope
GSU3201	protein glutamine deamidase and protein glutamate methylesterase CheD associated with MCPs of class 44H	*cheD44H*	7.83	0.28	Chemotaxis
GSU2639	hypothetical protein		7.83	0.18	Hypothetical protein
GSU1452	23S rRNA m(5)U-1939 methyltransferase (EC 2.1.1.190)		7.83	0.12	Protein synthesis
GSU2686	ribosome-associated ATPase and membrane protein RbbA	*rbbA*	7.83	0.11	Protein synthesis
GSU1215	thiol reductant ABC exporter, ATP-binding protein CydD	*cydD*	7.83	0.11	Transport and binding proteins
GSU2885	NHL repeat domain protein		7.83	0.10	Unknown function
GSU1835	glutamine synthetase, type I	*glnA*	7.82	0.50	Amino acid biosynthesis
GSU0350	NADH dehydrogenase I subunit M	*nuoM-1*	7.82	0.41	Energy metabolism
GSU0812	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.82	0.30	Signal transduction
GSU0884	radical SAM domain protein		7.82	0.10	Unknown function
GSU3072	phospho-N-acetylmuramoyl-pentapeptide transferase	*mraY*	7.81	0.35	Cell envelope
GSU1035	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-9*	7.81	0.40	Chemotaxis
GSU0785	periplasmically oriented, membrane-bound [NiFe]-hydrogenase large subunit	*hybL*	7.81	0.20	Energy metabolism
GSU1254	hypothetical protein		7.81	0.10	Hypothetical protein
GSU0125	hypothetical protein		7.81	0.70	Hypothetical protein
GSU0448	hydrolase, putative		7.81	0.53	Unknown function
GSU0281	Signal transduction histidine kinase, core		7.80	0.27	Signal transduction mechanisms
GSU2484	winged-helix transcriptional response regulator KdpE	*kdpE*	7.80	0.31	Signal transduction mechanisms
GSU2049	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	*argJ*	7.79	0.53	Amino acid biosynthesis
GSU2383	anthranilate synthase, catalytic subunit	*trpE*	7.79	0.20	Amino acid biosynthesis
GSU0400	methyl-accepting chemotaxis sensory transducer, class 40H, Cache_2 domain-containing	*mcp40H-11*	7.79	0.30	Chemotaxis
GSU0509	NADPH oxidoreductase subunit alpha	*sfrA*	7.79	0.18	Energy metabolism
GSU0622	hypothetical protein		7.79	0.17	Hypothetical protein
GSU0953	hypothetical protein		7.79	0.53	Hypothetical protein
GSU3518	sensor histidine kinase		7.79	0.10	Signal transduction

GSU3118	DNA-binding response regulator		7.79	0.10	Signal transduction mechanisms
GSU0811	two component, sigma54 specific, transcriptional regulator, Fis family		7.79	0.10	Transcriptional regulation
GSU1505	ABC transporter ATP-binding protein	*xapH*	7.79	0.40	Transport and binding protein
GSU2375	tryptophan synthase subunit beta	*trpB1*	7.78	0.53	Amino acid biosynthesis
GSU1332	heavy metal efflux pump, CzcA family		7.78	0.24	Defense mechanisms
GSU1359	helicase, putative		7.78	0.03	DNA replication, recombination and repair
GSU1305	glutamate dehydrogenase	*gdhA*	7.78	0.22	Energy metabolism
GSU2019	acetyl-CoA carboxylase, biotin carboxylase component	*accC*	7.78	0.15	Fatty acid and phospholipid metabolism
GSU2771	hypothetical protein		7.78	0.21	Hypothetical protein
GSU3595	hypothetical protein		7.78	0.10	Hypothetical protein
GSU1312	radical SAM domain protein, selenocysteine-containing		7.78	0.43	Unknown function
GSU2611	flagellar FliL protein		7.77	0.10	Cell motility
GSU1304	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-12*	7.77	0.40	Chemotaxis
GSU3126	oxidoreductase, aldo/keto reductase family		7.77	0.28	Energy metabolism
GSU3186	hypothetical protein		7.77	0.28	Hypothetical protein
GSU1811	hypothetical protein		7.77	0.28	Hypothetical protein
GSU2690	phospholipid-binding lipoprotein MlaA		7.77	0.17	Lipid transport and metabolism
GSU3136	isoleucyl-tRNA ligase	*ileS*	7.77	0.29	Protein synthesis
GSU1635	phosphoribosylformylglycinamidine synthase	*purQ*	7.77	0.07	Purines, pyrimidines, nucleosides, and nucleotides
GSU0296	sensor histidine kinase CheA associated with MCPs of classes 40H and 40+24H	*cheA64H*	7.77	0.48	Signal transduction
GSU1119	response regulator receiver sensor signal transduction histidine kinase (EC 2.7.13.3)		7.77	0.47	Signal transduction
GSU1302	Hpt sensor hybrid histidine kinase (EC 2.7.13.3)		7.77	0.27	Signal transduction mechanisms
GSU1348	sulfate ABC transporter membrane protein CysW	*cysW*	7.77	0.07	Transport and binding proteins
GSU0286	PBS lyase HEAT-like repeat protein		7.77	0.33	Unknown function
GSU1105	xaa-pro dipeptidase	*pepQ-1*	7.76	0.47	Amino acid metabolism
GSU3029	2-acyl-glycerophospho-ethanolamine acyltransferase		7.76	0.40	Fatty acid and phospholipid metabolism
GSU3171	hypothetical protein		7.76	0.34	Hypothetical protein
GSU0927	peptidase, M16 family		7.76	0.09	Protein fate
GSU1403	23S rRNA pseudouridine 2605 synthase	*rluB*	7.76	0.25	Protein synthesis
GSU0656	branched-chain amino acid aminotransferase	*ilvE*	7.75	0.42	Amino acid biosynthesis
GSU3246	peroxiredoxin, typical 2-Cys subfamily	*prx-2*	7.75	0.53	Electron transport
GSU1538	methylamine utilization protein MauG, putative		7.75	0.66	Energy metabolism
GSU1023	glycogen synthase	*glgA-1*	7.75	0.25	Energy metabolism

GSU1314	hypothetical protein		7.75	0.70	Hypothetical protein
GSU2948	hypothetical protein		7.75	0.16	Hypothetical protein
GSU0601	alpha amylase family protein		7.75	0.17	Polysaccharide metabolism
GSU1790	ATP-dependent Lon protease (La)	*lon-2*	7.75	0.14	Protein fate
GSU1873	oligoendopeptidase F	*pepF*	7.75	0.28	Protein fate
GSU1617	LexA family transcriptional repressor	*lexA-2*	7.74	0.53	DNA replication, recombination, and repair
GSU2801	cytochrome c family protein		7.74	0.39	Energy metabolism
GSU0688	squalene-hopene cyclase	*shc-1*	7.74	0.05	Fatty acid and phospholipid metabolism
GSU2297	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.74	0.25	Signal transduction
GSU2477	TPR domain/radical SAM/B12 binding domain protein		7.74	0.31	Unknown function
GSU3277	lysM domain protein		7.74	0.10	Unknown function
GSU1812	arginyl-tRNA ligase	*argS*	7.73	0.41	Amino acid biosynthesis
GSU3200	protein phosphoaspartate phosphatase CheC associated with MCPs of class 44H	*cheC44H*	7.73	0.53	Chemotaxis
GSU2675	hypothetical protein		7.73	0.28	Hypothetical protein
GSU1436	hypothetical protein		7.73	0.28	Hypothetical protein
GSU2944	(R)-2-hydroxyglutaryl-CoA dehydratase alpha-subunit, putative		7.73	0.17	Secondary metabolites biosynthesis
GSU2352	sodium/solute symporter family protein	*aplC*	7.73	0.21	Transport and binding proteins
GSU0010	flagellar biogenesis master response receiver sensor histidine kinase, PAS and GAF domain-containing	*fgrL*	7.72	0.27	Cell motility
GSU1638	hypothetical protein		7.72	0.70	Hypothetical protein
GSU3417	dioxygenase, putative		7.72	0.15	Secondary metabolites biosynthesis, transport and catabolism
GSU0122	periplasmically oriented, membrane-bound [NiFe]-hydrogenase large subunit	*hyaL*	7.71	0.12	Energy metabolism
GSU1944	hypothetical protein		7.71	0.10	Hypothetical protein
GSU2232	methionyl-tRNA ligase	*metG*	7.71	0.68	Protein synthesis
GSU1038	sensory box histidine kinase/response regulator		7.71	0.25	Signal transduction
GSU2337	trehalose-6-phosphate synthase	*otsA*	7.70	0.43	Carbohydrate transport and metabolism
GSU0683	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-6*	7.70	0.14	Chemotaxis
GSU0437	3-octaprenyl-4hydroxybenzoate decarboxylase (EC 4.1.1.-)	*ubiD*	7.70	0.70	Coenzyme transport and metabolism
GSU2191	aldehyde ferredoxin oxidoreductase, tungsten-containing		7.70	0.15	Energy metabolism
GSU2617	preprotein translocase subunit SecD	*secD*	7.70	0.17	Protein and peptide secretion and trafficking
GSU1290	sensor histidine kinase CheA associated with MCPs of class 34H	*cheA34H*	7.70	0.32	Signal transduction

GSU0475	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.70	0.22	Signal transduction
GSU1341	ABC transporter, ATP-binding protein		7.70	0.70	Transport and binding protein
GSU2350	potassium uptake protein, Kup system		7.70	0.36	Transport and binding protein
GSU1925	transport-associated domain protein		7.70	0.39	Unknown function
GSU1007	GAF domain/HD domain protein		7.70	0.32	Unknown function
GSU0766	methyl-accepting chemotaxis sensory transducer, class 40+24H	*mcp64H-8*	7.69	0.42	Chemotaxis
GSU2549	DNA topoisomerase I	*topA*	7.69	0.13	DNA replication
GSU2605	cytidylate kinase	*cmk*	7.69	0.52	Purines, pyrimidines, nucleosides, and nucleotides
GSU2523	transcriptional regulator, LysR family		7.69	0.40	Transcriptional regulator
GSU2286	enolase	*eno*	7.68	0.18	Energy metabolism
GSU1952	hypothetical protein		7.68	0.53	Hypothetical protein
GSU0144	sensory box histidine kinase		7.68	0.23	Signal transduction
GSU3419	sensor histidine kinase		7.68	0.17	Signal transduction
GSU3485	ABC transporter membrane protein		7.68	0.38	Transport and binding protein
GSU3393	amino acid/amide ABC transporter membrane protein 2, HAAT family (TC 3.A.1.4.-)		7.67	0.40	Amino acid transporter
GSU0410	flagellar M-ring mounting plate protein FliF	*fliF*	7.67	0.25	Cell motility
GSU1000	hypothetical protein		7.67	0.08	Hypothetical protein
GSU2224	response regulator		7.67	0.42	Signal transduction
GSU3418	sigma-54 dependent DNA-binding response regulator		7.67	0.16	Transcriptional regulator
GSU2458	penicillin-binding protein, putative		7.67	0.30	Unknown function
GSU2004	3-octaprenyl-4-hydroxybenzoate carboxy-lyase family protein	*ubiD*	7.66	0.33	Coenzyme transport and metabolism
GSU2494	cytochrome c family protein		7.66	0.47	Energy metabolism
GSU0912	hypothetical protein		7.66	0.70	Hypothetical protein
GSU2836	adenylate kinase	*adk*	7.66	0.33	Purines, pyrimidines, nucleosides, and nucleotides
GSU1630	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.66	0.33	Signal transduction
GSU2367	lipopolysaccharide biogenesis outer membrane protein LptD	*lptD*	7.66	0.21	Transport and binding protein
GSU2584	lipoprotein, putative		7.66	0.10	Unknown function
GSU1058	succinyl-CoA synthetase subunit beta	*sucC*	7.65	0.23	Energy metabolism
GSU0460	3-oxoacyl-(acyl carrier protein) synthase II	*fabF-1*	7.65	0.28	Fatty acid and phospholipid metabolism
GSU2603	30S ribosomal protein S1	*rpsA*	7.65	0.14	Protein synthesis
GSU1504	ABC transporter membrane protein, ABC-2 family	*xapG*	7.65	0.28	Transport and binding protein
GSU1137	phosphodiesterase	*rny*	7.65	0.29	Unknown function
GSU3096	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	*hisA*	7.64	0.70	Amino acid biosynthesis
GSU2795	iron-sulfur cluster-binding protein		7.64	0.25	Energy metabolism

GSU2501	cytochrome c family protein		7.64	0.53	Energy metabolism
GSU2941	transcriptional regulator, LysR family		7.64	0.40	Transcriptional regulator
GSU0952	GGDEF domain protein		7.64	0.47	Unknown function
GSU1937	GGDEF domain/HAMP domain protein		7.64	0.53	Unknown function
GSU0356	Protein of unknown function DUF3365		7.64	0.70	Unknown function
GSU0994	fumarate hydratase	*fumB*	7.63	0.18	Energy metabolism
GSU2899	high-molecular-weight cytochrome c		7.63	0.18	Energy metabolism
GSU2345	serine phosphatase		7.62	0.70	Amino acid transport and metabolism
GSU3257	glycogen synthase	*glgA-2*	7.62	0.40	Energy metabolism
GSU3414	hypothetical protein		7.62	0.29	Hypothetical protein
GSU0302	hypothetical protein		7.62	0.24	Hypothetical protein
GSU0956	hypothetical protein		7.62	0.53	Hypothetical protein
GSU1043	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.62	0.10	Signal transduction
GSU0267	transcriptional regulator, GntR family		7.62	0.70	Transcriptional regulator
GSU2696	RND family efflux pump inner membrane protein	*acrB*	7.62	0.31	Transport and binding proteins
GSU1029	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-4*	7.61	0.44	Chemotaxis
GSU0545	hypothetical protein		7.61	0.07	Hypothetical protein
GSU2160	hypothetical protein		7.61	0.40	Hypothetical protein
GSU1895	CTP synthetase	*pyrG*	7.61	0.47	Purines, pyrimidines, nucleosides, and nucleotides
GSU1531	phosphoribosyl-AMP cyclohydrolase	*hisI*	7.60	0.70	Amino acid biosynthesis
GSU2366	dTDP-glucose 4,6-dehydratase	*rfbB*	7.60	0.21	Cell envelope
GSU2957	thioredoxin family protein	*trx-2*	7.60	0.70	Energy metabolism
GSU0775	sensor histidine kinase		7.60	0.53	Signal transduction
GSU1230	putative ABC transport system substrate-binding protein		7.60	0.40	Transport and binding protein
GSU1028	agmatine deiminase	*aguA*	7.59	0.59	Amino acid metabolism
GSU3431	NADH dehydrogenase I subunit L	*nuoL-2*	7.59	0.07	Energy metabolism
GSU2586	hypothetical protein		7.59	0.38	Hypothetical protein
GSU2107	hypothetical protein		7.59	0.33	Hypothetical protein
GSU1810	tRNA(Ile)-lysidine synthase TilS/MesJ	*tilS*	7.59	0.28	Protein synthesis
GSU2507	Cache sensor signal transduction histidine kinase (EC 2.7.13.3)		7.59	0.41	Signal transduction mechanisms
GSU2475	sigma-54 dependent transcriptional regulator		7.59	0.48	Transcriptional regulator
GSU0937	trans-homoaconitate synthase	*nifV*	7.58	0.28	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2268	outer membrane protein assembly complex protein YaeT	*yaeT*	7.58	0.28	Cell envelope
GSU0078	hypothetical protein		7.58	0.53	Hypothetical protein
GSU0456	hypothetical protein		7.58	0.26	Hypothetical protein
GSU0033	molecular chaperone DnaK	*dnaK*	7.58	0.21	Protein fate
GSU2581	sigma-54 dependent transcriptional regulator		7.58	0.53	Transcriptional regulator

GSU3059	radical SAM domain protein		7.58	0.08	Unknown function
GSU3312	ferrochelatase	*hemH*	7.57	0.07	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1311	glucose-6-phosphate isomerase	*pgi*	7.57	0.10	Carbohydrate transport and metabolism
GSU0416	flagellar hook-length control protein FliK	*fliK*	7.57	0.27	Cell motility
GSU0386	DNA replication and repair protein RadC		7.57	0.53	DNA replication
GSU0102	selenocysteine-specific translation elongation factor	*selB*	7.57	0.07	Protein synthesis
GSU0527	trkA domain protein		7.57	0.35	Unknown function
GSU1560	radical SAM domain protein		7.57	0.10	Unknown function
GSU1533	exodeoxyribonuclease V subunit gamma	*recC*	7.56	0.10	DNA metabolism
GSU2450	hypothetical protein		7.56	0.70	Hypothetical protein
GSU2567	sensor histidine kinase		7.56	0.29	Signal transduction
GSU0842	sensory box histidine kinase/response regulator		7.56	0.23	Signal transduction
GSU1657	DNA internalization-related competence protein ComEC/Rec2		7.55	0.22	Bacterial conjugation
GSU2423	methyl-accepting chemotaxis sensory transducer	*mvhV*	7.55	0.16	Chemotaxis
GSU1140	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-3*	7.55	0.43	Chemotaxis
GSU0235	S1 RNA-binding domain-containing transcriptional accessory protein	*tex*	7.55	0.51	DNA transformation
GSU3395	proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase	*putA*	7.55	0.26	Energy metabolism
GSU3154	cytochrome c nitrite and sulfite reductase, catalytic subunit lipoprotein	*nrfA*	7.55	0.17	Energy metabolism
GSU1527	hypothetical protein		7.55	0.35	Hypothetical protein
GSU0359	sensory box protein/sigma-54 dependent transcriptional regulator		7.55	0.47	Signal transduction
GSU1129	two component, sigma54 specific, transcriptional regulator, Fis family		7.55	0.17	Transcriptional regulation
GSU0211	ABC transporter, permease protein, putative		7.55	0.39	Transport and binding protein
GSU1700	bifunctional malic enzyme oxidoreductase/phosphotransacetylase	*maeB*	7.54	0.34	Energy metabolism
GSU3465	tRNA modification GTPase TrmE	*mnmE*	7.54	0.17	Protein synthesis
GSU1036	sensor histidine kinase		7.54	0.25	Signal transduction
GSU2497	lipoprotein, putative		7.54	0.28	Unknown function
GSU2079	peptidoglycan transpeptidase	*mrdA*	7.53	0.54	Cell envelope
GSU2443	pyruvate dehydrogenase E1 component subunit alpha	*pdhA*	7.53	0.07	Energy metabolism
GSU1182	4-alpha-glucanotransferase	*malQ*	7.53	0.30	Energy metabolism
GSU1434	peptide ABC transporter, permease protein		7.53	0.07	Transport and binding proteins
GSU2017	chorismate dehydratase	*mqnA*	7.52	0.10	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU3075	peptidoglycan transglycosylase and transpeptidase FtsI	*ftsI*	7.52	0.07	Cell envelope
GSU3102	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	*murA*	7.52	0.42	Cell envelope
GSU1896	3-deoxy-manno-octulosonate cytidylyltransferase	*kdsB*	7.52	0.17	Cell envelope
GSU1298	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-2*	7.52	0.31	Chemotaxis
GSU2862	DNA-directed RNA polymerase subunit beta'	*rpoC*	7.52	0.44	Transcription

GSU3346	potassium uptake protein, Kup system		7.52	0.17	Transport and binding protein
GSU1884	UPF0042 nucleotide-binding protein		7.52	0.39	Unknown function
GSU1653	sigma-54 dependent DNA-binding response regulator		7.51	0.22	Transcriptional regulator
GSU1147	NitT/TauT family transport system substrate-binding protein		7.51	0.37	Transport and binding proteins
GSU2555	melittin resistance protein, putative		7.50	0.70	Cell envelope
GSU3023	glycosyl transferase, group 1/2 family protein		7.50	0.23	Cell envelope
GSU2215	protein glutamate methyltransferase CheR associated with MCPs of class 40H	*cheR40H*	7.50	0.39	Chemotaxis
GSU0002	DNA replication and repair protein RecF	*recF*	7.50	0.48	DNA replication
GSU0536	conserved hypothetical protein TIGR00268		7.50	0.70	Hypothetical protein
GSU3205	30S ribosomal protein S12 methylthiotransferase	*rimO*	7.50	0.19	Protein synthesis
GSU1306	PHP domain protein		7.50	0.42	Unknown function
GSU1092	GH3 auxin-responsive promoter family protein		7.50	0.12	Unknown function
GSU2102	pyruvate formate-lyase-activating enzyme, putative		7.49	0.25	Energy metabolism
GSU2710	hypothetical protein		7.49	0.53	Hypothetical protein
GSU1677	AMP-binding enzyme/acyltransferase		7.49	0.19	Lipid transport and metabolism
GSU3347	peptidase, U32 family		7.49	0.22	Protein fate
GSU0373	sensor histidine kinase		7.49	0.17	Signal transduction
GSU2669	sensor histidine kinase		7.49	0.40	Signal transduction
GSU0742	Ech-hydrogenase-related complex, HyfF-like integral membrane subunit	*ehrD*	7.48	0.21	Energy metabolism
GSU2503	cytochrome c	*omcT*	7.48	0.42	Energy metabolism
GSU2106	hypothetical protein		7.48	0.21	Hypothetical protein
GSU3275	hypothetical protein		7.48	0.28	Hypothetical protein
GSU2526	hypothetical protein		7.48	0.53	Hypothetical protein
GSU1310	pyridine nucleotide-disulphide oxidoreductase family protein		7.48	0.53	Inorganic ion transport and metabolism
GSU2194	GMP synthase	*guaA*	7.48	0.21	Purines, pyrimidines, nucleosides, and nucleotides
GSU2695	outer membrane efflux protein		7.48	0.32	Transport and binding proteins
GSU0731	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	*lpxC*	7.47	0.70	Cell envelope
GSU1492	twitching motility pilus retraction protein	*pilT-4*	7.47	0.25	Cell motility
GSU2579	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H-14*	7.47	0.27	Chemotaxis
GSU3228	cytochrome c family protein		7.47	0.15	Energy metabolism
GSU2504	cytochrome c	*omcS*	7.47	0.42	Energy metabolism
GSU2726	hypothetical protein		7.47	0.42	Hypothetical protein
GSU3163	hypothetical protein		7.47	0.53	Hypothetical protein
GSU0642	signal recognition particle protein	*ffh*	7.47	0.28	Protein fate
GSU0332	multifunctional aminopeptidase A	*pepA*	7.47	0.33	Protein fate

GSU1953	asparagine synthetase	*asnB*	7.46	0.25	Amino acid biosynthesis
GSU2483	osmosensitive potassium channel sensor histidine kinase KdpD, KdpD and USP_OKCHK domain-containing	*kdpD*	7.46	0.36	Signal transduction mechanisms
GSU1820	nitrogen regulatory protein P-II uridylyltransferase, GlnD	*glnD*	7.45	0.26	Central intermediary metabolism
GSU2829	Deoxyribodipyrimidine photo-lyase type II (EC 4.1.99.3)		7.45	0.28	DNA repair
GSU0148	alanyl-tRNA ligase	*alaS*	7.45	0.42	Protein synthesis
GSU0521	tRNA (N7-methyl-G46)-methyltransferase	*trmB*	7.45	0.28	Protein synthesis
GSU0913	DNA-binding ATPase Uup	*uup*	7.45	0.17	Transport and binding proteins
GSU0784	hydrogenase 2 b cytochrome subunit	*hybB*	7.44	0.42	Energy metabolism
GSU0713	hypothetical protein		7.44	0.22	Hypothetical protein
GSU0047	transposase/IS protein		7.44	0.17	Mobilome: prophages, transposons
GSU2594	transposase/IS protein		7.44	0.17	Mobilome: prophages, transposons
GSU0037	seryl-tRNA ligase	*serS*	7.44	0.28	Protein synthesis
GSU2524	sigma-54 dependent DNA-binding response regulator		7.44	0.35	Transcriptional regulator
GSU2381	anthranilate phosphoribosyltransferase	*trpD*	7.43	0.07	Amino acid biosynthesis
GSU3167	type VI secretion system protein VasJ		7.43	0.31	Bacterial secretion
GSU1509	glycosyl transferase, group 2 family protein		7.43	0.20	Cell envelope
GSU2564	hypothetical protein		7.43	0.28	Hypothetical protein
GSU1262	hypothetical protein		7.43	0.42	Hypothetical protein
GSU0273	radical SAM domain protein		7.43	0.25	Unknown function
GSU1113	carbohydrate kinase, PfkB family		7.42	0.25	Carbohydrate transport and metabolism
GSU0501	outer membrane protein assembly lipoprotein YfiO	*yfiO*	7.42	0.53	Cell envelope
GSU2244	glycosyl transferase, group 2 family protein		7.42	0.17	Cell envelope
GSU3015	flagellar protein FlaG	*flaG*	7.42	0.53	Cell motility
GSU1761	lipoprotein cytochrome c	*pgcA*	7.42	0.33	Energy metabolism
GSU0925	ABC transporter, ATP-binding protein		7.42	0.53	Transport and binding protein
GSU3158	cysteine synthase B	*cysM*	7.41	0.53	Amino acid biosynthesis
GSU1457	polysaccharide deacetylase domain protein		7.41	0.53	Carbohydrate transport and metabolism
GSU2264	UDP-N-acetylglucosamine acyltransferase	*lpxA-1*	7.41	0.53	Cell envelope
GSU0924	ABC transporter, permease protein, putative		7.41	0.53	Transport and binding protein
GSU2761	glycerol-3-phosphate dehydrogenase	*glpA*	7.40	0.53	Energy metabolism
GSU0650	conserved hypothetical protein TIGR00252		7.40	0.53	Hypothetical protein
GSU0584	hypothetical protein		7.39	0.23	Hypothetical protein
GSU0975	phage tail sheath protein, putative		7.39	0.17	Mobilome: prophages, transposons
GSU0878	glycosyl transferase, group 2 family protein		7.38	0.07	Cell envelope
GSU2819	nitrogenase molybdenum-iron protein subunit beta	*nifK*	7.38	0.67	Central intermediary metabolism
GSU0935	methyl-accepting chemotaxis sensory transducer, class 40H dimer with helix-swapped heme-binding	*mcp40H-20*	7.38	0.33	Chemotaxis

GSU2616	preprotein translocase subunit SecF	*secF*	7.38	0.10	Protein and peptide secretion and trafficking
GSU0698	PBS lyase HEAT-like repeat protein		7.38	0.07	Unknown function
GSU1294	methyl-accepting chemotaxis sensory transducer, class 34H	*mcp34H-7*	7.37	0.35	Chemotaxis
GSU0001	DNA polymerase III subunit beta	*dnaN*	7.37	0.40	DNA replication
GSU3061	squalene cyclase	*shc-2*	7.37	0.07	Fatty acid and phospholipid metabolism
GSU2955	hypothetical protein		7.37	0.30	Hypothetical protein
GSU2833	30S ribosomal protein S11	*rpsK*	7.37	0.53	Protein synthesis
GSU2789	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.37	0.40	Signal transduction
GSU0886	radical SAM domain protein		7.37	0.28	Unknown function
GSU1858	IPT/TIG domain protein		7.37	0.25	Unknown function
GSU1783	type II secretion system ATPase PulE	*pulE*	7.36	0.43	Bacterial secretion
GSU1392	CRISPR-associated endodeoxyribonuclease Cas1	*cas1-2*	7.36	0.10	Mobilome:prophages, transposons
GSU0138	peptide chain release factor 3	*prfC*	7.36	0.08	Protein synthesis
GSU1945	fibronectin type III domain protein		7.36	0.43	Unknown function
GSU1705	3-methyl-2-oxobutanoate hydroxymethyltransferase	*panB*	7.35	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU1660	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	*acnB*	7.35	0.15	Energy metabolism
GSU0377	glycine dehydrogenase subunit 1	*gcvP1*	7.35	0.28	Energy metabolism
GSU1564	glutamate dehydrogenase (NAD) (EC 1.4.1.2)		7.35	0.51	Energy metabolism
GSU3033	hypothetical protein		7.35	0.53	Hypothetical protein
GSU1678	cation-transport ATPase, E1-E2 family		7.35	0.19	Transport and binding proteins
GSU0123	periplasmically oriented, membrane-bound [NiFe]-hydrogenase small subunit	*hyaS*	7.34	0.07	Energy metabolism
GSU0533	cytochrome c family protein, putative		7.34	0.53	Energy metabolism
GSU3342	hypothetical protein		7.34	0.28	Hypothetical protein
GSU0715	hypothetical protein		7.34	0.53	Hypothetical protein
GSU2157	hypothetical protein		7.34	0.53	Hypothetical protein
GSU0103	sensory box histidine kinase		7.34	0.28	Signal transduction
GSU0328	type II secretion system ATPase GspE	*gspE*	7.33	0.61	Bacterial secretion
GSU3070	cell division protein FtsW	*ftsW*	7.33	0.07	Cell division
GSU1287	methyl-accepting chemotaxis sensory transducer	*mcp34H-1*	7.33	0.10	Chemotaxis
GSU0344	NADH dehydrogenase I subunit G	*nuoG-1*	7.33	0.40	Energy metabolism
GSU2671	hypothetical protein		7.33	0.47	Hypothetical protein
GSU3366	glutaminyl-tRNA ligase	*glnS*	7.33	0.24	Protein synthesis
GSU2041	two component, sigma54 specific, transcriptional regulator, Fis family		7.33	0.28	Transcriptional regulation
GSU1280	nickel ABC transporter membrane protein NikQ	*nikQ*	7.33	0.53	Transport and binding protein
GSU0580	pyruvate phosphate dikinase	*ppdK*	7.32	0.30	Energy metabolism
GSU1871	ribonucleotide-diphosphate reductase subunit alpha	*nrdJ*	7.32	0.39	Purines, pyrimidines, nucleosides,

					and nucleotides
GSU2388	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		7.32	0.07	Signal transduction
GSU1412	hypothetical protein		7.31	0.53	Hypothetical protein
GSU0759	hypothetical protein		7.31	0.33	Hypothetical protein
GSU2404	pentapeptide repeat domain protein		7.31	0.35	Unknown function
GSU2276	hypothetical protein		7.30	0.53	Hypothetical protein
GSU0963	two component, sigma54 specific, transcriptional regulator, Fis family		7.30	0.28	Transcriptional regulation
GSU1340	ABC transporter, permease protein		7.30	0.40	Transport and binding protein
GSU0830	heavy metal efflux pump, CzcA family		7.29	0.33	Defense mechanisms
GSU3245	DNA polymerase II, putative		7.29	0.11	DNA replication
GSU3016	hypothetical protein		7.29	0.15	Hypothetical protein
GSU1529	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)		7.29	0.24	Signal transduction
GSU1285	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)		7.29	0.07	Signal transduction
GSU3256	UDP-glucose--galactose-1-phosphate uridylyltransferase	*galT*	7.28	0.09	Cell envelope
GSU2365	dTDP-4-dehydrorhamnose reductase	*rmlD*	7.28	0.53	Cell envelope
GSU1088	2-octaprenylphenol hydroxylase (EC 1.14.13.-)	*aarF*	7.28	0.53	Coenzyme transport and metabolism
GSU2721	bidirectional NAD-reducing hydrogenase, diaphorase subunit	*hoxF*	7.28	0.15	Energy metabolism
GSU1164	ABC transporter, permease protein		7.28	0.07	Transport and binding protein
GSU1397	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1.4.-)		7.27	0.33	Amino acid transporter
GSU2604	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	*lytB*	7.27	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0918	S-adenosylmethionine synthetase	*metK-2*	7.27	0.40	Coenzyme transport and metabolism
GSU1015	hypothetical protein		7.27	0.53	Hypothetical protein
GSU1928	Hpt sensor hybrid histidine kinase (EC 2.7.13.3)		7.27	0.29	Signal transduction mechanisms
GSU1005	TIM barrel oxidoreductase NifR3	*nifR3*	7.27	0.10	Unknown function
GSU2806	bifunctional nitrogenase molybdenum-cofactor biosynthesis protein NifE/NifN	*nifEN*	7.26	0.40	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0928	peptidase, M16 family		7.26	0.28	Protein fate
GSU1461	orotidine 5'-phosphate decarboxylase	*pyrF*	7.26	0.28	Purines, pyrimidines, nucleosides, and nucleotides
GSU2531	sensory box histidine kinase		7.26	0.56	Signal transduction
GSU1070	sodium/solute symporter family protein	*aplB*	7.26	0.10	Transport and binding proteins
GSU0634	glycosyl transferase, group 1 family protein		7.25	0.40	Cell envelope
GSU1144	protein glutamine deamidase and protein glutamate methylesterase CheD associated with MCPs of class 34H	*cheD34H*	7.25	0.70	Chemotaxis
GSU0862	5,10-methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	*folD-2*	7.25	0.53	Coenzyme transport and metabolism

GSU0739	Ech-hydrogenase-related complex, NuoL-like integral membrane subunit	*ehrA-1*	7.25	0.10	Energy metabolism
GSU0874	hypothetical protein		7.25	0.03	Hypothetical protein
GSU0186	Protein of unknown function DUF1579		7.25	0.70	Unknown function
GSU2992	cobalt-precorrin-3 C17-methyltransferase and adenosylcobyric acid synthase	*cobQ*	7.24	0.13	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0351	NADH dehydrogenase I subunit N	*nuoN-1*	7.24	0.21	Energy metabolism
GSU0345	NADH dehydrogenase I subunit H	*nuoH-1*	7.24	0.53	Energy metabolism
GSU1198	D-3-phosphoglycerate dehydrogenase	*serA*	7.23	0.23	Amino acid biosynthesis
GSU3460	glycosyl transferase, group 2 family protein		7.23	0.10	Cell envelope
GSU3247	iron-sulfur cluster-binding protein		7.23	0.28	Energy metabolism
GSU0702	cytochrome c family protein		7.23	0.27	Energy metabolism
GSU1223	hypothetical protein		7.23	0.53	Hypothetical protein
GSU3143	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative		7.23	0.53	Protein fate
GSU0653	16S rRNA (2'-O-methyl-C1402)-methyltransferase	*rsmI*	7.23	0.47	Protein synthesis
GSU2529	elongation factor G	*fusA-2*	7.23	0.39	Protein synthesis
GSU0363	ATP-dependent DNA helicase DinG	*dinG*	7.22	0.30	DNA replication, recombination and repair
GSU1462	23S rRNA (2'-O-methyl-G2251)-methyltransferase	*rlmB*	7.22	0.28	Protein synthesis
GSU0385	NADH dehydrogenase subunit, putative		7.21	0.53	Energy metabolism
GSU3254	phosphoglucomutase/phosphomannomutase family protein		7.21	0.40	Energy metabolism
GSU2016	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)		7.21	0.28	Signal transduction mechanisms
GSU3292	transcriptional regulator, Fur family		7.21	0.53	Transcriptional regulator
GSU1266	GTP-binding protein LepA	*lepA*	7.21	0.13	Unknown function
GSU2609	type IV pilus assembly protein, putative		7.20	0.25	Cell motility
GSU1323	hypothetical protein		7.20	0.53	Hypothetical protein
GSU0609	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	*purH*	7.20	0.42	Purines, pyrimidines, nucleosides, and nucleotides
GSU2055	extracellular solute-binding protein, family 7		7.19	0.10	Carbohydrate transport and metabolism
GSU0990	hypothetical protein		7.19	0.17	Hypothetical protein
GSU0309	hydrogenase expression/formation protein HypE	*hypE*	7.18	0.70	Energy metabolism
GSU0243	KDO2-lipid IV(A) lauroyltransferase		7.18	0.53	Lipid transport and metabolism
GSU2384	GAF sensor signal transduction histidine kinase (EC 2.7.13.3)		7.18	0.07	Signal transduction mechanisms
GSU2245	UDP-N-acetylglucosamine 2-epimerase		7.17	0.25	Cell envelope
GSU0003	DNA gyrase subunit B	*gyrB*	7.17	0.39	DNA replication
GSU1252	hypothetical protein		7.17	0.35	Hypothetical protein
GSU1342	transcriptional regulator, LysR family		7.17	0.53	Transcriptional regulator
GSU1130	condensin subunit Smc		7.16	0.30	Bacterial conjugation
GSU0380	lipoyl synthase	*lipA*	7.16	0.53	Biosynthesis of cofactors,

					prosthetic groups, and carriers
GSU2463	glycosyl transferase, group 1 family protein		7.16	0.70	Cell envelope
GSU0867	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase (EC 2.1.1.-)/demethylmenaquinone methyltransferase (EC 2.1.1.163)	*ubiE*	7.16	0.28	Coenzyme transport and metabolism
GSU0005	hypothetical protein		7.16	0.41	Hypothetical protein
GSU0253	sensory box histidine kinase		7.16	0.12	Signal transduction
GSU3619	hypothetical protein		7.15	0.53	Hypothetical protein
GSU3315	major facilitator family transporter		7.15	0.14	Transport and binding protein
GSU2914	NHL repeat protein		7.15	0.30	Unknown function
GSU2044	diguanylate cyclase/phosphodiesterase		7.14	0.25	Regulatory functions
GSU2137	metal ion efflux outer membrane protein family protein, putative		7.14	0.40	Transport and binding proteins
GSU2361	trehalose/maltose transglucosylase and maltokinase	*treS*	7.13	0.14	Carbohydrate transport and metabolism
GSU1064	type IV pilus minor pilin PilW	*pilW-1*	7.13	0.10	Cell motility
GSU3216	sensor histidine kinase, putative		7.13	0.30	Signal transduction
GSU3608	ABC transporter ATP-binding protein	*ybhF-N*	7.13	0.53	Transport and binding protein
GSU1987	TPR domain protein		7.13	0.16	Unknown function
GSU3166	type VI secretion system ATPase and inner membrane protein TssM	*tssM*	7.12	0.18	Bacterial secretion
GSU2158	cobS protein, putative	*cobS*	7.12	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2917	type II secretion system pseudopilin TklG	*tklG*	7.11	0.70	Bacterial secretion
GSU3297	D-lactate/glycolate dehydrogenase, iron-sulfur cluster-binding protein	*glcF-1*	7.11	0.28	Energy metabolism
GSU0044	salmonella virulence plasmid 65kDa B protein /YD repeat protein		7.11	0.36	Unknown function
GSU1827	L-aspartate oxidase	*nadB*	7.10	0.22	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2064	DNA repair ATPase RecN	*recN*	7.10	0.42	DNA repair
GSU2098	carbon monoxide dehydrogenase, catalytic subunit	*cooS*	7.10	0.33	Energy metabolism
GSU3141	hypothetical protein		7.10	0.53	Hypothetical protein
GSU0603	hypothetical protein		7.10	0.53	Hypothetical protein
GSU2619	queuine tRNA-ribosyltransferase	*tgt-2*	7.09	0.10	Protein synthesis
GSU0088	heterodisulfide oxidoreductase, iron-sulfur cluster-binding subunit D	*hdrD*	7.08	0.35	Energy metabolism
GSU1055	hypothetical protein		7.08	0.10	Hypothetical protein
GSU2401	multi-sensor hybrid histidine kinase (EC 2.7.13.3)		7.08	0.43	Signal transduction mechanisms
GSU2093	ABC transporter, ATP-binding protein		7.08	0.28	Transport and binding protein
GSU1966	hypothetical protein		7.07	0.07	Hypothetical protein
GSU2285	metal dependent phosphohydrolase		7.07	0.25	Signal transduction mechanisms
GSU1922	lipopolysaccharide ABC transporter membrane protein LptF	*lptF*	7.07	0.30	Transport and binding protein
GSU3071	UDP-N-acetylmuramylalanine--D-glutamate ligase	*murD*	7.06	0.07	Cell envelope
GSU1364	HNH endonuclease family protein		7.06	0.53	DNA recombination, replication, and repair

GSU2883	cytochrome c	*omcH*	7.06	0.07	Energy metabolism
GSU0969	periplasmic carboxy-terminal processing protease lipoprotein	*ctpA-1*	7.06	0.07	Protein fate
GSU1842	polysaccharide biosynthesis/export domain protein		7.05	0.11	Carbohydrate transport and metabolism
GSU2436	pyruvate dehydrogenase E1 component subunit beta	*pdhB*	7.05	0.53	Energy metabolism
GSU0080	periplasmic trypsin-like serine protease lipoprotein	*degQ*	7.05	0.30	Protein fate
GSU1175	queuine tRNA-ribosyltransferase	*tgt-1*	7.05	0.70	Protein synthesis
GSU2433	ATP-dependent protease, putative		7.04	0.25	Protein fate
GSU1555	sensory box histidine kinase/response regulator		7.04	0.18	Signal transduction
GSU1656	sensory box/response regulator		7.04	0.17	Signal transduction
GSU3212	glutamate 5-kinase	*proB*	7.03	0.70	Amino acid biosynthesis
GSU3090	DNA primase	*dnaG*	7.03	0.42	DNA replication
GSU1739	indolepyruvate:ferredoxin oxidoreductase subunit alpha	*iorA-1*	7.03	0.42	Energy metabolism
GSU1240	hypothetical protein		7.03	0.53	Hypothetical protein
GSU1276	carbamyl-phosphate synthase, large subunit lipoprotein, glutamine-dependent	*carB*	7.03	0.09	Purines, pyrimidines, nucleosides, and nucleotides
GSU2506	sensory box protein/sigma-54 dependent DNA-binding response regulator		7.03	0.28	Signal transduction
GSU2351	cation-transport ATPase, E1-E2 family		7.03	0.09	Transport and binding proteins
GSU1968	nucleotidyltransferase family protein		7.02	0.40	Cell envelope
GSU2737	lipoprotein cytochrome c	*omcB*	7.02	0.45	Energy metabolism
GSU2066	glycogen phosphorylase	*glgP*	7.02	0.22	Energy metabolism
GSU0434	hypothetical protein		7.02	0.53	Hypothetical protein
GSU1939	GAF sensor signal transduction histidine kinase (EC 2.7.13.3)		7.02	0.48	Signal transduction mechanisms
GSU0707	quaternary ammonium compound resistance transporter SugE	*uge*	7.02	0.53	Transport and binding proteins
GSU0341	NADH dehydrogenase I subunit D	*nuoD*	7.01	0.10	Energy metabolism
GSU2911	hypothetical protein		7.01	0.25	Hypothetical protein
GSU1454	glycosyl transferase, group 2 family protein		7.00	0.07	Cell envelope
GSU1401	DNA polymerase III subunit alpha	*dnaE*	7.00	0.23	DNA replication
GSU3325	excinuclease ABC subunit A	*uvrA*	6.99	0.50	DNA metabolism
GSU1378	beta-lactamase		6.99	0.53	Unknown function
GSU2028	type IV pilus secretin lipoprotein PilQ	*pilQ*	6.98	0.23	Cell motility
GSU2471	group II intron, maturase		6.97	0.43	Mobilome: prophages, transposons
GSU0955	group II intron, maturase		6.97	0.43	Mobilome:prophages, transposons
GSU2288	sensor histidine kinase		6.97	0.53	Signal transduction
GSU2502	spermine/spermidine synthase family protein		6.95	0.20	Amino acid biosynthesis
GSU1156	asparaginyl-tRNA ligase	*asnS*	6.95	0.41	Protein synthesis
GSU2291	phospho-2-dehydro-3-deoxyheptonate aldolase	*aroF*	6.94	0.53	Amino acid biosynthesis
GSU2030	type IV pilus biogenesis protein PilO	*pilO*	6.94	0.70	Cell motility
GSU0185	hypothetical protein		6.94	0.22	Hypothetical protein

GSU0970	hypothetical protein		6.94	0.15	Hypothetical protein
GSU2895	hypothetical protein		6.94	0.53	Hypothetical protein
GSU3284	glutamyl-tRNA reductase	*hemA*	6.93	0.32	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0097	pyruvate:ferredoxin/flavodoxin oxidoreductase	*por*	6.93	0.04	Energy metabolism
GSU0686	1-deoxy-D-xylulose-5-phosphate synthase	*dxs-1*	6.91	0.42	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU0890	NAD-dependent DNA ligase	*ligA*	6.91	0.35	DNA replication, recombination, and repair
GSU2187	ABC transporter, permease protein		6.91	0.10	Transport and binding protein
GSU2782	AcrB/AcrD/AcrF family protein		6.90	0.07	Defense mechanisms
GSU1838	ATP-dependent helicase HrpB	*hrpB*	6.90	0.10	DNA replication, recombination and repair
GSU2934	cytochrome c family protein		6.90	0.10	Energy metabolism
GSU1571	hypothetical protein		6.90	0.53	Hypothetical protein
GSU1097	phosphate ABC transporter membrane protein PstA	*pstA*	6.90	0.28	Inorganic ion transporter protein
GSU0658	ATP-dependent chaperone ClpB	*clpB*	6.90	0.15	Protein fate
GSU0314	general secretion protein E N-terminal domain protein		6.89	0.53	Bacterial secretion
GSU0337	glutamate-1-semialdehyde aminotransferase	*hemL*	6.88	0.10	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2045	valyl-tRNA ligase	*valS*	6.88	0.39	Protein synthesis
GSU2898	lipoprotein cytochrome c	*omcN*	6.87	0.30	Energy metabolism
GSU0493	pyridine nucleotide-disulphide oxidoreductase family protein		6.87	0.70	Inorganic ion transport and metabolism
GSU3464	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	*gidA*	6.87	0.28	Protein synthesis
GSU1632	adenylosuccinate lyase	*purB*	6.87	0.10	Purines, pyrimidines, nucleosides, and nucleotides
GSU0371	maltodextrin phosphorylase		6.86	0.21	Carbohydrate transport and metabolism
GSU1424	hypothetical protein		6.86	0.53	Hypothetical protein
GSU1121	hypothetical protein		6.85	0.40	Hypothetical protein
GSU2320	hypothetical protein		6.85	0.53	Hypothetical protein
GSU2728	hypothetical protein		6.85	0.53	Hypothetical protein
GSU1520	phenylalanyl-tRNA ligase subunit beta	*pheT*	6.85	0.38	Protein synthesis
GSU1636	glutamine--phosphoribosylpyrophosphate amidotransferase	*purF*	6.85	0.25	Purines, pyrimidines, nucleosides, and nucleotides
GSU1643	response regulator receiver modulated diguanylate cyclase		6.85	0.28	Signal transduction
GSU2664	outer membrane efflux protein		6.85	0.23	Transport and binding proteins
GSU1784	type II secretion system inner membrane protein PulF	*pulF*	6.84	0.17	Bacterial secretion
GSU1748	23S rRNA m(5)U-1939 methyltransferase (EC 2.1.1.190)		6.84	0.10	Protein synthesis

GSU1581	adenosine-specific tRNA nucleotidyltransferase	*ccaA*	6.84	0.10	Protein synthesis
GSU1891	response regulator		6.84	0.53	Signal transduction
GSU1480	drug resistance transporter, EmrB/QacA family		6.84	0.09	Transport and binding proteins
GSU1593	polynucleotide phosphorylase/polyadenylase	*pnp*	6.83	0.22	Degradation of RNA
GSU3321	phosphoglucomutase/phosphomannomutase family protein		6.83	0.36	Energy metabolism
GSU2816	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)		6.83	0.10	Signal transduction
GSU0922	ABC transporter, ATP-binding protein		6.83	0.28	Transport and binding protein
GSU0146	twitching motility pilus retraction protein	*pilT-1*	6.82	0.53	Cell motility
GSU1101	phosphate sensor histidine kinase, HAMP and PAS domain-containing	*phoR*	6.82	0.59	Inorganic ion transporter protein
GSU1330	metal ion efflux outer membrane protein family protein, putative		6.82	0.52	Transport and binding proteins
GSU0689	efflux pump, RND superfamily	*hpnN*	6.82	0.41	Transport and binding proteins
GSU0270	glucosamine--fructose-6-phosphate aminotransferase	*glmS*	6.81	0.24	Cell envelope
GSU0417	flagellar hook capping protein FlgD	*flgD*	6.81	0.70	Cell motility
GSU0756	methyl-accepting chemotaxis sensory transducer,class 40H	*mcp40H-24*	6.81	0.40	Chemotaxis
GSU3233	cytochrome c family protein		6.81	0.14	Energy metabolism
GSU2011	nitrogen fixation iron-sulfur cluster assembly cysteine desulfurase NifS	*nifS-1*	6.80	0.53	Central intermediary metabolism
GSU1213	hypothetical protein		6.80	0.70	Hypothetical protein
GSU1770	hypothetical protein		6.80	0.10	Hypothetical protein
GSU3086	23S rRNA (2-N-methyl-G2445)-methyltransferase	*rlmL*	6.80	0.53	Protein synthesis
GSU3350	sensor histidine kinase/GGDEF domain protein		6.80	0.53	Signal transduction
GSU2656	branched-chain alpha-keto acid dehydrogenase E2 subunit	*bkdF*	6.79	0.53	Energy metabolism
GSU0734	Ech-hydrogenase-related complex, NuoL-like integral membrane lipoprotein subunit	*ehrA-2*	6.79	0.43	Energy metabolism
GSU3255	hypothetical protein		6.78	0.26	Hypothetical protein
GSU0482	cardiolipin synthase	*cls-1*	6.78	0.53	Lipid transport and metabolism
GSU1690	3,4-dihydroxy-2-butanone-4-phosphate synthase and GTP cyclohydrolase II	*ribA*	6.77	0.53	Biosynthesis of cofactors, prosthetic groups, and carriers
GSU2314	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)		6.77	0.17	Signal transduction
GSU2325	cation-transport ATPase, E1-E2 family		6.77	0.10	Transport and binding proteins
GSU1326	ATP-dependent DNA helicase RecG	*recG*	6.76	0.13	DNA replication, recombination and repair
GSU0678	ABC transporter, ATP-binding protein		6.76	0.70	Transport and binding protein
GSU0204	radical SAM domain protein		6.76	0.70	Unknown function
GSU0892	ATP-dependent DNA helicase Rep	*rep*	6.75	0.28	DNA replication, recombination and repair
GSU2164	hypothetical protein		6.75	0.07	Hypothetical protein
GSU2921	5-methyltetrahydrofolate--homocysteine S-methyltransferase, cobalamin-dependent	*metH*	6.74	0.47	Amino acid biosynthesis
GSU0921	RNAse E (EC 3.1.26.12)		6.74	0.47	Degradation of RNA

GSU3450	ferredoxin/NAD(P)H-dependent glutamate synthase, large subunit	*gltS*	6.74	0.20	Energy metabolism
GSU0579	glycyl-tRNA ligase subunit beta	*glyS*	6.74	0.28	Protein synthesis
GSU2144	sensor histidine kinase		6.74	0.70	Signal transduction
GSU0175	transcriptional regulator, TetR family		6.74	0.53	Transcriptional regulator
GSU0189	ATP-dependent RNA helicase DbpA	*dbpA*	6.73	0.70	DNA replication, recombination and repair
GSU1875	S-adenosyl-L-homocysteine hydrolase	*ahcY*	6.73	0.10	Energy metabolism
GSU0388	hypothetical protein		6.73	0.53	Hypothetical protein
GSU1588	translation initiation factor IF-2	*infB*	6.73	0.50	Protein synthesis
GSU1587	RNA-binding protein YlxRQ	*ylxRQ*	6.73	0.53	Unknown function
GSU0429	type VI secretion system protein TssK	*tssK*	6.72	0.70	Bacterial secretion
GSU2640	hypothetical protein		6.72	0.70	Hypothetical protein
GSU0932	uracil transporter	*uraA*	6.71	0.53	Transport and binding proteins
GSU0868	conserved hypothetical protein TIGR00159		6.70	0.70	Hypothetical protein
GSU3484	ABC transporter ATP-binding protein		6.70	0.70	Transport and binding protein
GSU3323	polyphosphate kinase	*ppk-1*	6.69	0.23	Central intermediary metabolism
GSU1624	D-lactate/glycolate dehydrogenase, iron-sulfur cluster-binding protein	*glcF-2*	6.69	0.47	Energy metabolism
GSU2851	30S ribosomal protein S3	*rpsC*	6.68	0.53	Protein synthesis
GSU3196	chemotaxis sensory transducer	*mcp44H*	6.67	0.53	Chemotaxis
GSU0608	hypothetical protein		6.67	0.53	Hypothetical protein
GSU2125	conjugative transfer pilus assembly protein TraH		6.67	0.10	Mobilome: prophages, transposons
GSU1482	outer membrane efflux protein		6.67	0.53	Transport and binding proteins
GSU0279	cadherin domain/calx-beta domain protein		6.67	0.22	Unknown function
GSU2606	3-phosphoshikimate 1-carboxyvinyltransferase	*aroA*	6.66	0.53	Amino acid biosynthesis
GSU3400	heavy metal efflux pump, CzcA family		6.63	0.22	Defense mechanisms
GSU0140	hypothetical protein		6.62	0.70	Hypothetical protein
GSU2278	peptide chain release factor 2	*prfB*	6.62	0.28	Protein synthesis
GSU3330	NADH-dependent flavin oxidoreductase, Oye family		6.61	0.28	Energy metabolism
GSU2673	hypothetical protein		6.61	0.53	Hypothetical protein
GSU3217	sigma-54 dependent DNA-binding response regulator		6.61	0.70	Transcriptional regulator
GSU3627	triosephosphate isomerase	*tpi*	6.60	0.70	Energy metabolism
GSU2653	MATE efflux family protein		6.60	0.10	Transport and binding proteins
GSU0754	fibronectin type III domain protein		6.60	0.03	Unknown function
GSU3055	flagellar biogenesis protein FlhF	*flhF*	6.59	0.53	Cell motility
GSU3278	hypothetical protein		6.59	0.19	Hypothetical protein
GSU1458	TPR domain protein		6.59	0.10	Unknown function
GSU1821	N-acetylmuramoyl-L-alanine amidase, family 3		6.58	0.53	Cell envelope
GSU0301	lytic murein transglycosylase, putative		6.58	0.70	Mobilome: prophages, transposons
GSU0372	sigma-54 dependent DNA-binding response regulator		6.58	0.53	Transcriptional regulator
GSU1554	GGDEF domain protein		6.56	0.28	Unknown function

GSU3263	response regulator		6.55	0.53	Signal transduction
GSU3391	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.-)		6.54	0.53	Amino acid transporter
GSU2866	50S ribosomal protein L1	*rplA*	6.54	0.53	Protein synthesis
GSU0452	sensor histidine kinase		6.54	0.53	Signal transduction
GSU3057	dihydropyrimidine dehydrogenase subunit A	*nfnA*	6.53	0.53	Amino acid biosynthesis
GSU1253	hypothetical protein		6.51	0.40	Hypothetical protein
GSU3313	thiolase, putative		6.51	0.70	Lipid transport and metabolism
GSU2073	EF hand domain/PKD domain protein		6.50	0.22	Unknown function
GSU3381	aspartyl/glutamyl-tRNA amidotransferase subunit A	*gatA*	6.49	0.53	Protein synthesis
GSU0283	GAF sensor signal transduction histidine kinase (EC 2.7.13.3)		6.49	0.25	Signal transduction mechanisms
GSU1209	hypothetical protein		6.48	0.53	Hypothetical protein
GSU2975	putative manganese-dependent inorganic pyrophosphatase		6.48	0.70	Transport and binding protein
GSU2894	hypothetical protein		6.47	0.53	Hypothetical protein
GSU0673	hypothetical protein		6.46	0.53	Hypothetical protein
GSU0941	nitrogen fixation transcript antitermination sensor histidine kinase	*gnfK*	6.45	0.53	Central intermediary metabolism
GSU1281	nickel ABC transporter ATP-binding protein	*nikO*	6.45	0.53	Transport and binding protein
GSU2063	HD domain protein		6.43	0.70	Unknown function
GSU3014	HD domain protein		6.43	0.70	Unknown function
GSU1034	nitrate/nitrite-sensing methyl-accepting chemotaxis sensory transducer, class 40H, NIT domain-containing	*mcp40H-8*	6.42	0.41	Chemotaxis
GSU1901	hypothetical protein		6.42	0.53	Hypothetical protein
GSU2517	rhodanese-like domain/cysteine-rich domain protein		6.42	0.28	Unknown function
GSU3392	amino acid/amide ABC transporter ATP-binding protein 1, HAAT family (TC 3.A.1.4.-)		6.41	0.53	Amino acid transporter
GSU0174	succinyl:acetate coenzyme A transferase	*ato-2*	6.39	0.53	Energy metabolism
GSU0500	translation-regulating membrane GTPase	*typA*	6.38	0.16	Protein synthesis
GSU1249	sensory box histidine kinase		6.38	0.53	Signal transduction
GSU2873	radical SAM domain protein		6.38	0.10	Unknown function
GSU0004	DNA gyrase subunit A	*gyrA*	6.37	0.34	DNA replication
GSU2277	lipoprotein, NLP/P60 family, putative		6.35	0.53	Unknown function
GSU0750	methyl-accepting chemotaxis sensory transducer, class 40H	*mcp40H*	6.34	0.53	Chemotaxis
GSU3343	SpoVR-like family protein		6.33	0.53	Cell division
GSU2982	TonB dependent receptor, putative		6.31	0.17	Transport and binding proteins
GSU3038	flagellin	*fliC*	6.30	0.53	Cell motility
GSU2576	HD domain protein		6.24	0.53	Unknown function
GSU3356	GGDEF domain/HAMP domain protein		6.24	0.28	Unknown function
GSU0876	diacylglycerol kinase catalytic domain protein		6.23	0.53	Lipid transport and metabolism
GSU0051	CRISPR-associated helicase Cas3	*cas3-1*	6.22	0.22	Mobilome:prophages, transposons
GSU2991	sensor histidine kinase		6.22	0.10	Signal transduction

GSU3341	protein serine/threonine kinase PrkA	*prkA*	6.20	0.10	Signal transduction mechanisms
GSU3219	fibronectin type III domain protein		6.19	0.38	Unknown function
GSU1154	surface repeat protein, putative		6.12	0.35	Unknown function
GSU0822	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)		6.11	0.10	Signal transduction
GSU2768	hypothetical protein		6.04	0.28	Hypothetical protein
GSU0556	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU0761	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU1356	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU1848	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU2128	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU2140	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU2171	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU2279	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU2391	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU3083	ISGsu7, transposase OrfB		6.02	0.21	Mobilome:prophages, transposons
GSU0803	phosphoenolpyruvate synthase	*ppsA*	5.97	0.10	Energy metabolism
GSU2912	cytochrome c	*omcO*	5.85	0.07	Energy metabolism

Supplementary Table S7. Genes that mapped to the *Methanothrix concillii* genome that were significantly transcribed in RNAseq libraries assembled with mRNA extracted from methanogenic rice paddy soils. Transcript reads with expression levels ≥ median $\log_2$ RPKM values (6.5) were considered significant. All log2 RPKM values represent average expression values from six different transcriptomic libraries; SEM is the standard error of the mean.

Locus ID	Gene annotation	Gene abbr	Average log2 RPKM	SEM	Functional Categories
MCON_0760	Methyl-coenzyme M reductase (MCR) gamma subunit	*mcrG*	13.81	0.17	Energy metabolism- methanogenesis
MCON_2517	V-type ATP synthase subunit F	*atpF*	13.49	0.26	Energy metabolism
MCON_0762	methyl-coenzyme M reductase subunit beta	*mcrB*	13.01	0.11	Energy metabolism- methanogenesis
MCON_1755	hypothetical protein		12.83	0.25	Hypothetical proteins
MCON_1667	Non-histone chromosomal MC1	*mc1*	12.57	0.55	Unknown function
MCON_0759	methyl-coenzyme M reductase subunit alpha	*mcrA*	12.32	0.16	Energy metabolism- methanogenesis
MCON_3295	ferredoxin		12.31	0.85	Energy metabolism
MCON_0450	hypothetical protein		12.23	0.89	Hypothetical proteins
MCON_0235	hypothetical protein		12.18	0.25	Hypothetical proteins
MCON_1161	hypothetical protein		12.13	0.44	Hypothetical proteins
MCON_2612	superoxide dismutase	*sod*	12.08	0.44	Inorganic ion transport and metabolism
MCON_3357	Flavin-binding protein dodecin		12.03	0.02	Unknown functions
MCON_1280	transcription elongation factor NusA	*nusA*	11.99	0.42	Transcriptional regulation
MCON_2389	F420H2 dehydrogenase subunit	*fpoO*	11.88	0.46	Energy metabolism
MCON_2514	V-type ATP synthase subunit D	*atpD*	11.85	0.23	Energy metabolism
MCON_1705	30S ribosomal protein S28e	*rps28e*	11.82	0.34	Protein synthesis
MCON_1141	hypothetical protein		11.75	0.40	Hypothetical proteins
MCON_RS05535	hypothetical protein		11.74	0.84	Hypothetical proteins
MCON_3185	DNA-directed RNA polymerase subunit E"	*rpoE2*	11.70	0.58	Transcription
MCON_0917	nucleoid protein MC1	*mc1A*	11.55	0.46	Defense mechanisms
MCON_2115	hypothetical protein		11.47	0.08	Hypothetical proteins
MCON_1700	cold-shock protein	*cspA*	11.47	1.14	Transcription
MCON_RS13325	rRNA metabolism protein		11.47	0.06	Unknown function
MCON_2295	6,7-dimethyl-8-ribityllumazine synthase	*ribH*	11.46	1.03	Biosynthesis of secondary metabolites- riboflavin synthesis
MCON_2515	V-type ATP synthase subunit B	*atpB*	11.33	0.31	Energy metabolism
MCON_RS12430	hypothetical protein		11.31	0.18	Hypothetical proteins
MCON_1694	gar1 RNA-binding protein		11.31	0.36	Protein synthesis
MCON_0311	asparaginyl/glutamyl-tRNA amidotransferase subunit C	*gatC*	11.30	0.59	Protein synthesis
MCON_2751	50S ribosomal protein L21e	*rplU*	11.29	0.49	Protein synthesis
MCON_1729	translation initiation factor		11.27	0.31	Protein synthesis
MCON_2519	V-type ATP synthase subunit E	*atpE*	11.24	0.35	Energy metabolism
MCON_3282	heterodisulfide reductase	*hdrC*	11.24	0.32	Energy metabolism-Methanogenesis
MCON_1706	50S ribosomal protein L7ae	*rpl7ae*	11.11	0.39	Protein synthesis
MCON_1618	proteasome assembly chaperone family protein		11.09	1.03	Protein fate
MCON_0559	acetyl-coenzyme A synthetase	*acsA*	7.66	0.39	Energy metabolism- methanogenesis
MCON_1330	acetyl-CoA synthase subunit beta	*cdhC*	10.81	0.20	Energy metabolism- methanogenesis
MCON_2516	ATP synthase subunit A	*atpA*	11.05	0.19	Energy metabolism
MCON_RS04360	hypothetical protein		11.05	0.33	Hypothetical proteins
MCON_1703	nucleoside-diphosphate kinase	*ndk*	11.05	0.02	Nucleotide transport and metabolism
MCON_0637	30S ribosomal protein S13	*rpsM*	11.04	1.12	Protein synthesis

MCON_1153	S-layer protein		11.03	0.22	Cell envelope
MCON_2012	transcription factor		10.99	0.45	Transcriptional regulation
MCON_2696	50S ribosomal protein L29	*rpmC*	10.96	0.69	Protein synthesis
MCON_2693	50S ribosomal protein L14	*rplN*	10.94	0.54	Protein synthesis
MCON_2624	hypothetical protein		10.93	0.41	Hypothetical proteins
MCON_2567	50S ribosomal protein L18e	*rplR*	10.93	0.32	Protein synthesis
MCON_2520	ATP synthase C subunit, lipid-binding protein	*atpL*	10.92	0.55	Energy metabolism
MCON_1472	formylmethanofuran-tetrahydromethanopterin formyltransferase	*ftr*	10.92	0.64	Energy metabolism- methanogenesis
MCON_2991	transcriptional regulator		10.92	0.26	Transcriptional regulation
MCON_0767	mRNA surveillance protein pelota	*pelA*	10.91	0.03	Protein synthesis
MCON_2649	hypothetical protein		10.90	0.29	Hypothetical proteins
MCON_1969	phosphoribosyl-AMP cyclohydrolase	*hisI*	10.88	0.94	Amino acid biosynthesis
MCON_2917	transcriptional regulator		10.88	1.03	Transcriptional regulation
MCON_2018	CBS domain-containing protein		10.88	0.25	Unknown function
MCON_0431	hypothetical protein		10.87	0.76	Hypothetical proteins
MCON_1279	50S ribosomal protein L30e	*rpl30e*	10.86	0.23	Protein synthesis
MCON_2694	30S ribosomal protein S17	*rps17p*	10.85	0.25	Protein synthesis
MCON_0531	large conductance mechanosensitive channel protein MscL	*mscL*	10.84	0.69	Cell envelope
MCON_3471	30S ribosomal protein S3ae	*rpsC*	10.84	1.03	Protein synthesis
MCON_2518	ATP synthase subunit C	*atpC*	10.83	0.27	Energy metabolism
MCON_2279	aspartate aminotransferase	*aspC*	10.82	0.74	Amino acid transport and metabolism
MCON_0624	nitrogen regulatory protein P-II 1		10.78	0.94	Signal transduction mechanisms
MCON_2699	30S ribosomal protein S19	*rps19p*	10.76	0.37	Protein synthesis
MCON_2776	translation initiation factor IF-5A		10.76	0.46	Protein synthesis
MCON_1959	heat-shock protein Hsp20	*hsp20*	10.75	0.43	Defense mechanisms
MCON_1732	formylmethanofuran dehydrogenase, subunit G	*fwdG*	10.75	1.53	Energy metabolism- methanogenesis
MCON_2690	50S ribosomal protein L5	*rpl5p*	10.75	0.84	Protein synthesis
MCON_1693	transcription initiation factor IIB		10.74	0.89	Transcriptional regulation
MCON_1365	nucleoside triphosphatase		10.73	0.85	Nucleotide transport and metabolism
MCON_1887	30S ribosomal protein S8e	*rpsH*	10.73	0.41	Protein synthesis
MCON_0501	pyridoxamine 5'-phosphate oxidase		10.72	0.73	Unknown function
MCON_3321	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase	*aroA*	10.71	0.20	Carbohydrate transport and metabolism
MCON_3158	Transcription factor Pcc1	*ppc1*	10.71	0.47	Transcriptional regulation
MCON_1137	hypothetical protein		10.67	0.44	Hypothetical proteins
MCON_1347	PBS lyase HEAT-like repeat-containing protein		10.66	0.45	Unknown function
MCON_1281	30S ribosomal protein S12	*rps12P*	10.65	0.82	Protein synthesis
MCON_2995	thioredoxin family protein		10.65	0.47	Unknown function
MCON_1926	hypothetical protein		10.64	0.96	Hypothetical proteins
MCON_0520	hypothetical protein		10.62	0.47	Hypothetical proteins
MCON_1139	hypothetical protein		10.61	0.29	Hypothetical proteins
MCON_3442	CoB--CoM heterodisulfide reductase subunit D	*hdrD*	10.60	0.20	Energy metabolism-Methanogenesis
MCON_2856	proteasome endopeptidase complex, archaeal, beta subunit	*psmB*	10.60	0.24	Protein fate
MCON_0551	hypothetical protein		10.57	0.34	Hypothetical proteins
MCON_2101	proline--tRNA ligase	*proS*	10.57	0.10	Protein synthesis
MCON_0398	methanogenesis marker protein 17		10.56	0.89	Energy metabolism- methanogenesis
MCON_1925	Fe-S cluster protein		10.55	0.44	Energy metabolism
MCON_0934	hypothetical protein		10.54	0.31	Hypothetical proteins
MCON_1725	hypothetical protein		10.54	0.30	Hypothetical proteins
MCON_0921	translation initiation factor IF-2	*eif2b*	10.53	0.18	Protein synthesis

MCON_2655	iron-sulfur cluster assembly scaffold protein NifU	*nifU*	10.52	0.42	Biosynthesis of cofactors, prosthetic groups, and carriers
MCON_0246	hypothetical protein		10.51	0.25	Hypothetical proteins
MCON_2049	methyltransferase		10.50	0.33	Unknown function
MCON_1499	hypothetical protein		10.49	0.78	Hypothetical proteins
MCON_1474	hypothetical protein		10.47	0.38	Hypothetical proteins
MCON_2976	hypothetical protein		10.47	0.94	Hypothetical proteins
MCON_2522	ATP synthase archaeal subunit H	*atpH*	10.45	0.43	Energy metabolism
MCON_1134	hypothetical protein		10.45	0.25	Hypothetical proteins
MCON_3298	hypothetical protein		10.44	0.43	Hypothetical proteins
MCON_2394	5,10-Methylenetetrahydromethanopterin reductase	*mer*	10.42	0.99	Energy metabolism- Methanogenesis
MCON_0586	transcriptional regulator		10.41	0.46	Transcriptional regulation
MCON_0411	acetolactate synthase small subunit	*ilvH*	10.40	0.46	Amino acid biosynthesis
MCON_1037	molecular chaperone DnaK	*dnaK*	10.40	0.41	Protein fate
MCON_2684	50S ribosomal protein L18	*rpl18p*	10.40	0.74	Protein synthesis
MCON_0471	hypothetical protein		10.39	0.94	Hypothetical proteins
MCON_0639	30S ribosomal protein S11	*rps11p*	10.35	0.35	Protein synthesis
MCON_3159	prefoldin subunit beta		10.32	0.52	Protein fate
MCON_1146	30S ribosomal protein S6e	*rpsF*	10.32	0.60	Protein synthesis
MCON_0761	methyl-coenzyme M reductase operon protein D	*mcrD*	10.31	0.28	Energy metabolism- methanogenesis
MCON_1831	dTDP-glucose pyrophosphorylase		10.28	0.96	Cell envelope
MCON_2565	30S ribosomal protein S9	*rpsI*	10.27	0.57	Protein synthesis
MCON_1519	phosphate ABC transporter permease subunit PstC	*pstC*	10.27	1.15	Transport and binding proteins
MCON_2916	LSU ribosomal protein L24A	*rplX*	10.26	0.44	Protein synthesis
MCON_0807	hypothetical protein		10.25	0.41	Hypothetical proteins
MCON_1282	30S ribosomal protein S7	*rpsG*	10.25	0.52	Protein synthesis
MCON_3445	ABC transporter		10.25	0.93	Transport and binding proteins
MCON_2912	50S ribosomal protein P1	*rpl12p*	10.24	0.47	Protein synthesis
MCON_1743	transposase		10.23	0.09	Mobilome:prophages and transposons
MCON_1653	cobalamin biosynthesis protein CobN	*cooC*	10.23	0.18	Posttranslational modification, protein turnover, chaperones
MCON_0905	amino acid-binding protein		10.22	0.60	Unknown functions
MCON_0167	hypothetical protein		10.21	0.51	Hypothetical proteins
MCON_3287	hypothetical protein		10.20	0.25	Hypothetical proteins
MCON_1244	B12-binding domain-containing radical SAM protein		10.20	0.46	Unknown function
MCON_1150	2'-5' RNA ligase		10.19	0.94	Transcription- RNA processing
MCON_2031	hypothetical protein		10.17	0.51	Hypothetical proteins
MCON_1255	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	*ppiB*	10.17	0.58	Protein fate
MCON_0292	serine/threonine protein kinase		10.17	1.05	Signal transduction mechanisms
MCON_0208	phosphoribosylformylglycinamidine synthase I	*purQ*	10.15	1.05	Purines, pyrimidines, nucleosides, and nucleotides
MCON_2860	transposase		10.14	0.74	Mobilome:prophages and transposons
MCON_2988	adenine phosphoribosyltransferase	*apt1*	10.14	0.47	Nucleotide transport and metabolism
MCON_3146	50S ribosomal protein L15e	*rplJ*	10.14	0.46	Protein synthesis
MCON_0827	hypothetical protein		10.13	0.45	Hypothetical proteins
MCON_2418	LL-diaminopimelate aminotransferase apoenzyme		10.11	0.13	Amino acid transport and metabolism
MCON_2351	pyridoxal biosynthesis lyase PdxS	*pdxS*	10.11	0.58	Biosynthesis of cofactors, prosthetic groups, and carriers
MCON_1182	transposase		10.11	0.27	Mobilome:prophages and transposons

MCON_0708	MFS transporter		10.11	0.94	Transport and binding proteins
MCON_1911	DUF342 domain protein		10.08	0.23	Unknown function
MCON_2613	peroxiredoxin		10.06	0.55	Defense mechanisms
MCON_0922	50S ribosomal protein L16	*rplP*	10.06	1.15	Protein synthesis
MCON_3064	4Fe-4S ferredoxin		10.05	0.17	Energy metabolism
MCON_3154	RNA-binding protein		10.04	0.40	Unknown function
MCON_3149	ribonuclease P		10.03	0.34	RNA degradation
MCON_0409	2-isopropylmalate synthase	*leuA*	10.02	0.25	Amino acid biosynthesis
MCON_0178	hypothetical protein		10.02	0.58	Hypothetical proteins
MCON_3465	tRNA methyltransferase		10.02	0.98	Unknown function
MCON_3188	translation initiation factor IF-2 subunit gamma		10.01	0.67	Protein synthesis
MCON_3070	F420H2 dehydrogenase subunit N	*fpoN*	10.00	0.19	Energy metabolism
MCON_3204	sugar phosphate isomerase		9.99	0.52	Carbohydrate transport and metabolism
MCON_2691	30S ribosomal protein S4e	*rpsD*	9.98	0.73	Protein synthesis
MCON_0443	PHP domain-containing protein		9.97	0.46	Unknown function
MCON_3152	RNA-binding protein		9.96	0.42	Unknown function
MCON_0800	amino acid-binding protein		9.96	0.45	Unknown functions
MCON_1634	rubrerythrin	*rbrB*	9.95	0.57	Energy metabolism
MCON_2851	transposase		9.95	0.41	Mobilome:prophages and transposons
MCON_3216	transposase		9.95	0.31	Mobilome:prophages and transposons
MCON_0157	phosphopyruvate hydratase	*eno*	9.94	0.39	Energy metabolism
MCON_2176	integrase		9.94	0.39	Mobilome:prophages and transposons
MCON_1768	ABC transporter ATP-binding protein	*sufC*	9.94	0.54	Transport and binding proteins
MCON_RS13320	proteasome subunit alpha		9.93	0.42	Protein fate
MCON_1542	CTP synthetase	*pyrG*	9.93	0.50	Purines, pyrimidines, nucleosides, and nucleotides
MCON_RS00010	IS256 family transposase		9.92	0.38	Mobilome:prophages and transposons
MCON_2623	hypothetical protein		9.91	0.62	Hypothetical proteins
MCON_3186	DNA-directed RNA polymerase	*rpoE*	9.91	1.03	Transcription
MCON_2914	50S ribosomal protein L1	*rplA*	9.88	0.23	Protein synthesis
MCON_3427	transcription factor		9.88	0.51	Transcriptional regulation
MCON_2511	pyridoxal-phosphate dependent TrpB-like enzyme	*trpB*	9.87	0.13	Amino acid transport and metabolism
MCON_0093	hypothetical protein		9.87	0.05	Hypothetical proteins
MCON_2571	hypothetical protein		9.86	0.48	Hypothetical proteins
MCON_0428	preprotein translocase subunit SecF	*secF*	9.84	0.40	Secretion
MCON_3195	hypothetical protein		9.84	0.83	Hypothetical proteins
MCON_1721	hypothetical protein		9.84	0.46	Hypothetical proteins
MCON_2561	30S ribosomal protein S2	*rpsB*	9.84	1.15	Protein synthesis
MCON_2654	N-acetylglutamate kinase	*argB*	9.83	0.54	Amino acid biosynthesis
MCON_1172	sulfite reductase	*nirB*	9.83	0.71	Central intermediary metabolism
MCON_3441	CoB--CoM heterodisulfide reductase subunit E	*hdrE*	9.83	0.34	Energy metabolism- Methanogenesis
MCON_1622	hypothetical protein		9.82	0.52	Hypothetical proteins
MCON_2823	sulfonate ABC transporter permease	*tauC*	9.82	0.25	Inorganic ion transport and metabolism
MCON_1082	thiolase		9.82	0.26	Lipid transport and metabolism
MCON_3474	translation initiation factor 2B subunit I family (IF-2BI)	*mtnA*	9.82	0.96	Protein synthesis
MCON_1434	TIGR01210 family radical SAM protein		9.82	0.85	Unknown functions
MCON_0350	hypothetical protein		9.81	0.04	Hypothetical proteins
MCON_3181	hypothetical protein		9.80	0.41	Hypothetical proteins
MCON_2214	hypothetical protein		9.80	0.88	Hypothetical proteins

MCON_1619	translation initiation factor IF-2 subunit alpha	*eif2a*	9.80	0.82	Protein synthesis
MCON_2915	50S ribosomal protein L11	*rpl11p*	9.79	0.40	Protein synthesis
MCON_3176	hypothetical protein		9.78	1.03	Hypothetical proteins
MCON_2619	prefoldin subunit alpha		9.78	0.69	Protein fate
MCON_1649	elongation factor 1-alpha	*tuf*	9.78	0.54	Protein synthesis
MCON_2282	RimK domain-containing protein ATP-grasp		9.77	0.55	Coenzyme transport and metabolism
MCON_2010	antibiotic resistance protein MarC	*marC*	9.76	1.03	Amino acid transport and metabolism
MCON_3345	hypothetical protein		9.76	0.56	Hypothetical proteins
MCON_2314	transposase		9.76	0.46	Mobilome:prophages and transposons
MCON_2631	aspartate carbamoyltransferase	*pyrB*	9.75	0.04	Purines, pyrimidines, nucleosides, and nucleotides
MCON_1136	hypothetical protein		9.74	0.46	Hypothetical proteins
MCON_1068	tetrahydromethanopterin S-methyltransferase subunit H	*mtrH*	9.73	0.25	Energy metabolism- methanogenesis
MCON_2577	UDP-N-acetylglucosamine 2-epimerase	*wecB*	9.72	0.03	Cell envelope
MCON_0432	phosphoesterase, RecJ domain-containing protein	*recJ*	9.72	0.14	DNA replication, recombination and repair
MCON_1557	cell division protein FtsZ	*ftsZ-2*	9.68	0.02	Cell division
MCON_0238	formylmethanofuran dehydrogenase, subunit B	*fmdB*	9.67	0.45	Energy metabolism- methanogenesis
MCON_2703	50S ribosomal protein L3	*rpl3p*	9.67	0.40	Protein synthesis
MCON_RS12980	NADH dehydrogenase subunit D		9.66	0.23	Energy metabolism
MCON_2040	efflux ABC transporter permease		9.66	0.27	Transport and binding proteins
MCON_0718	B12-binding domain-containing radical SAM protein		9.65	0.22	Unknown function
MCON_1457	NAD-dependent epimerase/dehydratase		9.63	0.59	Cell envelope
MCON_2704	hypothetical protein		9.63	0.42	Hypothetical proteins
MCON_0542	GTP-binding protein		9.63	0.49	Unknown function
MCON_3063	F420H2 dehydrogenase subunit H	*fpoH*	9.62	0.40	Energy metabolism
MCON_1128	transposase		9.62	0.89	Mobilome:prophages and transposons
MCON_2955	hypothetical protein		9.60	0.46	Hypothetical proteins
MCON_1018	hypothetical protein		9.60	0.18	Hypothetical proteins
MCON_3163	deoxyhypusine synthase	*dysB*	9.60	0.34	Protein fate
MCON_2596	2-isopropylmalate synthase 1	*leuA*	9.58	0.32	Amino acid biosynthesis
MCON_0223	serine hydroxymethyltransferase	*glyA*	9.58	0.21	Amino acid biosynthesis
MCON_3169	methanogenesis marker protein 11		9.58	0.25	Energy metabolism- methanogenesis
MCON_1906	manganese-dependent inorganic pyrophosphatase	*ppaC*	9.58	0.29	Inorganic ion transport and metabolism
MCON_0804	4-hydroxy-tetrahydrodipicolinate synthase	*dapA*	9.57	0.28	Amino acid biosynthesis
MCON_2883	phosphoenolpyruvate synthase	*ppsA*	9.57	0.89	Energy metabolism
MCON_2683	30S ribosomal protein S5	*rps5p*	9.57	0.50	Protein synthesis
MCON_2575	transferase hexapeptide repeat containing protein		9.57	0.28	Unknown functions
MCON_2525	fructose 1,6-bisphosphatase	*fbp*	9.56	0.59	Carbohydrate transport and metabolism
MCON_0572	glycerophosphoryl diester phosphodiesterase	*glpQ*	9.56	0.82	Lipid transport and metabolism
MCON_1268	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-monophosphate synthetase		9.56	0.41	Nucleotide transport and metabolism
MCON_0583	AMP phosphorylase		9.56	0.22	Nucleotide transport and metabolism
MCON_1964	adenylate kinase	*adk*	9.56	0.30	Purines, pyrimidines, nucleosides, and nucleotides
MCON_1510	DNA polymerase sliding clamp	*pcnA*	9.54	0.44	DNA replication, recombination and repair
MCON_1783	hypothetical protein		9.54	0.25	Hypothetical proteins
MCON_0587	proteasome-activating nucleotidase	*panA*	9.54	0.47	Protein fate
MCON_1547	DNA topoisomerase VI subunit A	*top6a*	9.53	0.05	DNA replication, recombination and repair
MCON_2816	hypothetical protein		9.53	0.07	Hypothetical proteins

MCON_1325	acetyl-CoA decarbonylase/synthase gamma subunit	*cdhE*	9.52	0.18	Energy metabolism- methanogenesis
MCON_2741	formate/nitrite family transporter		9.51	0.46	Transport and binding proteins
MCON_0412	ketol-acid reductoisomerase	*ilvC*	9.50	0.40	Amino acid biosynthesis
MCON_2673	cell filamentation protein Fic	*fic*	9.50	0.39	Cell division
MCON_1760	peroxiredoxin		9.50	0.38	Defense mechanisms
MCON_2371	hypothetical protein		9.50	0.28	Hypothetical proteins
MCON_1221	NAD dependent epimerase/dehydratase		9.49	0.58	Cell envelope
MCON_1878	wyosine biosynthesis protein TYW1	*taw1*	9.49	0.42	Protein synthesis
MCON_1566	ammonium transporter	*amtB*	9.49	0.89	Transport and binding proteins
MCON_2526	hypothetical protein		9.48	0.19	Hypothetical proteins
MCON_2304	Ribonuclease BN, tRNA processing enzyme	*elaC*	9.47	0.35	RNA degradation
MCON_0613	nitrogenase molybdenum-iron protein subunit beta	*nifK*	9.46	0.96	Inorganic ion transport and metabolism
MCON_1052	Methylenetetrahydromethanopterin dehydrogenase	*mtd*	9.45	0.23	Energy metabolism- methanogenesis
MCON_1668	aspartate--tRNA(Asn) ligase	*aspC*	9.44	0.22	Protein synthesis
MCON_0771	transcriptional regulator, AsnC family		9.44	0.46	Transcriptional regulation
MCON_1331	acetyl-CoA decarbonylase/synthase epsilon subunit	*cdhB*	9.43	0.29	Energy metabolism- methanogenesis
MCON_1803	exodeoxyribonuclease VII large subunit	*xseA*	9.42	0.76	DNA replication, recombination, and repair
MCON_3037	Metal-binding trascriptional regulator	*arsR*	9.42	0.24	Transcriptional regulation
MCON_0264	dUTP pyrophosphatase		9.40	0.46	Purines, pyrimidines, nucleosides, and nucleotides
MCON_1672	cell division control protein Cdc6	*cdc6*	9.39	0.43	Cell division
MCON_2441	condensin subunit ScpA	*scpA*	9.39	0.28	Cell division
MCON_0535	hypothetical protein		9.38	0.46	Hypothetical proteins
MCON_1313	hypothetical protein		9.38	0.46	Hypothetical proteins
MCON_3291	CopG family transcriptional regulator		9.38	0.31	Transcriptional regulation
MCON_2017	CBS domain-containing protein		9.38	0.32	Unknown function
MCON_3087	cache domain-containing protein		9.38	0.67	Unknown function
MCON_0151	hypothetical protein		9.37	0.73	Hypothetical proteins
MCON_2521	V-type ATP synthase subunit I	*atpI*	9.36	0.43	Energy metabolism
MCON_1327	CO dehydrogenase nickel-insertion accessory protein	*cooC*	9.36	0.28	Energy metabolism
MCON_1183	hypothetical protein		9.36	0.05	Hypothetical proteins
MCON_1548	DNA topoisomerase VI subunit B	*top6b*	9.35	0.30	DNA replication, recombination and repair
MCON_2581	IS4 family transposase		9.35	0.37	Mobilome:prophages and transposons
MCON_2700	50S ribosomal protein L2	*rplB*	9.35	0.18	Protein synthesis
MCON_2117	tryptophan--tRNA ligase	*trpS*	9.35	0.85	Protein synthesis
MCON_0640	DNA-directed RNA polymerase, subunit D	*rpoD*	9.35	0.16	Transcription
MCON_1368	phosphoribosylaminoimidazolecarboxamide formyltransferase	*purH*	9.33	0.85	Purines, pyrimidines, nucleosides, and nucleotides
MCON_2286	hypothetical protein		9.32	0.41	Hypothetical proteins
MCON_3059	deoxyhypusine synthase	*dysA*	9.32	0.37	Protein fate
MCON_2106	histidine--tRNA ligase	*hisS*	9.32	0.57	Protein synthesis
MCON_0422	exodeoxyribonuclease III	*exoA*	9.31	0.57	DNA replication, recombination, and repair
MCON_0135	sugar kinase		9.27	0.28	Unknown function
MCON_0397	hypothetical protein		9.26	0.35	Hypothetical proteins
MCON_2483	2-isopropylmalate synthase	*cimA*	9.25	0.98	Amino acid biosynthesis
MCON_0129	glutamine synthetase	*glnA*	9.25	0.24	Amino acid biosynthesis
MCON_1081	hydroxymethylglutaryl-CoA synthase		9.25	0.36	Fatty acid and phospholipid metabolism
MCON_2164	IS630 family transposase		9.25	0.47	Mobilome:prophages and transposons
MCON_2211	transposase		9.25	0.24	Mobilome:prophages and transposons

MCON_2557	isopentenyl-diphosphate delta-isomerase	*fni*	9.24	0.46	Biosynthesis of cofactors, prosthetic groups, and carriers
MCON_2824	S-adenosylmethionine synthetase	*mat*	9.22	0.29	Coenzyme transport and metabolism
MCON_0904	AAA ATPase family protein		9.22	0.25	Unknown functions
MCON_0012	4Fe-4S ferredoxin, iron-sulfur binding domain-containing protein		9.21	0.25	Energy metabolism
MCON_2891	AAA family ATPase, CDC48 subfamily; TIGR01243		9.21	0.63	Unknown functions
MCON_0584	Predicted nucleotidyltransferase		9.20	1.15	Unknown function
MCON_2921	aminoglycoside phosphotransferase		9.20	0.94	Unknown functions
MCON_2574	oxidoreductase domain-containing protein		9.19	0.24	Energy metabolism
MCON_3271	CRISPR-associated endonuclease Cas1	*cas1*	9.18	0.25	Mobile and extrachromosomal element functions
MCON_0503	Mo-nitrogenase iron protein subunit NifH	*nifH*	9.16	0.18	Central intermediary metabolism
MCON_2753	DNA-binding protein		9.16	0.46	Unknown function
MCON_3028	cytochrome c biogenesis protein	*ccdA*	9.15	0.62	Energy metabolism
MCON_1382	transposase		9.15	0.40	Mobilome:prophages and transposons
MCON_3412	pentapeptide repeat-containing protein		9.14	0.25	Unknown function
MCON_1286	lipoprotein-releasing system, ABC transporter permease	*lolE*	9.13	0.46	Cell envelope
MCON_0399	hypothetical protein		9.13	0.16	Hypothetical proteins
MCON_1879	hypothetical protein		9.13	0.05	Hypothetical proteins
MCON_2977	glucose-6-phosphate isomerase	*pgiA*	9.12	0.69	Coenzyme transport and metabolism
MCON_0440	hypothetical protein		9.12	0.81	Hypothetical proteins
MCON_3069	NADH:ubiquinone oxidoreductase subunit M	*fpoM*	9.11	0.78	Energy metabolism
MCON_2737	glutamate synthase (NADPH), homotetrameric	*gltA*	9.10	0.40	Amino acid biosynthesis
MCON_2653	pyruvate carboxylase subunit B	*pycB*	9.10	0.53	Transport and binding proteins
MCON_2103	hypothetical protein		9.09	0.46	Hypothetical proteins
MCON_2095	ribonucleoside-triphosphate reductase class III catalytic subunit	*nrdD*	9.09	0.37	Purines, pyrimidines, nucleosides, and nucleotides
MCON_3135	phosphoserine-tRNA(Cys) ligase	*sepS*	9.08	0.40	Amino acid biosynthesis
MCON_3068	F420H2 dehydrogenase subunit L	*fpoL*	9.08	0.27	Energy metabolism
MCON_2599	adenosylcobyric acid synthase	*cobQ*	9.05	0.68	Biosynthesis of cofactors, prosthetic groups, and carriers
MCON_0638	SSU ribosomal protein S4P	*rpsD*	9.03	0.71	Protein synthesis
MCON_2697	30S ribosomal protein S3	*rpsC*	9.02	0.73	Protein synthesis
MCON_1975	phenylalanyl-tRNA synthetase beta subunit	*pheT*	9.02	0.18	Protein synthesis
MCON_1764	cation transporting P-type ATPase		9.02	0.67	Transport and binding proteins
MCON_1651	aspartate kinase		8.99	0.59	Amino acid biosynthesis
MCON_2913	LSU ribosomal protein L10P	*rplJ*	8.98	0.35	Protein synthesis
MCON_1551	single-stranded DNA-binding replication protein A	*rpa*	8.97	0.48	DNA recombination, replication, and repair
MCON_0595	integral membrane protein		8.97	0.47	Unknown function
MCON_2750	tRNA pseudouridine(54/55) synthase Pus10	*pus10*	8.96	0.51	Protein synthesis
MCON_2296	aspartate aminotransferase	*aspC*	8.95	1.03	Amino acid transport and metabolism
MCON_2327	ISL3 family transposase		8.95	0.69	Mobilome:prophages and transposons
MCON_1712	CoA-binding domain-containing protein	*accS*	8.94	0.31	Energy metabolism
MCON_3279	CoB--CoM heterodisulfide reductase subunit A	*hdrA*	8.94	0.02	Energy metabolism- Methanogenesis
MCON_0025	Myo-inositol-1-phosphate synthase		8.94	0.21	Lipid transport and metabolism
MCON_2853	putative transcriptional regulator		8.94	0.37	Transcriptional regulation
MCON_2892	ATP-dependent protease LonB	*lonB*	8.93	0.52	Protein fate
MCON_1103	DNA gyrase subunit A	*gyrA*	8.92	0.63	DNA replication, recombination and repair
MCON_2271	DNA polymerase I	*polA*	8.92	0.02	DNA replication, recombination and repair
MCON_0313	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	*gatB*	8.92	0.74	Protein synthesis

MCON_1851	IS481 family transposase		8.90	0.49	Mobilome:prophages and transposons
MCON_3356	hypothetical protein		8.89	0.47	Hypothetical proteins
MCON_2618	signal recognition particle-docking protein FtsY	*ftsY*	8.88	1.15	Protein fate
MCON_2284	hypothetical protein		8.87	0.46	Hypothetical proteins
MCON_0645	IS481 family transposase		8.87	0.37	Mobilome:prophages and transposons
MCON_0312	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A	*gatA*	8.87	0.42	Protein synthesis
MCON_RS04130	hypothetical protein		8.86	0.51	Hypothetical proteins
MCON_RS07660	hypothetical protein		8.86	0.51	Hypothetical proteins
MCON_RS13655	hypothetical protein		8.86	0.51	Hypothetical proteins
MCON_RS14035	hypothetical protein		8.86	0.51	Hypothetical proteins
MCON_3519	integrase		8.86	0.63	Mobilome:prophages and transposons
MCON_3466	RecJ-like exonuclease		8.85	0.43	DNA recombination, replication, and repair
MCON_1962	glycine--tRNA ligase	*glyS*	8.85	0.57	Protein synthesis
MCON_1252	AAA family ATPase		8.85	0.19	Unknown functions
MCON_2442	chromosome segregation protein SMC	*smc*	8.83	0.04	Cell division
MCON_0256	ATPase AAA		8.83	0.18	Unknown function
MCON_1345	indolepyruvate ferredoxin oxidoreductase subunit alpha	*iorA*	8.81	0.04	Energy metabolism
MCON_1326	acetyl-CoA decarbonylase/synthase delta subunit	*cdhD*	8.80	0.24	Energy metabolism- methanogenesis
MCON_2855	RNA-metabolising metallo-beta-lactamase		8.80	0.28	Unknown function
MCON_1278	DNA-directed RNA polymerase subunit A"	*rpoA2*	8.77	0.26	Transcription
MCON_1276	DNA-directed RNA polymerase, subunit B'	*rpoB1*	8.77	0.25	Transcription
MCON_2044	hydroxylamine reductase	*hcp*	8.76	0.36	Detoxification
MCON_0154	thermosome subunit	*thsA*	8.76	0.39	Protein fate
MCON_1442	thermosome subunit	*thsD*	8.76	0.39	Protein fate
MCON_2067	Na+/solute symporter		8.75	0.46	Transport and binding proteins
MCON_2732	anaerobic sulfatase-maturating enzyme		8.74	1.15	Protein fate
MCON_2089	seryl-tRNA synthetase	*serS*	8.73	0.31	Protein synthesis
MCON_0819	phenylacetate--CoA ligase	*paaK*	8.72	0.73	Coenzyme transport and metabolism
MCON_1158	valyl-tRNA synthetase	*valS*	8.72	0.52	Protein synthesis
MCON_1167	cell division protein FtsZ	*ftsZ*	8.71	0.18	Cell division
MCON_0393	methyl coenzyme M reductase system, component A2	*atwA*	8.71	0.28	Energy metabolism- methanogenesis
MCON_1292	elongation factor Tu, domain 2 protein		8.71	0.69	Protein synthesis
MCON_0418	DNA polymerase B	*dpo2*	8.70	0.32	DNA replication, recombination and repair
MCON_1942	acetyl-CoA decarbonylase/synthase beta subunit	*cdhC*	8.70	0.32	Energy metabolism- methanogenesis
MCON_2224	hypothetical protein		8.69	0.46	Hypothetical proteins
MCON_1215	hypothetical protein		8.68	0.69	Hypothetical proteins
MCON_1873	type I glutamate--ammonia ligase	*glnA*	8.65	0.55	Amino acid biosynthesis
MCON_2585	glycosyl transferase family 1		8.65	0.50	Cell envelope
MCON_2641	peptidase M42		8.63	0.46	Protein fate
MCON_0601	IS256 family transposase		8.61	0.50	Mobilome:prophages and transposons
MCON_1560	radical SAM protein		8.60	0.46	Unknown function
MCON_2922	adenosylhomocysteinase	*ahcY*	8.59	0.35	Energy metabolism
MCON_RS01900	ATP citrate synthase		8.58	0.31	Energy metabolism
MCON_2594	glucose-1-phosphate thymidylyltransferase	*rfbA*	8.57	0.69	Cell envelope
MCON_1470	pyruvate ferredoxin oxidoreductase, beta subunit	*porB*	8.57	0.46	Energy metabolism
MCON_1042	PhoU family transcriptional regulator	*phoU*	8.57	0.47	Transcriptional regulation
MCON_1517	glutamyl-tRNA(Gln) amidotransferase subunit E	*gatE*	8.56	0.28	Protein synthesis
MCON_0627	hypothetical protein		8.55	0.36	Hypothetical proteins
MCON_0209	phosphoribosylformylglycinamidine synthase II	*purL*	8.55	0.51	Purines, pyrimidines, nucleosides, and

					nucleotides
MCON_3433	ABC transporter ATP-binding protein	*gsiA*	8.55	0.74	Transport and binding proteins
MCON_2876	alpha glucan phosphorylase		8.51	0.04	Carbohydrate transport and metabolism
MCON_1974	phenylalanyl-tRNA synthetase, alpha subunit	*pheS*	8.51	1.15	Protein synthesis
MCON_1909	hypothetical protein		8.49	0.46	Hypothetical proteins
MCON_0558	acetyl-coenzyme A synthetase	*acsA*	7.47	0.34	Energy metabolism- methanogenesis
MCON_0995	transposase		8.46	1.05	Mobilome:prophages and transposons
MCON_1275	DNA-directed RNA polymerase, subunit B	*rpoB2*	8.46	0.33	Transcription
MCON_2731	sulfatase family protein		8.46	0.61	Unknown function
MCON_0703	hypothetical protein		8.45	0.69	Hypothetical proteins
MCON_1277	DNA-directed RNA polymerase, subunit A'	*rpoA1*	8.44	0.23	Transcription
MCON_2055	DNA methylase		8.38	0.74	DNA replication, recombination and repair
MCON_2869	GvpD gas vesicle	*gvpD*	8.37	0.50	Signal transduction mechanisms
MCON_0780	acyl-coenzyme A synthetase	*acsA*	7.36	0.44	Energy metabolism- methanogenesis
MCON_0172	amidohydrolase		8.33	0.38	Nucleotide transport and metabolism
MCON_2033	alanyl-tRNA synthetase	*alaS*	8.32	0.28	Protein synthesis
MCON_0894	glycosyltransferase family 57 protein		8.29	0.37	Cell envelope
MCON_1356	copper-translocating P-type ATPase		8.29	0.42	Transport and binding proteins
MCON_0109	metallo-beta-lactamase family protein		8.27	0.39	Unknown function
MCON_2352	WD40-like beta Propeller repeat-containing protein		8.27	1.03	Unknown functions
MCON_2723	peptidase, ArgE/DapE family		8.26	0.26	Protein fate
MCON_2419	leucyl-tRNA synthetase	*leuS*	8.26	0.37	Protein synthesis
MCON_RS01905	ATP citrate lyase citrate-binding		8.23	0.58	Energy metabolism
MCON_1670	sodium:solute symporter		8.23	0.20	Inorganic ion transport and metabolism
MCON_0002	IS256 family transposase		8.20	0.36	Mobilome:prophages and transposons
MCON_0772	aminotransferase		8.20	0.53	Unknown functions
MCON_2951	acetyl-CoA hydrolase/N-GNAT family acetyltransferase fusion protein		8.19	1.03	Energy metabolism
MCON_0325	hypothetical protein		8.19	1.03	Hypothetical proteins
MCON_3198	thiosulfate/3-mercaptopyruvate sulfurtransferase		8.18	0.46	Inorganic ion transport and metabolism
MCON_1258	transposase		8.18	0.46	Mobilome:prophages and transposons
MCON_0896	cation transport protein		8.18	0.18	Transport and binding proteins
MCON_1025	carbamoyl-phosphate synthase large subunit	*carB*	8.17	0.18	Purines, pyrimidines, nucleosides, and nucleotides
MCON_0241	formylmethanofuran dehydrogenase, subunit A	*fmdA*	8.16	0.44	Energy metabolism- methanogenesis
MCON_1073	tetrahydromethanopterin S-methyltransferase, subunit C	*mtrC*	8.15	0.04	Energy metabolism- methanogenesis
MCON_1135	hypothetical protein		8.14	0.46	Hypothetical proteins
MCON_1410	isoleucine--tRNA ligase	*ileS*	8.14	0.43	Protein synthesis
MCON_2355	phosphoglycerate kinase	*pgk*	8.11	0.46	Carbohydrate transport and metabolism
MCON_2433	helicase domain-containing protein		8.11	0.65	DNA recombination, replication, and repair
MCON_2817	hydrophobe/amphiphile efflux-3 (HAE3) family efflux transporter		8.11	0.47	Transport and binding proteins
MCON_3480	Phosphopantothenate-cysteine ligase (EC 6.3.2.5)/Phosphopantothenoylcysteine decarboxylase	*coaBC*	8.09	0.49	Biosynthesis of cofactors, prosthetic groups, and carriers
MCON_1102	DNA gyrase subunit B	*gyrB*	8.09	0.39	DNA replication, recombination and repair
MCON_0622	IS5 family transposase		8.07	0.35	Mobilome:prophages and transposons
MCON_1290	Methenyltetrahydromethanopterin cyclohydrolase	*mch*	8.05	0.33	Energy metabolism- methanogenesis
MCON_0894	glycosyltransferase family 57 protein		8.04	0.22	Cell envelope
MCON_0018	copper-translocating P-type ATPase		8.04	0.25	Transport and binding proteins
MCON_2326	ATP dependent helicase, Lhr family		8.03	0.47	DNA recombination, replication, and repair
MCON_1332	acetyl-CoA decarbonylase/synthase alpha subunit	*cdhA*	8.03	0.40	Energy metabolism- methanogenesis

MCON_1075	tetrahydromethanopterin S-methyltransferase, subunit E	*mtrE*	8.02	0.04	Energy metabolism- methanogenesis
MCON_0829	AAA family ATPase		7.98	0.49	Unknown functions
MCON_1650	elongation factor EF-2	*ef2*	7.90	0.27	Protein synthesis
MCON_3166	arginine decarboxylase	*speA*	7.86	0.47	Central intermediary metabolism
MCON_3111	two-component hybrid sensor and regulator		7.85	0.59	Signal transduction mechanisms
MCON_2417	putative Ski2-type helicase	*hel308*	7.84	0.52	DNA recombination, replication, and repair
MCON_3265	CRISPR-associated helicase/endonuclease Cas3	*cas3*	7.84	0.49	Mobile and extrachromosomal element functions
MCON_3371	D-3-phosphoglycerate dehydrogenase	*serA*	7.82	0.54	Amino acid biosynthesis
MCON_1490	pyruvate carboxylase subunit A	*accC*	7.81	0.46	Fatty acid and phospholipid metabolism
MCON_0764	DNA topoisomerase I	*topA*	7.75	0.35	DNA replication, recombination and repair
MCON_0086	carbamoyl-phosphate synthase large subunit	*carB*	7.74	0.83	Purines, pyrimidines, nucleosides, and nucleotides
MCON_1488	replication factor C large subunit	*rfcL*	7.70	0.46	DNA recombination, replication, and repair
MCON_0112	acetyl-CoA hydrolase/transferase		7.68	0.69	Energy metabolism
MCON_2320	Coenzyme F420 hydrogenase, subunit beta	*frhB*	7.68	0.69	Energy metabolism- methanogenesis
MCON_3104	Coenzyme F420 hydrogenase, subunit beta	*frhB*	7.68	0.69	Energy metabolism- methanogenesis
MCON_0996	restriction endonuclease subunit M		7.66	1.15	DNA metabolism
MCON_1408	multi-sensor hybrid histidine kinase		7.62	0.31	Signal transduction mechanisms
MCON_0242	formylmethanofuran dehydrogenase, subunit F	*fmdF*	7.60	0.60	Energy metabolism- methanogenesis
MCON_1569	ATPase, PilT family		7.60	0.18	Unknown function
MCON_0575	metal-dependent phosphohydrolase		7.51	0.46	Unknown function
MCON_1395	threonine--tRNA ligase	*thrS*	7.42	0.38	Protein synthesis
MCON_0548	DNA excision repair protein ERCC-2		7.38	0.57	DNA replication, recombination and repair
MCON_1119	hypothetical protein		7.37	0.46	Hypothetical proteins
MCON_2582	glutamine--fructose-6-phosphate transaminase	*glmS*	7.31	0.60	Cell envelope
MCON_0620	transposase		7.30	0.59	Mobilome:prophages and transposons
MCON_1022	transposase		7.30	0.59	Mobilome:prophages and transposons
MCON_1791	transposase		7.30	0.59	Mobilome:prophages and transposons
MCON_1072	tetrahydromethanopterin S-methyltransferase subunit B	*mtrB*	7.29	0.29	Energy metabolism- methanogenesis
MCON_0992	IS110 family transposase		7.23	0.58	Mobilome:prophages and transposons
MCON_2047	transposase		7.21	0.76	Mobilome:prophages and transposons
MCON_3206	transposase		7.21	0.76	Mobilome:prophages and transposons
MCON_3419	transposase		7.15	0.59	Mobilome:prophages and transposons
MCON_1071	tetrahydromethanopterin S-methyltransferase subunit A	*mtrA*	7.13	0.13	Energy metabolism- methanogenesis
MCON_2603	transposase		7.11	0.45	Mobilome:prophages and transposons
MCON_0957	transposase		7.10	0.46	Mobilome:prophages and transposons
MCON_3325	transposase		7.10	0.46	Mobilome:prophages and transposons
MCON_0495	transposase		7.08	0.76	Mobilome:prophages and transposons
MCON_1412	transposase		7.08	0.76	Mobilome:prophages and transposons
MCON_1582	transposase		7.08	0.76	Mobilome:prophages and transposons
MCON_2674	helicase domain-containing protein		7.00	0.60	DNA recombination, replication, and repair
MCON_2308	transposase, IS116/IS110/IS902 family		7.00	0.57	Mobilome:prophages and transposons
MCON_0603	transposase		6.99	0.45	Mobilome:prophages and transposons
MCON_1384	transposase		6.99	0.45	Mobilome:prophages and transposons
MCON_1572	DNA mismatch repair protein MutS	*mutS*	6.98	0.46	DNA replication, recombination and repair
MCON_1032	Cna B domain-containing protein		6.96	0.47	Unknown functions
MCON_3389	transposase		6.91	0.51	Mobilome:prophages and transposons
MCON_0090	hypothetical protein		6.82	0.47	Hypothetical proteins
MCON_0628	transposase		6.82	0.44	Mobilome:prophages and transposons

MCON_2947	transposase		6.73	0.53	Mobilome:prophages and transposons
MCON_1362	IS110 family transposase		6.65	0.47	Mobilome:prophages and transposons
MCON_2264	DNA polymerase II large subunit	*polC*	6.61	0.46	DNA replication, recombination and repair
MCON_2638	IS110 family transposase		6.61	0.80	Mobilome:prophages and transposons
MCON_3224	IS110 family transposase		6.59	0.78	Mobilome:prophages and transposons
MCON_0924	transposase		6.58	1.26	Mobilome:prophages and transposons
MCON_0629	transposase		6.54	1.03	Mobilome:prophages and transposons