

Supplementary Table S2 List of identified proteins by LC-MS/MS using the monolithic silica column and the 41 hour gradient

Accession number	Gene name	Product	GO annotation	GRAVY score	Membrane proteins	Number of predicted transmembrane domains (TMHMM)	Number of identified peptides	Protein score
JW3951	rpoC	RNA polymerase, beta prime subunit	GO:0005737 cytoplasm	-0.240	0	0	76	5523
JW3950	rpoB	RNA polymerase, beta subunit	GO:0005737 cytoplasm	-0.394	0	0	68	5260
JW1215	narG	nitrate reductase 1, alpha subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.512	1	0	67	4507
JW2573	clpB	protein disaggregation chaperone	GO:0005737 cytoplasm	-0.358	0	0	54	4068
JW0999	putA	fused DNA-binding transcriptional regulator -!- proline dehydrogenase -!- pyrroline-5-carboxylate dehydrogenase	GO:0005737 cytoplasm	-0.131	0	0	60	4047
JW0110	aceE	pyruvate dehydrogenase, decarboxylase component E1, thiamin-	0	-0.437	0	0	55	3988
JW2541	purL	phosphoribosylformyl-glycineamide synthetase	GO:0005737 cytoplasm	-0.235	0	0	58	3744
JW2871	gcvP	glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	0	-0.066	0	0	46	3739
JW0013	dnaK	chaperone Hsp70, co-chaperone with DnaJ	GO:0005737 cytoplasm	-0.409	0	0	46	3734
JW2667	alaS	alanyl-tRNA synthetase	GO:0005737 cytoplasm	-0.303	0	0	50	3647
JW0031	carB	carbamoyl-phosphate synthase large subunit	0	-0.162	0	0	55	3623
JW0114	acnB	bifunctional aconitate hydratase 2 -!- 2-methylisocitrate dehydratase	0	-0.117	0	0	46	3579
JW1268	acnA	aconitate hydratase 1	0	-0.234	0	0	48	3371
JW1228	adhE	fused acetaldehyde-CoA dehydrogenase -!- iron-dependent alcohol dehydrogenase -!- pyruvate-	0	-0.066	0	0	46	3336
JW3302	fusA	protein chain elongation factor EF-G	GO:0005737 cytoplasm	-0.286	0	0	38	3283
JW0886	pflB	pyruvate formate lyase I	GO:0005737 cytoplasm	-0.380	0	0	41	3272
JW3914	katG	catalase/hydroperoxidase HPI(I)	0	-0.372	0	0	42	3092
JW0894	rpsA	30S ribosomal subunit protein S1	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.300	0	0	39	3008
JW0715	sucA	2-oxoglutarate decarboxylase, thiamin-requiring	0	-0.441	0	0	44	3006
JW1703	pheT	phenylalanine tRNA synthetase, beta subunit	GO:0005737 cytoplasm	-0.097	0	0	44	2971
JW5689	malP	maltodextrin phosphorylase	0	-0.348	0	0	44	2957
JW0096	secA	preprotein translocase subunit, ATPase that targets protein precursors to the SecYE core translocon	GO:0005737 cytoplasm	-0.467	0	0	44	2926
JW3530	glyS	glycine tRNA synthetase, beta subunit	GO:0005737 cytoplasm	-0.219	0	0	38	2910
JW0915	pepN	aminopeptidase N	0	-0.325	0	0	41	2844

JW4103	groL	Cpn60 chaperonin GroEL, large subunit of GroESL	GO:0005737 cytoplasm	-0.009	0	0	35	2832
JW0024	ileS	isoleucyl-tRNA synthetase	GO:0005737 cytoplasm	-0.263	0	0	43	2798
JW4215	valS	valyl-tRNA synthetase	GO:0005737 cytoplasm	-0.380	0	0	48	2731
JW3974	aceB	malate synthase A	GO:0005737 cytoplasm	-0.316	0	0	36	2709
JW0429	lon	DNA-binding ATP-dependent protease	GO:0005737 cytoplasm	-0.312	0	0	44	2703
JW3928	ppc	phosphoenolpyruvate carboxylase	GO:0005737 cytoplasm	-0.277	0	0	49	2676
JW4354	yjjK	fused predicted transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.478	0	0	37	2675
JW1855	aspS	aspartyl-tRNA synthetase	GO:0005737 cytoplasm	-0.265	0	0	39	2647
JW2225	gyrA	DNA gyrase (type II topoisomerase), subunit A	GO:0005737 cytoplasm	-0.240	0	0	43	2642
JW0637	leuS	leucyl-tRNA synthetase	GO:0005737 cytoplasm	-0.368	0	0	45	2627
JW3137	infB	fused protein chain initiation factor 2,	GO:0005737 cytoplasm	-0.533	0	0	36	2600
JW0462	htpG	molecular chaperone HSP90 family		-0.524	0	0	35	2594
JW3970	purH	fused IMP cyclohydrolase -!- phosphoribosylaminoimidazolecarboxamide formyltransferase	GO:0005737 cytoplasm	-0.126	0	0	35	2571
JW1488	gadB	glutamate decarboxylase B, PLP-dependent	GO:0005737 cytoplasm	-0.297	0	0	32	2557
JW1772	yeaG	conserved protein with nucleoside triphosphate hydrolase domain		-0.529	0	0	37	2549
JW1071	rne	fused ribonucleaseE endoribonuclease -!- scaffold for formation of degradosome	GO:0005737 cytoplasm	-0.645	0	0	35	2493
JW2278	nuoG	NADH:ubiquinone oxidoreductase,	GO:0005737 cytoplasm	-0.318	0	0	36	2489
JW3710	atpD	F1 sector of membrane-bound ATP synthase, beta subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.118	1	0	27	2477
JW0713	sdhA	succinate dehydrogenase, flavoprotein subunit	GO:0005737 cytoplasm	-0.324	0	0	30	2450
JW3712	atpA	F1 sector of membrane-bound ATP synthase, alpha subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.045	1	0	29	2425
JW3686	tnaA	tryptophanase/L-cysteine desulfhydrase, PLP-dependent		-0.216	0	0	30	2424
JW2491	guaA	GMP synthetase (glutamine aminotransferase)	GO:0005737 cytoplasm	-0.096	0	0	33	2407
JW0172	yaeT	conserved protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.483	1	0	36	2390
JW5375	nuoC	NADH:ubiquinone oxidoreductase, chain C,D	GO:0005737 cytoplasm	-0.307	0	0	33	2368
JW0907	mukB	fused chromosome partitioning proteins		-0.599	0	0	45	2361
JW0111	aceF	pyruvate dehydrogenase, dihydrolipoyltransacetylase component		0.004	1	0	30	2348

JW2447	maeB	fused malic enzyme predicted oxidoreductase - - predicted phosphotransacetylase	0	0.054	1	0	33	2339
JW3835	polA	fused DNA polymerase I 5'->3' exonuclease - - 3'->5' polymerase - - 3'->5' exonuclease	GO:0005737 cytoplasm	-0.264	0	0	38	2333
JW5625	gyrB	DNA gyrase, subunit B	GO:0005737 cytoplasm	-0.454	0	0	39	2326
JW2449	tktB	transketolase 2, thiamin-binding	0	-0.309	0	0	32	2316
JW2101	metG	methionyl-tRNA synthetase	GO:0005737 cytoplasm	-0.303	0	0	33	2311
JW3138	nusA	transcription termination/antitermination L factor	GO:0005737 cytoplasm	-0.278	0	0	27	2283
JW0190	proS	prolyl-tRNA synthetase	GO:0005737 cytoplasm	-0.243	0	0	32	2269
JW2409	ptsI	PEP-protein phosphotransferase of PTS system (enzyme I)	0	-0.120	0	0	30	2264
JW4090	lysU	lysine tRNA synthetase, inducible	GO:0005737 cytoplasm	-0.399	0	0	33	2257
JW1266	topA	DNA topoisomerase I, omega subunit	GO:0005737 cytoplasm	-0.609	0	0	38	2246
JW1666	pykF	pyruvate kinase I	0	-0.082	0	0	28	2240
JW1604	fumA	aerobic Class I fumarate hydratase (fumarase A)	0	-0.368	0	0	27	2211
JW3366	pck	phosphoenolpyruvate carboxykinase	0	-0.315	0	0	26	2207
JW4115	frdA	fumarate reductase (anaerobic) catalytic and NAD/ flavoprotein subunit	GO:0005737 cytoplasm	-0.365	0	0	35	2196
JW3975	aceA	isocitrate lyase	GO:0005737 cytoplasm	-0.224	0	0	25	2191
JW0675	pgm	phosphoglucomutase	GO:0005737 cytoplasm	-0.168	0	0	30	2167
JW2228	nrdA	ribonucleoside diphosphate reductase 1, alpha subunit	0	-0.337	0	0	37	2159
JW2011	gnd	gluconate-6-phosphate dehydrogenase, decarboxylating	0	-0.200	0	0	26	2157
JW0955	hyaB	hydrogenase 1, large subunit	GO:0019866 inner membrane	-0.210	1	0	31	2148
JW5741	rnr	exoribonuclease R, RNase R	0	-0.551	0	0	38	2137
JW1709	thrS	threonyl-tRNA synthetase	GO:0005737 cytoplasm	-0.494	0	0	37	2129
JW3145	ftsH	protease, ATP-dependent zinc-metallo	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.263	1	2	35	2125
JW2943	glcB	malate synthase G	0	-0.327	0	0	31	2119
JW3465	prlC	oligopeptidase A	0	-0.416	0	0	32	2099
JW0426	tig	peptidyl-prolyl cis/trans isomerase (trigger factor)	GO:0005737 cytoplasm	-0.428	0	0	29	2097
JW4135	purA	adenylosuccinate synthetase	GO:0005737 cytoplasm	-0.200	0	0	26	2093
JW1692	pps	phosphoenolpyruvate synthase	0	-0.243	0	0	34	2091
JW1412	aldA	aldehyde dehydrogenase A, NAD-linked	0	-0.056	0	0	27	2084
JW2294	pta	phosphate acetyltransferase	0	-0.080	0	0	28	2073
JW5851	pnp	polynucleotide phosphorylase/polyadenylase	GO:0005737 cytoplasm	-0.169	0	0	31	2060
JW1843	pykA	pyruvate kinase II	0	-0.025	0	0	29	2031
JW3897	glpK	glycerol kinase	0	-0.292	0	0	28	2014
JW3841	glnA	glutamine synthetase	GO:0005737 cytoplasm	-0.292	0	0	27	2011

JW1372	ydbK	fused predicted Fe-S subunit of pyruvate-flavodoxin oxidoreductase	0	-0.191	0	0	40	1991
JW0866	clpA	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity	GO:0005737 cytoplasm	-0.298	0	0	31	1986
JW1235	oppA	oligopeptide transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 periplasmic space	-0.436	1	1	26	1977
JW4019	uvrA	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC	GO:0005737 cytoplasm	-0.289	0	0	37	1971
JW1865	argS	arginyl-tRNA synthetase	GO:0005737 cytoplasm	-0.258	0	0	30	1969
JW3707	glmS	L-glutamine:D-fructose-6-phosphate aminotransferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737	-0.101	0	0	28	1962
JW2395	gltX	glutamyl-tRNA synthetase	GO:0005737 cytoplasm	-0.528	0	0	28	1932
JW0717	sucC	succinyl-CoA synthetase, beta subunit	0	0.024	1	0	24	1918
JW0431	ppiD	peptidyl-prolyl cis-trans isomerase (rotamase D)	0	-0.405	1	1	32	1893
JW2893	pgk	phosphoglycerate kinase	GO:0005737 cytoplasm	0.072	1	0	21	1880
JW3994	malE	maltose transporter subunit -!- periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.251	0	0	23	1869
JW2535	glyA	serine hydroxymethyltransferase	GO:0005737 cytoplasm	-0.233	0	0	23	1860
JW3301	tufA	protein chain elongation factor EF-Tu (duplicate of tufB)	GO:0005737 cytoplasm	-0.196	0	0	24	1859
JW1606	ydgA	conserved protein	0	-0.299	1	1	22	1848
JW2637	gabT	4-aminobutyrate aminotransferase, PLP-dependent	0	0.002	1	0	26	1848
JW0666	glnS	glutamyl-tRNA synthetase	GO:0005737 cytoplasm	-0.518	0	0	30	1846
JW0053	imp	exported protein required for envelope biosynthesis and integrity	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.657	1	0	31	1837
JW0165	tsf	protein chain elongation factor EF-Ts	GO:0005737 cytoplasm	-0.118	0	0	23	1821
JW2858	lysS	lysine tRNA synthetase, constitutive	GO:0005737 cytoplasm	-0.396	0	0	27	1819
JW3865	fdoG	formate dehydrogenase-O, large	GO:0005737 cytoplasm	-0.346	0	0	30	1819
JW0599	ahpF	alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding	0	-0.123	0	0	26	1816
JW1100	mfd	transcription-repair coupling factor	GO:0005737 cytoplasm	-0.292	0	0	41	1783
JW2750	eno	enolase	GO:0005737 cytoplasm	-0.158	0	0	20	1783
JW2194	napA	nitrate reductase, periplasmic, large subunit	GO:0042597 periplasmic space	-0.438	0	0	32	1771
JW2751	pyrG	CTP synthetase	0	-0.139	1	1	29	1770
JW4030	acs	bifunctional acetyl-CoA synthetase -!- propionyl-CoA synthetase	0	-0.291	0	0	28	1764
JW3756	rho	transcription termination factor	GO:0005737 cytoplasm	-0.298	0	0	26	1742
JW5238	sfcA	malate dehydrogenase, NAD-requiring (malic enzyme)	0	-0.180	0	0	25	1738

JW2137	mglB	methyl-galactoside transporter subunit -! periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.273	1	1	22	1735
JW0911	aspC	aspartate aminotransferase, PLP-dependent	GO:0005737 cytoplasm	-0.202	0	0	27	1723
JW3205	mdh	malate dehydrogenase, NAD(P)-binding	0	0.194	1	0	19	1715
JW1122	icd	e14 prophage; isocitrate dehydrogenase, specific for NADP+	0	-0.154	0	0	27	1711
JW5551	sthA	pyridine nucleotide transhydrogenase, soluble	GO:0005737 cytoplasm	-0.227	0	0	23	1703
JW4346	deoB	phosphopentomutase	0	-0.271	0	0	24	1699
JW0112	lpd	lipoamide dehydrogenase, E3 component is part of three enzyme	GO:0005737 cytoplasm	-0.011	0	0	22	1684
JW0058	hepA	RNA polymerase-associated helicase protein (ATPase and RNA polymerase recycling factor)	0	-0.355	0	0	34	1680
JW2499	ispG	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	0	-0.157	0	0	25	1679
JW0157	degP	serine endoprotease (protease Do), membrane-associated	GO:0042597 periplasmic space	-0.067	0	0	21	1673
JW5118	dmsA	dimethyl sulfoxide reductase, anaerobic, subunit A	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.436	1	0	31	1667
JW4345	deoA	thymidine phosphorylase	0	0.011	1	0	24	1660
JW5401	quaB	IMP dehydrogenase	GO:0005737 cytoplasm	-0.098	0	0	21	1654
JW3902	hslU	molecular chaperone and ATPase component of HslUV protease	GO:0005737 cytoplasm	-0.363	0	0	26	1652
JW0913	asnS	asparaginyl tRNA synthetase	GO:0005737 cytoplasm	-0.257	0	0	25	1641
JW5344	fbaB	fructose-bisphosphate aldolase class I	0	-0.148	0	0	23	1627
JW3513	dppA	dipeptide transporter -! periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.463	0	0	22	1621
JW1905	fliY	cystine transporter subunit -! periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.302	0	0	22	1616
JW4001	plsB	glycerol-3-phosphate O-acyltransferase	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.179	1	0	32	1614
JW1216	narH	nitrate reductase 1, beta (Fe-S) subunit	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.477	1	0	26	1610
JW0855	poxB	pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAD-	GO:0005737 cytoplasm	0.008	1	0	23	1599
JW4194	pmbA	predicted peptidase required for the maturation and secretion of the antibiotic peptide MccB17	GO:0005737 cytoplasm	-0.160	0	0	22	1597
JW0710	gltA	citrate synthase	0	-0.231	0	0	21	1596
JW0317	yahK	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	-0.183	0	0	23	1595
JW0007	talB	transaldolase B	GO:0005737 cytoplasm	-0.210	0	0	21	1593
JW1531	dcp	dipeptidyl carboxypeptidase II	0	-0.331	0	0	25	1591

JW2636	gabD	succinate-semialdehyde dehydrogenase I, NADP-dependent	0	-0.071	0	0	22	1584
JW1841	zwf	glucose-6-phosphate dehydrogenase	GO:0005737 cytoplasm	-0.374	0	0	25	1578
JW3179	gltB	glutamate synthase, large subunit	0	-0.224	0	0	33	1566
JW2403	ligA	DNA ligase, NAD(+)-dependent	GO:0005737 cytoplasm	-0.137	0	0	28	1545
JW4220	yjgR	predicted ATPase	0	-0.150	0	0	25	1540
JW5478	tktA	transketolase 1, thiamin-binding	0	-0.228	0	0	25	1535
JW0876	serS	seryl-tRNA synthetase, also charges selenocysteinyI-tRNA with serine	GO:0005737 cytoplasm	-0.447	0	0	25	1531
JW2082	gatZ	D-tagatose 1,6-bisphosphate aldolase 2, subunit	0	-0.121	0	0	18	1529
JW1721	katE	hydroperoxidase HPiI(III) (catalase)	GO:0005737 cytoplasm	-0.498	0	0	25	1528
JW2766	ygdH	conserved protein	0	-0.107	0	0	22	1525
JW2486	ppk	polyphosphate kinase, component of RNA degradosome	0	-0.341	0	0	31	1517
JW3140	argG	argininosuccinate synthetase	GO:0005737 cytoplasm	-0.371	0	0	25	1513
JW3481	mdtE	multidrug resistance efflux transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.207	1	0	19	1507
JW0658	miaB	isopentenyl-adenosine A37 tRNA methylthiolase	GO:0005737 cytoplasm	-0.378	0	0	24	1501
JW0797	dps	Fe-binding and storage protein	GO:0005737 cytoplasm	-0.214	0	0	19	1498
JW2320	fabB	3-oxoacyl-[acyl-carrier-protein] synthase	GO:0005737 cytoplasm	0.008	1	0	17	1497
JW1677	ydiJ	predicted FAD-linked oxidoreductase	0	-0.160	0	0	38	1496
JW1186	treA	periplasmic trehalase	GO:0042597 periplasmic space	-0.580	0	0	25	1493
JW5905	hrpA	ATP-dependent helicase	GO:0005737 cytoplasm	-0.439	0	0	32	1487
JW4099	aspA	aspartate ammonia-lyase	GO:0005737 cytoplasm	-0.066	0	0	21	1479
JW1035	mdoG	glucan biosynthesis protein, periplasmic	GO:0042597 periplasmic space	-0.541	0	0	23	1470
JW3592	kbl	glycine C-acetyltransferase	0	-0.049	0	0	19	1469
JW3594	rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding	0	-0.284	0	0	18	1469
JW2498	hisS	histidyl tRNA synthetase	GO:0005737 cytoplasm	-0.272	0	0	22	1465
JW4347	deoD	purine-nucleoside phosphorylase	0	0.070	1	0	19	1465
JW0428	clpX	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease	GO:0005737 cytoplasm	-0.238	0	0	21	1464
JW0093	ftsZ	GTP-binding tubulin-like cell division	GO:0005737 cytoplasm	-0.005	0	0	17	1463
JW5571	bipA	GTP-binding protein	0	-0.298	0	0	23	1462
JW3580	lldD	L-lactate dehydrogenase, FMN-linked	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.037	1	0	22	1454
JW4171	cpdB	2':3'-cyclic-nucleotide 2'-phosphodiesterase	GO:0005737 cytoplasm	-0.285	0	0	24	1446
JW2504	yfhM	conserved protein	0	-0.321	0	0	30	1438
JW2293	ackA	acetate kinase A and propionate kinase	GO:0005737 cytoplasm	-0.047	0	0	17	1430
JW2448	talA	transaldolase A	0	-0.315	0	0	20	1425
JW0227	pepD	aminoacyl-histidine dipeptidase (peptidase D)	GO:0005737 cytoplasm	-0.146	0	0	19	1421
JW2970	yghZ	aldo-keto reductase	0	-0.389	0	0	21	1420

JW3039	rpoD	RNA polymerase, sigma 70 (sigma D) factor	GO:0005737 cytoplasm	-0.589	0	0	22	1413
JW3969	purD	phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase	GO:0005737 cytoplasm	-0.071	0	0	19	1409
JW2962	hybC	hydrogenase 2, large subunit	GO:0019866 inner membrane	-0.140	1	0	23	1408
JW3143	glmM	phosphoglucosamine mutase	GO:0009274 cell wall (sensu Bacteria) - - GO:0009274 cell wall (sensu Bacteria) - - GO:0005737	0.013	1	0	22	1404
JW2869	bglA	6-phospho-beta-glucosidase A	0	-0.452	0	0	22	1398
JW5867	aidB	isovaleryl CoA dehydrogenase	0	-0.136	0	0	23	1398
JW2909	metK	methionine adenosyltransferase 1	GO:0005737 cytoplasm	-0.189	0	0	19	1391
JW3482	mdtF	multidrug transporter, RpoS-dependent	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	0.318	1	11	23	1388
JW1279	rnb	ribonuclease II	0	-0.277	0	0	24	1387
JW2569	pssA	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	-0.429	1	0	26	1380
JW5907	yncB	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	-0.268	0	0	16	1379
JW1178	dadA	D-amino acid dehydrogenase	0	-0.216	0	0	19	1377
JW2136	mglA	fused methyl-galactoside transporter subunitsl - - ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.155	0	0	24	1377
JW0001	thrA	fused aspartokinase I - - homoserine dehydrogenase I	GO:0005737 cytoplasm	0.035	1	0	22	1374
JW0473	copA	copper transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.205	1	8	24	1367
JW2279	nuoF	NADH:ubiquinone oxidoreductase,	GO:0005737 cytoplasm	-0.318	0	0	20	1364
JW0052	surA	peptidyl-prolyl cis-trans isomerase (PPIase)	GO:0009279 external outer membrane (sensu Gram-negative	-0.382	1	0	19	1360
JW2553	lepA	GTP binding membrane protein	0	-0.200	0	0	22	1359
JW2905	speA	biosynthetic arginine decarboxylase, PLP-binding	GO:0042597 periplasmic space	-0.296	0	0	22	1359
JW1117	purB	adenylosuccinate lyase	GO:0005737 cytoplasm	-0.243	0	0	24	1356
JW2133	yeiT	predicted oxidoreductase	0	-0.089	0	0	18	1349
JW0762	uvrB	excinulease of nucleotide excision repair, DNA damage recognition	GO:0005737 cytoplasm	-0.358	0	0	29	1342
JW3730	rbsB	D-ribose transporter subunit - - periplasmic-binding compoent of ABC superfamily	GO:0042597 periplasmic space	-0.031	0	0	16	1341
JW5100	tolB	periplasmic protein	GO:0042597 periplasmic space	-0.215	0	0	15	1326
JW4204	pyrB	aspartate carbamoyltransferase, catalytic subunit	GO:0005737 cytoplasm	-0.105	0	0	19	1322

JW0890	serC	3-phosphoserine/phosphohydroxythreonine aminotransferase	GO:0005737 cytoplasm	-0.113	0	0	18	1313
JW5312	otsA	trehalose-6-phosphate synthase	0	-0.281	0	0	21	1311
JW5873	prfC	peptide chain release factor RF-3	GO:0005737 cytoplasm	-0.326	0	0	22	1308
JW4344	deoC	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked	GO:0005737 cytoplasm	-0.014	0	0	17	1307
JW2317	pdxB	erythronate-4-phosphate	0	-0.037	0	0	26	1305
JW1198	prsA	phosphoribosylpyrophosphate synthase	0	0.096	1	0	14	1304
JW3224	accC	acetyl-CoA carboxylase, biotin carboxylase subunit	GO:0005737 cytoplasm	-0.173	0	0	21	1299
JW1420	mdoD	glucan biosynthesis protein, periplasmic	GO:0042597 periplasmic space	-0.414	0	0	23	1296
JW1596	ydgH	predicted protein	0	-0.324	0	0	18	1291
JW1737	astC	succinylornithine transaminase, PLP-dependent	0	-0.064	0	0	20	1287
JW5427	ygaT	predicted protein	0	-0.375	0	0	22	1286
JW3063	uxaC	uronate isomerase	0	-0.429	0	0	30	1285
JW4198	treC	trehalose-6-P hydrolase	GO:0005737 cytoplasm	-0.560	0	0	22	1281
JW0451	acrB	multidrug efflux system protein	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.266	1	11	25	1280
JW3073	yqjG	predicted S-transferase	0	-0.368	0	0	18	1280
JW0987	agp	glucose-1-phosphatase/inositol phosphatase	GO:0042597 periplasmic space	-0.325	0	0	17	1279
JW2309	purF	amidophosphoribosyltransferase	GO:0005737 cytoplasm	-0.243	0	0	19	1277
JW3574	mtlD	mannitol-1-phosphate dehydrogenase, NAD(P)-binding	0	-0.040	0	0	20	1272
JW1113	pepT	peptidase T	0	-0.215	0	0	21	1267
JW3890	tpiA	triosephosphate isomerase	0	0.010	1	0	18	1267
JW5499	dkgA	2,5-diketo-D-gluconate reductase A	GO:0005737 cytoplasm	-0.375	0	0	21	1267
JW1819	prc	carboxy-terminal protease for penicillin-binding protein 3	GO:0009274 cell wall (sensu Bacteria)	-0.482	0	0	24	1259
JW3573	mtlA	fused mannitol-specific PTS enzyme IIABC components	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.329	1	8	17	1249
JW5536	arcB	hybrid sensory histidine kinase in two-component regulatory system with ArcA	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.251	1	2	21	1249
JW2866	ygfZ	predicted folate-dependent regulatory protein	0	-0.247	0	0	17	1246
JW3429	ftsY	fused Signal Recognition Particle (SRP) receptor	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.335	1	0	20	1245
JW3391	glgP	glycogen phosphorylase	GO:0005737 cytoplasm	-0.339	0	0	28	1243
JW3222	yhdH	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	-0.004	0	0	15	1242
JW2306	hisJ	histidine/lysine/arginine/ornithine transporter subunit - - periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.299	1	1	16	1237
JW2663	gshA	gamma-glutamate-cysteine ligase	0	-0.310	0	0	22	1234

JW3024	rfaE	fused heptose 7-phosphate kinase -!- heptose 1-phosphate adenylyltransferase	0	-0.004	0	0	21	1233
JW4355	slt	lytic murein transglycosylase, soluble	GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597	-0.503	0	0	26	1229
JW2978	yqhD	alcohol dehydrogenase, NAD(P)-dependent	0	-0.129	0	0	20	1226
JW5277	pheS	phenylalanine tRNA synthetase, alpha subunit	GO:0005737 cytoplasm	-0.324	0	0	18	1223
JW3418	ugpB	glycerol-3-phosphate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.503	0	0	21	1222
JW0469	ushA	bifunctional UDP-sugar hydrolase -!- 5'-nucleotidase	GO:0005737 cytoplasm	-0.411	0	0	19	1216
JW0718	sucD	succinyl-CoA synthetase, NAD(P)-binding, alpha subunit	0	0.162	1	0	16	1215
JW2120	bgIX	beta-D-glucoside glucohydrolase, periplasmic	GO:0042597 periplasmic space	-0.260	0	0	25	1215
JW3587	gpml	phosphoglycerate mutase III, cofactor-independent	GO:0005737 cytoplasm	-0.195	0	0	18	1215
JW0515	cysS	cysteinyl-tRNA synthetase	GO:0005737 cytoplasm	-0.415	0	0	18	1214
JW3203	degQ	serine endoprotease, periplasmic	0	0.055	1	1	14	1211
JW2514	iscS	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent	0	-0.273	0	0	20	1209
JW0233	proA	gamma-glutamylphosphate reductase	GO:0005737 cytoplasm	-0.005	0	0	18	1208
JW0398	secD	SecYEG protein translocase auxillary subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.116	1	6	20	1208
JW1206	kdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.028	0	0	18	1208
JW1653	cfa	cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase)	0	-0.313	0	0	21	1205
JW0657	ybeZ	predicted protein with nucleoside triphosphate hydrolase domain	0	-0.370	0	0	19	1203
JW3684	trmE	GTPase	0	-0.095	0	0	19	1202
JW1239	oppF	oligopeptide transporter subunit -!- ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.041	0	0	20	1201
JW1095	ndh	respiratory NADH dehydrogenase 2/cupric reductase	GO:0005737 cytoplasm	-0.129	0	0	20	1200
JW1603	fumC	fumarate hydratase (fumarase C), aerobic Class II	0	-0.133	0	0	17	1199
JW1327	uspE	stress-induced protein	0	-0.207	0	0	18	1189
JW3257	rpoA	RNA polymerase, alpha subunit	GO:0005737 cytoplasm	-0.228	0	0	18	1184
JW4312	hsdM	DNA methylase M	GO:0005737 cytoplasm	-0.528	0	0	22	1181
JW3370	yhgF	predicted transcriptional accessory	0	-0.334	0	0	25	1179

JW3467	gor	glutathione oxidoreductase	GO:0005737 cytoplasm	-0.112	0	0	18	1179
JW0738	gpmA	phosphoglyceromutase 1		0 -0.568	0	0	18	1173
JW4285	uxuA	mannonate hydrolase		0 -0.402	0	0	20	1169
JW3393	glgC	glucose-1-phosphate	GO:0005737 cytoplasm	-0.267	0	0	17	1166
JW2424	yfeX	conserved protein		0 -0.322	0	0	18	1161
JW0739	galM	galactose-1-epimerase (mutarotase)	GO:0042597 periplasmic space	-0.466	0	0	14	1158
JW2972	yghA	predicted glutathionylspermidine synthase, with NAD(P)-binding Rossmann-fold domain		0 -0.178	0	0	16	1158
JW3947	rplA	50S ribosomal subunit protein L1	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.109	0	0	15	1155
JW1322	mppA	murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit - - periplasmic-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) - - GO:0042597 periplasmic space	-0.339	0	0	20	1154
JW1510	lsrF	predicted aldolase		0 -0.097	0	0	15	1154
JW0232	proB	gamma-glutamate kinase	GO:0005737 cytoplasm	0.007	1	0	20	1153
JW1194	yehF	predicted GTP-binding protein		0 -0.163	0	0	16	1149
JW3116	yraM	conserved protein		0 -0.272	0	0	23	1149
JW0150	hemL	glutamate-1-semialdehyde aminotransferase (aminomutase)		0 0.202	1	0	16	1146
JW1768	gapA	glyceraldehyde-3-phosphate dehydrogenase A	GO:0005737 cytoplasm	-0.133	0	0	20	1145
JW3706	pstS	phosphate transporter subunit - - periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.217	1	1	19	1138
JW1605	manA	mannose-6-phosphate isomerase	GO:0030113 capsule (sensu Bacteria) - - GO:0005737 cytoplasm	-0.126	0	0	15	1137
JW2797	ptsP	fused PEP-protein phosphotransferase (enzyme I) of PTS system		0 -0.094	0	0	23	1137
JW0823	dacC	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)	GO:0042597 periplasmic space	-0.078	0	0	15	1136
JW0714	sdhB	succinate dehydrogenase, FeS subunit	GO:0005737 cytoplasm	-0.299	0	0	15	1134
JW3775	hemX	uroporphyrinogen III methylase		0 -0.435	1	1	17	1134
JW2560	srmB	ATP-dependent RNA helicase	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.557	0	0	20	1133
JW5092	gltl	glutamate and aspartate transporter subunit - - periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.473	0	0	15	1133
JW3563	selB	selenocysteinyl-tRNA-specific translation factor	GO:0005737 cytoplasm	-0.354	0	0	23	1132
JW5414	ffh	Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)		0 -0.243	0	0	20	1132
JW3561	aldB	aldehyde dehydrogenase B		0 -0.116	0	0	15	1130

JW4011	qor	quinone oxidoreductase, NADPH-dependent	0	-0.059	0	0	17	1130
JW0229	frsA	hydrolase, binds to enzyme IIA(Glc)	0	-0.330	0	0	22	1128
JW2026	rfbB	dTDP-glucose 4,6 dehydratase, NAD(P)-binding	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.449	0	0	19	1128
JW0409	yajO	predicted oxidoreductase, NAD(P)-	0	-0.404	0	0	19	1127
JW4092	cadA	lysine decarboxylase 1	GO:0005737 cytoplasm	-0.260	0	0	24	1120
JW3711	atpG	F1 sector of membrane-bound ATP synthase, gamma subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.227	1	0	21	1116
JW2461	purC	phosphoribosylaminoimidazole-succinocarboxamide synthetase	GO:0005737 cytoplasm	-0.370	0	0	16	1114
JW0120	gcd	glucose dehydrogenase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.071	1	5	19	1109
JW4197	nrdD	anaerobic ribonucleoside-triphosphate reductase	0	-0.454	0	0	22	1104
JW4132	hflK	modulator for HflB protease specific for phage lambda cII repressor	0	-0.632	1	1	16	1102
JW5403	der	predicted GTP-binding protein	0	-0.334	0	0	19	1102
JW0663	nagA	N-acetylglucosamine-6-phosphate deacetylase	0	0.080	1	0	17	1097
JW2568	yfiQ	fused predicted acyl-CoA synthetase NAD(P)-binding subunit -!- ATP-binding subunit	0	-0.119	0	0	22	1097
JW5020	fadE	acyl coenzyme A dehydrogenase	0	0.006	1	2	22	1097
JW0083	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase	GO:0009274 cell wall (sensu Bacteria)	-0.051	0	0	18	1096
JW0452	acrA	multidrug efflux system	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.256	1	0	15	1092
JW2233	glpQ	periplasmic glycerophosphodiester phosphodiesterase	GO:0042597 periplasmic space	-0.553	0	0	19	1089
JW2876	pepP	proline aminopeptidase P II	0	-0.308	0	0	16	1089
JW1729	nadE	NAD synthetase, NH3/glutamine-	0	-0.370	0	0	15	1084
JW2229	nrdB	ribonucleoside diphosphate reductase 1, beta subunit, ferritin-like	0	-0.275	0	0	18	1084
JW3396	asd	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	0	-0.029	0	0	14	1082
JW1838	purT	phosphoribosylglycinamide formyltransferase 2	GO:0005737 cytoplasm	0.056	1	0	15	1077
JW2307	argT	lysine/arginine/ornithine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.231	0	0	14	1068
JW3985	pgi	glucosephosphate isomerase	GO:0005737 cytoplasm	-0.268	0	0	21	1067
JW1750	gdhA	glutamate dehydrogenase, NADP-	GO:0005737 cytoplasm	-0.158	0	0	18	1066
JW3347	trpS	tryptophanyl-tRNA synthetase	GO:0005737 cytoplasm	-0.320	0	0	16	1065
JW0627	dacA	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)	GO:0019866 inner membrane	-0.137	1	0	17	1058

JW2021	glf	UDP-galactopyranose mutase, FAD/NAD(P)-binding	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria)	-0.545	0	0	18	1058
JW2479	yfgC	predicted peptidase	0	-0.383	0	0	15	1055
JW1079	fabG	3-oxoacyl-[acyl-carrier-protein]	GO:0005737 cytoplasm	0.100	1	0	11	1054
JW1650	purR	DNA-binding transcriptional repressor, hypoxanthine-binding	GO:0005737 cytoplasm	-0.240	0	0	19	1054
JW2121	dld	D-lactate dehydrogenase, FAD-binding, NADH independent	GO:0005737 cytoplasm	-0.445	0	0	24	1052
JW0161	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	GO:0005737 cytoplasm	-0.054	0	0	15	1049
JW5287	ynjE	predicted thiosulfate sulfur transferase	0	-0.455	0	0	14	1048
JW1078	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	GO:0005737 cytoplasm	0.154	1	0	12	1039
JW2580	pheA	fused chorismate mutase P -!- prephenate dehydratase	GO:0005737 cytoplasm	-0.168	0	0	18	1039
JW2669	recA	DNA strand exchange and recombination protein with protease and	GO:0005737 cytoplasm	-0.175	0	0	14	1038
JW3823	pepQ	proline dipeptidase	0	-0.241	0	0	16	1038
JW0003	thrC	threonine synthase	GO:0005737 cytoplasm	-0.097	0	0	14	1037
JW2496	yfgL	protein assembly complex, lipoprotein component	0	0.009	1	0	13	1036
JW4131	hflX	predicted GTPase	0	-0.332	0	0	20	1036
JW0598	ahpC	alkyl hydroperoxide reductase, C22 subunit	0	-0.278	0	0	12	1033
JW3979	metH	homocysteine-N5-methyltetrahydrofolate transmethylase,	0	-0.249	0	0	23	1031
JW1238	oppD	oligopeptide transporter subunit -!- ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.009	0	0	17	1030
JW2873	gcvT	aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex	0	-0.159	0	0	15	1030
JW3249	fmt	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	GO:0005737 cytoplasm	-0.060	0	0	12	1030
JW1281	fabI	enoyl-[acyl-carrier-protein] reductase, NADH-dependent	GO:0005737 cytoplasm	0.163	1	0	15	1029
JW3708	glmU	fused N-acetyl glucosamine-1-phosphate uridylyltransferase -!- glucosamine-1-phosphate acetyl	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737	-0.176	0	0	16	1026
JW0030	carA	carbamoyl phosphate synthetase small subunit, glutamine amidotransferase	0	-0.199	0	0	14	1025
JW1403	ydbC	predicted oxidoreductase, NAD(P)-	0	0.047	1	0	13	1025
JW1439	ydcW	medium chain aldehyde dehydrogenase	0	-0.029	0	0	14	1024
JW5187	dhaK	dihydroxyacetone kinase, N-terminal domain	0	-0.113	0	0	14	1022
JW0463	adk	adenylate kinase	GO:0005737 cytoplasm	-0.383	0	0	16	1021

JW3220	mreB	cell wall structural complex MreBCD, actin-like component MreB	0	0.057	1	0	15	1019
JW1164	minD	membrane ATPase of the MinC-MinD-MinE system	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.118	1	0	16	1018
JW2892	fbaA	fructose-bisphosphate aldolase, class II	0	-0.224	0	0	13	1014
JW0716	sucB	dihydrolipoyltranssuccinase	0	-0.217	0	0	15	1013
JW1629	tyrS	tyrosyl-tRNA synthetase	GO:0005737 cytoplasm	-0.334	0	0	15	1012
JW5273	sufB	component of SufBCD complex	0	-0.298	0	0	16	1008
JW1081	fabF	3-oxoacyl-[acyl-carrier-protein] synthase	GO:0005737 cytoplasm	0.002	1	0	14	1007
JW0785	ybiB	predicted transferase/phosphorylase	0	-0.165	0	0	14	1003
JW0847	artI	arginine transporter subunit - - periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.329	0	0	13	999
JW4014	tyrB	tyrosine aminotransferase, tyrosine-repressible, PLP-dependent	GO:0005737 cytoplasm	0.009	1	0	16	997
JW1177	ycgB	conserved protein	0	-0.613	0	0	18	994
JW3395	glgB	1,4-alpha-glucan branching enzyme	GO:0005737 cytoplasm	-0.509	0	0	23	993
JW0722	cydA	cytochrome d terminal oxidase, subunit I	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.397	1	9	16	990
JW0931	ycbY	predicted methyltransferase	0	-0.359	0	0	23	990
JW1037	mdoH	glucan biosynthesis: glycosyl transferase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.046	1	6	18	989
JW3434	zntA	zinc, cobalt and lead efflux system	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.282	1	5	17	986
JW0404	ribD	fused diaminohydroxyphosphoribosylaminopyrimidine deaminase - - 5-amino-6-(5-phosphoribosylamino) uracil reductase	0	-0.229	0	0	18	985
JW0737	aroG	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine repressible	0	-0.182	0	0	14	985
JW0928	pyrD	dihydro-oroate oxidase, FMN-linked	GO:0005737 cytoplasm	-0.110	0	0	17	984
JW1803	sdaA	L-serine deaminase I	0	-0.051	0	0	18	983
JW5343	gatY	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit	0	-0.091	0	0	16	983
JW0180	accA	acetylCoA carboxylase, carboxytransferase, alpha subunit	GO:0005737 cytoplasm	-0.233	0	0	16	978
JW5067	ybbN	predicted thioredoxin domain-containing protein	0	-0.242	0	0	14	976
JW0940	ompA	outer membrane protein A (3a;II*;G;d)	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.339	1	0	14	975
JW1375	ldhA	fermentative D-lactate dehydrogenase, NAD-dependent	0	-0.101	0	0	15	974
JW2119	yehZ	predicted transporter subunit - - periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.066	0	0	14	972

JW3887	pfkA	6-phosphofructokinase I	GO:0005737 cytoplasm	0.000	1	0	16	972
JW0361	hemB	porphobilinogen synthase	0	-0.125	0	0	19	971
JW3298	bfr	bacterioferritin, iron storage and detoxification protein	GO:0005737 cytoplasm	-0.472	0	0	12	971
JW5146	ycdW	2-ketoacid reductase	0	-0.258	0	0	14	970
JW0811	moeA	molybdopterin biosynthesis protein	0	0.027	1	0	13	969
JW0963	appA	phosphoanhydride phosphorylase	GO:0042597 periplasmic space	-0.157	0	0	14	969
JW0212	lpcA	D-sedoheptulose 7-phosphate	GO:0005737 cytoplasm	-0.062	0	0	13	965
JW2517	suhB	inositol monophosphatase	GO:0005737 cytoplasm	-0.171	0	0	16	965
JW2462	nlpB	lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.265	1	0	16	962
JW0662	nagC	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.006	0	0	19	958
JW0029	dapB	dihydrodipicolinate reductase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	0.019	1	0	18	955
JW2640	ygaU	predicted protein	0	-0.458	0	0	14	954
JW2312	folC	bifunctional folylpolyglutamate synthase -!- dihydrofolate synthase	0	0.004	1	0	16	953
JW1077	fabH	3-oxoacyl-[acyl-carrier-protein] synthase	GO:0005737 cytoplasm	0.143	1	0	11	952
JW0796	glnH	glutamine transporter subunit -!- periplasmic binding component of ABC superfamily	GO:0042597 periplasmic space	-0.233	0	0	12	950
JW1806	manX	fused mannose-specific PTS enzyme IIAB components	GO:0005737 cytoplasm	-0.058	0	0	15	950
JW2703	mutS	methyl-directed mismatch repair protein	GO:0005737 cytoplasm	-0.238	0	0	19	950
JW1714	yniA	predicted phosphotransferase/kinase	0	-0.314	0	0	13	947
JW0750	ybhE	6-phosphogluconolactonase	0	-0.224	0	0	13	946
JW0871	trxB	thioredoxin reductase, FAD/NAD(P)-binding	GO:0005737 cytoplasm	-0.193	0	0	12	946
JW5280	pfkB	6-phosphofructokinase II	GO:0005737 cytoplasm	0.012	1	0	14	946
JW0746	modA	molybdate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.020	0	0	15	945
JW5058	yajQ	predicted nucleotide binding protein	0	-0.454	0	0	12	944
JW3352	aroB	3-dehydroquinate synthase	0	0.168	1	0	14	941
JW1447	yncE	conserved protein	0	-0.269	0	0	16	940
JW3619	yicC	conserved protein	0	-0.442	0	0	14	940
JW0413	thil	sulfurtransferase required for thiamine and 4-thiouridine biosynthesis	0	-0.222	0	0	19	932
JW0897	msbA	fused lipid transporter subunits -!- membrane component and ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.113	1	5	17	932
JW0164	rpsB	30S ribosomal subunit protein S2	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.268	0	0	13	931
JW3454	yhil	predicted HlyD family secretion protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.161	1	1	16	931
JW5243	ydeN	conserved protein	0	-0.575	0	0	16	931

JW0985	cbpA	curved DNA-binding protein, DnaJ homologue that functions as a co-chaperone of DnaK	GO:0005737 cytoplasm	-0.592	0	0	15	927
JW3753	rhIB	ATP-dependent RNA helicase	0	-0.346	0	0	18	927
JW5526	garR	tartronate semialdehyde reductase	0	0.264	1	0	14	927
JW0655	ybeX	predicted ion transport	GO:0009274 cell wall (sensu	-0.372	0	0	16	923
JW2914	gshB	glutathione synthetase	0	-0.261	0	0	12	923
JW3583	gpsA	glycerol-3-phosphate dehydrogenase (NAD+)	GO:0005737 cytoplasm	-0.025	0	0	13	923
JW0080	mraW	S-adenosyl-dependent methyltransferase activity on	0	-0.397	0	0	15	917
JW3250	rsmB	16S rRNA m5C967 methyltransferase, S-adenosyl-L-methionine-dependent	GO:0005737 cytoplasm	-0.394	0	0	16	915
JW4191	fbp	fructose-1,6-bisphosphatase I	GO:0005737 cytoplasm	-0.222	0	0	13	915
JW1753	selD	selenophosphate synthase	GO:0005737 cytoplasm	0.068	1	0	14	914
JW5522	tdcE	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	GO:0005737 cytoplasm	-0.294	0	0	21	911
JW0162	glnD	uridylyltransferase	GO:0005737 cytoplasm	-0.294	0	0	19	910
JW4192	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-	GO:0009274 cell wall (sensu Bacteria)	-0.051	0	0	18	910
JW1297	pspA	regulatory protein for phage-shock-protein operon	GO:0005737 cytoplasm	-0.722	0	0	15	907
JW2987	parC	DNA topoisomerase IV, subunit A	GO:0005737 cytoplasm	-0.369	0	0	20	905
JW0932	uup	fused predicted transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.467	0	0	20	899
JW3258	rpsD	30S ribosomal subunit protein S4	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.664	0	0	17	898
JW2024	rfaA	glucose-1-phosphate thymidyltransferase	GO:0005737 cytoplasm	-0.193	0	0	16	896
JW2483	upp	uracil phosphoribosyltransferase	0	0.073	1	0	11	896
JW3819	ubiD	3-octaprenyl-4-hydroxybenzoate decarboxylase	0	-0.248	0	0	17	896
JW2134	yeiA	predicted oxidoreductase	0	-0.111	0	0	16	893
JW4012	dnaB	replicative DNA helicase	GO:0005737 cytoplasm	-0.415	0	0	19	893
JW0660	asnB	asparagine synthetase B	GO:0005737 cytoplasm	-0.356	0	0	19	891
JW1963	amn	AMP nucleosidase	GO:0042597 periplasmic space	-0.295	0	0	16	890
JW1051	grxB	glutaredoxin 2 (Grx2)	0	-0.264	0	0	12	885
JW0665	nagE	fused N-acetyl glucosamine specific PTS enzyme IICBA components	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.584	1	10	15	883
JW3625	spoT	bifunctional (p)ppGpp synthetase II -!- guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase	GO:0005737 cytoplasm	-0.332	0	0	21	881
JW1253	trpB	tryptophan synthase, beta subunit	GO:0005737 cytoplasm	-0.191	0	0	16	880

JW3265	rpsE	30S ribosomal subunit protein S5	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.101	0	0	14	880
JW2385	glk	glucokinase	GO:0005737 cytoplasm	0.154	1	0	13	879
JW0804	ybiT	fused predicted transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.381	0	0	17	878
JW2174	yejK	nucleotide associated protein	GO:0005737 cytoplasm	-0.364	0	0	12	878
JW0410	dxs	1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, FAD-requiring	0	-0.081	0	0	15	872
JW2027	galF	predicted subunit with GalU	GO:0005737 cytoplasm	-0.092	0	0	14	872
JW5185	dhaH	fused predicted dihydroxyacetone-specific PTS enzyme HPr component -!- EI component	0	-0.017	0	0	14	872
JW4286	uxuB	D-mannonate oxidoreductase, NAD-	0	-0.141	0	0	15	871
JW3379	malQ	4-alpha-glucanotransferase (amylomaltase)	GO:0005737 cytoplasm	-0.393	0	0	19	869
JW3786	uvrD	DNA-dependent ATPase I and helicase	GO:0005737 cytoplasm	-0.458	0	0	18	869
JW5394	ucpA	predicted oxidoreductase, sulfate metabolism protein	0	0.046	1	0	14	867
JW1950	hchA	Hsp31 molecular chaperone	0	-0.224	0	0	12	866
JW4180	ytfN	conserved protein	0	-0.183	1	1	17	866
JW0347	frmA	alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase	GO:0005737 cytoplasm	-0.012	0	0	14	864
JW2755	relA	(p)ppGpp synthetase I/GTP pyrophosphokinase	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.337	0	0	20	864
JW5260	ynfF	oxidoreductase subunit	0	-0.447	0	0	17	864
JW3392	glgA	glycogen synthase	GO:0005737 cytoplasm	0.003	1	0	14	863
JW3495	yhjJ	predicted zinc-dependent peptidase	0	-0.340	0	0	16	862
JW0742	galE	UDP-galactose-4-epimerase	GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.311	0	0	12	861
JW2257	menB	dihydroxynaphthoic acid synthetase	0	-0.340	0	0	14	861
JW2773	fucl	L-fucose isomerase	0	-0.260	0	0	14	861
JW2956	gss	fused glutathionylspermidine amidase -!- glutathionylspermidine synthetase	0	-0.342	1	1	15	858
JW3389	glpD	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-	GO:0005737 cytoplasm	-0.384	0	0	25	858
JW2363	dsdA	D-serine ammonia-lyase	GO:0005737 cytoplasm	-0.087	0	0	14	857
JW1672	sufC	component of SufBCD complex, ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.205	0	0	14	856
JW2075	gatD	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding	0	0.139	1	0	12	855
JW2577	yfiO	predicted lipoprotein	0	-0.484	0	0	14	852
JW0396	tgt	tRNA-guanine transglycosylase	GO:0005737 cytoplasm	-0.412	0	0	15	851

JW1509	lsrB	A12 transporter -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.151	0	0	9	849
JW2313	accD	acetylCoA carboxylase, beta (carboxyltransferase) subunit	GO:0005737 cytoplasm	-0.129	0	0	15	847
JW3911	metL	fused aspartokinase II -!- homoserine dehydrogenase II	0	-0.101	0	0	16	846
JW1116	phoP	DNA-binding response regulator in two-component regulatory system with	GO:0005737 cytoplasm	-0.257	0	0	12	844
JW1889	araF	L-arabinose transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.186	0	0	17	843
JW2635	ygaF	predicted enzyme	0	-0.085	0	0	16	842
JW5932	hemC	hydroxymethylbilane synthase	0	-0.066	0	0	14	838
JW1648	sodB	superoxide dismutase, Fe	GO:0005737 cytoplasm	-0.169	0	0	11	834
JW3279	rplB	50S ribosomal subunit protein L2	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.699	0	0	14	834
JW5437	rpoS	RNA polymerase, sigma S (sigma 38) factor	GO:0005737 cytoplasm	-0.460	0	0	14	834
JW4161	rplI	50S ribosomal subunit protein L9	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	0.091	1	0	13	833
JW0600	uspG	universal stress protein UP12	0	-0.053	0	0	10	832
JW1224	galU	glucose-1-phosphate uridylyltransferase	GO:0030113 capsule (sensu	0.031	1	0	11	832
JW3403	yhhX	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	0	-0.346	0	0	13	831
JW1252	trpA	tryptophan synthase, alpha subunit	GO:0005737 cytoplasm	0.123	1	0	12	829
JW3492	yhjG	predicted outer membrane biogenesis protein	0	-0.227	1	1	18	829
JW3564	selA	selenocysteine synthase	GO:0005737 cytoplasm	-0.055	0	0	20	829
JW0167	frr	ribosome recycling factor	GO:0005737 cytoplasm	-0.534	0	0	12	828
JW2594	grpE	heat shock protein	GO:0005737 cytoplasm	-0.372	0	0	14	828
JW2049	asmA	predicted assembly protein	0	-0.422	1	1	18	827
JW2487	ppx	exopolyphosphatase	0	-0.239	0	0	19	827
JW1627	gst	glutathionine S-transferase	0	-0.220	0	0	12	826
JW2484	purM	phosphoribosylaminoimidazole	GO:0005737 cytoplasm	0.034	1	0	10	823
JW3025	glnE	fused deadenylyltransferase -!- adenylyltransferase for glutamine synthetase	0	-0.317	0	0	19	823
JW0384	rdgC	DNA-binding protein, non-specific	GO:0005737 cytoplasm	-0.222	0	0	12	822
JW0740	galK	galactokinase	GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.105	0	0	13	822
JW5581	ubiE	bifunctional 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase -!- S-adenosylmethionine:2-DMK methyltransferase	0	-0.168	0	0	12	822
JW0129	panC	pantothenate synthetase	GO:0005737 cytoplasm	-0.108	0	0	15	820

JW1317	tpx	lipid hydroperoxide peroxidase	GO:0042597 periplasmic space	0.256	1	0	9	820
JW3270	rplE	50S ribosomal subunit protein L5	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.282	0	0	10	820
JW1474	adhP	alcohol dehydrogenase, 1-propanol preferring	0	0.103	1	0	14	818
JW5702	crp	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.225	0	0	13	818
JW1054	yceH	conserved protein	0	-0.424	0	0	12	810
JW1611	hdhA	7alpha-hydroxysteroid dehydrogenase, NAD-dependent	GO:0005737 cytoplasm	0.139	1	0	14	810
JW2510	hscA	DnaK-like molecular chaperone specific for IscU	GO:0005737 cytoplasm	-0.028	0	0	19	804
JW3725	yieN	fused predicted transcriptional	0	-0.219	0	0	16	803
JW2505	sseA	3-mercaptopyruvate sulfurtransferase	0	-0.083	0	0	12	802
JW3267	rplF	50S ribosomal subunit protein L6	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.227	0	0	10	799
JW3822	fadB	fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase -!- 3-hydroxyacyl-CoA dehydrogenase	0	-0.094	0	0	21	798
JW3862	fdhE	formate dehydrogenase formation	0	-0.289	0	0	12	798
JW3485	gadA	glutamate decarboxylase A, PLP-dependent	GO:0005737 cytoplasm	-0.278	0	0	14	795
JW1938	yedP	conserved protein	0	-0.256	0	0	12	794
JW3879	sodA	superoxide dismutase, Mn	GO:0005737 cytoplasm	-0.429	0	0	11	794
JW5492	yghU	predicted S-transferase	0	-0.403	1	1	12	794
JW0659	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase	0	0.027	1	0	13	791
JW2536	hmp	fused nitric oxide dioxygenase -!- dihydropteridine reductase 2	0	-0.290	0	0	13	791
JW3180	gltD	glutamate synthase, 4Fe-4S protein, small subunit	0	-0.313	0	0	16	791
JW2497	yfgM	conserved protein	0	-0.222	1	1	13	790
JW0385	mak	manno(fructo)kinase	0	-0.202	0	0	12	788
JW4172	cysQ	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase	0	-0.251	0	0	11	787
JW0989	wrbA	predicted flavoprotein in Trp regulation	GO:0005737 cytoplasm	-0.082	0	0	9	786
JW1886	otsB	trehalose-6-phosphate phosphatase, biosynthetic	GO:0005737 cytoplasm	-0.145	0	0	12	786
JW3938	btuB	vitamin B12/cobalamin outer membrane transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.534	1	0	17	785

JW5786	yjiM	predicted 2-hydroxyglutaryl-CoA dehydratase		0	-0.187	0	0	12	785
JW4338	osmY	periplasmic protein	GO:0042597 periplasmic space		-0.292	0	0	9	782
JW0101	guaC	GMP reductase	GO:0005737 cytoplasm		-0.068	0	0	12	781
JW1532	ydfG	L-allo-threonine dehydrogenase, NAD(P)-binding		0	-0.175	0	0	12	779
JW3315	yheS	fused predicted transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm		-0.463	0	0	18	779
JW3213	tldD	predicted peptidase		0	-0.123	0	0	14	778
JW1816	kdgR	predicted DNA-binding transcriptional regulator	GO:0005737 cytoplasm		-0.278	0	0	13	775
JW4068	phnB	conserved protein		0	-0.243	0	0	12	774
JW0623	lipA	lipoate synthase	GO:0005737 cytoplasm		-0.330	0	0	15	772
JW1427	ydcL	predicted lipoprotein		0	-0.268	0	0	11	771
JW2291	yfbU	conserved protein		0	-0.579	0	0	14	771
JW0105	nadC	quinolinate phosphoribosyltransferase		0	-0.234	0	0	14	770
JW1595	pntA	pyridine nucleotide transhydrogenase, alpha subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.273	1	5	13	769
JW4169	ytfG	NAD(P)H:quinone oxidoreductase		0	0.052	1	0	12	769
JW2140	folE	GTP cyclohydrolase I		0	-0.121	0	0	13	768
JW3896	glpX	fructose 1,6-bisphosphatase II	GO:0005737 cytoplasm		-0.016	0	0	14	768
JW0893	cmk	cytidylate kinase	GO:0005737 cytoplasm		0.000	0	0	11	766
JW2662	luxS	S-ribosylhomocysteinease		0	-0.323	0	0	10	765
JW1419	ydcJ	conserved protein		0	-0.461	0	0	15	763
JW3148	greA	transcription elongation factor	GO:0005737 cytoplasm		-0.366	0	0	13	762
JW3948	rplJ	50S ribosomal subunit protein L10	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm		0.045	1	0	10	762
JW5556	gldA	glycerol dehydrogenase, NAD		0	0.171	1	0	10	762
JW0145	mrcB	fused glycosyl transferase -!- transpeptidase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.419	1	1	16	761
JW0664	nagB	glucosamine-6-phosphate deaminase		0	-0.185	0	0	12	761
JW2770	fucO	L-1,2-propanediol oxidoreductase		0	0.086	1	0	14	761
JW3309	fkpA	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	GO:0042597 periplasmic space		-0.458	0	0	12	761
JW4358	ytjC	phosphoglyceromutase 2, co-factor independent	GO:0005737 cytoplasm		-0.371	1	1	12	761
JW5656	tiaE	2-keto-D-gluconate reductase (glyoxalate reductase) (2-ketoaldonate	GO:0005737 cytoplasm		0.005	1	0	12	759
JW0567	nfnB	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive		0	-0.211	0	0	14	757
JW0835	nfsA	nitroreductase A, NADPH-dependent, FMN-dependent		0	-0.155	0	0	12	755
JW3303	rpsG	30S ribosomal subunit protein S7	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm		-0.460	0	0	13	755

JW3441	nikA	nickel transporter subunit -!- periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.261	0	0	18	754
JW5836	cld	regulator of length of O-antigen component of lipopolysaccharide chains	0	-0.265	1	2	11	754
JW3747	ilvC	ketol-acid reductoisomerase, NAD(P)-binding	GO:0005737 cytoplasm	-0.205	0	0	17	753
JW3722	asnA	asparagine synthetase A	GO:0005737 cytoplasm	-0.289	0	0	13	752
JW5126	ycbX	predicted 2Fe-2S cluster-containing	0	-0.180	0	0	12	749
JW2998	parE	DNA topoisomerase IV, subunit B	GO:0005737 cytoplasm	-0.345	0	0	13	748
JW2410	crr	glucose-specific enzyme IIA component of PTS	GO:0005737 cytoplasm	0.057	1	0	11	747
JW2563	yfiD	pyruvate formate lyase subunit	0	-0.332	0	0	10	747
JW0014	dnaJ	chaperone Hsp40, co-chaperone with DnaK	GO:0005737 cytoplasm	-0.634	0	0	11	746
JW0163	map	methionine aminopeptidase	0	-0.162	0	0	11	744
JW0372	ddlA	D-alanine-D-alanine ligase A	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	0.016	1	0	14	744
JW0454	kefA	fused mechanosensitive channel proteins	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.031	1	12	15	744
JW2205	rscB	DNA-binding response regulator in two-component regulatory system with RcsC and YojN	GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm	0.021	1	0	11	739
JW3198	sspA	stringent starvation protein A	GO:0005737 cytoplasm	-0.265	0	0	9	738
JW3714	atpF	F0 sector of membrane-bound ATP synthase, subunit b	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.213	1	1	9	737
JW3933	oxyR	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.088	0	0	13	735
JW2434	eutB	ethanolamine ammonia-lyase, large subunit, heavy chain	0	-0.070	0	0	15	732
JW0086	murD	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	0.005	1	1	12	731
JW2925	yggN	predicted protein	0	-0.469	0	0	12	731
JW3276	rpsC	30S ribosomal subunit protein S3	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.422	0	0	14	728
JW1225	hns	global DNA-binding transcriptional dual regulator H-NS	GO:0019861 flagellum -!- GO:0005737 cytoplasm	-0.751	0	0	9	726
JW3683	yidC	cytoplasmic insertase into membrane protein, Sec system	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.122	1	4	11	726
JW1654	ribC	riboflavin synthase, alpha subunit	0	-0.100	0	0	12	725
JW3774	hemY	predicted protoheme IX synthesis	0	-0.362	1	2	15	725
JW0638	ybeL	conserved protein	0	-0.604	0	0	10	724
JW3159	yrbC	predicted ABC-type organic solvent transporter	GO:0005737 cytoplasm	-0.416	0	0	11	723
JW3260	rpsM	30S ribosomal subunit protein S13	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.424	0	0	10	722

JW4133	hflC	modulator for HflB protease specific for phage lambda cII repressor	0	-0.365	1	1	12	721
JW1411	ycdF	conserved protein	0	-0.143	0	0	11	720
JW3026	ygiF	predicted adenylate cyclase	0	-0.260	0	0	17	720
JW4031	nrfA	nitrite reductase, formate-dependent, cytochrome	GO:0042597 periplasmic space	-0.589	0	0	13	720
JW2463	dapA	dihydrodipicolinate synthase	GO:0005737 cytoplasm	0.067	1	0	11	719
JW2988	ygiS	predicted transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.374	0	0	16	719
JW0885	pflA	pyruvate formate lyase activating enzyme 1	GO:0005737 cytoplasm	-0.361	0	0	15	718
JW2802	tas	predicted oxidoreductase, NADP(H)-dependent aldo-keto reductase	0	-0.323	0	0	12	716
JW1754	ydjA	predicted oxidoreductase	0	-0.168	0	0	9	713
JW4333	rsmC	16S RNA m2G1207 methylase	GO:0005737 cytoplasm	-0.111	0	0	12	713
JW5761	yjgB	predicted alcohol dehydrogenase, Zn-dependent and NAD(P)-binding	0	0.039	1	0	10	713
JW1656	ydhQ	conserved protein	0	0.025	1	0	11	712
JW1912	amyA	cytoplasmic alpha-amylase	GO:0005737 cytoplasm	-0.381	0	0	13	712
JW2316	usg	predicted semialdehyde dehydrogenase	0	0.061	1	0	10	711
JW3052	fadH	2,4-dienoyl-CoA reductase, NADH and FMN-linked	0	-0.064	0	0	15	710
JW4203	pyrI	aspartate carbamoyltransferase, regulatory subunit	GO:0005737 cytoplasm	-0.273	0	0	12	709
JW0460	ybaB	conserved protein	0	-0.473	0	0	8	707
JW0474	ybaS	predicted glutaminase	0	0.057	1	0	11	707
JW1700	btuE	predicted glutathione peroxidase	GO:0042597 periplasmic space	-0.131	0	0	8	707
JW0744	modE	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.021	0	0	11	705
JW1615	add	adenosine deaminase	0	-0.024	0	0	14	705
JW2204	rcsD	phosphotransfer intermediate protein in two-component regulatory system with RcsBC	0	-0.234	1	1	15	705
JW0891	aroA	5-enolpyruvylshikimate-3-phosphate synthetase	0	-0.005	0	0	17	702
JW2465	bcp	thiol peroxidase, thioredoxin-dependent	GO:0005737 cytoplasm	-0.431	0	0	10	700
JW3168	yhbG	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.124	0	0	10	698
JW3945	nusG	transcription termination factor	GO:0005737 cytoplasm	-0.391	0	0	10	698
JW1112	potA	polyamine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.338	0	0	12	697
JW1769	yeaD	conserved protein	0	-0.249	0	0	10	696
JW1998	yeeZ	predicted epimerase, with NAD(P)-binding Rossmann-fold domain	0	-0.100	0	0	11	696
JW3282	rplC	50S ribosomal subunit protein L3	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.235	0	0	12	693

JW4121	psd	phosphatidylserine decarboxylase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.093	1	0	10	693
JW5746	fkIB	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	0	-0.081	0	0	10	692
JW1200	lolB	chaperone for lipoproteins	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.644	1	0	12	691
JW3591	tdh	threonine 3-dehydrogenase, NAD(P)-binding	0	0.051	1	0	11	691
JW0732	ybgF	predicted protein	GO:0042597 periplasmic space	-0.468	0	0	10	690
JW2004	hisB	fused histidinol-phosphatase -!- imidazoleglycerol-phosphate	0	-0.365	0	0	13	689
JW0405	ribE	riboflavin synthase beta chain	0	0.294	1	0	7	688
JW1049	pyrC	dihydro-orotase	GO:0005737 cytoplasm	-0.123	0	0	15	687
JW0168	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0	-0.020	0	0	14	686
JW3324	fic	stationary-phase protein, cell division	0	-0.361	0	0	10	686
JW1106	cobB	deacetylase of acetyl-CoA synthetase, NAD-dependent	0	-0.354	0	0	9	685
JW3272	rplN	50S ribosomal subunit protein L14	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.128	0	0	8	685
JW3509	dppF	dipeptide transporter -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.428	0	0	11	685
JW3940	murB	UDP-N-acetylenolpyruvylglucosamine reductase, FAD-binding	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.204	0	0	12	685
JW5111	yliB	predicted peptide transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.253	0	0	14	679
JW5947	aroK	shikimate kinase I	0	-0.621	0	0	11	679
JW3150	obgE	GTPase involved in cell partitioning and DNA repair	0	-0.452	0	0	9	678
JW1738	xthA	exonuclease III	0	-0.555	0	0	14	677
JW5808	pcnB	poly(A) polymerase I	GO:0005737 cytoplasm	-0.531	0	0	17	676
JW0166	pyrH	uridylyate kinase	GO:0005737 cytoplasm	0.133	1	0	8	674
JW3368	ompR	DNA-binding response regulator in two-component regulatory system with EnvZ	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.346	0	0	12	674
JW0874	lolA	chaperone for lipoproteins	GO:0042597 periplasmic space	-0.492	0	0	8	673
JW0954	hyaA	hydrogenase 1, small subunit	GO:0019866 inner membrane	-0.205	1	2	10	672
JW1212	narL	DNA-binding response regulator in two-component regulatory system with NarX (or NarQ)	GO:0005737 cytoplasm	-0.153	0	0	12	672
JW0937	fabA	beta-hydroxydecanoyl thioester dehydrase	0	-0.012	0	0	10	669
JW0155	pfs	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	0	0.306	1	0	8	666

JW1202	prfA	peptide chain release factor RF-1	GO:0005737 cytoplasm	-0.660	0	0	17	666
JW1316	tyrR	DNA-binding transcriptional dual regulator, tyrosine-binding	GO:0005737 cytoplasm	-0.208	0	0	19	666
JW1250	yciF	conserved protein	0	-0.455	0	0	7	665
JW2748	ygcF	conserved protein	0	-0.260	0	0	10	664
JW4343	yjil	conserved protein	0	-0.280	0	0	13	664
JW0731	pal	peptidoglycan-associated outer membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.454	1	0	7	663
JW1670	sufS	selenocysteine lyase, PLP-dependent	0	-0.001	0	0	12	663
JW1839	eda	multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase -!- 2-keto-4-hydroxyglutarate aldolase -!- oxaloacetate decarboxylase	GO:0005737 cytoplasm	0.322	1	0	11	663
JW0570	ybdK	gamma-glutamyl:cysteine ligase	0	-0.224	0	0	9	662
JW2903	yggG	predicted peptidase	0	-0.204	0	0	8	661
JW3351	damX	predicted protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.935	1	1	15	661
JW1195	pth	peptidyl-tRNA hydrolase	GO:0005737 cytoplasm	-0.124	0	0	11	660
JW2964	hybA	hydrogenase 2 4Fe-4S ferredoxin-type component	0	-0.451	0	0	11	660
JW3194	nanA	N-acetylneuraminate lyase	0	-0.031	0	0	9	660
JW5692	hslO	heat shock protein Hsp33	0	-0.313	0	0	9	660
JW5756	yjgK	conserved protein	0	-0.249	0	0	10	660
JW0122	can	carbonic anhydrase	0	-0.231	0	0	10	658
JW2146	nfo	endonuclease IV with intrinsic 3'-5' exonuclease activity	0	-0.204	0	0	11	655
JW3624	rpoZ	RNA polymerase, omega subunit	GO:0005737 cytoplasm	-0.524	0	0	9	654
JW2131	cdd	cytidine/deoxycytidine deaminase	0	0.001	1	0	10	653
JW1263	yciK	predicted oxoacyl-(acyl carrier protein) reductase, EmrKY-TolC system	0	-0.321	0	0	11	652
JW4359	rob	DNA-binding transcriptional activator	GO:0005737 cytoplasm	-0.355	0	0	12	651
JW5854	yigL	predicted hydrolase	0	-0.185	0	0	12	651
JW0092	ftsA	ATP-binding cell division protein involved in recruitment of FtsK to Z ring	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.025	1	0	14	650
JW5733	yjdC	predicted transcriptional regulator	0	-0.305	0	0	12	648
JW2880	serA	D-3-phosphoglycerate dehydrogenase	GO:0005737 cytoplasm	0.025	1	0	13	647
JW2197	eco	ecotin, a serine protease inhibitor	GO:0042597 periplasmic space	-0.257	0	0	9	645
JW5240	ddpA	D-Ala-D-Ala transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.474	0	0	17	645
JW1264	sohB	predicted inner membrane peptidase	0	-0.354	1	2	12	644
JW0422	cyoA	cytochrome o ubiquinol oxidase subunit II	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.009	1	3	9	643
JW3402	yhhW	predicted protein	0	-0.471	0	0	12	642
JW0872	lrp	DNA-binding transcriptional dual regulator, leucine-binding	GO:0005737 cytoplasm	-0.420	0	0	10	640
JW1003	ycdO	conserved protein	0	-0.315	0	0	13	639

JW1968	erfK	conserved protein with NAD(P)-binding Rossmann-fold domain	0	-0.342	0	0	13	639
JW3510	dppD	dipeptide transporter -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.113	0	0	13	638
JW0822	yliJ	predicted glutathione S-transferase	0	-0.198	0	0	9	637
JW3263	rpIO	50S ribosomal subunit protein L15	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.250	0	0	9	637
JW3789	corA	magnesium/nickel/cobalt transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.156	1	2	11	636
JW4110	bIc	outer membrane lipoprotein (lipocalin)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.214	1	0	13	636
JW1087	ptsG	fused glucose-specific PTS enzyme IIBC components	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.618	1	10	11	635
JW1594	pntB	pyridine nucleotide transhydrogenase, beta subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.602	1	9	10	634
JW4186	ytfQ	predicted sugar transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.186	1	1	11	634
JW2100	mrp	antiporter inner membrane protein	0	-0.002	0	0	11	633
JW3176	elbB	isoprenoid biosynthesis protein with amidotransferase-like domain	0	0.267	1	0	8	633
JW3731	rbsK	ribokinase	GO:0005737 cytoplasm	0.046	1	0	10	633
JW3832	dsbA	periplasmic protein disulfide isomerase I	GO:0042597 periplasmic space	-0.131	0	0	9	632
JW2418	cysP	thiosulfate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.412	0	0	14	631
JW2565	yfiF	predicted methyltransferase	GO:0005737 cytoplasm	-0.682	0	0	12	630
JW0880	ycaC	predicted hydrolase	0	-0.127	0	0	8	628
JW1808	manZ	mannose-specific enzyme IID component of PTS	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.407	1	2	11	628
JW3713	atpH	F1 sector of membrane-bound ATP synthase, delta subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.063	1	0	8	628
JW3268	rpsH	30S ribosomal subunit protein S8	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.100	0	0	10	627
JW3531	glyQ	glycine tRNA synthetase, alpha subunit	GO:0005737 cytoplasm	-0.392	0	0	10	627
JW4049	alsB	D-allose transporter subunit -!- periplasmic-binding component of ABC	GO:0042597 periplasmic space	0.014	1	1	12	627
JW0803	ybiS	conserved protein	0	-0.116	1	1	10	626
JW1630	pdxH	pyridoxine 5'-phosphate oxidase	0	-0.621	0	0	12	626
JW1683	aroD	3-dehydroquininate dehydratase	0	0.065	1	0	12	626
JW2996	mdaB	NADPH quinone reductase	0	-0.356	0	0	11	626
JW0945	helD	DNA helicase IV	GO:0005737 cytoplasm	-0.413	0	0	18	625

JW1119	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	GO:0005737 cytoplasm	-0.285	0	0	12	625
JW2226	ubiG	bifunctional 3-demethylubiquinone-9 3-methyltransferase - - 2-octaprenyl-6-hydroxy phenol methylase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	-0.226	1	0	10	625
JW4125	yjeF	predicted carbohydrate kinase	0	-0.046	0	0	13	625
JW2301	yfcH	conserved protein with NAD(P)-binding Rossmann-fold domain	0	-0.060	0	0	13	624
JW2929	yggX	protein that protects iron-sulfur proteins against oxidative damage	0	-0.857	0	0	10	624
JW1767	yeaA	methionine sulfoxide reductase B	0	-0.738	0	0	10	623
JW2019	wbbI	conserved protein	0	-0.197	0	0	9	623
JW0078	fruR	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.346	0	0	12	622
JW4364	arcA	DNA-binding response regulator in two-component regulatory system with ArcB or CpxA	GO:0005737 cytoplasm	-0.487	0	0	10	622
JW3412	ggt	gamma-glutamyltranspeptidase	0	-0.220	0	0	13	621
JW5604	rep	DNA helicase and single-stranded DNA-dependent ATPase	GO:0005737 cytoplasm	-0.408	0	0	16	620
JW5829	infC	protein chain initiation factor IF-3	GO:0005737 cytoplasm	-0.671	0	0	9	620
JW0466	gsk	inosine/guanosine kinase	0	-0.346	0	0	14	619
JW3702	phoU	DNA-binding transcriptional regulator	0	-0.272	0	0	11	619
JW3864	fdoH	formate dehydrogenase-O, Fe-S subunit	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.361	1	0	12	616
JW2548	pdxJ	pyridoxine 5'-phosphate synthase	GO:0005737 cytoplasm	-0.091	0	0	10	615
JW1267	cysB	DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding	GO:0005737 cytoplasm	-0.077	0	0	11	614
JW3995	malK	fused maltose transport subunit, ATP-binding component of ABC superfamily - - regulatory protein	GO:0005737 cytoplasm	-0.030	0	0	12	614
JW3200	rplM	50S ribosomal subunit protein L13	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.540	0	0	9	613
JW2715	truD	pseudouridine synthase	0	-0.269	0	0	10	612
JW3216	rng	ribonuclease G	GO:0005737 cytoplasm	-0.279	0	0	15	612
JW0765	moaB	molybdopterin biosynthesis protein B	0	-0.225	0	0	8	611
JW1249	yciE	conserved protein	0	-0.409	0	0	9	611
JW5475	rpiA	ribosephosphate isomerase, constitutive	0	0.230	1	0	10	611
JW2002	hisD	bifunctional histidinal dehydrogenase - - histidinol dehydrogenase	0	-0.013	0	0	11	610
JW3119	yraP	predicted protein	GO:0042597 periplasmic space	0.045	1	1	8	608
JW0483	tesA	multifunctional acyl-CoA thioesterase I - - protease I - - lysophospholipase L1	GO:0042597 periplasmic space	-0.201	1	1	10	607
JW3040	ygfF	G/U mismatch-specific DNA	GO:0005737 cytoplasm	-0.298	0	0	9	606
JW5800	nadR	bifunctional DNA-binding transcriptional repressor - - NMN adenylyltransferase	0	-0.361	0	0	12	606

JW0401	tsx	nucleoside channel, receptor of phage T6 and colicin K	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.512	1	0	8	605
JW3630	yicH	conserved protein	0	-0.161	1	1	10	605
JW3997	malM	maltose regulon periplasmic protein	GO:0042597 periplasmic space	-0.021	0	0	9	605
JW5130	yccU	predicted CoA-binding protein with NAD(P)-binding Rossmann-fold domain	0	0.096	1	0	8	605
JW4158	rpsF	30S ribosomal subunit protein S6	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.745	0	0	9	604
JW1716	yniC	predicted hydrolase	0	0.102	1	0	13	601
JW1039	msyB	predicted protein	0	-0.833	0	0	6	600
JW0673	ybfF	conserved protein	0	-0.213	0	0	13	599
JW1477	osmC	osmotically inducible, stress-inducible membrane protein	0	-0.122	0	0	7	599
JW0779	ybhG	predicted membrane fusion protein (MFP) component of efflux pump, membrane anchor	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.364	1	1	10	597
JW0794	glnQ	glutamine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.138	0	0	8	597
JW1046	solA	N-methyltryptophan oxidase, FAD-	0	-0.234	0	0	11	597
JW3006	ygiC	predicted enzyme	0	-0.389	0	0	14	597
JW5282	astD	succinylglutamic semialdehyde dehydrogenase	0	-0.086	0	0	12	596
JW2326	aroC	chorismate synthase	0	-0.267	0	0	12	595
JW0669	fur	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.559	0	0	8	594
JW2861	dsbC	protein disulfide isomerase II	GO:0042597 periplasmic space	-0.103	0	0	10	594
JW0741	galT	galactose-1-phosphate uridylyltransferase	GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.524	0	0	13	593
JW3691	yieF	chromate reductase, Class I,	0	0.060	1	0	8	593
JW0849	ybjP	predicted lipoprotein	0	-0.459	0	0	6	592
JW2025	rfbD	dTDP-4-dehydrorhamnose reductase subunit, NAD(P)-binding, of dTDP-L-rhamnose synthase	GO:0005737 cytoplasm	-0.093	0	0	10	592
JW0443	ybaY	predicted outer membrane lipoprotein	0	0.176	1	0	5	591
JW5040	ykgC	predicted oxidoreductase with FAD/NAD(P)-binding domain and dimerization domain	0	-0.064	0	0	15	590
JW0202	gloB	predicted hydroxyacylglutathione hydrolase	0	-0.227	0	0	8	589
JW3115	yraL	predicted methyltransferase	0	-0.168	0	0	12	589
JW2513	iscU	scaffold protein	0	-0.355	0	0	8	587
JW3162	yrbF	predicted toluene transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	0.133	1	0	12	587

JW2001	hisG	ATP phosphoribosyltransferase	GO:0005737 cytoplasm	-0.145	0	0	9	586
JW2456	dapE	N-succinyl-diaminopimelate deacylase		0	-0.066	0	0	13
JW1853	yebC	conserved protein		0	-0.384	0	0	9
JW3097	garD	(D)-galactarate dehydrogenase		0	-0.014	0	0	14
JW5158	ycfP	conserved protein		0	-0.591	0	0	10
JW0304	betB	betaine aldehyde dehydrogenase, NAD-dependent		0	-0.079	0	0	15
JW3678	dnaN	DNA polymerase III, beta subunit	GO:0005737 cytoplasm		-0.133	0	0	14
JW5740	orn	oligoribonuclease		0	-0.372	0	0	11
JW0424	yajG	predicted lipoprotein		0	-0.090	0	0	6
JW1114	ycfD	conserved protein		0	-0.436	0	0	9
JW2407	cysK	cysteine synthase A, O-acetylserine sulfhydrylase A subunit	GO:0005737 cytoplasm		-0.078	0	0	10
JW4122	rsgA	ribosome small subunit-dependent GTPase A		0	-0.405	0	0	10
JW5578	fadA	3-ketoacyl-CoA thiolase (thiolase I)	GO:0005737 cytoplasm		0.131	1	0	12
JW0458	apt	adenine phosphoribosyltransferase	GO:0005737 cytoplasm		0.023	1	0	9
JW1241	cls	cardiolipin synthase 1	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.190	1	2	11
JW1834	ptrB	protease II		0	-0.507	0	0	12
JW2287	yfbQ	predicted aminotransferase		0	-0.163	0	0	13
JW2576	rluD	23S rRNA pseudouridine synthase	GO:0005737 cytoplasm		-0.416	0	0	12
JW4193	yjgA	conserved protein		0	-0.905	0	0	11
JW0905	mukF	Involved in chromosome partitioning, Ca2+ binding protein		0	-0.375	0	0	12
JW0554	ompT	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)		-0.645	1	0	15
JW2017	wbbK	lipopolysaccharide biosynthesis protein		0	-0.158	0	0	11
JW0159	yaeH	conserved protein		0	-0.811	0	0	10
JW1512	tam	trans-aconitate methyltransferase	GO:0005737 cytoplasm		-0.245	0	0	9
JW3838	hemN	coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen-		0	-0.346	0	0	12
JW2564	ung	uracil-DNA-glycosylase	GO:0005737 cytoplasm		-0.283	0	0	11
JW0786	ybiC	predicted dehydrogenase		0	-0.084	0	0	8
JW3038	dnaG	DNA primase	GO:0005737 cytoplasm		-0.389	0	0	16
JW5875	nuoB	NADH:ubiquinone oxidoreductase,	GO:0005737 cytoplasm		-0.320	0	0	11
JW2555	rseB	anti-sigma factor	GO:0005737 cytoplasm		-0.257	0	0	11
JW2889	yggE	conserved protein		0	-0.252	0	0	9
JW5950	yjbN	tRNA-dihydrouridine synthase A		0	-0.291	0	0	12
JW0130	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	GO:0005737 cytoplasm		0.138	1	0	9
JW1642	nemA	N-ethylmaleimide reductase, FMN-		0	-0.311	0	0	12
JW3413	yhhA	conserved protein		0	-1.049	0	0	7
JW5539	yhcB	conserved protein		0	-0.552	1	1	7
JW0181	ldcC	lysine decarboxylase 2, constitutive		0	-0.189	0	0	14

JW0661	nagD	UMP phosphatase		0	0.109	1	0	8	559
JW3281	rplD	50S ribosomal subunit protein L4	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm		-0.235	0	0	7	559
JW4114	frdB	fumarate reductase (anaerobic), Fe-S subunit	GO:0005737 cytoplasm		-0.224	0	0	8	559
JW5603	gpp	guanosine pentaphosphatase/exopolyphosphatase	GO:0005737 cytoplasm		-0.019	0	0	10	559
JW0099	yacF	conserved protein		0	-0.155	0	0	9	558
JW0854	ltaE	L-allo-threonine aldolase, PLP-	GO:0005737 cytoplasm		-0.128	0	0	13	557
JW1220	purU	formyltetrahydrofolate hydrolase	GO:0005737 cytoplasm		-0.166	0	0	8	557
JW2992	ygiW	conserved protein		0	-0.272	0	0	9	557
JW5601	wzzE	Entobacterial Common Antigen (ECA) polysaccharide chain length modulation protein	GO:0019866 inner membrane		-0.354	1	2	10	557
JW3976	aceK	isocitrate dehydrogenase kinase/phosphatase		0	-0.289	0	0	15	555
JW5300	proQ	predicted structural transport element		0	-0.776	0	0	8	555
JW1287	sapA	predicted antimicrobial peptide transporter subunit !- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space		-0.322	0	0	13	554
JW1668	ynhG	conserved protein		0	-0.235	0	0	10	554
JW5760	yjgQ	conserved inner membrane protein	GO:0009274 cell wall (sensu		0.320	1	6	8	553
JW5538	nanK	predicted N-acetylmannosamine kinase	GO:0005737 cytoplasm		0.272	1	0	8	552
JW3820	fre	flavin reductase		0	-0.123	0	0	9	551
JW1043	yceL	predicted protein		0	-0.423	0	0	9	550
JW2587	rplS	50S ribosomal subunit protein L19	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm		-0.527	0	0	9	550
JW3949	rplL	50S ribosomal subunit protein L7/L12	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm		0.295	1	0	8	550
JW5668	kdgK	ketodeoxygluconokinase		0	-0.195	0	0	8	550
JW5413	rimM	16S rRNA processing protein		0	-0.290	0	0	9	549
JW0377	proC	pyrroline-5-carboxylate reductase, NAD(P)-binding	GO:0005737 cytoplasm		0.318	1	0	7	548
JW2064	baeR	DNA-binding response regulator in two-component regulatory system with	GO:0005737 cytoplasm		-0.281	0	0	11	548
JW2509	fdx	[2Fe-2S] ferredoxin		0	-0.357	0	0	7	548
JW2260	menF	isochorismate synthase 2		0	-0.340	0	0	11	546
JW3474	slp	outer membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) !- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)		-0.140	1	0	6	546
JW4128	mutL	methyl-directed mismatch repair protein	GO:0005737 cytoplasm		-0.257	0	0	12	546
JW0755	ybhC	predicted pectinesterase	GO:0009279 external outer membrane (sensu Gram-negative		-0.358	1	0	8	545

JW0869	cydC	fused cysteine transporter subunits -! membrane component and ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner membrane	0.244	1	6	12	544
JW1489	pqqL	predicted peptidase	GO:0005737 cytoplasm	-0.397	1	1	15	542
JW3171	ptsN	sugar-specific enzyme IIA component of PTS	0	-0.167	0	0	8	541
JW2261	elaB	conserved protein	0	-0.520	1	1	8	540
JW5930	yihA	GTP-binding protein	0	-0.437	0	0	9	540
JW2003	hisC	histidinol-phosphate aminotransferase	0	-0.035	0	0	10	539
JW0902	ycbJ	conserved protein	0	-0.303	0	0	12	537
JW1370	uspF	stress-induced protein, ATP-binding protein	0	0.022	1	0	8	537
JW0050	ksgA	S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase	GO:0005737 cytoplasm	-0.101	0	0	10	536
JW2733	cysI	sulfite reductase, beta subunit, NAD(P)- binding	0	-0.434	0	0	15	535
JW1702	ihfA	integration host factor (IHF), DNA- binding protein, alpha subunit	GO:0005737 cytoplasm	-0.874	0	0	10	534
JW2712	nlpD	predicted outer membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.403	1	0	9	534
JW5642	dfp	fused 4'-phosphopantothenoilcysteine decarboxylase -! phosphopantothenoilcysteine synthetase, FMN-binding	GO:0005737 cytoplasm	0.030	1	0	9	534
JW1463	narZ	nitrate reductase 2 (NRZ), alpha subunit	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.443	1	0	14	533
JW3136	rbfA	30s ribosome binding factor	GO:0005737 cytoplasm	-0.398	0	0	7	533
JW3737	yifE	conserved protein	0	-1.069	0	0	9	532
JW1181	ldcA	L,D-carboxypeptidase A	GO:0009274 cell wall (sensu Bacteria) -! GO:0005737 cytoplasm	0.016	1	0	9	531
JW1639	ydhF	predicted oxidoreductase	0	-0.120	0	0	10	530
JW3623	gmk	guanylate kinase	GO:0005737 cytoplasm	-0.430	0	0	8	530
JW2500	yfgA	conserved protein	0	-0.391	1	1	8	529
JW5181	hlyE	hemolysin E	GO:0005576 extracellular	-0.212	1	1	8	529
JW0901	kdsB	3-deoxy-manno-octulosonate cytidyltransferase	GO:0009274 cell wall (sensu Bacteria) -! GO:0009274 cell wall (sensu Bacteria) -! GO:0030113 capsule (sensu Bacteria) -! GO:0005737 cytoplasm	-0.145	0	0	8	527
JW1693	ydiA	conserved protein	0	-0.093	0	0	9	527
JW0470	ybaK	conserved protein	0	-0.083	0	0	6	526
JW3674	yidA	predicted hydrolase	0	-0.002	0	0	7	526
JW0674	seqA	regulatory protein for replication initiation	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.286	1	0	9	525
JW5548	nudC	NADH pyrophosphatase	0	-0.337	0	0	11	525
JW0084	murF	UDP-N-acetylmuramoyl-tripeptide:D- alanyl-D-alanine ligase	GO:0009274 cell wall (sensu Bacteria) -! GO:0005737 cytoplasm	0.165	1	0	10	523

JW0090	ddIB	D-Alanine:D-alanine ligase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	0.077	1	0	11	523
JW1273	pyrF	orotidine-5'-phosphate decarboxylase	0	0.057	1	0	9	523
JW3027	htrG	predicted signal transduction protein (SH3 domain)	GO:0009274 cell wall (sensu Bacteria)	-0.430	1	1	9	522
JW3242	aroE	dehydroshikimate reductase, NAD(P)-binding	0	0.088	1	0	9	522
JW5682	dcrB	periplasmic protein	0	-0.229	0	0	8	521
JW0197	dkgB	2,5-diketo-D-gluconate reductase B	GO:0005737 cytoplasm	-0.114	0	0	10	520
JW0518	folD	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase -!- 5,10-methylene-tetrahydrofolate	0	0.048	1	0	8	520
JW1072	rluC	23S rRNA pseudouridylate synthase	GO:0005737 cytoplasm	-0.461	0	0	15	520
JW2765	yqcD	conserved protein	0	-0.530	0	0	10	520
JW4217	pepA	aminopeptidase A, a cyteinyglycinase	GO:0005737 cytoplasm	-0.217	0	0	10	519
JW3271	rplX	50S ribosomal subunit protein L24	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.381	0	0	8	518
JW1823	yebT	conserved protein	GO:0009274 cell wall (sensu Bacteria)	-0.098	1	1	14	517
JW5898	yccW	predicted methyltransferase	0	-0.190	0	0	14	517
JW4175	ytfJ	predicted transcriptional regulator	0	-0.205	0	0	8	513
JW1794	fadD	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)	GO:0009274 cell wall (sensu Bacteria)	-0.098	0	0	11	512
JW1982	flu	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter	0	-0.275	1	1	11	512
JW3311	slyD	FKBP-type peptidyl prolyl cis-trans isomerase (rotamase)	0	-0.383	0	0	5	512
JW3837	yihI	conserved protein	0	-1.377	0	0	7	511
JW1773	yeaH	conserved protein	0	-0.725	0	0	12	509
JW3895	fpr	ferredoxin-NADP reductase	0	-0.194	0	0	12	509
JW3538	xylF	D-xylose transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.128	0	0	11	508
JW1269	ribA	GTP cyclohydrolase II	0	-0.181	0	0	10	507
JW4349	lplA	lipoate-protein ligase A	GO:0005737 cytoplasm	-0.328	0	0	10	506
JW0671	fldA	flavodoxin 1	0	-0.285	0	0	7	505
JW0844	artJ	arginine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.281	0	0	10	504
JW2007	hisF	imidazole glycerol phosphate synthase, catalytic subunit with HisF	GO:0005737 cytoplasm	-0.044	0	0	10	504
JW3586	yibN	predicted rhodanese-related sulfurtransferase	0	0.064	1	1	7	504
JW1671	sufD	component of SufBCD complex	0	-0.343	0	0	10	503
JW1109	potD	polyamine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.445	0	0	11	502

JW3981	pepE	(alpha)-aspartyl dipeptidase	0	0.124	1	0	8	502
JW5186	dhaL	dihydroxyacetone kinase, C-terminal domain	0	-0.106	0	0	8	502
JW0597	dsbG	periplasmic disulfide isomerase/thiol-disulphide oxidase	GO:0042597 periplasmic space	-0.218	0	0	10	501
JW1633	slyB	outer membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.114	1	0	6	501
JW3932	argH	argininosuccinate lyase	GO:0005737 cytoplasm	-0.189	0	0	11	501
JW5265	ydgJ	predicted oxidoreductase	0	-0.221	0	0	11	500
JW5860	yidR	conserved protein	0	-0.463	0	0	9	500
JW1318	ycjG	L-Ala-D/L-Glu epimerase	0	0.092	1	0	10	499
JW2578	yfiA	cold shock protein associated with 30S ribosomal subunit	GO:0009281 cytosolic ribosome (sensu Bacteria)	-0.535	0	0	6	499
JW3961	hemE	uroporphyrinogen decarboxylase	0	-0.156	0	0	11	498
JW0198	yafC	predicted DNA-binding transcriptional regulator	0	-0.122	0	0	12	497
JW3466	yhiR	predicted DNA (exogenous) processing protein	0	-0.361	0	0	13	497
JW3929	argE	acetylornithine deacetylase	GO:0005737 cytoplasm	-0.181	0	0	8	497
JW3156	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	GO:0009274 cell wall (sensu Bacteria)	0.070	1	0	11	496
JW3904	ftsN	essential cell division protein	GO:0019866 inner membrane	-1.024	1	1	9	496
JW0888	ycaO	conserved protein	0	-0.196	0	0	10	495
JW1093	nagZ	beta N-acetyl-glucosaminidase	0	-0.293	0	0	9	495
JW2795	thyA	thymidylate synthetase	GO:0005737 cytoplasm	-0.382	0	0	8	495
JW1084	tmk	thymidylate kinase	0	-0.202	0	0	10	494
JW1893	ftn	ferritin iron storage protein (cytoplasmic)	GO:0005737 cytoplasm	-0.568	0	0	8	494
JW2789	ptr	protease III	0	-0.369	0	0	16	494
JW3326	ppiA	peptidyl-prolyl cis-trans isomerase A (rotamase A)	0	-0.135	0	0	7	494
JW5878	csiE	stationary phase inducible protein	0	-0.231	0	0	9	494
JW3763	rffH	glucose-1-phosphate thymidyltransferase	0	-0.186	0	0	7	493
JW2077	gatB	galactitol-specific enzyme IIB component of PTS	GO:0005737 cytoplasm	0.306	1	0	5	491
JW0123	yadG	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.237	0	0	12	490
JW1913	yedD	predicted protein	0	-0.195	0	0	8	490
JW3779	cyaY	frataxin, iron-binding and oxidizing	0	-0.592	0	0	7	490
JW5267	slyA	DNA-binding transcriptional activator	GO:0005737 cytoplasm	-0.277	0	0	7	490
JW2502	ndk	multifunctional nucleoside diphosphate kinase -!- apyrimidinic endonuclease -!- 3'-phosphodiesterase	GO:0042597 periplasmic space	-0.082	0	0	6	489
JW2551	rnc	RNase III	0	-0.449	0	0	12	489
JW3169	rpoN	RNA polymerase, sigma 54 (sigma N) factor	0	-0.435	0	0	8	489
JW5559	yiiM	conserved protein	0	-0.417	0	0	10	488

JW5841	prmB	N5-glutamine methyltransferase		0	-0.153	0	0	9	487
JW0478	ybbK	predicted protease, membrane	GO:0009274 cell wall (sensu		-0.020	1	1	7	486
JW4178	msrA	methionine sulfoxide reductase A		0	-0.333	0	0	6	486
JW1226	tdk	thymidine kinase/deoxyuridine kinase		0	-0.320	0	0	8	485
JW0210	ivy	inhibitor of vertebrate C-lysozyme		0	-0.103	0	0	6	484
JW1860	yecP	predicted methyltransferase		0	-0.241	0	0	10	484
JW2173	rplY	50S ribosomal subunit protein L25	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm		-0.468	0	0	8	484
JW3172	yhbJ	predicted protein with nucleoside triphosphate hydrolase domain		0	-0.316	0	0	10	484
JW3859	yiiD	predicted acetyltransferase		0	-0.354	0	0	8	483
JW2782	ygdK	predicted Fe-S metabolism protein		0	-0.086	0	0	6	482
JW1896	yecA	conserved metal-binding protein		0	-0.392	0	0	5	481
JW3125	yhbS	predicted acyltransferase with acyl-CoA N-acyltransferase domain	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.075	1	0	7	481
JW0459	dnaX	DNA polymerase III/DNA elongation factor III, tau and gamma subunits	GO:0005737 cytoplasm		-0.258	0	0	13	480
JW1789	yeaU	predicted dehydrogenase		0	-0.221	0	0	13	480
JW2501	yfgB	predicted enzyme		0	-0.291	0	0	10	478
JW0116	speD	S-adenosylmethionine decarboxylase		0	-0.313	0	0	10	477
JW0934	pqiB	paraquat-inducible protein B		0	-0.280	1	1	11	477
JW2243	yfaY	conserved protein		0	-0.055	0	0	9	477
JW3009	ribB	3,4 dihydroxy-2-butanone-4-phosphate synthase		0	-0.147	0	0	6	477
JW5362	yeiP	predicted elongation factor		0	-0.379	0	0	8	476
JW0434	ybaX	predicted aluminum resistance protein		0	-0.095	0	0	10	475
JW0089	murC	UDP-N-acetylmuramate:L-alanine ligase	GO:0009274 cell wall (sensu		-0.161	0	0	12	474
JW2758	gudD	(D)-glucarate dehydratase 1		0	-0.222	0	0	11	474
JW3883	cpxR	DNA-binding response regulator in two-component regulatory system with CpxA	GO:0005737 cytoplasm		-0.344	0	0	8	474
JW3058	ygjR	predicted NAD(P)-binding		0	0.046	1	0	7	473
JW3129	yhbW	predicted enzyme		0	-0.166	0	0	11	472
JW1167	ycgK	predicted protein		0	-0.634	0	0	7	470
JW3252	mscL	mechanosensitive channel	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.499	1	2	7	470
JW1964	yeeN	conserved protein		0	-0.258	0	0	7	469
JW1529	ydeI	conserved protein		0	-0.298	0	0	6	468
JW2376	yfdZ	predicted aminotransferase, PLP-dependent		0	-0.187	0	0	9	467
JW1254	trpC	fused indole-3-glycerolphosphate synthetase -!- N-(5-phosphoribosyl)anthranilate isomerase	GO:0005737 cytoplasm		-0.025	0	0	11	466
JW1781	yeaO	conserved protein		0	-0.641	0	0	9	466
JW3251	trkA	NAD-binding component of Trk potassium transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.015	1	0	11	466
JW1261	rluB	23S rRNA pseudouridylate synthase		0	-0.585	0	0	11	465

JW3322	argD	bifunctional acetylornithine aminotransferase -/- succinyldiaminopimelate	GO:0005737 cytoplasm	0.045	1	0	10	465
JW0514	ppiB	peptidyl-prolyl cis-trans isomerase B (rotamase B)	GO:0005737 cytoplasm	-0.312	0	0	8	464
JW3377	gntY	predicted gluconate transport associated protein	0	-0.256	0	0	7	463
JW0601	ybdR	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	-0.011	0	0	11	462
JW2050	dcd	2'-deoxycytidine 5'-triphosphate deaminase	0	-0.162	0	0	9	462
JW0067	tbpA	thiamin transporter subunit -/- periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.176	0	0	7	461
JW1248	ompW	outer membrane protein W	GO:0009274 cell wall (sensu Bacteria) -/- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.027	1	0	7	461
JW3277	rplV	50S ribosomal subunit protein L22	GO:0009281 cytosolic ribosome (sensu Bacteria) -/- GO:0005737 cytoplasm	-0.349	0	0	6	460
JW3480	gadE	DNA-binding transcriptional activator	0	-0.198	0	0	8	460
JW3805	metE	5-methyltetrahydropteroyltrimethylglutamate-homocysteine S-methyltransferase	GO:0005737 cytoplasm	-0.258	0	0	9	460
JW0511	purK	N5-carboxyaminoimidazole ribonucleotide synthase	GO:0005737 cytoplasm	-0.139	0	0	11	459
JW1032	ymdB	conserved protein	0	0.007	1	0	8	457
JW0819	yltG	predicted SAM-dependent methyltransferase	0	-0.280	0	0	10	456
JW3900	rraA	ribonuclease E (RNase E) inhibitor	0	0.054	1	0	6	456
JW3703	pstB	phosphate transporter subunit -/- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.270	0	0	9	455
JW4003	lexA	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.241	0	0	8	455
JW3427	ftsX	predicted transporter subunit -/- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner	0.192	1	4	10	454
JW1163	minE	cell division topological specificity factor	GO:0005737 cytoplasm	-0.294	0	0	7	453
JW2674	srlD	sorbitol-6-phosphate dehydrogenase	0	0.130	1	0	8	452
JW4080	mela	alpha-galactosidase, NAD(P)-binding	0	-0.182	0	0	11	452
JW4083	fumB	anaerobic class I fumarate hydratase (fumarase B)	0	-0.316	0	0	9	452
JW1836	yebF	predicted protein	0	-0.411	0	0	7	451
JW3839	glnG	fused DNA-binding response regulator in two-component regulatory system with GlnL, nitrogen regulator I (NRI)	GO:0005737 cytoplasm	-0.246	0	0	12	451
JW3328	nirB	nitrite reductase, large subunit, NAD(P)H-binding	GO:0005737 cytoplasm	-0.211	0	0	15	450
JW0590	cstA	carbon starvation protein	GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner	0.782	1	18	8	449

JW1658	ydhS	conserved protein with FAD/NAD(P)-binding domain	0	-0.318	0	0	12	449
JW1576	speG	spermidine N1-acetyltransferase	0	-0.439	0	0	9	447
JW1579	ynfE	oxidoreductase subunit	0	-0.443	0	0	11	447
JW2171	rsuA	16S rRNA pseudouridylate 516 synthase	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.363	0	0	7	447
JW3164	kdsD	D-arabinose 5-phosphate isomerase	GO:0030113 capsule (sensu	0.223	1	0	8	447
JW4340	yjiU	predicted esterase	0	-0.152	0	0	6	447
JW5165	hflD	predicted lysogenization regulator	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.127	1	0	7	447
JW5376	yfbT	predicted hydrolase or phosphatase	0	0.142	1	0	9	447
JW0756	ybhB	predicted kinase inhibitor	0	-0.180	0	0	7	446
JW0768	moaE	molybdopterin synthase, large subunit	0	-0.497	0	0	5	446
JW2125	yohF	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	0	0.079	1	0	6	446
JW3946	rplK	50S ribosomal subunit protein L11	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.061	0	0	7	446
JW1314	ycjX	conserved protein with nucleoside triphosphate hydrolase domain	0	-0.243	0	0	11	445
JW3199	rpsI	30S ribosomal subunit protein S9	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.687	0	0	8	445
JW3830	yihD	conserved protein	0	-0.424	0	0	6	445
JW5606	ilvE	branched-chain amino-acid aminotransferase	0	-0.165	0	0	7	445
JW5600	rffE	UDP-N-acetyl glucosamine-2-epimerase	GO:0005737 cytoplasm	-0.151	0	0	10	444
JW5019	yafV	predicted C-N hydrolase family amidase, NAD(P)-binding	0	-0.213	0	0	7	443
JW1732	spy	envelope stress induced periplasmic protein	GO:0042597 periplasmic space	-0.758	0	0	8	442
JW2280	nuoE	NADH:ubiquinone oxidoreductase,	GO:0005737 cytoplasm	-0.392	0	0	6	442
JW3496	dctA	C4-dicarboxylic acid, orotate and citrate transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.872	1	8	9	442
JW4311	hsdS	specificity determinant for hsdM and	GO:0005737 cytoplasm	-0.261	0	0	11	442
JW5831	znuA	zinc transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.211	0	0	8	442
JW0636	rlpB	minor lipoprotein	GO:0019866 inner membrane	-0.252	1	0	9	441
JW5529	yhbO	predicted intracellular protease	0	-0.242	0	0	7	441
JW3144	folP	7,8-dihydropteroate synthase	0	-0.022	0	0	11	440
JW3256	rplQ	50S ribosomal subunit protein L17	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.565	0	0	8	440
JW1276	yciT	predicted DNA-binding transcriptional regulator	0	-0.092	0	0	10	439

JW1771	mipA	scaffolding protein for murein synthesizing machinery	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.402	1	0	6	438
JW2276	nuoI	NADH:ubiquinone oxidoreductase,	GO:0005737 cytoplasm	-0.327	0	0	9	438
JW5009	hpt	hypoxanthine phosphoribosyltransferase	GO:0005737 cytoplasm	-0.069	0	0	7	438
JW5155	yceF	predicted protein	0	-0.302	0	0	7	437
JW0494	allR	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	0.073	1	0	8	436
JW1530	ydeJ	conserved protein	0	0.116	1	0	6	436
JW3536	xylB	xylulokinase	0	-0.092	0	0	10	435
JW3903	hslV	peptidase component of the HslUV protease	GO:0005737 cytoplasm	-0.034	0	0	8	435
JW5655	yiaF	conserved protein	0	-0.151	1	1	7	435
JW0427	clpP	proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine	GO:0005737 cytoplasm	-0.154	0	0	7	434
JW2460	ypfJ	conserved protein	0	-0.512	1	1	6	434
JW2575	yfiH	conserved protein	0	-0.141	0	0	7	434
JW3831	yihE	predicted kinase	0	-0.317	0	0	12	434
JW1179	dadX	alanine racemase 2, PLP-binding	0	-0.026	0	0	10	433
JW5946	gntR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.104	0	0	10	433
JW2913	yggJ	predicted protein	0	-0.216	0	0	8	432
JW3394	glgX	glycogen debranching enzyme	GO:0005737 cytoplasm	-0.341	0	0	14	432
JW0048	apaH	diadenosine tetrphosphatase	GO:0005737 cytoplasm	-0.246	0	0	9	431
JW0395	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	GO:0005737 cytoplasm	-0.129	0	0	8	431
JW2144	yeiE	predicted DNA-binding transcriptional regulator	0	0.017	1	0	10	431
JW5157	ycfM	predicted outer membrane lipoprotein	0	-0.215	0	0	5	431
JW1272	yciM	conserved protein	0	-0.365	0	0	10	430
JW1776	yeaK	conserved protein	0	0.165	1	0	8	430
JW2927	yggH	tRNA (m7G46) methyltransferase, SAM-dependent	0	-0.397	0	0	8	430
JW5531	deaD	ATP-dependent RNA helicase	GO:0005737 cytoplasm	-0.586	0	0	7	430
JW2700	hypE	carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein	0	0.329	1	0	10	429
JW5790	yjiA	predicted GTPase	0	-0.085	0	0	8	428
JW1338	ydaO	predicted C32 tRNA thiolase	0	-0.455	0	0	7	427
JW2697	hypB	GTP hydrolase involved in nickel liganding into hydrogenases	0	-0.238	0	0	7	427
JW2985	sufI	repressor protein for FtsI	0	-0.175	0	0	10	427
JW3646	ilvB	acetolactate synthase I, large subunit	0	0.041	1	0	10	427
JW1755	sppA	protease IV (signal peptide peptidase)	0	-0.111	1	1	12	426
JW0051	pdxA	4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent	GO:0005737 cytoplasm	0.192	1	0	8	425
JW5057	yajL	conserved protein	0	0.323	1	0	7	425
JW1756	ansA	cytoplasmic L-asparaginase I	GO:0005737 cytoplasm	-0.187	0	0	7	424

JW2716	ispF	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	GO:0005737 cytoplasm	0.089	1	0	6	424
JW5566	yihX	predicted hydrolase		0	-0.158	0	0	7
JW2874	visC	predicted oxidoreductase, FAD/NAD(P)-binding domain		0	-0.132	0	0	9
JW2644	stpA	DNA binding protein, nucleoid-	GO:0005737 cytoplasm	-0.794	0	0	7	422
JW4020	ssb	Single-stranded DNA-binding protein	GO:0005737 cytoplasm	-0.708	0	0	7	422
JW5676	rbbA	fused ribosome-associated ATPases	GO:0005737 cytoplasm	0.077	1	5	11	422
JW0387	sbcC	exonuclease, dsDNA, ATP-dependent	GO:0005737 cytoplasm	-0.635	0	0	9	421
JW1694	aroH	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible		0	-0.315	0	0	9
JW5769	yjhc	KpLE2 phage-like element; predicted oxidoreductase		0	-0.266	0	0	8
JW2339	yfcY	beta-ketoacyl-CoA thiolase, anaerobic, subunit		0	0.039	1	0	9
JW2924	ansB	periplasmic L-asparaginase II	GO:0042597 periplasmic space	-0.114	1	1	7	418
JW1821	yebR	conserved protein		0	0.168	1	0	8
JW2566	trxC	thioredoxin 2		0	-0.200	0	0	7
JW3135	truB	tRNA pseudouridine synthase	GO:0005737 cytoplasm	-0.368	0	0	9	415
JW3331	cysG	fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase/siroheme ferrocyclase -!- uroporphyrinogen methyltransferase		0	-0.042	0	0	11
JW5339	yegP	predicted protein		0	-0.711	0	0	6
JW0467	ybaL	predicted transporter with NAD(P)-binding Rossmann-fold domain	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.805	1	12	9	413
JW1426	tehB	predicted S-adenosyl-L-methionine-dependent methyltransferase		0	-0.376	0	0	9
JW2156	fruB	fused fructose-specific PTS enzyme IIA component -!- HPr component	GO:0005737 cytoplasm	-0.029	0	0	7	413
JW0603	rna	ribonuclease I	GO:0005737 cytoplasm	-0.412	0	0	9	412
JW2076	gatC	galactitol-specific enzyme IIC component of PTS	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.824	1	11	5	411
JW2552	lepB	leader peptidase (signal peptidase I)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.156	1	2	9	411
JW0421	cyoB	cytochrome o ubiquinol oxidase subunit I	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.658	1	14	7	409
JW2234	glpT	sn-glycerol-3-phosphate transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.493	1	12	9	409
JW5196	yciO	conserved protein		0	-0.311	0	0	7
JW5804	ycjY	predicted hydrolase		0	-0.387	0	0	9
JW2066	yegQ	predicted peptidase		0	-0.410	0	0	10
JW3195	nanR	DNA-binding transcriptional dual		0	-0.408	0	0	8
JW3259	rpsK	30S ribosomal subunit protein S11	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.446	0	0	6	408

JW5060	bolA	regulator of penicillin binding proteins and beta lactamase transcription	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.190	0	0	5	407
JW3154	ispB	octaprenyl diphosphate synthase	0	-0.095	0	0	8	406
JW3909	metJ	DNA-binding transcriptional repressor, S-adenosylmethionine-binding	GO:0005737 cytoplasm	-0.748	0	0	7	406
JW4072	proP	proline/glycine betaine transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.558	1	12	7	406
JW5302	yebV	predicted protein	0	-0.451	0	0	5	406
JW5264	ynfK	predicted dethiobiotin synthetase	0	0.135	1	0	8	405
JW5558	cpxP	periplasmic protein combats stress	GO:0005737 cytoplasm -!- GO:0042597 periplasmic space	-0.787	0	0	6	405
JW3160	yrbD	predicted ABC-type organic solvent transporter	0	-0.068	1	1	7	404
JW3428	ftsE	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.077	0	0	8	404
JW5162	lolD	outer membrane-specific lipoprotein transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.182	0	0	6	404
JW1646	ydhD	conserved protein	0	-0.272	0	0	4	403
JW2051	udk	uridine/cytidine kinase	0	-0.258	0	0	9	403
JW3283	rpsJ	30S ribosomal subunit protein S10	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.352	0	0	6	403
JW0908	ycbB	predicted carboxypeptidase	0	-0.276	0	0	13	401
JW5672	yhiQ	predicted SAM-dependent methyltransferase	0	-0.009	0	0	7	401
JW1213	narX	sensory histidine kinase in two-component regulatory system with NarL	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.213	1	2	9	400
JW1993	sbcb	exonuclease I	0	-0.401	0	0	13	400
JW2155	fruK	fructose-1-phosphate kinase	0	0.060	1	0	9	400
JW2768	sdaB	L-serine deaminase II	0	0.052	1	0	11	400
JW3964	hupA	HU, DNA-binding transcriptional regulator, alpha subunit	GO:0005737 cytoplasm	-0.228	0	0	4	400
JW1644	rnt	ribonuclease T (RNase T)	0	-0.051	0	0	6	399
JW3028	cca	fused tRNA nucleotidyl transferase -!- 2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase	GO:0005737 cytoplasm	-0.313	0	0	12	399
JW3266	rpIR	50S ribosomal subunit protein L18	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.395	0	0	6	397
JW0117	speE	spermidine synthase (putrescine aminopropyltransferase)	0	-0.170	0	0	7	396
JW0939	ycbG	conserved protein	0	-0.779	0	0	8	396
JW0958	hyaE	protein involved in processing of HyaA and HyaB proteins	0	-0.282	0	0	7	396
JW5853	ysgA	predicted hydrolase	0	-0.210	0	0	6	396

JW0870	cydD	fused cysteine transporter subunits -! membrane component and ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner membrane	0.162	1	5	12	395
JW2493	xseA	exonuclease VII, large subunit		0	-0.528	0	9	395
JW1017	ycdX	predicted zinc-binding hydrolase		0	-0.118	0	7	394
JW0188	nlpE	lipoprotein involved with copper homeostasis and adhesion	GO:0009274 cell wall (sensu Bacteria) -! GO:0009279 external outer membrane (sensu Gram- negative Bacteria)	-0.311	1	0	7	393
JW0878	dmsB	dimethyl sulfoxide reductase, anaerobic, subunit B	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.484	1	0	7	393
JW1409	azoR	NADH-azoreductase, FMN-dependent		0	0.067	1	7	392
JW5374	menD	bifunctional 2-oxoglutarate decarboxylase -! SHCHC synthase		0	-0.127	0	10	392
JW0264	yagH	CP4-6 prophage; predicted xylosidase/arabinosidase		0	-0.465	0	6	391
JW0407	thiL	thiamin-monophosphate kinase		0	0.075	1	10	391
JW3462	uspA	universal stress global response	GO:0005737 cytoplasm	-0.056	0	0	5	391
JW0119	cueO	multicopper oxidase (laccase)		0	-0.165	0	10	390
JW1089	hinT	purine nucleoside phosphoramidase		0	-0.062	0	7	390
JW1487	gadC	predicted glutamate:gamma- aminobutyric acid antiporter	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.846	1	12	8	390
JW2965	hybO	hydrogenase 2, small subunit	GO:0019866 inner membrane	-0.194	1	1	7	390
JW3894	yiiT	stress-induced protein		0	-0.221	0	5	390
JW4199	treB	fused trehalose(maltose)-specific enzyme IIBC component of PTS	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.648	1	10	7	390
JW3585	grxC	glutaredoxin 3		0	-0.314	0	6	389
JW4314	mrr	methylated adenine and cytosine restriction protein	GO:0005737 cytoplasm	-0.359	0	0	9	389
JW5599	rffD	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	GO:0009274 cell wall (sensu Bacteria)	0.065	1	0	9	389
JW2081	gatA	galactitol-specific enzyme IIA component of PTS		0	-0.025	0	5	388
JW0027	ispH	1-hydroxy-2-methyl-2-(E)-butenyl 4- diphosphate reductase, 4Fe-4S protein	GO:0005737 cytoplasm	-0.173	0	0	9	387
JW0193	metQ	DL-methionine transporter subunit -! periplasmic-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -! GO:0042597 periplasmic space	-0.138	0	0	7	387
JW0766	moaC	molybdopterin biosynthesis, protein C		0	-0.037	0	9	387
JW5431	gutQ	predicted phosphosugar-binding protein	GO:0030113 capsule (sensu	0.144	1	0	10	387
JW1505	ydeW	predicted DNA-binding transcriptional regulator		0	0.129	1	9	385
JW3262	secY	preprotein translocase membrane subunit	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.602	1	10	8	385
JW3615	dut	deoxyuridinetriphosphatase		0	0.005	1	4	385
JW5309	yecM	predicted metal-binding enzyme		0	-0.380	0	6	385
JW5547	nfi	endonuclease V		0	-0.064	0	7	385

JW3808	udp	uridine phosphorylase		0	0.022	1	0	8	384
JW0430	hupB	HU, DNA-binding transcriptional regulator, beta subunit	GO:0005737 cytoplasm		-0.042	0	0	5	383
JW1265	yciN	predicted protein		0	-0.380	0	0	5	383
JW1674	sufA	Fe-S cluster assembly protein		0	-0.103	0	0	6	383
JW2516	yfhQ	predicted methyltransferase		0	-0.133	0	0	7	383
JW2660	emrA	multidrug efflux system	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.129	1	1	8	383
JW3963	yjaG	conserved protein		0	-0.241	0	0	7	383
JW5927	ygiB	conserved outer membrane protein		0	-0.601	0	0	7	383
JW1176	fadR	DNA-binding transcriptional dual	GO:0005737 cytoplasm		-0.283	0	0	7	381
JW3679	dnaA	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator	GO:0005737 cytoplasm		-0.364	0	0	10	381
JW3719	gidA	glucose-inhibited cell-division protein		0	-0.308	0	0	9	381
JW0176	lpxA	UDP-N-acetylglucosamine acetyltransferase	GO:0005737 cytoplasm		0.002	1	0	7	380
JW2427	ypeA	predicted acyltransferase with acyl-CoA N-acyltransferase domain		0	-0.405	0	0	7	380
JW0005	yaaA	conserved protein		0	-0.403	0	0	9	378
JW1849	ruvB	ATP-dependent DNA helicase, component of RuvABC resolvosome	GO:0005737 cytoplasm		-0.089	0	0	10	378
JW2006	hisA	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase	GO:0005737 cytoplasm		0.063	1	0	8	378
JW3348	gph	phosphoglycolate phosphatase		0	-0.133	0	0	6	378
JW5567	yihW	predicted DNA-binding transcriptional regulator		0	-0.054	0	0	7	378
JW0702	ybgK	predicted enzyme subunit		0	-0.347	0	0	9	377
JW1706	rplT	50S ribosomal subunit protein L20	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm		-0.336	0	0	8	377
JW5090	ybeB	predicted protein		0	0.034	1	0	5	377
JW3192	nanE	predicted N-acetylmannosamine-6-P epimerase	GO:0005737 cytoplasm		0.162	1	0	7	376
JW3899	yiiU	conserved protein		0	-0.980	0	0	5	376
JW0023	ribF	bifunctional riboflavin kinase -!- FAD synthetase	GO:0005737 cytoplasm		-0.067	0	0	9	375
JW0173	hlpA	periplasmic chaperone	GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597		-0.473	0	0	6	375
JW4120	yjeP	predicted mechanosensitive channel	GO:0042597 periplasmic space		0.018	1	11	14	375
JW0028	rihC	ribonucleoside hydrolase 3		0	0.289	1	0	6	374
JW0399	secF	SecYEG protein translocase auxillary subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.401	1	6	6	374
JW2485	purN	phosphoribosylglycinamide formyltransferase 1	GO:0005737 cytoplasm		-0.124	0	0	6	374

JW4102	groS	Cpn10 chaperonin GroES, small subunit of GroESL	GO:0005737 cytoplasm	-0.004	0	0	6	374
JW0988	yccJ	predicted protein	0	-0.649	0	0	4	373
JW2975	metC	cystathionine beta-lyase, PLP-	GO:0005737 cytoplasm	0.024	1	0	7	373
JW4138	rlmB	23S rRNA (Gm2251)-methyltransferase	0	-0.033	0	0	8	373
JW5755	yjgF	ketoacid-binding protein	0	0.086	1	0	6	373
JW3304	rpsL	30S ribosomal subunit protein S12	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.623	0	0	6	372
JW3907	rpmE	50S ribosomal subunit protein L31	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.649	0	0	5	372
JW4366	yjtD	predicted rRNA methyltransferase	0	0.005	1	0	9	372
JW5856	trxA	thioredoxin 1	0	0.025	1	0	4	372
JW2868	yqfB	conserved protein	0	-0.373	0	0	6	371
JW3248	def	peptide deformylase	0	-0.290	0	0	6	371
JW1050	yceB	predicted lipoprotein	0	-0.142	0	0	7	369
JW2404	zipA	cell division protein involved in Z ring assembly	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.606	1	1	6	369
JW3167	yhbN	predicted transporter subunit -!- periplasmic-binding component of ABC superfamily	0	-0.444	0	0	5	369
JW5505	yqiC	conserved protein	0	-0.818	0	0	8	369
JW3718	gidB	methyltransferase, glucose-inhibited cell-division protein	0	-0.154	0	0	9	368
JW2974	exbB	membrane spanning protein in TonB-ExbB-ExbD complex	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.265	1	3	7	367
JW3153	rplU	50S ribosomal subunit protein L21	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.369	0	0	7	367
JW3582	cysE	serine acetyltransferase	GO:0005737 cytoplasm	0.002	1	0	8	367
JW3748	ppiC	peptidyl-prolyl cis-trans isomerase C (rotamase C)	0	-0.105	0	0	7	366
JW0088	murG	N-acetylglucosaminyl transferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.040	1	0	9	365
JW3645	ilvN	acetolactate synthase I, small subunit	0	-0.201	0	0	6	365
JW1328	fnr	DNA-binding transcriptional dual regulator, global regulator of anaerobic	GO:0005737 cytoplasm	-0.274	0	0	6	364
JW1638	sodC	superoxide dismutase, Cu, Zn	GO:0042597 periplasmic space	-0.277	0	0	6	364
JW2915	yqgE	predicted protein	0	-0.072	0	0	4	364
JW3460	pitA	phosphate transporter, low-affinity	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.523	1	10	7	364
JW1795	yeaY	predicted lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.120	1	0	6	363

JW1236	oppB	oligopeptide transporter subunit -! membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -! GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner membrane	0.767	1	6	6	362
JW5605	ilvD	dihydroxyacid dehydratase		0	-0.136	0	0	12
JW5008	yacG	conserved protein		0	-0.615	0	0	5
JW4106	yjeK	predicted lysine aminomutase		0	-0.189	0	0	6
JW0141	dksA	transcriptional regulator of rRNA transcription, DnaK suppressor protein	GO:0005737 cytoplasm		-0.866	0	0	6
JW3765	rffA	TDP-4-oxo-6-deoxy-D-glucose transaminase		0	-0.067	0	0	8
JW3882	cpxA	sensory histidine kinase in two- component regulatory system with	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner		-0.264	1	2	9
JW0806	ybiV	predicted hydrolase		0	-0.168	0	0	5
JW2181	narP	DNA-binding response regulator in two- component regulatory system with NarQ or NarX	GO:0005737 cytoplasm		-0.014	0	0	5
JW5129	mgsA	methylglyoxal synthase	GO:0005737 cytoplasm		0.038	1	0	5
JW0440	glnK	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB		0	0.067	1	0	5
JW1812	cspC	stress protein, member of the CspA-		0	-0.190	0	0	4
JW0230	crl	DNA-binding transcriptional regulator	GO:0009289 fimbria -! GO:0005737 cytoplasm		-0.511	0	0	7
JW2480	yfgD	predicted oxidoreductase		0	-0.361	0	0	4
JW4356	trpR	DNA-binding transcriptional repressor, tryptophan-binding	GO:0005737 cytoplasm		-0.424	0	0	7
JW5592	dapF	diaminopimelate epimerase	GO:0005737 cytoplasm		-0.090	0	0	8
JW5503	tolC	transport channel	GO:0009274 cell wall (sensu Bacteria) -! GO:0009279 external outer membrane (sensu Gram- negative Bacteria)		-0.427	1	0	7
JW0900	ycaR	conserved protein		0	-0.127	0	0	6
JW3959	rsd	stationary phase protein, binds sigma 70 RNA polymerase subunit	GO:0005737 cytoplasm		-0.277	0	0	5
JW2008	hisI	fused phosphoribosyl-AMP cyclohydrolase -! phosphoribosyl-ATP	GO:0005737 cytoplasm		-0.331	0	0	6
JW2659	mprA	DNA-binding transcriptional regulator	GO:0005737 cytoplasm		-0.638	0	0	7
JW3076	yhaJ	predicted DNA-binding transcriptional regulator		0	-0.161	0	0	7
JW5669	hdeB	acid-resistance protein		0	-0.242	0	0	3
JW5042	ykgG	predicted transporter		0	-0.135	0	0	5
JW0185	yaeP	conserved protein		0	0.026	1	0	3
JW0071	leuC	3-isopropylmalate isomerase subunit, dehydratase component	GO:0005737 cytoplasm		-0.174	0	0	8
JW3132	nlpl	conserved protein		0	-0.321	0	0	7
JW5608	yieP	predicted transcriptional regulator		0	-0.079	0	0	6

JW2235	glpA	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit, FAD/NAD(P)-binding	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	-0.134	1	0	11	347	
JW2647	ygaM	predicted protein		0	-0.501	1	1	5	347
JW4360	creA	conserved protein		0	-0.032	0	0	8	347
JW1120	ymfB	bifunctional thiamin pyrimidine pyrophosphate hydrolase -!- thiamin pyrophosphate hydrolase		0	-0.148	0	0	7	346
JW2433	eutC	ethanolamine ammonia-lyase, small subunit (light chain)		0	-0.101	0	0	7	346
JW3278	rpsS	30S ribosomal subunit protein S19	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.620	0	0	7	346	
JW0895	ihfB	integration host factor (IHF), DNA-binding protein, beta subunit	GO:0005737 cytoplasm	-0.784	0	0	6	345	
JW5284	ynjB	conserved protein		0	-0.302	0	0	8	345
JW3069	ycjD	conserved protein		0	-0.545	1	1	6	344
JW3893	yiiS	conserved protein		0	-0.007	0	0	3	344
JW3728	rbsA	fused D-ribose transporter subunits -!- ATP-binding components ABC	GO:0005737 cytoplasm	-0.088	0	0	7	343	
JW3486	yhjA	predicted cytochrome C peroxidase		0	-0.395	1	1	10	342
JW2343	vacJ	predicted lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.291	1	0	6	341	
JW5795	yjjA	conserved protein		0	-0.210	0	0	5	341
JW2273	nuoL	NADH:ubiquinone oxidoreductase, membrane subunit L	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.868	1	16	6	339	
JW3827	hemG	protoporphyrin oxidase, flavoprotein		0	-0.587	0	0	7	339
JW3993	malF	maltose transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.290	1	8	6	339	
JW0626	ybeD	conserved protein		0	-0.166	0	0	4	337
JW2878	zapA	protein that localizes to the cytokinetic		0	-0.733	0	0	5	337
JW3584	secB	protein export chaperone	GO:0005737 cytoplasm	-0.188	0	0	5	337	
JW1214	narK	nitrate/nitrite transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.678	1	12	6	336	
JW4185	ppa	inorganic pyrophosphatase	GO:0005737 cytoplasm	-0.272	0	0	9	336	
JW0179	dnaE	DNA polymerase III alpha subunit	GO:0005737 cytoplasm	-0.241	0	0	12	335	
JW2721	cysN	sulfate adenylyltransferase, subunit 1		0	-0.184	0	0	8	335
JW3065	exuR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.524	0	0	9	335	
JW5473	ygfB	predicted protein		0	-0.362	0	0	5	335
JW1534	ydfZ	conserved protein		0	-0.281	0	0	4	334
JW2761	yqcA	predicted flavoprotein		0	-0.117	0	0	4	334
JW5513	ygjO	predicted methyltransferase small		0	-0.181	0	0	7	332
JW2425	yfeY	predicted protein		0	-0.351	0	0	5	331
JW5180	ycgN	conserved protein		0	-0.530	0	0	5	331
JW1462	narY	nitrate reductase 2 (NRZ), beta subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.434	1	0	9	330	

JW4250	fecB	KpLE2 phage-like element; iron-dictrate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	0.026	1	0	8	330
JW3459	yhiN	predicted oxidoreductase, FAD/NAD(P)-binding domain	0	-0.036	1	1	6	328
JW1018	yedY	conserved protein	0	-0.166	0	0	5	327
JW1105	yefX	predicted DNA-binding transcriptional regulator	0	-0.071	0	0	7	327
JW1863	cutC	copper homeostasis protein	GO:0005737 cytoplasm	0.016	1	0	8	327
JW2322	yfcL	predicted protein	0	-0.148	0	0	5	327
JW0485	ybbP	predicted inner membrane protein	0	0.255	1	10	8	326
JW0618	cspE	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.213	0	0	5	326
JW0867	infA	translation initiation factor IF-1	GO:0005737 cytoplasm	-0.354	0	0	4	326
JW1511	lsrG	conserved protein	0	-0.529	0	0	5	325
JW2296	yfcD	predicted NUDIX hydrolase	0	-0.427	0	0	5	325
JW3149	dacB	D-alanyl-D-alanine carboxypeptidase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597	-0.051	0	0	8	325
JW3776	hemD	uroporphyrinogen III synthase	0	-0.124	0	0	7	325
JW5291	yeaJ	predicted diguanylate cyclase	0	-0.207	1	2	9	325
JW0860	ybjD	conserved protein with nucleoside triphosphate hydrolase domain	0	-0.326	0	0	8	324
JW2639	csiR	DNA-binding transcriptional dual	0	-0.127	0	0	10	324
JW3095	garL	alpha-dehydro-beta-deoxy-D-glucarate aldolase	0	0.071	1	0	7	324
JW1288	ymjA	predicted protein	0	-0.469	0	0	5	323
JW2300	folX	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase	0	-0.426	0	0	6	323
JW3152	rpmA	50S ribosomal subunit protein L27	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.638	0	0	5	322
JW3770	rffM	UDP-N-acetyl-D-mannosaminuronic acid transferase	0	-0.322	0	0	7	321
JW3809	rnuC	predicted recombination limiting protein	0	-0.651	1	1	9	321
JW0960	appC	cytochrome bd-II oxidase, subunit I	GO:0019866 inner membrane	0.358	1	9	6	320
JW2141	yeiG	predicted esterase	0	-0.320	0	0	8	320
JW2176	yejM	predicted hydrolase, inner membrane	0	-0.122	1	5	6	320
JW2714	surE	broad specificity 5'(3')-nucleotidase and polyphosphatase	0	-0.075	0	0	6	320
JW3264	rpmD	50S ribosomal subunit protein L30	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.137	0	0	6	320
JW5703	yheO	predicted DNA-binding transcriptional regulator	0	-0.163	0	0	4	320
JW1844	lpxM	myristoyl-acyl carrier protein (ACP)-dependent acyltransferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.450	1	1	9	319

JW0196	gmhB	D,D-heptose 1,7-bisphosphate phosphatase	0	-0.251	0	0	5	318
JW2421	yfeU	predicted PTS component	0	0.134	1	0	7	318
JW3217	yhdE	conserved protein	0	-0.187	0	0	5	318
JW5940	bisC	biotin sulfoxide reductase	0	-0.301	0	0	9	318
JW0938	ycbZ	predicted peptidase	0	-0.162	0	0	8	317
JW4126	yjeE	ATPase with strong ADP affinity	0	-0.086	0	0	4	317
JW0406	nusB	transcription antitermination protein	GO:0005737 cytoplasm	-0.219	0	0	6	316
JW0736	ybgS	conserved protein	0	-0.711	0	0	3	316
JW0345	yaiL	nucleoprotein/polynucleotide-associated enzyme	GO:0005737 cytoplasm	-0.473	0	0	7	315
JW3201	yhcM	conserved protein with nucleoside triphosphate hydrolase domain	0	-0.289	0	0	7	315
JW5295	yoaB	conserved protein	0	0.024	1	0	5	315
JW0445	ybaA	conserved protein	0	-0.393	0	0	4	314
JW2154	fruA	fused fructose-specific PTS enzyme IIB'BC components	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.585	1	9	7	314
JW5533	yhbC	conserved protein	0	0.047	1	0	5	314
JW2550	era	membrane-associated, 16S rRNA-binding GTPase	0	-0.192	0	0	10	313
JW1074	yceD	conserved protein	0	-0.192	0	0	5	311
JW3785	yigB	predicted hydrolase	0	-0.329	0	0	5	311
JW0174	lpxD	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	0	0.125	1	0	6	310
JW0701	ybgJ	predicted enzyme subunit	0	0.018	1	0	6	310
JW1315	ycjF	conserved inner membrane protein	0	-0.247	1	3	6	310
JW1556	relB	Qin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin system -!- transcriptional repressor	GO:0005737 cytoplasm	-0.359	0	0	5	310
JW3478	hdeA	stress response protein acid-resistance protein	0	-0.208	1	1	4	310
JW0213	yafJ	predicted amidotransfease	0	-0.313	0	0	7	309
JW1086	ycfH	predicted metallodependent hydrolase	0	-0.212	0	0	7	309
JW1256	trpE	component I of anthranilate synthase	0	-0.190	0	0	8	309
JW1728	osmE	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.265	1	1	3	308
JW2537	glnB	regulatory protein P-II for glutamine synthetase	GO:0005737 cytoplasm	0.009	1	0	6	308
JW5283	ydjY	predicted protein	0	-0.242	0	0	6	308
JW5832	yedQ	predicted diguanylate cyclase	0	-0.287	1	2	8	308
JW1394	paaX	DNA-binding transcriptional regulator, aryl-CoA responsive	0	0.004	1	0	7	307
JW1757	pncA	nicotinamidase/pyrazinamidase	GO:0005737 cytoplasm	-0.249	0	0	4	307
JW2894	epd	D-erythrose 4-phosphate	GO:0005737 cytoplasm	-0.041	0	0	7	307
JW2338	yfcX	fused enoyl-CoA hydratase-!- epimerase-!-isomerase -!- 3-hydroxyacyl-CoA dehydrogenase, subunit of anaerobic fatty acid oxidation	0	-0.050	0	0	9	306

JW0054	djIA	DnaJ-like protein, membrane anchored	0	-0.341	1	1	8	305
JW0442	tesB	acyl-CoA thioesterase II	0	-0.253	0	0	7	305
JW1859	yecO	predicted methyltransferase	0	-0.145	0	0	7	305
JW1902	yecC	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.147	0	0	5	305
JW0171	yaeL	zinc metalloproteinase	0	0.265	1	4	8	303
JW0192	rcsF	predicted outer membrane protein,	GO:0030113 capsule (sensu	-0.190	0	0	4	302
JW1600	rstA	DNA-binding response regulator in two-component regulatory system with RstB	GO:0005737 cytoplasm	-0.064	0	0	7	302
JW5317	yodD	predicted protein	0	-0.731	0	0	4	302
JW1991	sbmC	DNA gyrase inhibitor	GO:0005737 cytoplasm	-0.363	0	0	4	301
JW1199	ispE	4-diphosphocytidyl-2-C-methylerythritol kinase	GO:0005737 cytoplasm	-0.060	0	0	6	300
JW0265	yagl	CP4-6 prophage; predicted DNA-binding transcriptional regulator	0	-0.132	0	0	6	299
JW2870	ygfF	predicted NAD(P)-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain	0	0.118	1	0	6	299
JW3424	yhhK	conserved protein	0	-0.360	0	0	5	299
JW0321	yahO	predicted protein	0	-0.286	0	0	4	297
JW1734	astB	succinylarginine dihydrolase	0	-0.273	0	0	7	297
JW2713	pcm	L-isoaspartate protein carboxylmethyltransferase type II	0	-0.158	0	0	7	297
JW5550	murl	glutamate racemase	GO:0009274 cell wall (sensu	0.187	1	0	7	296
JW0848	artP	arginine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.134	0	0	6	295
JW2511	hscB	DnaJ-like molecular chaperone specific for IscU	0	-0.598	0	0	6	295
JW3318	prkB	predicted phosphoribulokinase	0	-0.165	0	0	7	295
JW5652	avtA	valine-pyruvate aminotransferase	0	-0.065	0	0	7	295
JW3375	bioH	carboxylesterase of pimeloyl-CoA synthesis	0	0.039	1	0	6	294
JW5127	ymbA	conserved protein	0	-0.158	0	0	4	294
JW5791	yjiY	predicted inner membrane protein	0	0.725	1	16	6	294
JW0906	mukE	protein involved in chromosome	0	-0.495	0	0	7	293
JW3275	rplP	50S ribosomal subunit protein L16	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.384	0	0	3	293
JW5089	lipB	lipoyl-protein ligase	0	-0.178	0	0	7	293
JW1614	malY	bifunctional beta-cystathionase, PLP-dependent -!- regulator of maltose	GO:0005737 cytoplasm	-0.101	0	0	7	292
JW3891	yiiQ	conserved protein	0	-0.294	0	0	6	291
JW0094	lpxC	UDP-3-O-acyl N-acetylglucosamine deacetylase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.050	0	0	8	290
JW1899	uvrY	DNA-binding response regulator in two-component regulatory system with BarA	0	-0.056	0	0	7	290

JW0216	dinJ	predicted antitoxin of YafQ-DinJ toxin-antitoxin system	0	-0.142	0	0	6	289
JW1053	rimJ	ribosomal-protein-S5-alanine N-acetyltransferase	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.524	0	0	7	289
JW2734	cysJ	sulfite reductase, alpha subunit, flavoprotein	0	-0.256	0	0	6	288
JW0152	yadR	conserved protein	0	-0.089	0	0	4	287
JW1075	rpmF	50S ribosomal subunit protein L32	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.974	0	0	4	287
JW5449	amiC	N-acetylmuramoyl-L-alanine amidase	GO:0009274 cell wall (sensu	-0.210	0	0	7	287
JW0156	dgt	deoxyguanosine triphosphate triphosphohydrolase	GO:0005737 cytoplasm	-0.451	0	0	6	286
JW0780	ybiH	predicted DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.113	0	0	6	286
JW1242	kch	voltage-gated potassium channel	GO:0019866 inner membrane	0.422	1	7	4	286
JW2512	iscA	FeS cluster assembly protein	0	-0.103	0	0	6	286
JW4351	serB	3-phosphoserine phosphatase	GO:0005737 cytoplasm	0.091	1	0	7	286
JW4352	radA	predicted repair protein	0	0.038	1	0	6	286
JW1958	yeel	conserved protein	0	-0.142	0	0	5	285
JW2070	yegS	conserved protein	0	0.030	1	0	5	285
JW2857	idi	isopentenyl diphosphate isomerase	GO:0005737 cytoplasm	-0.292	0	0	5	285
JW1718	ydjN	predicted transporter	0	0.816	1	9	4	284
JW2161	yeiR	predicted enzyme	0	-0.229	0	0	8	284
JW2764	syd	predicted protein	GO:0005737 cytoplasm	-0.276	0	0	6	284
JW3269	rpsN	30S ribosomal subunit protein S14	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.795	0	0	5	284
JW3720	mioC	FMN-binding protein MioC	0	-0.159	0	0	5	283
JW0628	rlpA	minor lipoprotein	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.245	1	0	6	281
JW1506	ego	fused A12 transporter subunits - - ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.051	0	0	7	281
JW2408	ptsH	phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)	0	-0.166	0	0	3	281
JW2732	cysH	3'-phosphoadenosine 5'-phosphosulfate reductase	0	-0.439	0	0	7	280
JW4299	yjiN	conserved inner membrane protein	GO:0009274 cell wall (sensu	-0.048	1	3	7	280
JW2875	ubiH	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding	0	0.023	1	0	8	279
JW0403	ybaD	conserved protein	0	-0.395	0	0	8	278
JW1217	narJ	molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1	0	-0.259	0	0	6	278
JW1643	gloA	glyoxalase I, Ni-dependent	0	-0.346	0	0	5	278

JW2428	amiA	N-acetylmuramoyl-L-alanine amidase I	GO:0009274 cell wall (sensu	-0.318	0	0	8	278
JW3042	yqjI	predicted transcriptional regulator	0	-0.760	0	0	9	278
JW5253	gnsB	Qin prophage; predicted protein	0	-0.481	0	0	4	278
JW5714	zur	DNA-binding transcriptional activator, Zn(II)-binding	GO:0005737 cytoplasm	-0.250	0	0	5	278
JW0115	yacL	conserved protein	0	-0.471	0	0	5	277
JW2808	ygeA	predicted racemase	0	0.077	1	0	7	277
JW1380	feaB	phenylacetaldehyde dehydrogenase	0	-0.037	0	0	6	276
JW4087	yjdl	conserved protein	0	-0.339	0	0	4	276
JW4129	miaA	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	GO:0005737 cytoplasm	-0.158	0	0	9	276
JW1435	ydcS	predicted spermidine/putrescine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.324	0	0	10	275
JW1835	yebE	conserved protein	0	-0.237	1	2	6	275
JW3170	yhbH	predicted ribosome-associated, sigma 54 modulation protein	0	-0.398	0	0	4	275
JW0325	prpD	2-methylcitrate dehydratase	0	-0.136	0	0	6	274
JW1796	yeaZ	predicted peptidase	0	-0.071	0	0	5	274
JW2796	lgt	phosphatidylglycerol-prolipoprotein diacylglycerol transferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.444	1	5	6	274
JW3942	coaA	pantothenate kinase	0	-0.247	0	0	6	274
JW5070	ybcJ	predicted RNA-binding protein	0	0.101	1	0	5	274
JW0100	coaE	dephospho-CoA kinase	0	-0.116	0	0	5	273
JW2005	hisH	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	0	-0.071	0	0	7	273
JW2366	evgA	DNA-binding response regulator in two-component regulatory system with EvgS	GO:0005737 cytoplasm	-0.094	0	0	4	273
JW2451	yffH	predicted NUDIX hydrolase	0	-0.335	0	0	4	273
JW3071	yqjK	conserved protein	0	-0.544	1	1	7	273
JW3204	degS	serine endoprotease, periplasmic	GO:0042597 periplasmic space	0.115	1	1	5	273
JW4013	alr	alanine racemase 1, PLP-binding, biosynthetic	0	-0.106	0	0	7	273
JW1423	rimL	ribosomal-protein-L7/L12-serine acetyltransferase	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.370	0	0	5	272
JW2926	yggL	predicted protein	0	-0.678	0	0	4	272
JW3134	rpsO	30S ribosomal subunit protein S15	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.673	0	0	4	272
JW2883	argP	DNA-binding transcriptional activator, replication initiation inhibitor	GO:0005737 cytoplasm	-0.173	0	0	5	271
JW1441	ydcY	predicted protein	0	-0.636	0	0	6	270
JW4005	yjbJ	predicted stress response protein	0	-1.526	0	0	4	270

JW2671	mltB	membrane-bound lytic murein transglycosylase B	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.331	1	0	6	269
JW3372	feoB	fused ferrous iron transporter, protein B	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.422	1	10	5	269
JW5247	yneI	predicted aldehyde dehydrogenase	0	-0.032	0	0	8	269
JW5307	yecD	predicted hydrolase	0	-0.031	0	0	6	269
JW1989	yeeX	conserved protein	0	-0.694	0	0	5	268
JW2464	gcvR	DNA-binding transcriptional repressor, regulatory protein accessory to GcvA	GO:0005737 cytoplasm	-0.017	0	0	4	268
JW3227	prmA	methylase for 50S ribosomal subunit protein L11	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.065	0	0	6	268
JW1080	acpP	acyl carrier protein (ACP)	0	-0.346	0	0	4	267
JW1898	uvrC	excinuclease UvrABC, endonuclease subunit	GO:0005737 cytoplasm	-0.344	0	0	7	267
JW2997	ygiN	quinol monooxygenase	0	0.015	1	0	6	267
JW3093	garK	glycerate kinase I	0	0.079	1	0	7	267
JW3941	birA	bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase -!- DNA-binding transcriptional repressor, bio-5'-AMP-binding	GO:0005737 cytoplasm	-0.031	0	0	5	267
JW5952	yjH	KpLE2 phage-like element; predicted DNA-binding transcriptional regulator	0	-0.025	0	0	7	267
JW1153	ymgB	predicted protein	0	0.031	1	0	3	266
JW2347	yfdH	CPS-53 (KpLE1) prophage; bactoprenol glucosyl transferase	0	0.079	1	2	6	266
JW4179	ytfM	predicted outer membrane protein and surface antigen	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.415	1	0	8	266
JW5920	rscC	hybrid sensory kinase in two-component regulatory system with RcsB and YojN	0	-0.114	1	2	8	266
JW0324	prpC	2-methylcitrate synthase	GO:0005737 cytoplasm	-0.289	0	0	7	265
JW2277	nuoH	NADH:ubiquinone oxidoreductase, membrane subunit H	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.810	1	8	5	265
JW3937	trmA	tRNA (uracil-5-)-methyltransferase	GO:0005737 cytoplasm	-0.322	0	0	7	265
JW2777	ygdE	predicted methyltransferase	0	-0.292	0	0	7	264
JW5161	lolC	outer membrane-specific lipoprotein transporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.319	1	4	7	264
JW1842	yebK	predicted DNA-binding transcriptional regulator	0	-0.129	0	0	6	263
JW2833	ygeR	Tetratricopeptide repeat transcriptional regulator	GO:0009279 external outer membrane (sensu Gram-negative	-0.254	1	0	6	263
JW3577	yibL	conserved protein	0	-0.628	0	0	5	263

JW3905	cytR	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.143	0	0	6	263
JW2665	yqaB	predicted hydrolase	0	-0.027	0	0	5	262
JW3280	rplW	50S ribosomal subunit protein L23	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.373	0	0	4	262
JW0729	tolA	membrane anchored protein in TolA-TolQ-TolR complex	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.610	1	1	7	261
JW4026	yjcE	predicted cation/proton antiporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.633	1	11	5	261
JW5857	rbsD	predicted cytoplasmic sugar-binding protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.101	1	0	4	261
JW0142	sfsA	predicted DNA-binding transcriptional regulator	0	-0.340	0	0	6	260
JW3675	yidB	conserved protein	0	-0.006	0	0	3	260
JW0348	frmR	regulator protein that represses frmRAB operon	0	-0.502	0	0	6	259
JW5377	yfcE	predicted phosphatase	0	0.024	1	0	4	259
JW0584	fepB	iron-enterobactin transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.068	0	0	5	258
JW1301	pspE	thiosulfate:cyanide sulfurtransferase (rhodanese)	0	-0.188	0	0	3	258
JW1944	dcm	DNA cytosine methylase	GO:0005737 cytoplasm	-0.450	0	0	8	258
JW2263	elaC	binuclear zinc phosphodiesterase	0	-0.061	0	0	8	258
JW4069	phnA	predicted phosphonate metabolizing protein	0	-0.532	0	0	5	258
JW5156	plsX	fatty acid/phospholipid synthesis protein	0	0.113	1	0	4	258
JW5580	tatB	TatABCE protein translocation system subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.380	1	1	6	258
JW0984	cbpM	modulator of CbpA co-chaperone	0	0.086	1	0	3	257
JW3576	yibT	predicted protein	GO:0005737 cytoplasm	-0.535	0	0	3	257
JW0412	xseB	exonuclease VII small subunit	GO:0005737 cytoplasm	-0.735	0	0	4	256
JW0464	hemH	ferrochelatase	0	-0.187	0	0	5	256
JW1713	ydiZ	predicted protein	0	-0.470	0	0	5	256
JW3612	rpmB	50S ribosomal subunit protein L28	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.650	0	0	6	256
JW0047	folA	dihydrofolate reductase	0	-0.294	0	0	4	255
JW2596	uppS	NAD kinase	0	-0.072	0	0	4	255
JW1210	ychn	conserved protein	0	0.190	1	0	4	254
JW3000	cpdA	cyclic 3',5'-adenosine monophosphate phosphodiesterase	GO:0005737 cytoplasm	-0.203	0	0	4	254
JW3524	viaG	predicted transcriptional regulator	0	-0.397	0	0	5	254
JW5415	yfjD	predicted inner membrane protein	0	0.025	1	3	7	254
JW0904	smtA	S-adenosylmethionine-dependent methyltransferase	0	-0.402	0	0	8	253

JW1082	pabC	4-amino-4-deoxychorismate lyase component of para-aminobenzoate synthase multienzyme complex	0	-0.054	0	0	6	253
JW1169	ycgM	predicted isomerase/hydrolase	0	-0.106	0	0	5	253
JW3565	yibF	predicted glutathione S-transferase	0	-0.027	0	0	9	253
JW5063	ylaC	predicted inner membrane protein	0	0.103	1	2	4	253
JW2203	ompC	outer membrane porin protein C	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.533	1	0	5	252
JW2256	menC	o-succinylbenzoyl-CoA synthase	0	-0.117	0	0	7	252
JW2214	atoC	fused response regulator of ato operon, in two-component system with AtoS	GO:0005737 cytoplasm	-0.168	0	0	10	251
JW2840	ygeY	predicted peptidase	0	-0.251	0	0	7	251
JW2590	rpsP	30S ribosomal subunit protein S16	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.329	0	0	4	250
JW3598	rfaK	lipopolysaccharide core biosynthesis	GO:0019866 inner membrane	-0.176	1	0	9	249
JW5641	ttk	division inhibitor	0	-0.306	0	0	5	249
JW3146	rrmJ	23S rRNA methyltransferase	0	-0.244	0	0	7	248
JW0461	recR	gap repair protein	GO:0005737 cytoplasm	-0.184	0	0	6	247
JW0602	rnk	regulator of nucleoside diphosphate	0	-0.029	0	0	5	247
JW2112	yehS	conserved protein	0	-0.327	0	0	6	247
JW3319	yhfA	conserved protein	0	0.069	1	0	6	247
JW0749	ybhA	predicted hydrolase	0	-0.126	0	0	4	246
JW3568	yibA	lyase containing HEAT-repeat	0	-0.386	0	0	8	246
JW4196	nrdG	anaerobic ribonucleotide reductase activating protein	0	-0.376	0	0	6	246
JW4335	rimI	acetylase for 30S ribosomal subunit protein S18	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.184	0	0	5	246
JW0182	yaeR	predicted lyase	0	-0.198	0	0	3	244
JW0380	yaiA	predicted protein	0	-1.275	0	0	5	244
JW5346	yohN	predicted protein	0	-0.238	1	1	4	244
JW2411	pdxK	pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase	0	0.090	1	0	5	243
JW2556	rseA	anti-sigma factor	GO:0005737 cytoplasm	-0.600	0	0	5	243
JW0186	yaeQ	conserved protein	0	-0.357	0	0	4	242
JW1759	ydjF	predicted DNA-binding transcriptional regulator	0	-0.189	0	0	7	242
JW2115	mlrA	DNA-binding transcriptional regulator	0	-0.349	0	0	6	242
JW2756	rumA	23S rRNA (uracil-5)-methyltransferase	0	-0.230	0	0	8	242
JW3070	yqjE	conserved inner membrane protein	0	0.346	1	2	6	242
JW3525	cspA	major cold shock protein	GO:0005737 cytoplasm	-0.251	0	0	5	242
JW4201	mgTA	magnesium transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.159	1	7	9	242
JW5041	ykgE	predicted oxidoreductase	0	0.037	1	0	6	242

JW5107	ybiN	predicted SAM-dependent methyltransferase	0	-0.382	0	0	5	242
JW1632	ydhH	conserved protein	0	0.057	1	0	6	241
JW2328	yfcN	conserved protein	0	-0.482	0	0	6	241
JW4216	holC	DNA polymerase III, chi subunit	GO:0005737 cytoplasm	-0.372	0	0	6	241
JW0026	fkpB	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	GO:0005737 cytoplasm	-0.095	0	0	3	240
JW0743	modF	fused subunits of molybdate transporter -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.216	0	0	8	240
JW4018	yjbR	conserved protein	0	-0.392	0	0	4	240
JW4148	yjfP	predicted hydrolase	0	-0.036	0	0	4	240
JW5113	ybjI	conserved protein	0	-0.137	0	0	4	240
JW0411	ispA	geranyltranstransferase	GO:0005737 cytoplasm	-0.121	0	0	6	239
JW0864	cspD	cold shock protein homolog	GO:0005737 cytoplasm	-0.197	0	0	3	239
JW0008	mog	predicted molybdochelataase	GO:0005737 cytoplasm	-0.013	0	0	5	238
JW2581	tyrA	fused chorismate mutase T -!- prephenate dehydrogenase	GO:0005737 cytoplasm	-0.090	0	0	8	238
JW2788	recB	exonuclease V (RecBCD complex), beta subunit	0	-0.319	0	0	7	238
JW2288	yfbR	deoxyribonucleoside 5'-	0	-0.216	0	0	6	237
JW2507	pepB	aminopeptidase B	0	-0.214	0	0	5	237
JW3595	rfaF	ADP-heptose:LPS heptosyltransferase	0	-0.185	0	0	6	237
JW5535	yrbB	predicted protein	0	0.032	1	0	4	237
JW5735	dcuA	C4-dicarboxylate antiporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.800	1	9	3	237
JW5777	yjhT	conserved protein	0	-0.348	0	0	5	237
JW2717	ispD	4-diphosphocytidyl-2C-methyl-D-erythritol synthase	GO:0005737 cytoplasm	-0.174	0	0	7	236
JW3386	glpR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.213	0	0	6	236
JW4177	ytfL	predicted inner membrane protein	0	0.238	1	4	5	236
JW2340	yfcZ	conserved protein	0	-0.094	0	0	3	235
JW2989	ygiT	predicted DNA-binding transcriptional regulator	0	-0.322	0	0	6	235
JW1208	chaB	predicted cation regulator	GO:0005737 cytoplasm	-1.478	0	0	5	234
JW1283	sapF	predicted antimicrobial peptide transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.242	0	0	6	234
JW1811	rrmA	23S rRNA m1G745 methyltransferase	GO:0005737 cytoplasm	-0.284	0	0	4	234
JW0389	phoB	DNA-binding response regulator in two-component regulatory system with PhoR (or CreC)	GO:0005737 cytoplasm	-0.372	0	0	4	233
JW0557	nfrA	bacteriophage N4 receptor, outer membrane subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.454	1	0	6	233
JW0700	ybgl	conserved metal-binding protein	0	-0.125	0	0	4	233

JW4212	yjgD	conserved protein	0	-0.605	0	0	4	233
JW0415	panE	2-dehydropantoate reductase, NADPH-specific	0	-0.119	0	0	6	232
JW1575	ynfB	predicted protein	0	-0.746	0	0	4	232
JW2588	trmD	tRNA (guanine-1-)-methyltransferase	GO:0005737 cytoplasm	-0.309	0	0	5	232
JW3274	rpmC	50S ribosomal subunit protein L29	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm	-0.657	0	0	3	232
JW1504	ydeV	predicted sugar kinase	0	0.047	1	0	7	231
JW3273	rpsQ	30S ribosomal subunit protein S17	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm	-0.293	0	0	4	231
JW3360	nudE	ADP-ribose diphosphatase	0	-0.254	0	0	3	231
JW1733	astE	succinylglutamate desuccinylase	0	-0.069	0	0	4	230
JW2918	yggS	predicted enzyme	0	-0.200	0	0	6	230
JW3423	livK	leucine transporter subunit !- periplasmic-binding component of ABC	GO:0042597 periplasmic space	-0.227	0	0	6	230
JW0801	mntR	transcriptional regulator of mntH	0	-0.377	0	0	6	229
JW2262	elaA	predicted acyltransferase with acyl-CoA N-acyltransferase domain	0	-0.218	0	0	4	229
JW5785	yjiL	predicted ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase	0	0.133	1	0	5	229
JW0944	yccF	conserved inner membrane protein	0	0.777	1	3	4	228
JW2142	cirA	ferric iron-catecholate outer membrane transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.600	1	0	4	228
JW1915	yedF	conserved protein	0	-0.271	0	0	4	227
JW3310	slyX	conserved protein	0	-0.478	0	0	3	227
JW5847	prfB	peptide chain release factor RF-2	GO:0005737 cytoplasm	-1.008	0	0	7	227
JW0183	tilS	tRNA(Ile)-lysidine synthetase	0	-0.134	0	0	6	226
JW0654	Int	apolipoprotein N-acyltransferase	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.273	1	6	6	226
JW3537	xylA	D-xylose isomerase	GO:0005737 cytoplasm	-0.442	0	0	6	226
JW4127	amiB	N-acetylmuramoyl-l-alanine amidase II	GO:0009274 cell wall (sensu	-0.297	0	0	7	226
JW2078	gatA	galactitol-specific enzyme IIA component of PTS	0	-0.056	0	0	3	225
JW2757	barA	hybrid sensory histidine kinase, in two-component regulatory system with UvrY	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	-0.109	1	2	8	225
JW3490	yhjD	conserved inner membrane protein	0	0.210	1	6	3	225
JW0378	yail	conserved protein	0	-0.211	0	0	6	224
JW1243	ycil	predicted enzyme	0	-0.031	0	0	4	224
JW1431	ydcP	predicted peptidase	0	-0.311	0	0	9	224
JW3709	atpC	F1 sector of membrane-bound ATP synthase, epsilon subunit	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	-0.095	1	0	4	224

JW1255	trpD	fused glutamine amidotransferase (component II) of anthranilate synthase -!- anthranilate phosphoribosyl	GO:0005737 cytoplasm	-0.007	0	0	5	223
JW5131	yccX	predicted acylphosphatase	0	-0.393	0	0	6	223
JW5296	yoaC	predicted protein	0	-0.253	0	0	3	223
JW0184	rof	modulator of Rho-dependent transcription termination	GO:0005737 cytoplasm	-0.410	0	0	3	222
JW0397	yajC	SecYEG protein translocase auxillary subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.395	1	1	4	222
JW0697	ybgA	conserved protein	0	-0.489	0	0	5	222
JW3243	yrdC	dsRNA-binding protein	0	-0.057	0	0	3	222
JW5598	rffG	dTDP-glucose 4,6-dehydratase	0	-0.270	0	0	6	222
JW0316	yahJ	predicted deaminase with metallo-dependent hydrolase domain	0	-0.245	0	0	7	221
JW0369	yaiW	predicted DNA-binding transcriptional regulator	0	-0.377	0	0	7	221
JW0647	gltL	glutamate and aspartate transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.063	0	0	6	221
JW1284	sapD	predicted antimicrobial peptide transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.357	0	0	5	221
JW1669	sufE	sulfur acceptor protein	0	-0.171	0	0	5	221
JW1914	yedE	predicted inner membrane protein	0	0.586	1	10	5	221
JW3147	yhbY	predicted RNA-binding protein	0	-0.182	0	0	4	221
JW5794	mdbB	phosphoglycerol transferase I	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.236	1	4	9	221
JW5943	yhjK	predicted diguanylate cyclase	0	0.187	1	2	6	221
JW0022	rpsT	30S ribosomal subunit protein S20	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.705	0	0	3	219
JW0106	ampD	N-acetyl-anhydromuranmyl-L-alanine amidase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.309	0	0	6	219
JW0479	ybbL	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.212	0	0	6	219
JW1165	minC	cell division inhibitor	GO:0005737 cytoplasm	-0.051	0	0	5	219
JW3889	cdh	CDP-diacylglycerol	0	-0.304	1	1	6	219
JW0910	ycbL	predicted metal-binding enzyme	0	-0.145	0	0	5	218
JW1121	ymfC	23S rRNA pseudouridine synthase	0	-0.669	0	0	5	218
JW3002	nudF	ADP-ribose pyrophosphatase	0	-0.216	0	0	6	217
JW3606	rfaG	glucosyltransferase I	GO:0019866 inner membrane	-0.341	1	0	6	217
JW4017	yjbQ	conserved protein	0	-0.396	0	0	4	217
JW0704	nei	endonuclease VIII -!- 5-formyluracil/5-hydroxymethyluracil DNA glycosylase	GO:0005737 cytoplasm	-0.349	0	0	5	216
JW3037	rpsU	30S ribosomal subunit protein S21	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-1.090	0	0	4	216

JW3778	cyaA	adenylate cyclase	GO:0005737 cytoplasm	-0.292	0	0	8	216
JW1884	yecG	universal stress protein	0	0.127	1	0	4	215
JW1041	lpxL	lauryl-acyl carrier protein (ACP)-dependent acyltransferase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.205	1	1	6	214
JW2863	fldB	flavodoxin 2	0	-0.231	0	0	4	214
JW4111	ampC	beta-lactamase/D-alanine carboxypeptidase	GO:0009274 cell wall (sensu Bacteria) - - GO:0042597	-0.184	0	0	4	214
JW5372	yfbE	uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase, PLP-dependent	0	-0.044	0	0	5	214
JW1818	htpX	predicted endopeptidase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.344	1	4	4	213
JW5596	rffT	TDP-Fuc4NAc:lipidIII transferase	0	-0.138	0	0	7	213
JW0177	lpxB	tetraacyldisaccharide-1-P synthase	GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 cytoplasm	-0.007	0	0	6	212
JW1334	ydaL	conserved protein	0	-0.600	0	0	8	212
JW2138	galS	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	0.029	1	0	6	212
JW2601	smpB	trans-translation protein	0	-0.581	0	0	4	212
JW2860	recJ	ssDNA exonuclease, 5' --> 3'-specific	0	-0.069	0	0	8	212
JW4136	yjeB	predicted DNA-binding transcriptional regulator	0	0.055	1	0	5	212
JW4160	rpsR	30S ribosomal subunit protein S18	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.775	0	0	3	212
JW3487	treF	cytoplasmic trehalase	GO:0005737 cytoplasm	-0.563	0	0	6	211
JW3813	tatA	TatABCE protein translocation system subunit	0	-0.470	1	1	3	211
JW0070	leuD	3-isopropylmalate isomerase subunit	GO:0005737 cytoplasm	-0.175	0	0	5	210
JW0795	glnP	glutamine transporter subunit - - membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.877	1	3	5	210
JW1941	yedI	conserved inner membrane protein	GO:0009274 cell wall (sensu	0.804	1	5	4	210
JW3036	ygjD	predicted peptidase	0	0.015	1	0	4	209
JW5396	ypfH	predicted hydrolase	0	-0.009	0	0	4	209
JW1655	mdtK	multidrug efflux system transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.760	1	12	3	208
JW3219	mreC	cell wall structural complex MreBCD transmembrane component MreC	GO:0009274 cell wall (sensu Bacteria)	-0.152	1	1	5	208
JW0279	yagS	predicted oxidoreductase with FAD-binding domain	0	-0.010	0	0	5	207
JW0336	lacI	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	0.032	1	0	6	207
JW0566	ybdG	predicted mechanosensitive channel	GO:0042597 periplasmic space	0.301	1	5	7	206
JW3414	ugpQ	glycerophosphodiester phosphodiesterase, cytosolic	GO:0005737 cytoplasm	-0.213	0	0	4	206
JW3844	yihM	predicted sugar phosphate isomerase	0	-0.350	0	0	7	206
JW5588	yigl	conserved protein	0	-0.008	0	0	5	206
JW5646	envC	protease with a role in cell division	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.688	1	1	6	206

JW5949	yrdD	predicted DNA topoisomerase		0	-0.315	0	0	5	206
JW0781	rhIE	RNA helicase		0	-0.506	0	0	7	205
JW4089	yjdK	predicted protein		0	-0.150	0	0	2	205
JW5482	speC	ornithine decarboxylase, constitutive		0	-0.162	0	0	5	205
JW5823	ycdH	predicted protein		0	-1.024	0	0	4	205
JW1319	mpaA	murein peptide amidase A		0	-0.146	0	0	6	204
JW2455	yffB	conserved protein		0	-0.338	0	0	5	204
JW2801	ygdR	predicted protein		0	-0.200	1	1	2	204
JW3626	trmH	tRNA (Guanosine-2'-O)-		0	-0.223	0	0	6	204
JW3866	fdhD	formate dehydrogenase formation	GO:0005737 cytoplasm		-0.173	0	0	4	204
JW5096	kdpE	DNA-binding response regulator in two-component regulatory system with	GO:0005737 cytoplasm		-0.147	0	0	7	204
JW0109	pdhR	DNA-binding transcriptional dual	GO:0005737 cytoplasm		-0.551	0	0	4	203
JW3664	ibpA	heat shock chaperone		0	-0.525	0	0	4	203
JW1586	dgsA	DNA-binding transcriptional repressor	GO:0005737 cytoplasm		0.096	1	0	6	202
JW2701	fhlA	DNA-binding transcriptional activator	GO:0005737 cytoplasm		-0.244	0	0	7	202
JW4149	ulaR	DNA-binding transcriptional dual		0	-0.179	0	0	5	201
JW2599	yjfF	predicted protein		0	-0.584	0	0	5	200
JW2921	yggV	dITP/XTP pyrophosphatase		0	-0.122	0	0	3	200
JW3359	mrcA	fused penicillin-binding protein 1a murein transglycosylase -!- murein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.255	1	1	5	200
JW5448	ygdI	predicted protein		0	-0.523	1	1	3	200
JW0805	ybiU	predicted protein		0	-0.395	0	0	5	199
JW2804	aas	fused 2-acylglycerophospho-ethanolamine acyl transferase -!- acyl-acyl carrier protein synthetase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane		-0.042	1	0	9	199
JW3609	coaD	pantetheine-phosphate adenylyltransferase		0	0.006	1	0	4	198
JW0810	moeB	molybdopterin synthase sulfurlyase		0	0.164	1	0	4	197
JW0862	macA	macrolide transporter subunit, membrane fusion protein (MFP)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.184	1	1	8	197
JW5262	dmsD	twin-arginine leader-binding protein for DmsA and TorA		0	-0.089	0	0	5	197
JW0195	metN	DL-methionine transporter subunit -!- ATP-binding component of ABC	GO:0005737 cytoplasm		-0.072	0	0	4	196
JW0821	yliI	predicted dehydrogenase		0	-0.374	0	0	6	195
JW2508	yfhJ	conserved protein		0	-0.520	0	0	2	195
JW3312	yheV	predicted protein	GO:0005737 cytoplasm		-0.611	0	0	3	195
JW4107	efp	Elongation factor EF-P	GO:0005737 cytoplasm		-0.221	0	0	3	194
JW1218	narI	nitrate reductase 1, gamma (cytochrome b(NR)) subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.575	1	5	3	193
JW2790	recC	exonuclease V (RecBCD complex), gamma chain		0	-0.288	0	0	7	193
JW5054	psiF	conserved protein		0	-0.570	1	1	3	193
JW2088	yegW	predicted DNA-binding transcriptional regulator		0	-0.306	0	0	5	192

JW3197	sspB	ClpXP protease specificity-enhancing factor	0	-0.432	0	0	3	192
JW5736	yjel	conserved protein	0	-0.076	0	0	2	192
JW0373	yaiB	predicted protein	0	-0.458	0	0	3	191
JW2023	rfbC	dTDP-4-deoxyrhamnose-3,5-epimerase	GO:0005737 cytoplasm -! GO:0005737 cytoplasm	-0.204	0	0	5	191
JW3811	yigP	conserved protein	0	0.021	1	0	3	191
JW0107	ampE	predicted inner membrane protein	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.474	1	4	4	190
JW1667	lpp	murein lipoprotein	GO:0009274 cell wall (sensu Bacteria) -! GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner membrane	-0.314	1	0	2	190
JW3980	yjbB	predicted transporter	0	0.432	1	8	6	190
JW0482	ybbO	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	0	-0.043	0	0	5	189
JW2872	gcvH	glycine cleavage complex lipoylprotein	0	-0.139	0	0	3	189
JW3307	yheN	predicted intracellular sulfur oxidation protein	0	0.166	1	0	3	189
JW5521	tdcF	predicted L-PSP (mRNA)	0	0.120	1	0	3	189
JW1336	ydaN	predicted Zn(II) transporter	0	-0.050	1	2	5	188
JW3098	sohA	predicted regulator	0	-0.578	0	0	3	188
JW3512	dppB	dipeptide transporter-!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.692	1	6	3	188
JW5819	ybjS	predicted NAD(P)H oxidoreductase with NAD(P)-binding Rossmann-fold domain	0	-0.290	0	0	3	187
JW0079	mraZ	conserved protein	0	-0.247	0	0	4	186
JW0400	yajD	conserved protein	0	-0.830	0	0	3	186
JW0788	ybil	conserved protein	0	-0.882	0	0	5	186
JW1083	yceG	predicted aminodeoxychorismate lyase	0	-0.236	1	1	5	186
JW1274	yciH	conserved protein	0	-0.419	0	0	3	186
JW4085	dcuR	DNA-binding response regulator in two-component regulatory system with	GO:0005737 cytoplasm	-0.250	0	0	4	185
JW4054	phnO	predicted acyltransferase with acyl-CoA N-acyltransferase domain	0	-0.316	0	0	4	184
JW2916	yqgF	predicted Holliday junction resolvase	0	-0.257	0	0	3	183
JW3446	nikR	DNA-binding transcriptional regulator, Ni-binding	GO:0005737 cytoplasm	-0.532	0	0	4	183
JW0382	yaiE	conserved protein	0	-0.039	0	0	3	182
JW1617	ydgT	predicted regulator	0	-0.470	0	0	5	182
JW5745	ytfB	predicted cell envelope opacity-associated protein	0	-0.574	0	0	4	182
JW0727	tolQ	membrane spanning protein in TolA-TolQ-TolR complex	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.226	1	3	4	181
JW2299	yfcG	predicted glutathione S-transferase	0	-0.382	0	0	4	181
JW3223	accB	acetyl CoA carboxylase, BCCP subunit	0	0.010	1	0	3	181
JW0533	ybcL	DLP12 prophage; predicted kinase	0	-0.121	0	0	3	180

JW1782	yoaF	conserved outer membrane protein		0	-0.167	0	0	2	180
JW4116	poxA	predicted lysyl-tRNA synthetase		0	-0.291	0	0	5	180
JW5116	ybjT	conserved protein with NAD(P)-binding Rossmann-fold domain		0	-0.064	1	1	4	180
JW0936	rnf	ribosome modulation factor	GO:0009281 cytosolic ribosome (sensu Bacteria) !- GO:0005737 cytoplasm		-1.136	0	0	4	179
JW2805	galR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm		-0.069	0	0	5	179
JW3784	xerC	site-specific tyrosine recombinase		0	-0.379	0	0	4	179
JW1676	ydil	conserved protein		0	-0.064	0	0	3	178
JW0046	kefC	potassium:proton antiporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		0.457	1	13	5	177
JW2515	iscR	DNA-binding transcriptional activator		0	-0.256	0	0	3	177
JW2767	sdaC	predicted serine transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		0.807	1	11	3	177
JW3470	arsC	arsenate reductase		0	-0.280	0	0	4	177
JW5657	yaD	predicted outer membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		-0.073	1	3	2	177
JW0560	cusR	DNA-binding response regulator in two-component regulatory system with		0	0.075	1	0	5	176
JW2557	rpoE	RNA polymerase, sigma 24 (sigma E) factor	GO:0005737 cytoplasm		-0.254	0	0	4	176
JW5758	yjgM	predicted acetyltransferase		0	-0.122	0	0	4	176
JW0712	sdhD	succinate dehydrogenase, membrane subunit, binds cytochrome b556	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		1.369	1	3	3	175
JW5528	yraR	predicted nucleoside-diphosphate-sugar epimerase		0	-0.095	0	0	2	175
JW1237	oppC	oligopeptide transporter subunit !- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) !- GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner membrane		0.675	1	6	4	174
JW2687	hycl	protease involved in processing C-terminal end of HycE		0	0.023	1	0	3	174
JW2999	yqiA	predicted esterase		0	-0.034	0	0	3	174
JW4166	cycA	D-alanine/D-serine/glycine transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		0.831	1	12	3	173
JW0456	priC	primosomal replication protein N"	GO:0005737 cytoplasm		-0.551	0	0	6	172
JW1168	ycgL	conserved protein		0	-0.669	0	0	5	172
JW1807	manY	mannose-specific enzyme IIC component of PTS	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner		1.007	1	7	2	172
JW2284	IrhA	DNA-binding transcriptional repressor	GO:0005737 cytoplasm		-0.011	0	0	5	172
JW3608	kdtA	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	GO:0009274 cell wall (sensu Bacteria) !- GO:0030113 capsule (sensu Bacteria)		0.022	1	0	5	172
JW0703	ybgL	predicted lactam utilization protein		0	0.022	1	0	4	171
JW1581	ynfG	oxidoreductase, Fe-S subunit		0	-0.418	0	0	3	171

JW3863	fdol	formate dehydrogenase-O, cytochrome b556 subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.499	1	4	2	171
JW2961	hybD	predicted maturation element for hydrogenase 2	0	0.298	1	0	4	170
JW3602	rfal	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase	0	-0.221	0	0	6	170
JW1436	ycdT	predicted spermidine/putrescine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.121	0	0	5	169
JW0976	gnsA	predicted regulator of phosphatidylethanolamine synthesis	GO:0005737 cytoplasm	-0.546	0	0	2	168
JW1610	uidR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.037	0	0	4	168
JW1699	btuD	vitamin B12 transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.132	0	0	4	168
JW2960	hybE	hydrogenase 2-specific chaperone	0	-0.054	0	0	3	168
JW3644	uhpA	DNA-binding response regulator in two-component regulatory system with	GO:0005737 cytoplasm	0.182	1	0	4	168
JW3840	glnL	sensory kinase in two-component regulatory system with GlnG	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.174	1	0	6	168
JW0077	ilvH	acetolactate synthase III, thiamin-dependent, small subunit	0	-0.055	0	0	3	167
JW0767	moaD	molybdopterin synthase, small subunit	0	0.202	1	0	2	167
JW1828	yebY	predicted protein	0	0.010	1	1	2	167
JW3426	rpoH	RNA polymerase, sigma 32 (sigma H) factor	GO:0005737 cytoplasm	-0.502	0	0	3	167
JW1891	yecJ	predicted protein	GO:0005737 cytoplasm	0.082	1	0	4	166
JW4325	dnaC	DNA biosynthesis protein	0	-0.481	0	0	3	166
JW5553	argB	acetylglutamate kinase	GO:0005737 cytoplasm	0.207	1	0	3	166
JW5962	sra	30S ribosomal subunit protein S22	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-1.269	0	0	4	166
JW1222	rssA	conserved protein	GO:0009274 cell wall (sensu	0.084	1	0	3	165
JW3118	yraO	DnaA initiator-associating factor for replication initiation	0	0.023	1	0	4	165
JW3130	mtr	tryptophan transporter of high affinity	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.863	1	11	2	165
JW4113	frdC	fumarate reductase (anaerobic), membrane anchor subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.554	1	3	3	165
JW4181	ytfP	conserved protein	0	-0.514	0	0	3	165
JW1152	ymgA	predicted protein	0	-0.600	0	0	5	164
JW1251	yciG	predicted protein	0	-1.673	0	0	3	164
JW2837	ygeV	predicted DNA-binding transcriptional regulator	0	-0.130	0	0	5	164
JW3102	agaV	N-acetylgalactosamine-specific enzyme IIB component of PTS	GO:0005737 cytoplasm	0.226	1	0	4	164

JW3611	rpmG	50S ribosomal subunit protein L33	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.804	0	0	2	164
JW0388	sbcD	exonuclease, dsDNA, ATP-dependent	GO:0005737 cytoplasm	-0.244	0	0	5	163
JW2117	yehX	predicted transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.119	0	0	7	163
JW2283	nuoA	NADH:ubiquinone oxidoreductase, membrane subunit A	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.565	1	3	2	163
JW1727	chbB	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	0	0.251	1	0	3	162
JW5241	yddV	predicted diguanylate cyclase	0	-0.277	0	0	4	162
JW5816	ybfE	LexA regulated protein	0	-0.907	0	0	3	162
JW1001	putP	proline:sodium symporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.785	1	12	5	161
JW2389	nupC	nucleoside (except guanosine) transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.903	1	8	3	161
JW3367	envZ	sensory histidine kinase in two-component regulatory system with	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.060	1	2	6	159
JW3484	gadX	DNA-binding transcriptional dual	0	-0.077	0	0	4	159
JW4002	dgkA	diacylglycerol kinase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.881	1	2	3	159
JW5338	mdtA	multidrug efflux system, subunit A	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.223	1	1	3	159
JW0002	thrB	homoserine kinase	GO:0005737 cytoplasm	0.024	1	0	5	158
JW4167	ytfE	predicted regulator of cell morphogenesis and cell wall	0	-0.352	0	0	4	158
JW0773	ybhP	predicted DNase	0	-0.295	0	0	3	157
JW1517	yneH	predicted glutaminase	0	0.133	1	0	3	157
JW1602	tus	inhibitor of replication at Ter, DNA-binding protein	GO:0005737 cytoplasm	-0.471	0	0	7	157
JW1657	ydhR	predicted protein	0	-0.215	0	0	2	157
JW1954	yedY	predicted reductase	0	-0.289	0	0	5	157
JW3208	yhcO	predicted barnase inhibitor	0	-0.376	0	0	3	157
JW0952	yccK	predicted sulfite reductase subunit	0	-0.304	0	0	3	156
JW2545	yfhH	predicted DNA-binding transcriptional regulator	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.007	1	0	4	156
JW2600	yfjG	conserved protein	0	0.129	1	0	4	156
JW5336	yegH	fused predicted membrane proteins	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.177	1	7	2	156
JW5660	eptB	predicted metal dependent hydrolase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.110	1	5	5	156
JW3142	secG	preprotein translocase membrane subunit	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.375	1	2	2	155
JW3906	priA	Primosome factor n' (replication factor)	GO:0005737 cytoplasm	-0.186	0	0	6	155
JW5017	yafD	conserved protein	0	-0.154	0	0	4	155
JW5117	hcr	HCP oxidoreductase, NADH-dependent	0	-0.066	0	0	3	155
JW0957	hyaD	protein involved in processing of HyaA and HyaB proteins	0	-0.114	0	0	3	154
JW1223	rssB	response regulator of RpoS	GO:0005737 cytoplasm	0.071	1	0	4	154

JW3581	yibK	predicted rRNA methylase	0	-0.243	0	0	4	154
JW3716	atpB	F0 sector of membrane-bound ATP synthase, subunit a		0.807	1	5	3	154
JW0057	rluA	pseudouridine synthase for 23S rRNA (position 746) and tRNA ^{phe} (position 32)	0	-0.428	0	0	3	153
JW1275	osmB	lipoprotein	0	0.511	1	0	1	153
JW2779	gcvA	DNA-binding transcriptional dual		-0.143	0	0	4	153
JW5182	dsbB	oxidoreductase that catalyzes reoxidation of DsbA protein disulfide isomerase I		0.638	1	4	4	153
JW0393	malZ	maltodextrin glucosidase		-0.449	0	0	5	152
JW1262	btuR	cob(I)alamin adenosyltransferase/cobinamide ATP-dependent adenosyltransferase		-0.440	0	0	2	152
JW3100	agaR	DNA-binding transcriptional dual	0	-0.232	0	0	3	152
JW5159	ycfQ	predicted DNA-binding transcriptional regulator	0	-0.254	0	0	3	152
JW5479	yggU	conserved protein	0	-0.074	0	0	3	152
JW2298	yfcF	predicted enzyme	0	-0.215	0	0	4	151
JW4073	basS	sensory histidine kinase in two-component regulatory system with		-0.050	1	2	6	151
JW0630	mrdA	transpeptidase involved in peptidoglycan synthesis (penicillin-		-0.353	1	1	6	150
JW1696	ydiU	conserved protein	0	-0.425	0	0	5	150
JW5486	glcF	glycolate oxidase iron-sulfur subunit	0	-0.275	0	0	4	150
JW0772	ybhO	cardiolipin synthase 2	0	-0.392	0	0	6	149
JW2274	nuoK	NADH:ubiquinone oxidoreductase, membrane subunit K		0.929	1	3	2	149
JW2538	yfhA	predicted DNA-binding response regulator in two-component system	0	-0.156	0	0	4	149
JW3610	mutM	formamidopyrimidine/5-formyluracil/ 5-hydroxymethyluracil DNA glycosylase		-0.272	0	0	4	149
JW5226	ydcl	predicted DNA-binding transcriptional regulator	0	-0.022	0	0	5	149
JW1562	dicA	Qin prophage; predicted regulator for	0	-0.789	0	0	4	148
JW2922	yggW	predicted oxidoreductase	0	-0.325	0	0	4	148
JW3363	hslR	ribosome-associated heat shock protein Hsp15		-0.941	0	0	5	148
JW3381	malT	DNA-binding transcriptional activator, maltotriose-ATP-binding		-0.273	0	0	4	148
JW0432	ybaV	conserved protein	0	0.019	1	0	4	147
JW0253	mmuM	CP4-6 prophage; S-methylmethionine:homocysteine methyltransferase	0	-0.030	0	0	3	146
JW0726	ybgC	predicted acyl-CoA thioesterase	0	-0.123	0	0	3	146

JW1351	racR	Rac prophage; predicted DNA-binding transcriptional regulator	0	-0.469	0	0	3	146		
JW5062	ylaB	conserved inner membrane protein	0	-0.136	1	2	6	146		
JW5216	ydbL	conserved protein	0	-0.125	1	1	5	146		
JW5380	trmC	fused 5-methylaminomethyl-2-thiouridine forming enzyme methyltransferase -!- FAD-dependent	0	-0.280	0	0	4	146		
JW0138	folK	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	0	-0.213	0	0	2	145		
JW0475	ybaT	predicted transporter			GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.038	1	12	3	145
JW0912	ompF	outer membrane porin 1a (Ia;b;F)			GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.398	1	0	4	145
JW0959	hyaF	protein involved in nickel incorporation into hydrogenase-1 proteins	0	-0.159	0	0	2	145		
JW1278	gmr	modulator of Rnase II stability	0	-0.190	0	0	4	145		
JW3046	ebgR	DNA-binding transcriptional repressor			GO:0005737 cytoplasm	-0.153	0	0	5	145
JW5871	mcrB	5-methylcytosine-specific restriction enzyme McrBC, subunit McrB			GO:0005737 cytoplasm	-0.456	0	0	6	145
JW0723	cydB	cytochrome d terminal oxidase, subunit II			GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.658	1	8	2	144
JW1149	ycgE	predicted DNA-binding transcriptional regulator	0	-0.405	0	0	2	144		
JW2018	wbbJ	predicted acyl transferase	0	0.103	1	0	3	144		
JW2919	yggT	predicted inner membrane protein	0	1.191	1	4	2	144		
JW3361	yrfF	predicted inner membrane protein	0	-0.097	1	5	6	144		
JW4259	yjhG	KpLE2 phage-like element; predicted dehydratase	0	-0.111	0	0	7	144		
JW5259	ynfD	predicted protein	0	-0.122	0	0	2	144		
JW0512	purE	N5-carboxyaminoimidazole ribonucleotide mutase			GO:0005737 cytoplasm	0.086	1	0	2	143
JW1471	fdnH	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible			GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.271	1	1	3	143
JW1623	rsxG	predicted oxidoreductase	0	-0.129	0	0	3	143		
JW3206	argR	DNA-binding transcriptional dual regulator, L-arginine-binding			GO:0005737 cytoplasm	-0.007	0	0	4	143
JW3596	rfaC	ADP-heptose:LPS heptosyl transferase			GO:0019866 inner membrane	-0.219	1	0	3	143
JW3829	mobA	molybdopterin-guanine dinucleotide synthase	0	-0.191	0	0	4	143		
JW5701	yhfK	conserved inner membrane protein			GO:0005737 cytoplasm	0.047	1	9	4	143
JW0204	rnhA	ribonuclease HI, degrades RNA of DNA-RNA hybrids			GO:0005737 cytoplasm	-0.631	0	0	4	142
JW0556	ybcH	predicted protein	0	-0.158	1	1	3	142		

JW1131	ymfK	e14 prophage; repressor protein phage e14	0	-0.411	0	0	5	142
JW3603	rfaB	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase	0	-0.143	0	0	4	142
JW3982	yjbC	23S rRNA pseudouridine synthase	0	-0.522	0	0	4	142
JW0381	aroM	conserved protein	0	0.166	1	0	3	141
JW4287	uxuR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.405	0	0	6	140
JW1115	phoQ	sensory histidine kinase in two-component regulatory system with PhoP	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.140	1	2	4	139
JW2771	fucA	L-fucose-1-phosphate aldolase	0	-0.046	0	0	3	139
JW1329	ogt	O-6-alkylguanine-DNA:cysteine-protein methyltransferase	GO:0005737 cytoplasm	-0.253	0	0	2	138
JW1533	ydfH	predicted DNA-binding transcriptional regulator	0	-0.496	0	0	5	138
JW3475	yhiF	predicted DNA-binding transcriptional regulator	0	0.269	1	0	5	138
JW5807	leuB	3-isopropylmalate dehydrogenase	GO:0005737 cytoplasm	-0.113	0	0	4	138
JW1175	nhaB	sodium:proton antiporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.806	1	12	3	137
JW3305	yheL	predicted intracellular sulfur oxidation protein	0	0.091	1	0	2	137
JW3640	ade	cryptic adenine deaminase	0	-0.035	0	0	6	137
JW1900	yecF	predicted protein	0	-0.258	0	0	3	136
JW2175	yejL	conserved protein	0	-0.184	0	0	2	136
JW3165	kdsC	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	0	0.239	1	0	2	135
JW3818	rfaH	DNA-binding transcriptional antiterminator	GO:0009289 fimbria -!- GO:0005737 cytoplasm	-0.141	0	0	3	135
JW5575	mobB	molybdopterin-guanine dinucleotide biosynthesis protein B	0	-0.082	0	0	3	135
JW2185	ccmE	periplasmic heme chaperone	GO:0019866 inner membrane	-0.275	1	1	3	134
JW3021	glgS	predicted glycogen synthesis protein	GO:0005737 cytoplasm	-0.544	0	0	3	134
JW5378	dedD	conserved protein	0	-0.306	1	1	3	134
JW2182	ccmH	heme lyase, CcmH subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.169	1	3	4	133
JW2891	mscS	mechanosensitive channel	0	0.494	1	3	2	133
JW5368	yojL	predicted thiamine biosynthesis	0	-0.282	0	0	4	133
JW5487	glcE	glycolate oxidase FAD binding subunit	0	-0.148	0	0	2	133
JW0085	mraY	phospho-N-acetylmuramoyl-pentapeptide transferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.824	1	10	4	132
JW0281	yagU	conserved inner membrane protein	0	0.337	1	3	3	132
JW2798	nudH	nucleotide hydrolase	0	-0.674	0	0	2	132
JW5136	ymdF	conserved protein	GO:0005737 cytoplasm	-1.712	0	0	3	132
JW0328	codA	cytosine deaminase	GO:0005737 cytoplasm	-0.222	0	0	3	131

JW1752	topB	DNA topoisomerase III	GO:0005737 cytoplasm	-0.370	0	0	4	131
JW2367	evgS	hybrid sensory histidine kinase in two-component regulatory system with EvgA	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.199	1	0	4	131
JW3369	greB	transcription elongation factor	GO:0005737 cytoplasm	-0.692	0	0	5	131
JW3984	lysC	aspartokinase III	GO:0005737 cytoplasm	0.210	1	0	4	131
JW4108	ecnB	entericidin B membrane lipoprotein	0	0.419	1	1	1	131
JW5965	yicS	predicted protein	0	-0.319	0	0	4	131
JW0711	sdhC	succinate dehydrogenase, membrane subunit, binds cytochrome b556	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.837	1	3	2	130
JW3546	yiaJ	predicted DNA-binding transcriptional repressor	0	-0.162	0	0	6	130
JW0300	ykgF	predicted amino acid dehydrogenase with NAD(P)-binding domain and ferridoxin-like domain	0	-0.313	0	0	4	129
JW0824	deoR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.182	0	0	4	129
JW3415	ugpC	glycerol-3-phosphate transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.224	0	0	2	129
JW3812	ubiB	2-octaprenylphenol hydroxylase	0	-0.140	1	2	4	129
JW4218	yjgP	conserved inner membrane protein	GO:0009274 cell wall (sensu	0.465	1	6	4	129
JW5446	exo	exonuclease IX (5'-3' exonuclease)	0	-0.208	0	0	3	129
JW1609	uidA	beta-D-glucuronidase	0	-0.383	0	0	4	128
JW2394	yfeD	predicted DNA-binding transcriptional regulator	0	-0.498	0	0	2	128
JW2835	xdhB	xanthine dehydrogenase, FAD-binding subunit	0	-0.115	0	0	4	128
JW5258	ynfC	predicted protein	0	-0.411	0	0	2	128
JW1374	hslJ	heat-inducible protein	0	-0.131	0	0	2	127
JW3161	yrbE	predicted toluene transporter subunit-!- membrane component of ABC	0	0.847	1	5	4	127
JW3927	yijP	conserved inner membrane protein	GO:0009274 cell wall (sensu	-0.323	1	5	5	127
JW4348	yjjJ	predicted DNA-binding transcriptional regulator	0	-0.249	0	0	7	127
JW5510	ygjG	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent	0	0.016	1	0	6	127
JW0833	grxA	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)	0	-0.571	0	0	3	126
JW2582	aroF	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase, tyrosine-	0	-0.297	0	0	3	126
JW1916	yedK	predicted protein	0	-0.388	0	0	3	125
JW2643	ygaP	predicted inner membrane protein with hydrolase activity	0	0.239	1	2	5	125
JW3157	yrbA	predicted DNA-binding transcriptional regulator	0	-0.265	0	0	4	125
JW4152	ulaB	L-ascorbate-specific enzyme IIB component of PTS	0	0.091	1	0	3	125
JW1940	yodC	predicted protein	0	-0.407	0	0	4	124

JW2063	baeS	sensory histidine kinase in two-component regulatory system with	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.208	1	2	3	124
JW2378	ypdB	predicted response regulator in two-component system with YpdA	0	-0.180	0	0	3	124
JW5353	yehU	predicted sensory kinase in two-component system with YehT	0	0.175	1	6	5	124
JW2654	proX	glycine betaine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.321	0	0	4	123
JW3127	yhbU	predicted peptidase (collagenase-like)	0	-0.271	0	0	4	123
JW3600	rfaY	lipopolysaccharide core biosynthesis protein	GO:0019866 inner membrane	-0.517	1	0	4	123
JW5402	yfgJ	predicted protein	0	-0.179	0	0	3	123
JW5633	yidQ	conserved outer membrane protein	0	-0.035	0	0	3	123
JW5645	yibQ	predicted polysaccharide deacetylase	0	-0.229	1	1	3	123
JW1298	pspB	transcriptional regulator of psp operon	GO:0005737 cytoplasm	-0.223	1	1	2	122
JW2254	pmrD	polymyxin resistance protein B	0	-0.264	0	0	2	122
JW5627	dgoR	predicted DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.355	0	0	4	122
JW0261	yagE	CP4-6 prophage; predicted	0	0.105	1	0	3	121
JW3323	pabA	aminodeoxychorismate synthase,	0	-0.022	0	0	3	121
JW3746	ilvY	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.141	0	0	3	121
JW5897	yliA	fused predicted peptide transport subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.040	0	0	2	121
JW0635	holA	DNA polymerase III, delta subunit	GO:0005737 cytoplasm	-0.099	0	0	4	120
JW1805	yoaE	fused predicted membrane proteins	GO:0009274 cell wall (sensu	0.452	1	7	3	120
JW2592	ypjD	predicted inner membrane protein	0	0.822	1	8	2	120
JW3745	ilvA	threonine deaminase	0	-0.048	0	0	4	120
JW5083	ybdF	conserved protein	0	-0.365	0	0	3	120
JW5367	napB	nitrate reductase, small, cytochrome C550 subunit, periplasmic	GO:0042597 periplasmic space	-0.412	0	0	3	119
JW5622	tnaB	tryptophan transporter of low affinity	0	0.719	1	7	2	119
JW1104	lolE	outer membrane-specific lipoprotein transporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.411	1	4	3	118
JW2993	qseB	DNA-binding response regulator in two-component regulatory system with	0	-0.234	0	0	4	118
JW4025	yjcD	predicted permease	0	1.121	1	13	3	118
JW5466	guaD	guanine deaminase	0	-0.368	0	0	6	118
JW5542	yhdP	conserved membrane protein, predicted transporter	0	-0.279	1	1	6	118
JW0346	frmB	predicted esterase	0	-0.363	0	0	5	117
JW0875	ycaJ	recombination protein	0	-0.387	0	0	5	117
JW3425	livJ	leucine/isoleucine/valine transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.189	0	0	3	117

JW4028	actP	acetate transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.793	1	13	3	117
JW5066	ybbM	predicted inner membrane protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.726	1	7	2	117
JW2060	mdtB	multidrug efflux system, subunit B	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	0.376	1	11	5	116
JW2132	sanA	predicted protein		0	0.014	1	5	116
JW3166	yrbK	conserved protein		0	-0.372	1	4	116
JW3435	yhhP	conserved protein required for cell		0	-0.227	0	3	116
JW4206	yjgH	predicted mRNA endoribonuclease		0	-0.176	0	3	116
JW0873	ftsK	DNA-binding membrane protein required for chromosome resolution and	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.407	1	5	5	115
JW2315	truA	pseudouridylate synthase I	GO:0005737 cytoplasm	-0.314	0	0	4	115
JW2406	cysZ	predicted inner membrane protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.549	1	4	3	115
JW0453	acrR	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.186	0	0	2	114
JW0588	entA	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase		0	0.033	1	5	114
JW1871	cheY	chemotaxis regulator transmitting signal to flagellar motor component	GO:0005737 cytoplasm	0.027	1	0	2	114
JW2676	srlR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.125	0	0	3	114
JW2784	mltA	membrane-bound lytic murein transglycosylase A	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.409	1	0	4	114
JW3551	viaO	predicted transporter		0	-0.198	0	3	114
JW5013	cdaR	DNA-binding transcriptional regulator		0	-0.234	0	4	114
JW0275	intF	CP4-6 prophage; predicted phage integrase		0	-0.406	0	4	113
JW5272	ydhV	predicted oxidoreductase		0	-0.333	0	4	113
JW0049	apaG	protein associated with Co2+ and Mg2+ efflux		0	-0.045	0	2	112
JW0465	aes	acetyl esterase	GO:0005737 cytoplasm	-0.191	0	0	3	112
JW1459	yddE	conserved protein		0	-0.132	0	3	112
JW1802	yeaB	predicted NUDIX hydrolase		0	-0.028	0	3	112
JW4100	fxsA	inner membrane protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.385	1	3	2	111
JW5584	pldB	lysophospholipase L(2)		0	-0.336	0	5	111
JW3350	dam	DNA adenine methylase	GO:0005737 cytoplasm	-0.388	0	0	3	110
JW2775	fucU	L-fucose mutarotase		0	0.179	1	3	109
JW3314	kefG	component of potassium efflux complex with KefB		0	-0.251	0	3	109
JW5430	srlE	glucitol/sorbitol-specific enzyme IIB component of PTS		0	0.483	1	3	108
JW5516	yqjC	conserved protein		0	-0.987	0	3	108

JW0861	ybjX	conserved protein		0	-0.345	0	0	2	107
JW2165	yejA	predicted oligopeptide transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space		-0.433	1	1	3	107
JW3430	yhhF	predicted methyltransferase		0	-0.266	0	0	3	107
JW4279	fimC	chaperone, periplasmic	GO:0009289 fimbria -!- GO:0042597 periplasmic space		-0.208	1	1	2	107
JW0503	ylbA	conserved protein		0	-0.093	0	0	4	106
JW2762	yqcB	tRNA pseudouridine synthase		0	-0.495	0	0	3	106
JW2611	yfjN	CP4-57 prophage; predicted protein		0	-0.035	0	0	3	105
JW5201	puuA	gamma-Glu-putrescine synthase		0	-0.355	0	0	4	105
JW1296	pspF	DNA-binding transcriptional activator	GO:0005737 cytoplasm		-0.294	0	0	4	104
JW1665	ydhZ	predicted protein		0	-0.351	0	0	2	104
JW1675	ydiH	predicted protein		0	-0.315	0	0	2	104
JW2763	yqcC	conserved protein		0	-0.453	0	0	2	104
JW3622	ligB	DNA ligase, NAD(+)-dependent		0	-0.321	0	0	6	104
JW3681	rnpA	protein C5 component of RNase P	GO:0005737 cytoplasm		-0.464	0	0	3	104
JW0065	thiQ	thiamin transporter subunit -!- ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm		0.117	1	0	2	103
JW1770	yeaE	predicted oxidoreductase		0	-0.018	0	0	3	103
JW1085	holB	DNA polymerase III, delta prime subunit	GO:0005737 cytoplasm		-0.050	0	0	3	102
JW1833	exoX	DNA exonuclease X	GO:0005737 cytoplasm		-0.219	0	0	2	102
JW2052	yegE	predicted diguanylate cyclase, GGDEF domain signalling protein		0	0.166	1	11	4	102
JW5948	yhfZ	conserved protein		0	-0.140	0	0	4	102
JW3173	npr	phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr)	GO:0005737 cytoplasm		-0.087	0	0	1	101
JW3174	yrbL	predicted protein		0	-0.557	0	0	4	101
JW3983	yjbD	conserved protein		0	-1.186	0	0	2	101
JW2666	csrA	pleiotropic regulatory protein for carbon source metabolism	GO:0005737 cytoplasm		-0.257	0	0	2	100
JW3062	uxaA	altronate hydrolase		0	-0.232	0	0	5	100
JW4290	yjiE	predicted DNA-binding transcriptional regulator		0	-0.132	0	0	3	100
JW0018	nhaA	sodium-proton antiporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		1.005	1	11	2	99
JW2709	ygbM	conserved protein		0	-0.205	0	0	2	99
JW3635	nlpA	cytoplasmic membrane lipoprotein-28	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.165	1	0	2	99
JW5352	yehT	predicted response regulator in two-component system with YehU		0	-0.160	0	0	4	99
JW0433	ybaW	conserved protein		0	-0.104	0	0	2	98
JW1601	rstB	sensory histidine kinase in two-component regulatory system with RstA	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.026	1	2	3	98
JW3783	yigA	conserved protein		0	-0.149	0	0	3	98
JW0851	ybjR	predicted amidase and lipoprotein		0	-0.339	0	0	5	97

JW1271	yciS	conserved inner membrane protein	0	0.680	1	2	2	97
JW1514	uxaB	altronate oxidoreductase, NAD-	0	-0.188	0	0	2	97
JW2783	ygdl	conserved protein	0	0.089	1	1	5	97
JW3858	dtd	D-Tyr-tRNA(Tyr) deacylase	GO:0005737 cytoplasm	-0.173	0	0	2	97
JW4154	ulaD	3-keto-L-gulonate 6-phosphate decarboxylase	0	0.104	1	0	4	97
JW4334	holD	DNA polymerase III, psi subunit	GO:0005737 cytoplasm	-0.157	0	0	2	97
JW5391	yfeA	predicted diguanylate cyclase	0	0.306	1	8	2	97
JW5453	yqeF	predicted acyltransferase	0	0.109	1	0	2	97
JW5607	hdfR	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.284	0	0	2	97
JW0097	mutT	nucleoside triphosphate pyrophosphohydrolase, marked preference for dGTP	GO:0005737 cytoplasm	-0.475	0	0	4	96
JW0322	prpR	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.135	0	0	3	96
JW0863	macB	fused macrolide transporter subunits -!- ATP-binding component and membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.129	1	4	5	96
JW1801	pabB	aminodeoxychorismate synthase,	0	-0.289	0	0	3	96
JW1850	ruvA	component of RuvABC resolvosome, regulatory subunit	GO:0005737 cytoplasm	0.057	1	0	2	96
JW4039	yjcO	conserved protein	0	-0.289	0	0	2	96
JW5530	yhbV	predicted protease	0	-0.114	0	0	2	96
JW5713	ubiC	chorismate pyruvate lyase	GO:0005737 cytoplasm	-0.155	0	0	4	96
JW5776	sgcX	KpLE2 phage-like element; predicted endoglucanase with Zn-dependent exopeptidase domain	0	0.011	1	0	3	96
JW0323	prpB	2-methylisocitrate lyase	GO:0005737 cytoplasm	-0.015	0	0	3	95
JW0337	mhpR	DNA-binding transcriptional activator, 3HPP-binding	GO:0005737 cytoplasm	-0.181	0	0	3	95
JW2245	yfaO	predicted NUDIX hydrolase	0	-0.391	0	0	2	95
JW2341	fadL	long-chain fatty acid outer membrane transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.300	1	0	2	95
JW4112	frdD	fumarate reductase (anaerobic), membrane anchor subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.007	1	3	3	95
JW5877	ypeB	predicted protein	GO:0005737 cytoplasm	-0.194	0	0	2	95
JW0178	rnhB	ribonuclease HII, degrades RNA of DNA-RNA hybrids	GO:0005737 cytoplasm	-0.006	0	0	3	94
JW1621	rsxC	fused predicted 4Fe-4S ferredoxin-type protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.416	1	0	4	94
JW2444	eutQ	conserved protein	0	-0.115	0	0	3	94
JW0486	rhsD	rhsD element protein	0	-0.717	0	0	6	93
JW0728	tolR	membrane spanning protein in TolA-TolQ-TolR complex	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.204	1	1	2	93

JW1286	sapB	predicted antimicrobial peptide transporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.737	1	5	2	93
JW2092	yohL	conserved protein	0	-0.292	0	0	3	93
JW3857	rbn	tRNA processing exoribonuclease BN	GO:0005737 cytoplasm	0.615	1	6	2	93
JW4208	yjgJ	predicted transcriptional regulator	0	-0.167	0	0	3	93
JW0082	ftsI	transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	-0.150	1	1	6	92
JW1736	astA	arginine succinyltransferase	0	-0.197	0	0	3	92
JW3031	ygiH	conserved inner membrane protein	0	0.579	1	5	1	92
JW3325	yhfG	predicted protein	0	-0.924	0	0	2	92
JW3543	malS	alpha-amylase	GO:0042597 periplasmic space	-0.469	0	0	3	92
JW3815	tatC	TatABCE protein translocation system subunit	0	0.749	1	6	2	92
JW1800	yoaH	conserved protein	0	-0.468	0	0	2	91
JW3193	nanT	sialic acid transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.689	1	12	2	91
JW0476	cueR	DNA-binding transcriptional activator	0	-0.579	0	0	3	90
JW1299	pspC	transcriptional activator	GO:0005737 cytoplasm	0.281	1	1	2	90
JW2168	yejF	fused predicted oligopeptide transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.063	0	0	2	90
JW2598	smpA	small membrane lipoprotein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.087	1	0	1	90
JW3329	nirD	nitrite reductase, NAD(P)H-binding, small subunit	GO:0005737 cytoplasm	-0.211	0	0	2	90
JW5104	ybhF	fused predicted transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.183	0	0	3	90
JW5876	yfeH	predicted inner membrane protein	0	0.826	1	8	2	90
JW0154	btuF	vitamin B12 transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.120	0	0	4	89
JW0307	yahA	predicted DNA-binding transcriptional regulator	0	-0.045	0	0	3	89
JW0646	rihA	ribonucleoside hydrolase 1	0	0.105	1	0	3	89
JW1507	IsrC	A12 transporter -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.893	1	9	1	89
JW1598	folM	dihydrofolate reductase isozyme	0	-0.066	0	0	3	89
JW1857	yecE	conserved protein	0	-0.354	0	0	2	89
JW3677	recF	gap repair protein	GO:0005737 cytoplasm	-0.423	0	0	3	89
JW5801	yjxX	thiamin metabolism associated protein	0	0.034	1	0	3	89
JW1337	dbpA	ATP-dependent RNA helicase specific for 23S rRNA	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	0.014	1	0	3	88

JW2810	kduD	2-deoxy-D-gluconate 3-dehydrogenase	0	0.148	1	0	3	88
JW0222	yafN	predicted antitoxin of the YafO-YafN toxin-antitoxin system	0	-0.654	0	0	3	87
JW1424	ycdK	predicted enzyme	0	-0.033	0	0	4	87
JW1587	ynfL	predicted DNA-binding transcriptional regulator	0	-0.053	0	0	3	87
JW1742	ynjA	conserved protein	0	0.037	1	0	3	87
JW1953	yedX	conserved protein	0	-0.328	0	0	1	87
JW5408	yfhB	conserved protein	0	-0.040	1	1	2	87
JW5821	emtA	lytic murein endotransglycosylase E	GO:0009274 cell wall (sensu Bacteria) - - GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	-0.203	1	0	2	87
JW0059	polB	DNA polymerase II	GO:0005737 cytoplasm	-0.451	0	0	5	86
JW0205	dnaQ	DNA polymerase III epsilon subunit	GO:0005737 cytoplasm	-0.162	0	0	3	86
JW0491	ybbB	tRNA 2-selenouridine synthase, selenophosphate-dependent	0	-0.371	0	0	2	86
JW1056	mviN	predicted inner membrane protein	0	0.880	1	13	3	86
JW1203	prmC	N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2	0	-0.202	0	0	2	86
JW2457	ypfN	predicted protein	GO:0031225 anchored to	-0.689	1	1	2	86
JW2699	hypD	protein required for maturation of hydrogenases	0	-0.092	0	0	3	86
JW5670	yhiD	predicted Mg(2+) transport ATPase inner membrane protein	0	0.535	1	5	2	86
JW1854	nudB	dATP pyrophosphohydrolase	0	-0.268	0	0	3	85
JW3228	dusB	tRNA-dihydrouridine synthase B	0	-0.246	0	0	3	85
JW3254	zntR	DNA-binding transcriptional activator	GO:0005737 cytoplasm	-0.504	0	0	3	85
JW4053	phnP	carbon-phosphorus lyase complex accessory protein	0	-0.115	0	0	2	85
JW4200	treR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.085	0	0	1	85
JW5313	yedO	D-cysteine desulfhydrase, PLP-	0	0.123	1	0	3	85
JW0368	sbmA	predicted transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.535	1	8	2	84
JW2337	sixA	phosphohistidine phosphatase	0	0.200	1	0	1	84
JW3721	asnC	DNA-binding transcriptional dual	GO:0005737 cytoplasm	0.062	1	0	2	84
JW5173	icdC	conserved protein (pseudogene)	GO:0005737 cytoplasm	0.048	1	0	1	84
JW0191	yaeB	conserved protein	0	-0.149	0	0	3	83
JW0887	focA	formate transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.772	1	6	3	83
JW1590	ydgD	predicted peptidase	0	-0.207	0	0	3	83
JW1994	yeeD	conserved protein	0	0.215	1	0	1	83
JW4032	nrfB	nitrite reductase, formate-dependent, penta-heme cytochrome c	GO:0042597 periplasmic space	-0.540	0	0	2	83
JW1625	nth	DNA glycosylase and apyrimidinic (AP) lyase (endonuclease III)	GO:0005737 cytoplasm	-0.120	0	0	2	82

JW2061	mdtC	multidrug efflux system, subunit C	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	0.283	1	10	4	82
JW3781	yifL	predicted lipoprotein	GO:0016020 membrane	-0.437	1	1	3	82
JW4223	idnO	5-keto-D-gluconate-5-reductase	GO:0005737 cytoplasm	0.083	1	0	2	82
JW5501	ygiQ	conserved protein	0	-0.519	0	0	4	82
JW3384	rtcB	conserved protein	0	-0.221	0	0	3	81
JW3852	yihT	predicted aldolase	0	-0.048	0	0	2	81
JW5381	yfcM	conserved protein	0	-0.416	0	0	2	81
JW2128	dusC	tRNA-dihydrouridine synthase C	0	-0.164	0	0	4	80
JW3729	rbsC	D-ribose transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.924	1	8	1	80
JW4088	yjdJ	predicted acyltransferase with acyl-CoA N-acyltransferase domain	0	-0.704	0	0	2	80
JW5108	ybiO	predicted mechanosensitive channel	0	0.393	1	11	3	80
JW5308	yecN	predicted inner membrane protein	0	0.654	1	3	1	80
JW5389	ypdH	predicted enzyme IIB component of	0	-0.030	0	0	1	80
JW1500	hipA	regulator with hipB	GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.152	0	0	3	79
JW2862	xerD	site-specific tyrosine recombinase	0	-0.330	0	0	4	79
JW0634	nadD	nicotinic acid mononucleotide adenyltransferase, NAD(P)-dependent	0	-0.457	0	0	2	78
JW0846	artQ	arginine transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.718	1	4	2	78
JW0956	hyaC	hydrogenase 1, b-type cytochrome subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.297	1	4	2	78
JW1908	fliC	flagellar filament structural protein (flagellin)	GO:0019861 flagellum	-0.366	0	0	3	78
JW2705	ygbI	predicted DNA-binding transcriptional regulator	0	0.071	1	0	4	78
JW3511	dppC	dipeptide transporter -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.807	1	5	3	78
JW3627	recG	ATP-dependent DNA helicase	GO:0005737 cytoplasm	-0.127	0	0	2	78
JW4264	sgcA	KpLE2 phage-like element; predicted phosphotransferase enzyme IIA component	0	0.024	1	0	2	78
JW2543	tadA	tRNA-specific adenosine deaminase	0	-0.135	0	0	2	77
JW3604	rfaS	lipopolysaccharide core biosynthesis protein	GO:0019866 inner membrane	-0.339	1	0	4	77
JW5301	yebU	predicted methyltransferase	GO:0005737 cytoplasm	-0.195	0	0	3	77
JW5382	yfdI	CPS-53 (KpLE1) prophage; predicted inner membrane protein	0	0.488	1	10	2	77
JW0239	ykfB	CP4-6 prophage; predicted protein	0	-0.280	0	0	2	76
JW0587	entB	isochorismatase	GO:0005737 cytoplasm	-0.288	0	0	2	76
JW3506	bcsG	predicted inner membrane protein	0	0.022	1	4	2	76

JW2272	nuoM	NADH:ubiquinone oxidoreductase, membrane subunit M	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.821	1	14	3	75
JW2303	hisP	histidine/lysine/arginine/ornithine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.243	0	0	2	75
JW2318	flk	predicted flagella assembly protein	0	-0.308	1	1	3	75
JW4097	cutA	copper binding protein, copper	0	-0.026	0	0	2	75
JW0441	amtB	ammonium transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.937	1	12	1	74
JW0879	dmsC	dimethyl sulfoxide reductase, anaerobic, subunit C	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.064	1	8	2	74
JW2135	mglC	methyl-galactoside transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.002	1	9	2	74
JW2781	csdA	cysteine sulfinate desulfinate	0	0.041	1	0	2	74
JW4033	nrfC	formate-dependent nitrite reductase, 4Fe4S subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.162	1	0	2	74
JW4050	rpiR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	0.066	1	0	2	74
JW1460	narV	nitrate reductase 2 (NRZ), gamma subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.550	1	5	2	73
JW1897	pgsA	phosphatidylglycerophosphate synthetase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.824	1	4	3	73
JW2183	ccmG	periplasmic thioredoxin of cytochrome c-type biogenesis	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.188	1	1	2	73
JW2932	nupG	nucleoside transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.830	1	12	3	73
JW3996	lamB	maltose outer membrane porin (maltoporin)	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.516	1	0	1	73
JW5849	yqhC	predicted DNA-binding transcriptional regulator	0	-0.149	0	0	3	73
JW0420	cyoC	cytochrome o ubiquinol oxidase subunit III	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.721	1	5	1	72
JW1969	cobT	nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl transferase	0	0.342	1	0	1	72
JW2022	rfbX	predicted polysiprenol-linked O-antigen transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.917	1	10	2	72
JW2787	recD	exonuclease V (RecBCD complex), alpha chain	0	-0.201	0	0	3	72
JW5056	yajL	predicted lipoprotein	0	-0.129	0	0	2	72
JW5189	yehM	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.831	1	11	3	72
JW0763	ybhK	predicted transferase with NAD(P)-binding Rossmann-fold domain	0	0.039	1	0	3	71
JW1240	yciU	predicted protein	0	-0.328	0	0	2	71
JW1715	yniB	predicted inner membrane protein	0	0.504	1	3	2	71

JW2152	yeiN	conserved protein	0	0.194	1	0	2	71
JW5783	yjiH	conserved inner membrane protein	0	0.522	1	4	3	71
JW0278	yagR	predicted oxidoreductase with molybdenum-binding domain	0	-0.214	0	0	4	70
JW2271	nuoN	NADH:ubiquinone oxidoreductase, membrane subunit N	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.916	1	12	1	70
JW2865	ygfY	conserved protein	0	-0.559	0	0	2	70
JW5555	ptsA	fused predicted PTS enzymes Hpr component - - enzyme I component - - enzyme IIA component	0	-0.090	0	0	3	70
JW0578	entF	enterobactin synthase multienzyme complex component, ATP-dependent	GO:0005737 cytoplasm	-0.079	0	0	2	69
JW0903	ycbC	conserved inner membrane protein	0	0.044	1	2	1	69
JW2806	lysA	diaminopimelate decarboxylase, PLP-binding	0	-0.155	0	0	3	69
JW4029	yjch	conserved inner membrane protein involved in acetate transport	0	0.424	1	2	2	69
JW4326	dnaT	DNA biosynthesis protein (primosomal protein I)	GO:0005737 cytoplasm	-0.081	0	0	2	69
JW5298	yobH	predicted protein	0	0.601	1	1	1	69
JW2241	yfaW	predicted enolase	0	-0.208	0	0	3	68
JW0246	insI	CP4-6 prophage; IS30 transposase	0	-0.763	0	0	4	67
JW0586	entE	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex	GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 cytoplasm	-0.147	0	0	3	67
JW1707	rpml	50S ribosomal subunit protein L35	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm	-0.617	0	0	1	67
JW1971	cobU	bifunctional cobinamide kinase - - cobinamide phosphate	0	-0.135	0	0	1	67
JW2162	yeiU	undecaprenyl pyrophosphate	0	0.685	1	5	1	67
JW2289	yfbS	predicted transporter	0	0.730	1	10	2	67
JW2344	yfdC	predicted inner membrane protein	0	0.170	1	6	2	67
JW2546	yfhL	predicted 4Fe-4S cluster-containing	0	-0.310	0	0	2	67
JW5105	ybiX	conserved protein	0	-0.361	0	0	1	67
JW5404	sseB	rhodanase-like enzyme, sulfur transfer from thiosulfate	0	-0.176	0	0	2	67
JW0342	mhpF	acetaldehyde-CoA dehydrogenase II, NAD-binding	GO:0005737 cytoplasm	0.099	1	0	2	66
JW0998	ycdC	predicted DNA-binding transcriptional regulator	0	0.069	1	0	2	66
JW1221	ychJ	conserved protein	0	-0.280	0	0	2	66
JW2946	glcD	glycolate oxidase subunit, FAD-linked	0	0.051	1	0	3	66
JW3479	hdeD	acid-resistance membrane protein	0	1.271	1	6	2	66
JW3715	atpE	F0 sector of membrane-bound ATP synthase, subunit c	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	1.267	1	2	2	66

JW5086	fepA	iron-enterobactin outer membrane transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.581	1	0	2	66
JW5698	friR	predicted DNA-binding transcriptional regulator	0	-0.346	0	0	3	66
JW5942	bcsC	cellulose synthase subunit	0	-0.592	0	0	4	66
JW0063	araC	DNA-binding transcriptional dual	GO:0005737 cytoplasm	-0.315	0	0	2	65
JW1151	ycgZ	predicted protein	0	-0.362	0	0	1	65
JW1376	ydbH	predicted protein	0	-0.164	1	1	3	65
JW2167	yejE	predicted oligopeptide transporter subunit - - membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	0.378	1	6	2	64
JW2539	yfhG	conserved protein	0	-0.745	0	0	1	64
JW0390	phoR	sensory histidine kinase in two-component regulatory system with	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.305	1	1	4	63
JW1722	chbG	conserved protein	0	-0.051	0	0	2	63
JW1887	araH	fused L-arabinose transporter subunits - - membrane components of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	1.035	1	10	1	63
JW2029	wcaL	predicted glycosyl transferase	0	-0.108	0	0	3	63
JW2090	thiD	bifunctional hydroxy-methylpyrimidine kinase - - hydroxy-phosphomethylpyrimidine kinase	0	-0.037	0	0	2	63
JW2472	hyfG	hydrogenase 4, subunit	0	-0.284	0	0	4	63
JW2928	mutY	adenine DNA glycosylase	GO:0005737 cytoplasm	-0.146	0	0	1	63
JW3388	glpE	thiosulfate:cyanide sulfurtransferase (rhodanese)	0	-0.265	0	0	1	63
JW3617	pyrE	orotate phosphoribosyltransferase	GO:0005737 cytoplasm	-0.058	0	0	2	63
JW5434	ascG	DNA-binding transcriptional regulator	GO:0005737 cytoplasm	-0.066	0	0	3	63
JW5747	ytfH	predicted transcriptional regulator	0	-0.123	0	0	2	63
JW0144	hrpB	predicted ATP-dependent helicase	GO:0005737 cytoplasm	-0.171	0	0	3	62
JW0502	glxK	glycerate kinase II	0	0.335	1	0	2	62
JW0608	citE	citrate lyase, citryl-ACP lyase (beta) subunit	GO:0005737 cytoplasm	-0.165	0	0	3	62
JW1645	lhr	predicted ATP-dependent helicase	GO:0005737 cytoplasm	-0.174	0	0	4	62
JW1720	cedA	cell division modulator	0	-0.518	0	0	2	62
JW1760	ydjG	predicted oxidoreductase	0	-0.093	0	0	4	62
JW2236	glpB	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.062	1	0	4	62
JW5012	clcA	chloride channel, voltage-gated	0	0.636	1	11	2	62
JW5286	ynjD	predicted transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	0.024	1	0	2	62
JW0769	ybhL	predicted inner membrane protein	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.815	1	7	1	61
JW1058	flgM	anti-sigma factor for FliA (sigma 28)	GO:0019861 flagellum - - GO:0005737 cytoplasm	-0.504	0	0	1	61

JW1551	ydfT	Qin prophage; predicted antitermination protein Q	0	-0.313	0	0	4	61
JW1573	rspA	predicted dehydratase	0	-0.297	0	0	3	61
JW1970	cobS	cobalamin 5'-phosphate synthase	0	0.868	1	4	4	61
JW2884	yliK	methylmalonyl-CoA mutase	0	-0.122	0	0	4	61
JW3123	yhbP	conserved protein	0	-0.276	0	0	1	61
JW3317	yheU	conserved protein	0	-0.513	0	0	1	61
JW3843	yihL	predicted DNA-binding transcriptional regulator	0	-0.459	0	0	2	61
JW5366	ccmA	heme exporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.232	0	0	2	61
JW0656	ybeY	conserved protein	0	-0.311	0	0	1	60
JW0764	moaA	molybdopterin biosynthesis protein A	0	-0.354	0	0	3	60
JW2199	yojI	fused predicted multidrug transport subunits -!- membrane component and ATP-binding component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.194	1	6	2	60
JW4000	ubiA	p-hydroxybenzoate octaprenyltransferase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.690	1	7	1	60
JW5644	htrL	predicted protein	0	-0.268	0	0	2	60
JW0496	hyi	hydroxypyruvate isomerase	GO:0005737 cytoplasm	-0.343	0	0	2	59
JW0868	aat	leucyl/phenylalanyl-tRNA-protein transferase	GO:0005737 cytoplasm	-0.247	0	0	1	59
JW0974	cspG	DNA-binding transcriptional regulator	0	-0.363	0	0	1	59
JW0980	torR	DNA-binding response regulator in two-component regulatory system with TorS	GO:0005737 cytoplasm	-0.178	0	0	2	59
JW1456	ydcE	4-oxalocrotonate tautomerase	0	-0.262	0	0	1	59
JW1990	yeeA	conserved inner membrane protein	GO:0009274 cell wall (sensu	0.282	1	5	2	59
JW2248	yfbF	undecaprenyl phosphate-L-Ara4FN transferase	0	0.073	1	2	1	59
JW3518	tag	3-methyl-adenine DNA glycosylase I, constitutive	GO:0005737 cytoplasm	-0.280	0	0	1	59
JW5292	yeaP	predicted diguanylate cyclase	0	-0.235	0	0	1	59
JW5395	yfeW	predicted periplasmic esterase	0	-0.284	0	0	2	59
JW0203	yafS	predicted S-adenosyl-L-methionine-dependent methyltransferase	0	-0.126	0	0	1	58
JW2365	emrK	EmrKY-ToIC multidrug resistance efflux pump, membrane fusion protein	0	-0.237	1	1	4	58
JW2904	speB	agmatinase	0	-0.105	0	0	2	58
JW4074	basR	DNA-binding response regulator in two-component regulatory system with BasS	GO:0005737 cytoplasm	-0.150	0	0	1	58
JW5906	gapC	glyceraldehyde-3-phosphate dehydrogenase C, C-ter fragment (pseudogene)	0	0.028	1	0	3	58
JW0285	yagX	predicted aromatic compound	0	-0.351	0	0	3	57
JW0379	aroL	shikimate kinase II	GO:0005737 cytoplasm	-0.014	0	0	1	57
JW0800	ybiP	predicted hydrolase, inner membrane	GO:0009274 cell wall (sensu	-0.117	1	4	3	57

JW1788	yeaT	predicted DNA-binding transcriptional regulator		0	-0.007	0	0	2	57
JW2190	napC	nitrate reductase, cytochrome c-type, periplasmic	GO:0019866 inner membrane		-0.623	1	1	3	57
JW2571	kgpP	alpha-ketoglutarate transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.617	1	12	2	57
JW2910	galP	D-galactose transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.599	1	12	2	57
JW3241	yrdB	conserved protein		0	-0.748	0	0	2	57
JW3605	rfaP	kinase that phosphorylates core heptose of lipopolysaccharide	GO:0019866 inner membrane		-0.275	1	0	2	57
JW3886	fieF	zinc transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.378	1	6	2	57
JW5150	ymdC	predicted hydrolase		0	-0.163	0	0	2	57
JW0250	insH	CP4-6 prophage; IS5 transposase and trans-activator		0	-0.534	0	0	2	56
JW0449	hha	modulator of gene expression, with H-		0	-0.569	0	0	3	56
JW2237	glpC	sn-glycerol-3-phosphate dehydrogenase (anaerobic), small subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		-0.214	1	0	3	56
JW2670	ygaD	conserved protein		0	-0.114	0	0	2	56
JW3910	metB	cystathionine gamma-synthase, PLP-dependent	GO:0005737 cytoplasm		-0.021	0	0	1	56
JW0146	fhuA	ferrichrome outer membrane transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)		-0.481	1	0	3	55
JW1793	rnd	ribonuclease D	GO:0005737 cytoplasm		-0.150	0	0	2	55
JW5444	ygcE	predicted kinase		0	-0.103	0	0	2	55
JW1245	yciA	predicted hydrolase		0	0.118	1	0	2	54
JW1313	ycjW	predicted DNA-binding transcriptional regulator	GO:0042597 periplasmic space		-0.089	0	0	2	54
JW1377	ynbE	predicted lipoprotein		0	0.297	1	0	2	54
JW1749	ynjH	predicted protein		0	-0.104	0	0	1	54
JW1903	yecS	predicted transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.435	1	3	2	54
JW2966	yghW	predicted protein		0	-0.473	0	0	2	54
JW5061	mdIB	fused predicted multidrug transporter subunits -!- ATP binding components of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane		0.252	1	4	2	54
JW5729	yjzZ	conserved protein		0	-0.183	0	0	3	54
JW0484	ybbA	predicted transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm		-0.147	0	0	2	53
JW1830	yobA	conserved protein		0	-0.262	0	0	2	53
JW2160	yeiQ	predicted dehydrogenase, NAD-		0	-0.114	0	0	2	53
JW2187	ccmC	heme exporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner		0.586	1	6	2	53

JW3601	rfaJ	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase	0	-0.152	1	1	2	53
JW3992	malG	maltose transporter subunit -!- membrane component of ABC	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.836	1	6	1	53
JW4341	yjv	predicted DNase	0	-0.243	0	0	2	53
JW5970	yccV	DNA-binding protein, hemimethylated	0	-0.397	0	0	1	53
JW0341	mhpD	2-keto-4-pentenoate hydratase	0	-0.033	0	0	1	52
JW1247	yciC	predicted inner membrane protein	GO:0009274 cell wall (sensu	1.068	1	6	2	52
JW2030	wcaK	predicted pyruvyl transferase	0	-0.018	0	0	3	52
JW5917	rcsC	hybrid sensory kinase in two-component regulatory system with RcsB and YojN	0	-0.152	0	0	1	52
JW5931	tatD	DNase, magnesium-dependent	GO:0005737 cytoplasm	-0.156	0	0	2	52
JW0733	nadA	quinolinate synthase, subunit A	GO:0005737 cytoplasm	-0.141	0	0	1	51
JW1763	ydjJ	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	0.018	1	0	1	51
JW2432	eutL	predicted carboxysome structural protein with predicted role in ethanolamine utilization	0	0.191	1	0	2	51
JW5128	yccS	predicted inner membrane protein	0	0.098	1	9	3	51
JW5233	yncA	predicted acyltransferase with acyl-CoA N-acyltransferase domain	0	-0.217	0	0	2	51
JW5325	yeeL	predicted protein, C-ter fragment (pseudogene)	0	0.097	1	0	3	51
JW0076	ilvI	acetolactate synthase III, large subunit	0	-0.051	0	0	2	50
JW0438	mdlA	fused predicted multidrug transporter subunits -!- ATP-binding components of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.085	1	6	3	50
JW0817	yliE	conserved inner membrane protein	0	-0.083	1	2	3	50
JW0857	hcp	hybrid-cluster [4Fe-2S-2O] protein in anaerobic terminal reductases	0	0.035	1	0	3	50
JW2097	yehC	predicted periplasmic pilin chaperone	0	-0.136	1	1	3	50
JW2522	hcaE	3-phenylpropionate dioxygenase, large (alpha) subunit	0	-0.484	0	0	3	50
JW2813	yqeG	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.940	1	10	2	50
JW3599	rfaZ	lipopolysaccharide core biosynthesis protein	GO:0019866 inner membrane	-0.248	1	0	2	50
JW3758	rfe	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	0	0.767	1	11	2	50
JW1926	fliJ	flagellar protein	GO:0019861 flagellum	-0.981	0	0	3	49
JW1945	yedJ	predicted phosphohydrolase	0	-0.271	0	0	2	49
JW2275	nuoJ	NADH:ubiquinone oxidoreductase, membrane subunit J	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.913	1	5	1	49
JW2754	chpR	antitoxin of the ChpA-ChpR toxin-antitoxin system	0	-0.299	0	0	2	49

JW4034	nrfD	formate-dependent nitrite reductase, membrane subunit	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.995	1	8	1	49	
JW5251	ynfO	Qin prophage; predicted protein		0	-1.009	0	0	1	49
JW5887	yfdT	CPS-53 (KpLE1) prophage; predicted protein		0	-0.711	0	0	3	49
JW0045	kefF	flavoprotein subunit for the KefC potassium efflux system		0	-0.228	0	0	2	48
JW2559	yfiC	predicted methyltransferase		0	-0.095	0	0	1	48
JW2753	chpA	toxin of the ChpA-ChpR toxin-antitoxin system, endoribonuclease		0	-0.093	0	0	1	48
JW3120	yraQ	predicted permease		0	0.856	1	9	1	48
JW3221	yhdA	conserved inner membrane protein		0	-0.192	1	2	2	48
JW3261	rpmJ	50S ribosomal subunit protein L36	GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm		-0.611	0	0	1	48
JW3631	yicl	predicted alpha-glucosidase		0	-0.397	0	0	3	48
JW3978	iclR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm		-0.051	0	0	3	48
JW5540	yhcN	conserved protein		0	-0.087	0	0	1	48
JW5784	kptA	2'-phosphotransferase	GO:0005737 cytoplasm		-0.259	0	0	2	48
JW0147	fhuC	iron-hydroxamate transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm		0.015	1	0	3	47
JW0228	gpt	guanine-hypoxanthine phosphoribosyltransferase	GO:0005737 cytoplasm		-0.048	0	0	1	47
JW2172	yejH	predicted ATP-dependet helicase		0	-0.278	0	0	2	47
JW4159	priB	primosomal protein N	GO:0005737 cytoplasm		-0.101	0	0	1	47
JW4211	argI	ornithine carbamoyltransferase 1	GO:0005737 cytoplasm		-0.233	0	0	2	47
JW4362	creC	sensory histidine kinase in two-component regulatory system with CreB or PhoB, regulator of the CreBC regulon	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane		0.006	1	2	3	47
JW5010	yadD	predicted transposase		0	-0.269	0	0	3	47
JW5520	tdcG	L-serine dehydratase 3		0	0.071	1	0	3	47
JW0091	ftsQ	membrane anchored protein involved in growth of wall at septum	GO:0019866 inner membrane		-0.504	1	1	3	46
JW1678	ydiK	predicted inner membrane protein		0	1.029	1	9	1	46
JW2255	menE	o-succinylbenzoate-CoA ligase		0	-0.067	0	0	2	46
JW2619	yfjU	CP4-57 prophage; conserved protein		0	-0.190	0	0	1	46
JW2803	ygeD	predicted inner membrane protein		0	0.898	1	10	1	46
JW5087	citF	citrate lyase, citrate-ACP transferase (alpha) subunit	GO:0005737 cytoplasm		-0.094	0	0	2	46
JW5397	hda	ATPase regulatory factor involved in DnaA inactivation		0	-0.115	0	0	1	46
JW5433	hypF	carbamoyl phosphate phosphatase and maturation protein for [NiFe]	GO:0005737 cytoplasm		-0.091	0	0	2	46

JW5481	mltC	membrane-bound lytic murein transglycosylase C	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	-0.351	1	0	1	46
JW0280	yagT	predicted xanthine dehydrogenase, 2Fe-2S subunit	0	-0.126	0	0	1	45
JW0374	phoA	alkaline phosphatase	GO:0042597 periplasmic space	-0.313	0	0	3	45
JW1196	ychH	predicted inner membrane protein	0	-0.001	1	2	1	45
JW1464	narU	nitrate/nitrite transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.783	1	12	2	45
JW2358	yfdR	CPS-53 (KpLE1) prophage; conserved protein	0	-0.044	0	0	3	45
JW2400	yfeR	predicted DNA-binding transcriptional regulator	0	-0.054	0	0	3	45
JW2459	ypfl	predicted hydrolase	0	-0.223	0	0	2	45
JW2488	yfgF	predicted inner membrane protein	0	0.256	1	9	3	45
JW3099	yhaV	conserved protein	0	-0.758	0	0	2	45
JW3190	yhcH	conserved protein	0	-0.184	0	0	2	45
JW3433	yhhN	conserved inner membrane protein	0	0.974	1	6	2	45
JW4040	fdhF	formate dehydrogenase-H, selenopolypeptide subunit	0	-0.326	0	0	3	45
JW4224	idnD	L-idoonate 5-dehydrogenase, NAD-	0	-0.017	0	0	2	45
JW5059	yajR	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.691	1	12	2	45
JW5793	yjjN	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0	0.004	1	0	3	45
JW0081	ftsL	membrane bound cell division protein at septum containing leucine zipper motif	0	-0.026	1	1	3	44
JW0194	metI	DL-methionine transporter subunit -!- membrane component protein of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.994	1	5	2	44
JW0698	phr	deoxyribodipyrimidine photolyase, FAD-binding	GO:0005737 cytoplasm	-0.395	0	0	3	44
JW0748	modC	molybdate transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.050	0	0	2	44
JW1366	stfR	Rac prophage; predicted tail fiber	0	-0.327	0	0	3	44
JW2728	ygcJ	predicted protein	0	-0.241	0	0	2	44
JW2911	sprT	conserved protein	0	-0.522	0	0	2	44
JW3229	fis	global DNA-binding transcriptional dual regulator	GO:0005737 cytoplasm	-0.531	0	0	1	44
JW3405	yhhY	predicted acetyltransferase	0	-0.428	0	0	2	44
JW4288	yjiC	predicted protein	0	-0.290	0	0	3	44
JW5200	yciW	predicted oxidoreductase	0	-0.222	0	0	2	44
JW5205	abgA	predicted peptidase, aminobenzoyl-glutamate utilization protein	0	-0.096	0	0	3	44

JW0148	fhuD	iron-hydroxamate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	0.067	1	0	3	43
JW0169	ispU	undecaprenyl pyrophosphate synthase	GO:0005737 cytoplasm	-0.396	0	0	2	43
JW0579	fepE	regulator of length of O-antigen component of lipopolysaccharide chains	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.171	1	2	2	43
JW0649	gltJ	glutamate and aspartate transporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.605	1	5	3	43
JW1361	ynaA	Rac prophage; predicted tail protein		0 -0.413	0	0	2	43
JW1723	chbF	cryptic phospho-beta-glucosidase, NAD(P)-binding	GO:0005737 cytoplasm	-0.104	0	0	3	43
JW2776	fucR	DNA-binding transcriptional activator	GO:0005737 cytoplasm	-0.321	0	0	1	43
JW3313	kefB	potassium:proton antiporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.454	1	13	3	43
JW3385	rtcR	sigma 54-dependent transcriptional regulator of rtcBA expression	GO:0005737 cytoplasm	-0.363	0	0	3	43
JW3541	xylR	DNA-binding transcriptional activator, xylose-binding	GO:0005737 cytoplasm	-0.331	0	0	3	43
JW5011	ligT	2'-5' RNA ligase	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	-0.235	0	0	1	43
JW5177	ymgD	predicted protein		0 0.036	1	0	1	43
JW5892	yadB	glutamyl-Q tRNA(Asp) synthetase		0 -0.272	0	0	1	43
JW0922	ycbR	predicted periplasmic pilin chaperone		0 -0.057	0	0	2	42
JW1258	yciV	conserved protein		0 -0.301	0	0	2	42
JW1381	tynA	tyramine oxidase, copper-requiring	GO:0042597 periplasmic space	-0.390	0	0	2	42
JW2096	yehB	predicted outer membrane protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.493	1	0	2	42
JW2105	yehl	conserved protein		0 -0.330	0	0	3	42
JW2193	napG	ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB)		0 -0.155	0	0	1	42
JW2201	ada	fused DNA-binding transcriptional dual regulator -!- O6-methylguanine-DNA methyltransferase	GO:0005737 cytoplasm	-0.349	0	0	1	42
JW2222	yfaS	predicted protein, N-ter fragment (pseudogene)		0 -0.334	0	0	3	42
JW0021	insA	IS1 repressor protein InsA		0 -0.316	0	0	3	41
JW0358	tauB	taurine transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.034	0	0	3	41
JW1831	hoIE	DNA polymerase III, theta subunit	GO:0005737 cytoplasm	-0.454	0	0	1	41
JW1868	flhA	predicted flagellar export pore protein	GO:0019861 flagellum -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.378	1	7	2	41

JW2053	alkA	3-methyl-adenine DNA glycosylase II	GO:0005737 cytoplasm	-0.036	0	0	2	41
JW2164	rtn	conserved protein		0.105	1	2	2	41
JW2503	pbpC	fused transglycosylase -!	GO:0009274 cell wall (sensu	-0.218	1	1	3	41
JW1292	puuR	DNA-binding transcriptional repressor		-0.325	0	0	2	40
JW1321	ycjZ	predicted DNA-binding transcriptional regulator		-0.078	0	0	2	40
JW1631	ydhA	predicted lipoprotein		-0.314	0	0	2	40
JW3077	yhaK	predicted pirin-related protein		-0.269	0	0	1	40
JW3151	yhbE	conserved inner membrane protein	GO:0009274 cell wall (sensu	0.852	1	10	1	40
JW3234	acrF	multidrug efflux system protein	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.322	1	12	2	40
JW3235	yhdV	predicted outer membrane protein		0.396	1	1	1	40
JW3342	php	predicted hydrolase		-0.236	0	0	2	40
JW3400	gntK	gluconate kinase 2 -!- gluconate transport, GNT I system		-0.318	0	0	1	40
JW3845	yihN	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	0.731	1	12	3	40
JW3957	thiE	thiamin phosphate synthase (thiamin phosphate pyrophosphorylase)		0.032	1	0	2	40
JW5016	yaeF	predicted lipoprotein		-0.014	0	0	2	40
JW0923	ycbS	predicted outer membrane usher protein	GO:0009274 cell wall (sensu Bacteria) -! GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.364	1	1	2	39
JW1651	ydhB	predicted DNA-binding transcriptional regulator		-0.240	0	0	2	39
JW2249	yfbG	fused UDP-L-Ara4N formyltransferase -! -!- UDP-GlcA C-4'-decarboxylase		-0.183	0	0	2	39
JW2947	glcC	DNA-binding transcriptional dual regulator, glycolate-binding	GO:0005737 cytoplasm	-0.253	0	0	2	39
JW3698	bglH	carbohydrate-specific outer membrane porin, cryptic	GO:0009274 cell wall (sensu Bacteria) -! GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.588	1	0	2	39
JW4130	hfq	HF-I, host factor for RNA phage Q beta replication		-0.505	0	0	1	39
JW5174	ycgG	conserved inner membrane protein		0.149	1	2	2	39
JW5407	yfhK	predicted sensory kinase in two-component system		-0.140	1	2	2	39
JW0303	betA	choline dehydrogenase, a flavoprotein	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.468	1	0	2	38
JW2482	uraA	uracil transporter	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	1.045	1	12	1	38
JW2525	hcaB	2,3-dihydroxy-2,3-dihydrophenylpropionate		0.166	1	0	2	38
JW2864	ygfX	predicted protein		-0.059	1	1	1	38
JW3050	ygjJ	conserved protein		-0.476	0	0	2	38

JW3109	agaD	N-acetylgalactosamine-specific enzyme IID component of PTS	0	0.566	1	5	2	38
JW3662	yidE	predicted transporter	0	0.694	1	10	2	38
JW3930	argC	N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding	GO:0005737 cytoplasm	0.163	1	0	2	38
JW5757	yjgL	predicted protein	0	-0.596	0	0	2	38
JW0683	kdpD	fused sensory histidine kinase in two-component regulatory system with	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.090	1	4	2	37
JW1055	mviM	predicted oxidoreductase, NAD(P)-binding Rossmann-fold domain	0	-0.098	0	0	1	37
JW1295	puuE	GABA aminotransferase, PLP-	GO:0005737 cytoplasm	0.042	1	0	2	37
JW1472	fdnI	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.359	1	4	1	37
JW1571	intQ	Qin prophage; predicted defective integrase	0	-0.428	0	0	2	37
JW3023	yqiK	conserved protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.311	1	2	2	37
JW5363	bcr	bicyclomycin/multidrug efflux system	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.948	1	12	1	37
JW5469	ygfT	fused predicted oxidoreductase Fe-S subunit -!- nucleotide-binding subunit	0	-0.142	0	0	2	37
JW5775	yjhH	KpLE2 phage-like element; predicted lyase/synthase	0	0.096	1	0	2	37
JW0564	cusA	copper/silver efflux system, membrane component	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.283	1	12	2	36
JW0919	ssuA	alkanesulfonate transporter subunit -!- periplasmic-binding component of ABC superfamily	GO:0042597 periplasmic space	-0.077	0	0	2	36
JW1522	marC	predicted transporter	GO:0009274 cell wall (sensu	0.819	1	5	2	36
JW1995	yeeE	predicted inner membrane protein	0	0.716	1	9	2	36
JW2382	ypdF	predicted peptidase	0	-0.108	0	0	2	36
JW2531	yphE	fused predicted sugar transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.028	0	0	2	36
JW2849	xdhD	fused predicted xanthine/hypoxanthine oxidase, molybdopterin-binding subunit -!- Fe-S binding subunit	0	-0.132	0	0	2	36
JW3107	agaB	N-acetylgalactosamine-specific enzyme IIB component of PTS	GO:0005737 cytoplasm	-0.126	0	0	2	36
JW3575	mtlR	DNA-binding transcriptional repressor	GO:0005737 cytoplasm	-0.195	0	0	2	36
JW4124	yjeS	predicted Fe-S electron transport	0	-0.250	0	0	2	36
JW5065	ybbJ	conserved inner membrane protein	0	0.366	1	3	1	36
JW5507	yqiG	predicted outer membrane usher protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.526	1	0	2	36

JW5519	yhaO	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.894	1	11	1	36
JW1932	fliP	flagellar biosynthesis protein	GO:0019861 flagellum -!- GO:0009274 cell wall (sensu	0.801	1	5	2	35
JW1951	yedV	predicted sensory kinase in two-component regulatory system with	0	-0.051	1	2	2	35
JW2372	yfdX	predicted protein	0	-0.326	0	0	2	35
JW2467	hyfB	hydrogenase 4, membrane subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.888	1	16	2	35
JW2752	mazG	nucleoside triphosphate pyrophosphohydrolase	0	-0.515	0	0	2	35
JW3944	secE	preprotein translocase membrane subunit	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.876	1	3	1	35
JW4048	alsA	fused D-allose transporter subunits -!- ATP-binding components of ABC superfamily	GO:0005737 cytoplasm	-0.085	0	0	2	35
JW4059	phnJ	carbon-phosphorus lyase complex	0	-0.388	0	0	1	35
JW4329	yjjQ	predicted DNA-binding transcriptional regulator	0	-0.160	0	0	2	35
JW5018	mltD	predicted membrane-bound lytic murein transglycosylase D	GO:0005737 cytoplasm	-0.407	0	0	2	35
JW5923	ygfK	predicted oxidoreductase, Fe-S subunit	0	-0.291	0	0	2	35
JW0175	fabZ	(3R)-hydroxymyristol acyl carrier protein dehydratase	GO:0005737 cytoplasm	0.054	1	0	2	34
JW1042	yceA	conserved protein	0	-0.427	0	0	2	34
JW1134	ymfM	e14 prophage; predicted protein	0	-0.347	0	0	2	34
JW1389	paaG	acyl-CoA hydratase	0	-0.094	0	0	2	34
JW1434	ydcR	fused predicted DNA-binding transcriptional regulator -!- predicted amino transferase	0	-0.192	0	0	1	34
JW1502	ydeU	conserved protein, predicted	0	-0.754	0	0	2	34
JW2478	yfgO	predicted inner membrane protein	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.041	1	7	1	34
JW2952	yghR	predicted protein with nucleoside triphosphate hydrolase domain	0	-0.274	0	0	2	34
JW4086	dcuS	sensory histidine kinase in two-component regulatory system with DcuR, regulator of anaerobic fumarate	GO:0009274 cell wall (sensu Bacteria)	-0.109	1	2	2	34
JW5388	ypdA	predicted sensory kinase in two-component system with YpdB	0	0.283	1	6	2	34
JW5610	yieM	predicted von Willibrand factor containing protein	0	-0.306	0	0	1	34
JW5697	yhfU	predicted protein	0	0.153	1	1	2	34
JW0260	yagA	CP4-6 prophage; predicted DNA-binding transcriptional regulator	0	-0.656	0	0	2	33
JW0262	yagF	CP4-6 prophage; predicted dehydratase	0	-0.024	0	0	2	33

JW0437	ybaO	predicted DNA-binding transcriptional regulator	0	-0.001	0	0	2	33
JW1308	ycjS	predicted oxidoreductase, NADH-	0	-0.102	0	0	2	33
JW1470	fdnG	formate dehydrogenase-N, alpha subunit, nitrate-inducible	GO:0005737 cytoplasm	-0.421	0	0	2	33
JW1922	fliF	flagellar basal-body MS-ring and collar protein	GO:0019861 flagellum -! GO:0019866 inner membrane	-0.476	1	2	2	33
JW4070	yjdA	conserved protein with nucleoside triphosphate hydrolase domain	0	-0.293	0	0	2	33
JW4258	yjhF	KpLE2 phage-like element; predicted transporter	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	1.114	1	12	2	33
JW5103	ybhJ	predicted hydratase	0	-0.142	0	0	2	33
JW0964	yccC	cryptic autophosphorylating protein tyrosine kinase Etk	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.309	1	2	2	32
JW1023	csgD	DNA-binding transcriptional activator in two-component regulatory system	0	-0.415	0	0	1	32
JW1309	ycjT	predicted hydrolase	0	-0.324	0	0	2	32
JW1445	yncC	predicted DNA-binding transcriptional regulator	0	-0.142	0	0	1	32
JW1546	ydfQ	Qin prophage; predicted lysozyme	0	-0.401	1	1	2	32
JW1607	uidC	predicted outer membrane porin protein	GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner	-0.333	1	1	2	32
JW2609	yfjL	CP4-57 prophage; predicted protein	0	-0.407	0	0	2	32
JW3344	yhfX	predicted amino acid racemase	0	-0.001	0	0	2	32
JW3457	yhiL	predicted protein	0	-0.467	0	0	2	32
JW4015	aphA	acid phosphatase/phosphotransferase, class B, non-specific	GO:0005737 cytoplasm	-0.283	0	0	1	32
JW5084	hokE	toxic polypeptide, small	0	0.782	1	1	1	32
JW5925	yghJ	predicted inner membrane lipoprotein	0	-0.540	0	0	2	32
JW0504	allC	allantoate amidohydrolase	0	-0.230	0	0	2	31
JW0505	allD	ureidoglycolate dehydrogenase	0	-0.136	0	0	2	31
JW0695	ybfL	predicted transposase (pseudogene)	0	-0.320	0	0	2	31
JW0808	ybiY	predicted pyruvate formate lyase activating enzyme	0	-0.108	0	0	2	31
JW0916	ssuB	alkanesulfonate transporter subunit -! ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.009	0	0	2	31
JW1166	ycgJ	predicted protein	0	-0.208	0	0	2	31
JW1943	vsr	DNA mismatch endonuclease of very short patch repair	0	-0.360	0	0	2	31
JW2265	yfbK	conserved protein	0	-0.478	0	0	2	31
JW2314	dedA	conserved inner membrane protein	GO:0009274 cell wall (sensu	0.809	1	4	1	31
JW2345	intS	CPS-53 (KpLE1) prophage; predicted prophage CPS-53 integrase	0	-0.387	0	0	2	31
JW2759	gudX	predicted gluconate dehydratase	0	-0.195	0	0	2	31
JW3089	tdcA	DNA-binding transcriptional activator	GO:0005737 cytoplasm	0.092	1	0	2	31
JW3182	yhcA	predicted periplasmic chaperone protein	0	-0.366	0	0	2	31

JW3956	thiF	thiamin (thiazole moiety) biosynthesis protein	0	-0.039	1	1	2	31
JW4065	phnE	phosphonate/organophosphate ester transporter subunit -!- membrane component of ABC superfamily		0.313	1	3	2	31
JW4254	insA	KpLE2 phage-like element; IS1 repressor protein InsA	0	-0.376	0	0	2	31
JW5451	ppdB	conserved protein		0.032	1	1	2	31
JW5803	ybhR	predicted transporter subunit -!- membrane component of ABC		0.391	1	6	2	31
JW0073	leuA	2-isopropylmalate synthase		-0.188	0	0	1	30
JW1145	mcrA	e14 prophage; 5-methylcytosine-specific restriction endonuclease B	0	-0.436	0	0	2	30
JW1354	ydaU	Rac prophage; conserved protein	0	-0.539	0	0	2	30
JW1416	ydcA	predicted protein	0	0.084	1	0	1	30
JW1568	ydfE	Qin prophage; predicted protein	0	-0.452	0	0	2	30
JW2086	yegU	predicted hydrolase	0	0.031	1	0	1	30
JW2695	hycA	regulator of the transcriptional regulator FhIA		-0.356	0	0	2	30
JW2722	cysD	sulfate adenylyltransferase, subunit 2	0	-0.537	0	0	2	30
JW2811	kdul	predicted 5-keto 4-deoxyuronate isomerase	0	-0.190	0	0	1	30
JW3558	yaV	membrane fusion protein (MFP) component of efflux pump, signal		-0.028	1	2	2	30
JW3688	mdtL	multidrug efflux system protein		0.991	1	11	2	30
JW3989	yjbH	predicted porin	0	-0.502	0	0	2	30
JW4313	hsdR	endonuclease R		-0.489	0	0	2	30
JW5184	cvrA	predicted cation/proton antiporter		0.668	1	11	2	30
JW5228	ydcM	predicted transposase	0	-0.653	0	0	2	30
JW5406	yphH	predicted DNA-binding transcriptional regulator	0	-0.197	0	0	1	30
JW5688	rtcA	RNA 3'-terminal phosphate cyclase		0.130	1	0	2	30
JW5908	yddM	predicted DNA-binding transcriptional regulator	0	-0.161	0	0	1	30
JW0126	yadE	predicted polysaccharide deacetylase lipoprotein	0	-0.278	1	1	2	29
JW0498	ybbV	predicted protein	0	-0.023	1	1	2	29
JW0689	rhcC	rhcC element core protein RshC	0	-0.715	0	0	2	29
JW0850	ybjQ	conserved protein	0	0.034	1	0	1	29
JW0967	ymcA	conserved protein	0	-0.456	0	0	2	29
JW1007	ydcQ	predicted glycosyl transferase		0.296	1	5	2	29
JW1637	ydhK	conserved inner membrane protein	0	0.255	1	10	2	29
JW1766	yeaC	conserved protein	0	-0.369	0	0	2	29

JW1923	fliG	flagellar motor switching and energizing component	GO:0019861 flagellum	-0.108	0	0	2	29
JW1955	yedZ	conserved inner membrane protein	0	0.543	1	6	1	29
JW2054	yegD	predicted chaperone	0	-0.118	0	0	2	29
JW2192	napH	ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB)	0	0.397	1	4	2	29
JW2200	alkB	oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions	GO:0005737 cytoplasm	-0.286	0	0	1	29
JW2623	yfjW	CP4-57 prophage; predicted inner membrane protein	0	0.285	1	5	2	29
JW2686	ascB	cryptic 6-phospho-beta-glucosidase	0	-0.355	0	0	2	29
JW2912	endA	DNA-specific endonuclease I	0	-0.739	0	0	2	29
JW2923	yggM	conserved protein	0	-0.794	0	0	2	29
JW3029	bacA	undecaprenyl pyrophosphate phosphatase	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.930	1	7	1	29
JW3354	hofQ	predicted fimbrial transporter	0	-0.117	0	0	2	29
JW3455	yhiJ	predicted protein	0	-0.341	0	0	2	29
JW3643	uhpB	sensory histidine kinase in two-component regulatory system with UhpA	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.268	1	7	2	29
JW4261	yjhl	KpLE2 phage-like element; predicted DNA-binding transcriptional regulator	0	-0.233	0	0	2	29
JW5031	ykgK	predicted regulator	0	-0.522	0	0	2	29
JW5082	cusS	sensory histidine kinase in two-component regulatory system with CusR, senses copper ions	GO:0019866 inner membrane	0.012	1	2	2	29
JW5218	paaK	phenylacetyl-CoA ligase	0	-0.345	0	0	1	29
JW5316	fliO	flagellar biosynthesis protein	GO:0019861 flagellum	0.318	1	1	2	29
JW5512	ygiJ	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.787	1	12	2	29
JW5690	gntT	gluconate transporter, high-affinity GNT I system	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.029	1	11	2	29
JW0308	yahB	predicted DNA-binding transcriptional regulator	0	-0.102	0	0	2	28
JW0340	mhpC	2-hydroxy-6-keonona-2,4-dienedioic acid hydrolase	0	-0.202	0	0	1	28
JW0685	kdpB	potassium translocating ATPase, subunit B	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.358	1	7	2	28
JW0836	rimK	ribosomal protein S6 modification protein	GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm	0.022	1	0	2	28
JW1005	phoH	conserved protein with nucleoside triphosphate hydrolase domain	GO:0005737 cytoplasm	-0.242	0	0	2	28
JW1285	sapC	predicted antimicrobial peptide transporter subunit -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane	0.749	1	5	1	28

JW1355	ydaV	Rac prophage; predicted DNA replication protein	0	-0.476	0	0	2	28
JW1613	malX	fused maltose and glucose-specific PTS enzyme IIBC components	0	0.700	1	8	2	28
JW1684	ydiF	fused predicted acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit - - beta subunit	0	0.008	1	0	2	28
JW2368	yfdE	predicted CoA-transferase, NAD(P)-binding	0	-0.116	0	0	2	28
JW2415	cysA	sulfate/thiosulfate transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.273	0	0	1	28
JW2549	recO	gap repair protein	GO:0005737 cytoplasm	-0.257	0	0	2	28
JW2638	gabP	gamma-aminobutyrate transporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.826	1	12	2	28
JW3483	gadW	DNA-binding transcriptional activator	0	-0.154	0	0	2	28
JW3500	bcsB	regulator of cellulose synthase, cyclic di-GMP binding	0	-0.126	1	2	2	28
JW3901	menA	1,4-dihydroxy-2-naphthoate octaprenyltransferase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.664	1	9	1	28
JW3967	zraS	sensory histidine kinase in two-component regulatory system with ZraR	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	-0.061	1	2	1	28
JW5007	secM	regulator of secA translation	0	-0.281	1	1	1	28
JW5385	yfdN	CPS-53 (KpLE1) prophage; predicted protein	0	-0.815	0	0	2	28
JW5424	ypjC	predicted protein	0	-0.456	0	0	1	28
JW5707	gspD	general secretory pathway component, cryptic	0	-0.184	0	0	2	28
JW5710	yrdA	conserved protein	0	-0.206	0	0	1	28
JW5743	yjfO	conserved protein	0	-0.055	1	1	1	28
JW5748	ytfI	predicted protein	0	-0.374	0	0	2	28
JW5855	recQ	ATP-dependent DNA helicase	GO:0005737 cytoplasm	-0.269	0	0	2	28
JW5910	ydiD	short chain acyl-CoA synthetase, anaerobic	0	-0.060	0	0	2	28
JW5967	sgcB	predicted enzyme IIB component of	GO:0005737 cytoplasm	0.152	1	0	2	28
JW0444	ybaZ	predicted methyltransferase	0	-0.400	0	0	2	27
JW0629	mrdB	cell wall shape-determining protein	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.908	1	9	1	27
JW0783	ybiA	conserved protein	0	-0.764	0	0	2	27
JW1490	yddB	predicted porin protein	0	-0.584	0	0	2	27
JW1840	edd	6-phosphogluconate dehydratase	0	-0.023	0	0	2	27
JW1872	cheB	fused chemotaxis regulator - - protein-glutamate methyltransferase, in two-component regulatory system with	GO:0005737 cytoplasm	0.050	1	0	2	27
JW2047	wza	lipoprotein required for capsular polysaccharide translocation through the outer membrane	0	-0.216	0	0	2	27

JW2058	yegL	conserved protein	0	-0.083	0	0	2	27
JW2102	molR	DNA-binding transcriptional regulator, N-ter fragment (pseudogene)	0	-0.306	0	0	2	27
JW2143	lysP	lysine transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.616	1	12	1	27
JW2453	narQ	sensory histidine kinase in two-component regulatory system with NarP	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.152	1	2	1	27
JW2723	iap	aminopeptidase in alkaline phosphatase isozyme conversion	0	-0.372	0	0	1	27
JW2809	araE	arabinose transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.628	1	12	2	27
JW2841	hyuA	D-stereospecific phenylhydantoinase	0	-0.161	0	0	2	27
JW2843	yqeB	conserved protein with NAD(P)-binding Rossmann fold	0	0.125	1	0	2	27
JW2944	glcG	conserved protein	0	0.158	1	0	1	27
JW3357	yrfC	predicted fimbrial assembly protein	0	-0.345	1	1	2	27
JW3365	yhgE	predicted inner membrane protein	GO:0009274 cell wall (sensu	0.454	1	11	2	27
JW3528	insK	IS150 conserved protein InsB	0	-0.671	0	0	2	27
JW3965	yjaH	conserved protein	0	-0.539	0	0	1	27
JW4066	phnD	phosphonate/organophosphate ester transporter subunit -!- periplasmic binding component of ABC superfamily	GO:0042597 periplasmic space	-0.328	0	0	2	27
JW4101	yjeH	predicted transporter	0	0.960	1	11	2	27
JW4143	yjfM	conserved protein	0	-0.791	0	0	2	27
JW4247	fecE	KpLE2 phage-like element; iron-dicitrate transporter subunit -!- ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.065	0	0	2	27
JW5135	torS	hybrid sensory histidine kinase in two-component regulatory system with TorR	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.154	1	2	1	27
JW5142	ycdR	predicted enzyme associated with biofilm formation	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	-0.379	1	0	1	27
JW5188	dhaR	predicted DNA-binding transcriptional regulator, dihydroxyacetone	0	-0.085	0	0	1	27
JW5595	yifK	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.843	1	12	2	27
JW5749	ytfK	conserved protein	0	-0.157	0	0	1	27
JW0812	iaaA	L-asparaginase	0	0.101	1	0	2	26
JW1060	flgB	flagellar component of cell-proximal portion of basal-body rod	GO:0019861 flagellum -!- GO:0042597 periplasmic space	-0.469	0	0	2	26
JW1067	flgI	predicted flagellar basal body protein	GO:0019861 flagellum	0.055	1	0	2	26
JW1219	tpr	predicted protamine-like protein	GO:0005737 cytoplasm	-1.924	0	0	1	26
JW1294	puuB	gamma-Glu-putrescine oxidase, FAD/NAD(P)-binding	0	-0.244	0	0	2	26
JW1344	recE	Rac prophage; exonuclease VIII, 5' -> 3' specific dsDNA exonuclease	GO:0005737 cytoplasm	-0.578	0	0	2	26
JW1508	lsrD	A12 transporter -!- membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.103	1	9	2	26

JW2310	cvpA	membrane protein required for colicin V production	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.961	1	4	2	26
JW2973	exbD	membrane spanning protein in TonB-ExbB-ExbD complex	0	0.013	1	1	1	26
JW3096	garP	predicted (D)-galactarate transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.704	1	11	2	26
JW4008	yjbM	predicted protein	0	-0.419	0	0	2	26
JW4041	yjcP	predicted outer membrane factor of efflux pump	GO:0009274 cell wall (sensu Bacteria) !- GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.122	1	0	2	26
JW4304	yjiS	conserved protein	0	-0.976	0	0	2	26
JW4361	creB	DNA-binding response regulator in two-component regulatory system with CreC	GO:0005737 cytoplasm	-0.132	0	0	2	26
JW5455	yqeJ	predicted protein	0	-0.272	1	1	2	26
JW5858	yidX	predicted lipoproteinC	0	-0.122	1	1	1	26
JW0548	ybcW	DLP12 prophage; predicted protein	0	-0.113	0	0	1	25
JW0914	pncB	nicotinate phosphoribosyltransferase	GO:0042597 periplasmic space	-0.298	0	0	1	25
JW1731	ydjR	conserved protein	0	-0.134	0	0	1	25
JW2651	nrdF	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like	GO:0005737 cytoplasm	-0.255	0	0	1	25
JW3953	thiH	thiamin biosynthesis ThiGH complex subunit	0	-0.468	0	0	1	25
JW5412	yfiL	predicted protein	0	-0.440	0	0	1	25
JW5859	dgoT	D-galactonate transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.680	1	11	1	25
JW5881	yehS	predicted protein	0	0.014	1	0	1	25
JW0680	speF	ornithine decarboxylase isozyme,	0	-0.235	0	0	1	24
JW1597	ydgl	predicted arginine/ornithine antiporter transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.971	1	13	1	24
JW2454	acrD	aminoglycoside/multidrug efflux system	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.160	1	11	1	24
JW2490	yfgI	conserved protein	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	-1.118	1	0	1	24
JW2954	yghT	predicted protein with nucleoside triphosphate hydrolase domain	0	-0.151	0	0	1	24
JW3189	yhcG	conserved protein	0	-0.375	0	0	1	24
JW5046	mhpT	predicted 3-hydroxyphenylpropionic transporter	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.964	1	12	1	24
JW0042	fixC	predicted oxidoreductase, FAD/NAD(P)-binding domain	0	0.056	1	0	1	23
JW0831	ybjL	predicted transporter	0	0.554	1	9	1	23
JW1098	ycfR	predicted protein	0	0.029	1	0	1	23
JW2184	ccmF	heme lyase, CcmF subunit	GO:0009274 cell wall (sensu Bacteria) !- GO:0019866 inner	0.641	1	15	1	23

JW2380	ypdD	fused predicted PTS enzymes Hpr component - - enzyme I component - - enzyme IIA component	0	-0.148	0	0	1	23
JW2842	yqeA	predicted amino acid kinase	0	-0.019	0	0	1	23
JW3692	yieG	predicted inner membrane protein	0	0.997	1	13	1	23
JW5036	insE	IS3 element protein	0	-0.962	0	0	1	23
JW5422	ypjA	adhesin-like autotransporter	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.359	1	1	1	23
JW5818	potG	putrescine transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	-0.130	0	0	1	23
JW0068	sgrR	DNA-binding transcriptional regulator	GO:0042597 periplasmic space	-0.324	0	0	1	22
JW0455	ybaM	predicted protein	0	-0.391	0	0	1	22
JW0648	gltK	glutamate and aspartate transporter subunit - - membrane component of ABC superfamily	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane	0.868	1	5	1	22
JW1384	paaB	predicted multicomponent oxygenase/reductase subunit for phenylacetic acid degradation	0	-0.561	0	0	1	22
JW1395	paaY	predicted hexapeptide repeat acetyltransferase	0	-0.064	0	0	1	22
JW1402	ydbA	predicted outer membrane protein, C-terminal fragment (pseudogene)	0	-0.270	0	0	1	22
JW2330	yfcP	predicted fimbrial-like adhesin protein	GO:0009289 fimbria	0.064	1	1	1	22
JW2917	yggR	predicted transporter	0	-0.135	0	0	1	22
JW2986	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner	0.073	1	1	1	22
JW3689	yidZ	predicted DNA-binding transcriptional regulator	0	-0.226	0	0	1	22
JW0471	ybaP	conserved protein	0	-0.228	0	0	1	21
JW0609	citD	citrate lyase, acyl carrier (gamma)	GO:0005737 cytoplasm	0.028	1	0	1	21
JW0807	ybiW	predicted pyruvate formate lyase	0	-0.245	0	0	1	21
JW0884	ycaK	conserved protein	0	-0.381	0	0	1	21
JW1293	puuC	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase,	GO:0005737 cytoplasm	-0.116	0	0	1	21
JW1479	ddpD	D-Ala-D-Ala transporter subunit - - ATP-binding component of ABC superfamily	GO:0005737 cytoplasm	0.024	1	0	1	21
JW1779	yeaM	predicted DNA-binding transcriptional regulator	0	-0.142	0	0	1	21
JW2335	yfcU	predicted export usher protein	GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria)	-0.631	1	0	1	21
JW2547	acpS	holo-[acyl-carrier-protein] synthase 1	GO:0005737 cytoplasm	0.013	1	0	1	21
JW3101	kbaZ	tagatose 6-phosphate aldolase 1, kbaZ subunit	0	-0.175	0	0	1	21

JW3349	rpe	D-ribulose-5-phosphate 3-epimerase	0	0.066	1	0	1	21
JW3553	sgbH	3-keto-L-gulonate 6-phosphate decarboxylase	0	0.028	1	0	1	21
JW3700	bglF	fused beta-glucoside-specific PTS enzyme IIABC components	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.617	1	10	1	21
JW3701	bglG	transcriptional antiterminator of the bgl operon	GO:0005737 cytoplasm	-0.204	0	0	1	21
JW0133	yadL	predicted fimbrial-like adhesin protein	0	0.152	1	1	1	20
JW0332	cynX	predicted cyanate transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	0.857	1	12	1	20
JW0784	dinG	ATP-dependent DNA helicase	GO:0005737 cytoplasm	-0.243	0	0	1	20
JW1201	hemA	glutamyl tRNA reductase	GO:0005737 cytoplasm	-0.188	0	0	1	20
JW1555	relE	Qin prophage; toxin of the RelE-RelB toxin-antitoxin system	GO:0005737 cytoplasm	-0.348	0	0	1	20
JW2098	yehD	predicted fimbrial-like adhesin protein	GO:0009289 fimbria	0.048	1	1	1	20
JW2362	dsdX	predicted transporter	GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner	1.122	1	12	1	20
JW2608	yfjK	CP4-57 prophage; conserved protein	0	-0.184	0	0	1	20
JW2848	ygfM	predicted oxidoreductase	0	-0.127	0	0	1	20
JW2897	yggF	predicted hexoseP phosphatase	0	0.018	1	0	1	20
JW3685	tnaC	tryptophanase leader peptide	0	-0.117	0	0	1	20
JW3699	bglB	cryptic phospho-beta-glucosidase B	0	-0.304	0	0	1	20
JW3913	metF	5,10-methylenetetrahydrofolate	0	-0.235	0	0	1	20
JW5484	yghF	predicted secretion pathway protein, C-type protein	0	-0.218	0	0	1	20
JW5683	yhhL	conserved inner membrane protein	0	0.734	1	2	1	20
JW5737	ecnA	entericidin A membrane lipoprotein, antidote entericidin B	0	0.473	1	0	1	20