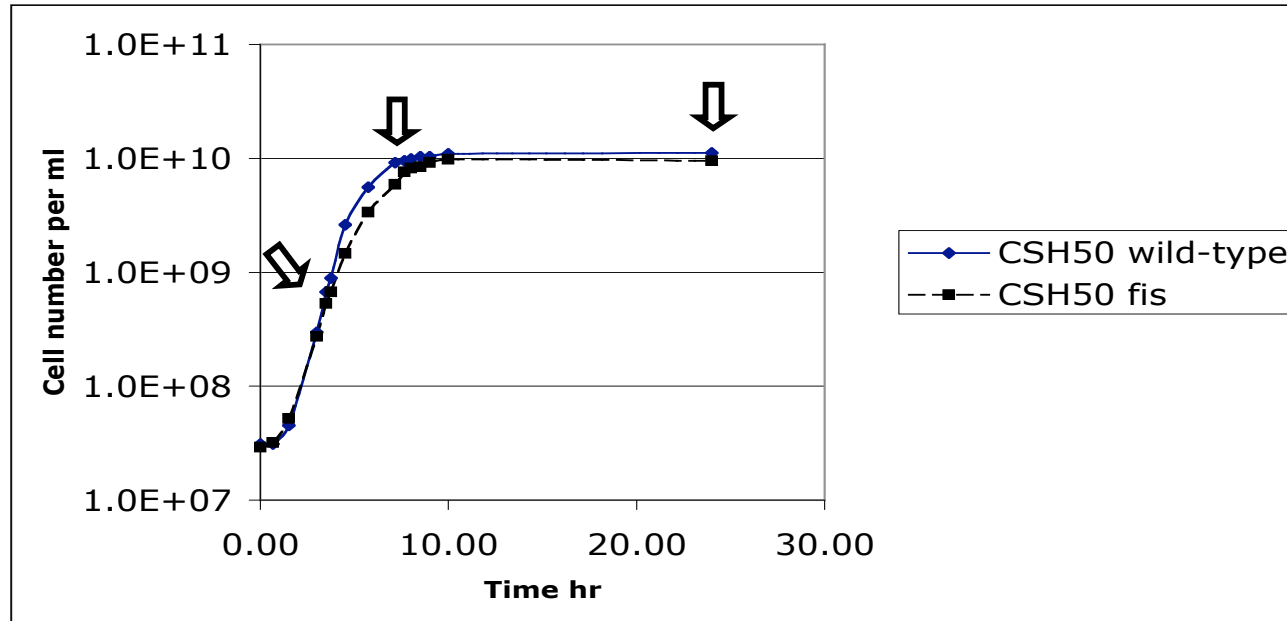


Supplementary information

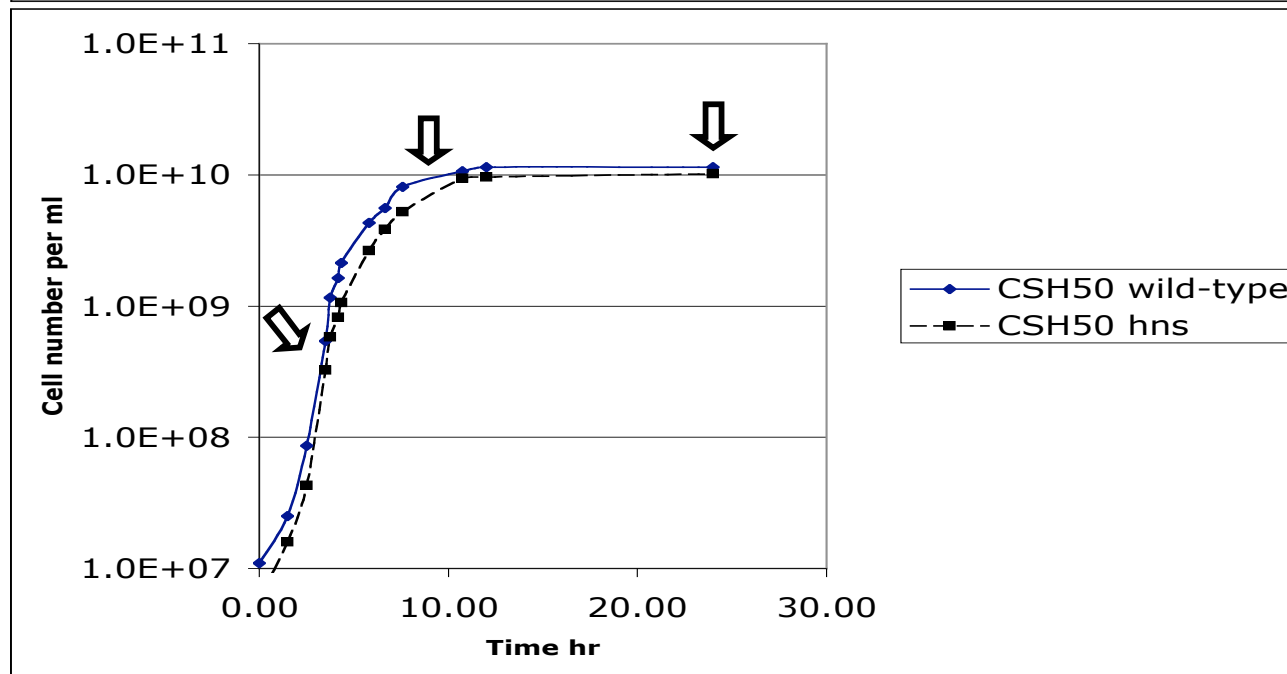
Blot et al. “Homeostatic regulation of supercoiling sensitivity coordinates transcription of the bacterial genome”.

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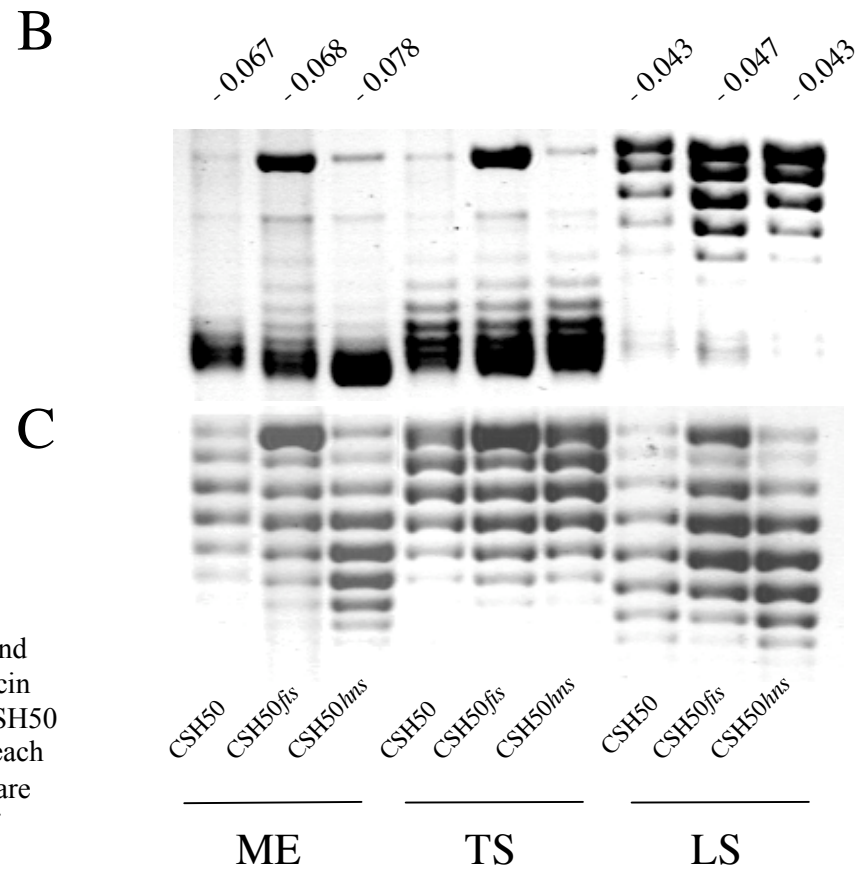
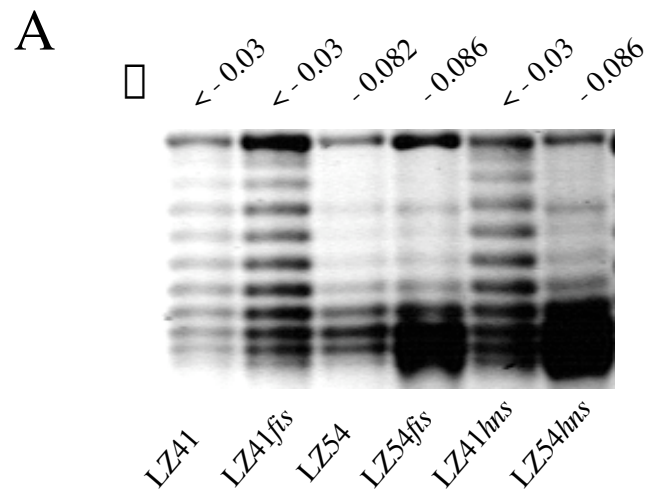
A



B



Supplementary Figure 1. The growth curves of CSH50 wild-type and mutant cells. (A) Growth curves of the wild-type and *fis* mutant (B) Growth curves of the wild-type and *hns* mutant. The growth curves are represented by solid and dashed lines for wild-type and (each) mutant, respectively. The arrows indicate the times of cell sampling for array analyses.



Supplementary Figure 2. Topoisomer distributions of plasmids (pUC18 DNA) isolated from growing cells. (A) Topoisomer distributions in LZ54 and LZ41 strains and their mutant derivatives (as indicated) 5 min after norfloxacin addition. (B) and (C) Topoisomer distributions of plasmids isolated from CSH50 strains and its mutant derivatives during the growth cycle. The $\langle \sigma \rangle$ values for each population (except for transition stage where no differences were observed) are indicated. High-resolution gel-electrophoresis was carried out in presence of 0.5 μ g/ml (B) and 2 μ g/ml (C) chloroquine. In (C) all topoisomers migrate as negatively supercoiled species except for the late stationary (LS) phase samples, which migrate as positively supercoiled species. The superhelical densities were determined by band counting method as previously described (Keller, W. 1975. *Proc.Nat.Acad.Sci.USA*, 72:4876-4880). Mean $\langle \sigma \rangle$ -values (\pm 15%) were calculated using a range of chloroquine concentrations (0.5 to 20 μ g/ml) according to the formula $\langle \sigma \rangle = \Delta Lk/Lk_0$, with $Lk_0 = 10.45$ bp/turn. The relaxed topoisomers of the samples isolated from LZ41 and its derivatives demonstrated a complex pattern making it difficult to derive precise figures for $\langle \sigma \rangle$.

Table I Genes demonstrating significant changes in expression

Scanned array images were analysed using the TM4 software package (Saeed AI *et al Biotechniques* **34**:374-378 (2003)). Spot intensities were quantified and quality of each spot was verified by calculating a quality control (QC) score depending on signal-to-noise ratio for every channel in spot and shape quality for each spot and calculating p-values for each channel as result of a t-test comparing the spot pixel set and surrounding background pixel set using the TIGR Spotfinder software. Data was normalized by locally weighted linear regression (Cleveland W *et al J Am Stat Assoc* **83**:596-609 (1988)) and a one-class t-test (Pan W *Bioinformatics* **18**: 546-554 (2002)) was applied to replicated experiments to obtain differentially regulated genes with significant p-values ($p < 0.05$) using the TIGR MIDAS software. Mean ratios and corresponding p-value from one-class t-test are indicated.

gene	blattner	ratio A/B	p-value	function
CSH50 (A) CSH50fs (B) in Mid-Exponential				
aceA	b4015	0,4993	0,0399	isocitrate lyase monomer
acnA	b1276	0,5979	0,0220	aconitase
add	b1623	0,7825	0,0299	deoxyadenosine deaminase / adenosine deaminase
adhP	b1478	0,5912	0,0138	ethanol dehydrogenase
adk	b0474	0,7212	0,0042	adenylate kinase
allR	b0506	0,5111	0,0224	AllR transcriptional regulator
ansA	b1767	0,5233	0,0335	asparaginase I
araC	b0064	0,6958	0,0157	AraC transcriptional dual regulator
argC	b3958	1,8029	0,0027	N-acetylglutamylphosphate reductase
argR	b3237	0,5625	0,0105	ArgR transcriptional dual regulator
argS	b1876	0,6906	0,0296	arginyl-tRNA synthetase
aroG	b0754	2,9967	0,0372	2-dehydro-3-deoxyphosphoheptonate aldolase
arsB	b3502	0,4948	0,0219	arsenite Ars transporter
artP	b0864	1,7795	0,0024	arginine ABC transporter
atoS	b2219	2,3222	0,0346	AtoS-Phis
b0259	b0259	1,7818	0,0203	IS5 protein
b0538	b0538	0,4888	0,0102	putative sensory transduction regulator
b1146	b1146	0,4913	0,0184	hypothetical protein
b3044	b3044	1,8424	0,0245	IS21 protein
bax	b3570	2,0569	0,0470	putative ATP-binding protein
bcsC	b3530	1,9134	0,0035	oxidase involved in cellulose synthesis
bcsE	b3536	2,7434	0,0002	putative protease
bcsF	b3537	2,2031	0,0199	hypothetical protein
bdm	b1481	0,4743	0,0212	hypothetical protein
bfd	b3337	3,4231	0,0057	bacterioferritin-associated ferredoxin
blc	b4149	1,5094	0,0488	Blc outer membrane lipoprotein (lipocalin)
bolA	b0435	3,8179	0,0135	BolA transcriptional regulator
caiB	b0038	0,5712	0,0445	CaiB monomer
carB	b0033	2,0837	0,0268	carbamoyl phosphate synthetase
chaC	b1218	0,5220	0,0378	cation transport regulator
cls	b1249	2,0209	0,0254	cardiolipin synthase
cmk	b0910	0,5068	0,0341	cytidylate kinase
codB	b0336	0,4890	0,0263	CodB cytosine NCS1 transporter
corA	b3816	0,6579	0,0224	CorA magnesium ion MIT transporter
csgA	b1042	0,4427	0,0472	curlin, major subunit
cspD	b0880	0,5276	0,0343	DNA replication inhibitor
cspF	b1558	0,4512	0,0391	cold shock protein CspF
cusF	b0573	1,4877	0,0197	periplasmic copper-binding protein
cusS	b0570	0,5047	0,0393	putative 2-component sensor protein
cyoB	b0431	1,9982	0,0279	cytochrome bo terminal oxidase subunit I
dcp	b1538	0,7555	0,0449	dipeptidyl carboxypeptidase II
dcuA	b4138	1,7199	0,0185	DcuA dicarboxylate Dcu transporter
dcuR	b4124	2,1501	0,0059	DcuR-Pasp56
dcuS	b4125	2,3146	0,0461	DcuS-Phis349
deoC	b4381	3,0453	0,0075	deoxyribose-phosphate aldolase
deoD	b4384	1,9030	0,0058	purine nucleoside phosphorylase
dgkA	b4042	1,3606	0,0128	diacylglycerol kinase
dgoA	b3692	0,1024	0,0302	dgoA 3871635-3871018 : '2-dehydro-3-deoxyphosphogalactonate aldolase / dgoD 3871021-3869873 : galactonate dehydratase
dgoR	b3694	0,2442	0,0306	regulator protein for dgo operon
dhaL	b1199	2,4480	0,0354	dihydroxyacetone kinase subunit L
dinB	b0231	0,5647	0,0273	DNA polymerase IV (Y-family DNA polymerase; translesion DNA synthesis)
dinI	b1061	0,5985	0,0137	damage-inducible protein I
dld	b2133	0,4244	0,0262	D-lactate:Quinone Oxidoreductase
dmsA	b0894	3,0559	0,0473	dimethyl sulfoxide reductase, chain A
dnaC	b4361	0,6833	0,0209	chromosome replication; initiation and chain elongation
dnaN	b3701	0,4388	0,0203	DNA polymerase III, beta-subunit

gene	blattner	ratio A/B	p-value	function
dos	b1489	0,4681	0,0009	heme-regulated phosphodiesterase monomer
dpiB	b0619	0,6938	0,0436	DpiB
dppA	b3544	2,6873	0,0270	dipeptide ABC transporter
dusB	b3260	0,1200	0,0055	tRNA dihydrouridine synthase
ecfL	b3095	1,4210	0,0186	putative integral membrane protein with possible extracytoplasmic function
eco	b2209	0,5356	0,0195	ecotin monomer; serine protease inhibitor
efp	b4147	1,6592	0,0497	elongation factor P (EF-P)
emrD	b3673	0,6508	0,0203	EmrD multidrug MFS transporter
eutD	b2458	0,4733	0,0002	putative phosphate acetyltransferase, ethanolamine utilization
eutK	b2438	0,4006	0,0142	hypothetical protein
exbB	b3006	3,7552	0,0314	ExbB protein; uptake of enterochelin; tonB-dependent uptake of B colicins
exbD	b3005	3,8008	0,0007	ExbD uptake of enterochelin; tonB-dependent uptake of B colicins
fadL	b2344	0,1834	0,0089	transport of long-chain fatty acids; sensitivity to phage T2
fbaB	b2097	0,1653	0,0131	fructose bisphosphate aldolase monomer
fbp	b4232	0,5580	0,0352	fructose 1,6 bisphosphatase monomer
fdx	b2525	0,5482	0,0090	oxidized ferredoxin
fecB	b4290	8,6991	0,0075	ferric dicitrate uptake system
fepD	b0590	8,7158	0,0041	Ferric Enterobactin Transport System
fhuF	b4367	4,4704	0,0311	acts in reduction of ferrioxamine B iron
fimC	b4316	0,4695	0,0364	periplasmic chaperone, required for type 1 fimbriae
fimI	b4315	0,4942	0,0141	fimbrial protein
flgJ	b1081	3,8116	0,0170	FlgJ
flgK	b1082	2,4424	0,0026	flagellar biosynthesis, hook-filament junction protein 1
fliM	b1945	19,0270	0,0382	flagellar motor switch protein FliM; component of motor switch and energizing, enabling rotation and determining its direction
fliQ	b1949	8,8017	0,0425	flagellar biosynthesis protein FliQ
fliS	b1925	9,2416	0,0232	flagellar biosynthesis protein FliS
fnr	b1334	0,4432	0,0445	FNR transcriptional dual regulator
folD	b0529	0,6351	0,0380	methyleneTHF enzyme / methenyltetrahydrofolate cyclohydrolase / methylenetetrahydrofolate dehydrogenase-(NADP+)
folK	b0142	0,7061	0,0168	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase
folP	b3177	0,3301	0,0096	dihydropteroate synthase
fpr	b3924	1,3795	0,0274	flavodoxin NADP+ reductase
frdC	b4152	2,7825	0,0397	fumarate reductase membrane protein
frtC	b3373	0,5854	0,0174	fructoselysine and psicoselysine degradation
ftnA	b1905	0,2818	0,0240	cytoplasmic ferritin, an iron storage protein)
ftsY	b3464	1,3557	0,0167	SRP receptor
fucR	b2805	1,7855	0,0380	FucR transcriptional activator
gadC	b1492	0,3529	0,0477	XasA GABA APC transporter
galK	b0757	0,5451	0,0491	galactokinase
galR	b2837	4,4098	0,0315	GalR-galactose
garK	b3124	2,4698	0,0490	glycerate kinase I
gatD	b2091	0,7554	0,0174	galactitol-1-phosphate dehydrogenase
gatY	b2096	1,6866	0,0090	tagatose-1,6-bisphosphate aldolase 2
gcvH	b2904	4,5473	0,0091	dihydrolipoyl-GcvH-protein
gcvT	b2905	5,7601	0,0109	aminomethyltransferase
gidB	b3740	0,4856	0,0237	protein with a methyltransferase fold; possible role in chromosome replication
glcB	b2976	0,6190	0,0452	malate synthase G
glmU	b3730	1,6033	0,0469	N-acetylglucosamine-1-phosphate uridyltransferase / glucosamine-1-phosphate acetyltransferase
glnH	b0811	0,4352	0,0140	glutamine ABC transporter
gloB	b0212	3,5188	0,0181	glyoxalase II
glpA	b2241	1,9558	0,0214	glycerol-3-phosphate-dehydrogenase, anaerobic
gnsA	b0991	4,7811	0,0050	YmcE
gntY	b3414	0,5552	0,0419	predicted membrane-bound protein that is involved in high-affinity gluconate transport
gspF	b3327	1,6223	0,0056	putative protein secretion protein for export
gssA	b2988	0,6968	0,0024	glutathionylspermidine synthetase / glutathionylspermidine amidase
guaA	b2507	0,3639	0,0040	GMP synthase / GMP synthase (ammonia dependent)
gutQ	b2708	2,2100	0,0352	protein with a sugar isomerase domain
hcaR	b2537	0,7416	0,0402	HcaR transcriptional activator
hchA	b1967	0,5528	0,0128	heat shock protein (Hsp) 31
hdhA	b1619	2,5786	0,0216	7-alpha-hydroxysteroid dehydrogenase
helD	b0962	0,5183	0,0290	DNA helicase IV
hepA	b0059	0,3051	0,0412	RNA Polymerase (RNAP)-binding ATPase and RNAP recycling factor
hflD	b1132	0,3468	0,0048	membrane protein in operon with purB
hisC	b2021	0,3221	0,0144	histidine-phosphate aminotransferase
hisD	b2020	0,3608	0,0326	histidinal dehydrogenase / histidinol dehydrogenase
hisF	b2025	0,6098	0,0314	imidazole glycerol phosphate synthase, HisF subunit
hns	b1237	2,0288	0,0189	H-NS transcriptional dual regulator
holB	b1099	0,7617	0,0287	DNA polymerase III, delta prime subunit
holD	b4372	0,6747	0,0191	DNA polymerase III, psi subunit
holE	b1842	0,5413	0,0155	DNA polymerase III, theta subunit

gene	blattner	ratio A/B	p-value	function
hslR	b3400	0,4968	0,0137	heat shock protein Hsp15
hslU	b3931	0,6792	0,0167	ATPase component of the HslVU protease
hslV	b3932	0,6182	0,0469	peptidase component of the HslVU protease
hupA	b4000	2,5232	0,0026	DNA-binding protein HU-alpha (HU-2)
hybO	b2997	1,6217	0,0148	Hyb0
hycF	b2720	0,4798	0,0143	formate hydrogenlyase complex
hypB	b2727	1,4176	0,0207	guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3
hypC	b2728	1,8523	0,0443	pleiotropic effects on 3 hydrogenase isozymes
ibpA	b3687	0,2895	0,0047	small heat shock protein IbpA
intA	b2622	0,3133	0,0364	prophage CP4-57 integrase
intB	b4271	1,5659	0,0241	prophage P4 integrase
intD	b0537	2,1932	0,0097	prophage DLP12 integrase
iscA	b2528	0,4418	0,0028	iron-sulfur cluster assembly protein
iscS	b2530	0,3669	0,0026	cysteine desulfurase monomer
iscU	b2529	0,4176	0,0013	scaffold protein involved in iron-sulfur cluster assembly
iscX	b2524	0,6472	0,0250	protein with possible role in iron-sulfur cluster biogenesis
ispB	b3187	0,6536	0,0347	octaprenyl diphosphate synthase
ispE	b1208	0,4973	0,0499	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
ivy	b0220	0,4552	0,0028	YkfE
kch	b1250	6,5771	0,0023	potassium VIC channel
kdgK	b3526	2,9680	0,0423	2-dehydro-3-deoxygluconokinase
kdgR	b1827	1,3175	0,0072	putative ICLR-type transcriptional regulator
kduD	b2842	1,7440	0,0252	2-deoxy-D-gluconate 3-dehydrogenase
kduI	b2843	1,5739	0,0360	homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase
lepA	b2569	0,4578	0,0106	GTP-binding elongation factor, may be inner membrane protein
leuA	b0074	0,4198	0,0265	2-isopropylmalate synthase
leuC	b0072	0,7154	0,0284	isopropylmalate isomerase
lspA	b0027	0,5391	0,0442	prolipoprotein signal peptidase (SPase II)
lsrB	b1516	0,5142	0,0288	YneA
malP	b3417	5,2986	0,0307	maltodextrin phosphorylase monomer
malX	b1621	0,4991	0,0496	EIIBCmalX
manA	b1613	0,5555	0,0306	mannose-6-phosphate isomerase
mcrB	b4346	2,7084	0,0157	MrcB subunit of 5-methylcytosine restriction system
menD	b2264	0,7410	0,0203	putative 2-hydroxyglutarate synthase / SHCHC synthase / 2-oxoglutarate decarboxylase
metA	b4013	0,2076	0,0209	homoserine O-succinyltransferase
metG	b2114	0,2830	0,0418	methionyl-tRNA synthetase
mgsA	b0963	2,1172	0,0134	methylglyoxal synthase
mhpB	b0348	0,4036	0,0047	3-(2,3-dihydroxyphenyl)propionate dioxygenase
mhpC	b0349	0,4068	0,0080	2-hydroxy-6-ketono-2,4-dienedioate hydrolase
mhpD	b0350	0,4575	0,0138	2-keto-4-pentenoate hydratase
mhpE	b0352	0,4565	0,0376	4-hydroxy-2-ketovaleate aldolase
mhpF	b0351	0,3457	0,0134	acetaldehyde dehydrogenase 2
mhpT	b0353	0,5565	0,0186	MhpT MFS transporter
miaB	b0661	0,2939	0,0013	hypothetical protein
mltA	b2813	0,6359	0,0136	membrane-bound lytic murein transglycosylase A
mltB	b2701	0,4337	0,0025	membrane-bound lytic murein transglycosylase B
mltD	b0211	0,3196	0,0035	membrane-bound lytic murein transglycosylase D
motB	b1889	6,4289	0,0485	MotB protein, enables flagellar motor rotation, linking torque machinery to cell wall
mppA	b1329	4,3955	0,0068	periplasmic murein tripeptide binding protein
mrcA	b3396	0,3396	0,0054	peptidoglycan synthetase; penicillin-binding protein 1A
msrB	b1778	0,3349	0,0304	methionine sulfoxide reductase B / protein-methionine-S-oxide reductase / methionine sulfoxide reductase
mtn	b0159	0,5806	0,0469	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase monomer
mtr	b3161	0,7656	0,0287	Mtr tryptophan ArAAP transporter
mug	b3068	0,4290	0,0023	stationary phase mismatch/uracil DNA glycosylase
mukE	b0923	1,6643	0,0073	protein involved in chromosome partitioning
murP	b2429	2,5027	0,0181	MurP
mutH	b2831	0,5136	0,0241	MutHLS complex, methyl-directed mismatch repair
mutS	b2733	0,4971	0,0195	MutHLS complex, methyl-directed mismatch repair
mutY	b2961	0,6703	0,0423	adenine glycosylase; G.C --> T.A transversions
nadE	b1740	1,4861	0,0474	NAD+ synthase, glutamine dependent / NAD+ synthase, NH3-dependent
napD	b2207	9,3356	0,0037	NapD protein
napF	b2208	9,2025	0,0031	ferredoxin-type protein
nfi	b3998	0,5850	0,0224	endonuclease V (deoxyinosine 3'endoclease)
nfrA	b0568	0,3170	0,0069	bacteriophage N4 receptor, outer membrane protein
nfrB	b0569	0,2637	0,0048	bacteriophage N4 receptor, outer membrane protein
nlpB	b2477	0,6974	0,0180	lipoprotein-34
nlpD	b2742	0,5841	0,0371	NlpD putative outer membrane lipoprotein
nmpC	b0553	5,5836	0,0159	outer membrane porin protein; locus of qsr prophage
nrfA	b4070	34,1708	0,0111	cytochrome C552

gene	blattner	ratio A/B	p-value	function
nudC	b3996	0,7120	0,0330	putative NAD ⁺ diphosphatase
nupG	b2964	3,7936	0,0032	NupG nucleoside MFS transporter
nusB	b0416	0,4621	0,0462	transcription termination; L factor
obgE	b3183	0,6444	0,0244	GTPase involved in chromosomal partitioning
ogrK	b2082	0,7617	0,0475	OgrK transcriptional regulator
ompN	b1377	0,6915	0,0136	putative outer membrane protein
ompT	b0565	3,4380	0,0014	outer membrane protein 3b (a), protease VII
osmB	b1283	0,2709	0,0014	OsmB osmotically inducible lipoprotein
paaB	b1389	0,3814	0,0222	putative subunit of phenylacetate-CoA oxygenase
paaJ	b1397	0,4901	0,0419	putative beta-keto-thiolase of phenylacetate degradation
paaX	b1399	0,6229	0,0058	PaaX transcriptional regulator
paaY	b1400	0,4875	0,0220	putative transferase
pabA	b3360	0,4832	0,0070	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
pcnB	b0143	0,6447	0,0227	poly(A) polymerase I
pflA	b0902	0,5773	0,0124	pyruvate formate-lyase activating enzyme
pgl	b0767	3,8773	0,0103	6-phosphogluconolactonase
phnK	b4097	1,4585	0,0490	PhnK
pldA	b3821	0,4974	0,0146	phospholipase A1
pldb	b3825	0,5697	0,0157	lysophospholipase L(2)
ppsA	b1702	0,4317	0,0283	phosphoenolpyruvate synthase
prmB	b2330	0,5513	0,0253	protein-(glutamine-N5) methyltransferase
prmC	b1212	0,4252	0,0039	protein-(glutamine-N5) methyltransferase
proP	b4111	1,6762	0,0033	ProP proline/betaine MFS transporter
proQ	b1831	0,8210	0,0472	protein that affects osmoregulation of ProP transporter
prsA	b1207	0,6550	0,0030	ribose-phosphate diphosphokinase
pstS	b3728	0,7215	0,0114	phosphate ABC transporter
ptrA	b2821	0,2729	0,0069	protease III
ptsG	b1101	0,6082	0,0302	EII _{Glc}
ptsP	b2829	1,9101	0,0202	PTS system, enzyme I, transcriptional regulator (with NPR and NTR proteins)
purB	b1131	0,3871	0,0008	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase / adenylosuccinate lyase
purU	b1232	1,8188	0,0292	formyltetrahydrofolate deformylase
puuD	b1298	0,6260	0,0406	probable amidotransferase subunit
pyrF	b1281	0,5616	0,0387	orotidine-5'-phosphate-decarboxylase
pyrI	b4244	1,8211	0,0362	aspartate carbamoyltransferase, PyrI subunit
rbn	b3886	2,4777	0,0058	tRNA processing exoribonuclease BN
rbsC	b3750	0,4430	0,0301	ribose ABC transporter
rbsD	b3748	0,3530	0,0401	D-ribose utilization
rcsD	b2216	0,8244	0,0460	putative 2-component sensor protein
recB	b2820	0,2328	0,0023	RecB; DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recD	b2819	0,4974	0,0325	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recJ	b2892	0,6227	0,0299	RecJ
recN	b2616	0,5404	0,0348	protein used in recombination and DNA repair
recT	b1349	0,6541	0,0142	recombinase, DNA renaturation
relE	b1563	0,9013	0,0436	toxin of the RelE-RelB toxin-antitoxin system; cleaves mRNA in ribosome
rep	b3778	0,5157	0,0285	rep helicase, a single-stranded DNA dependent ATPase
rfaC	b3621	1,7935	0,0235	lipopolysaccharide core biosynthesis; heptosyl transferase I
rfaL	b3622	1,6061	0,0258	lipopolysaccharide core biosynthesis; O-antigen ligase
rfe	b3784	3,5759	0,0000	undecaprenyl-phosphate α-N-acetylglucosaminyl transferase
ribD	b0414	0,6197	0,0299	pyrimidine reductase / pyrimidine deaminase
rihA	b0651	1,3869	0,0492	ribonucleoside hydrolase I (pyrimidine-specific)
rimI	b4373	0,6086	0,0452	acetylates N-terminal alanine of 30S ribosomal subunit protein S18 / ribosomal-protein-alanine N-acetyltransferase
rlmB	b4180	2,2471	0,0024	23S rRNA methyltransferase monomer
rluA	b0058	0,1900	0,0293	23S rRNA and tRNA pseudouridine synthase
rmhB	b0183	0,6624	0,0303	RNase HIII, degrades RNA of DNA-RNA hybrids
mk	b0610	0,5074	0,0130	regulator of nucleoside diphosphate kinase
rplP	b3313	1,4719	0,0001	50S ribosomal subunit protein L16
rplV	b3315	1,9726	0,0393	50S ribosomal subunit protein L22
rpoE	b2573	0,7058	0,0079	sigmaE
rpsE	b3303	1,4454	0,0390	30S ribosomal subunit protein S5
rsmB	b3289	0,6882	0,0279	16S rRNA m5C967 methyltransferase
ruvA	b1861	0,5638	0,0057	branch migration of Holliday structures; repair
sbcD	b0398	0,6260	0,0422	ATP-dependent dsDNA exonuclease
sdaA	b1814	0,5675	0,0065	L-threonine deaminase I / L-serine ammonia-lyase
sdaB	b2797	0,2485	0,0242	L-threonine deaminase II / L-serine deaminase 2
sdaC	b2796	0,2639	0,0054	SdaC serine STP transporter
selA	b3591	2,5277	0,0308	selenocysteine synthase monomer
seqA	b0687	1,4974	0,0332	SeqA, negative modulator of initiation of replication
setB	b2170	0,5500	0,0214	YeiO MFS transporter
setC	b3659	1,3277	0,0467	YicK MFS Transporter

gene	blattner	ratio A/B	p-value	function
shiA	b1981	2,3089	0,0071	ShiA shikimate MFS transporter
smtA	b0921	1,8104	0,0156	S-adenosylmethionine-dependent methyltransferase
sodA	b3908	2,2699	0,0356	superoxide dismutase (Mn)
soxS	b4062	4,6091	0,0238	SoxS transcriptional activator
speC	b2965	0,2222	0,0023	ornithine decarboxylase, biosynthetic
speD	b0120	0,2969	0,0050	adenosylmethionine decarboxylase, proenzyme
speE	b0121	0,2562	0,0023	spermidine synthase
speG	b1584	0,7323	0,0129	spermidine acetyltransferase
spr	b2175	1,9225	0,0066	putative lipoprotein
srmB	b2576	0,5873	0,0118	SrmB, DEAD-box RNA helicase
ssuD	b0935	0,5883	0,0008	alkanesulfonate monooxygenase
sufA	b1684	2,7742	0,0160	scaffold protein for iron-sulfur cluster assembly
sufB	b1683	2,7088	0,0255	component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex
sulA	b0958	0,5115	0,0067	suppressor of lon; inhibits cell division and ftsZ ring formation
tdcB	b3117	5,9813	0,0139	threonine dehydratase (catabolic)
thiG	b3991	0,8279	0,0346	ThiG
thiI	b0423	0,7960	0,0033	ThiI protein
thrC	b0004	4,5667	0,0131	threonine synthase
tldD	b3244	1,4990	0,0262	protease involved in Microcin B17 maturation and in sensitivity to the DNA gyrase inhibitor LetD
tolC	b3035	0,7151	0,0164	TolC outer membrane channel
tra5-5	b2089	1,7159	0,0251	IS3 element protein InsF
trpA	b1260	1,4667	0,0156	tryptophan synthase, alpha subunit / indoleglycerol phosphate aldolase
trpS	b3384	1,4491	0,0196	tryptophanyl-tRNA synthetase
tsgA	b3364	0,4974	0,0401	YhfC MFS transporter
tsr	b4355	2,1465	0,0180	MCP-I
ttk	b3641	0,6578	0,0296	Ttk transcriptional regulator
typA	b3871	0,5679	0,0271	protein possibly involved in LPS biosynthesis and host colonization
tyrR	b1323	1,8233	0,0206	TyrR-Phenylalanine transcriptional repressor
ubiX	b2311	0,4366	0,0267	3-octaprenyl-4-hydroxybenzoate decarboxylase 2
udk	b2066	0,6047	0,0102	uridine kinase / cytidine kinase
udp	b3831	2,1987	0,0472	uridine phosphorylase
ugpC	b3450	1,9691	0,0027	glycerol-3-P ABC transporter / transport
ulaB	b4194	0,8937	0,0050	eiiSga
ulaD	b4196	0,5940	0,0354	3-keto-L-gulonate 6-phosphate decarboxylase
ulaF	b4198	0,7134	0,0268	L-ribulose 5-phosphate 4-epimerase
uvrC	b1913	2,5330	0,0055	excinuclease ABC, subunit C; repair of UV damage to DNA
wbbK	b2032	1,1787	0,0066	putative transferase
wrbA	b1004	1,8606	0,0149	WrbA
wzxE	b3792	1,6853	0,0279	lipid III flippase
xthA	b1749	0,4507	0,0112	exonuclease III
xylR	b3569	2,2681	0,0011	XylR-Xylose transcriptional activator
yafK	b0224	0,6195	0,0023	conserved protein; in enteroaggregative E. coli, YafK is required for development of biofilms
yagN	b0280	0,6952	0,0146	hypothetical protein
yagT	b0286	1,7860	0,0035	putative oxidoreductase, Fe-S subunit
yagV	b0289	1,9412	0,0102	conserved hypothetical protein
yaiV	b0375	0,5910	0,0075	putative outer membrane protein, cAMP-binding
ybaD	b0413	0,6397	0,0464	conserved protein
ybaE	b0445	2,2337	0,0166	hypothetical protein
ybaN	b0468	2,0803	0,0260	hypothetical protein
ybeB	b0637	0,7033	0,0126	conserved hypothetical protein
ybeD	b0631	0,2523	0,0005	conserved hypothetical protein
ybeH	b0625	0,5572	0,0439	hypothetical protein
ybfD	b0706	0,3122	0,0215	conserved protein
ybhH	b0769	0,4829	0,0154	conserved hypothetical protein
ybiJ	b0802	0,4837	0,0237	conserved hypothetical protein
ybiM	b0806	0,3863	0,0240	conserved hypothetical protein
ybjI	b0844	1,9181	0,0193	conserved protein with a phosphatase-like domain
ycaM	b0899	0,3822	0,0104	YcaM APC amino acid transporter
ycaO	b0905	0,5753	0,0151	conserved hypothetical protein
ycbJ	b0919	0,5051	0,0363	conserved hypothetical protein
ycbX	b0947	2,2239	0,0044	putative Fe-S protein
yccK	b0969	0,5751	0,0496	putative sulfite reductase (EC 1.8.-.-)
yccS	b0960	0,5639	0,0338	hypothetical protein
yccV	b0966	0,5070	0,0014	hemimethylated DNA-binding protein
yceP	b1060	2,4225	0,0246	conserved hypothetical protein
ycfD	b1128	0,5605	0,0362	putative enzyme
ycgK	b1178	1,8393	0,0309	hypothetical protein
ycgV	b1202	0,3754	0,0210	putative adhesion and penetration protein
ychE	b1242	0,6093	0,0360	putative membrane protein

gene	blattner	ratio A/B	p-value	function
yciB	b1254	0,5700	0,0437	hypothetical protein
yciC	b1255	0,6624	0,0484	hypothetical protein
yciS	b1279	0,6175	0,0026	conserved hypothetical protein
ydbK	b1378	0,6806	0,0083	putative pyruvate synthase
ydcF	b1414	0,2689	0,0238	conserved hypothetical protein
ydcP	b1435	0,2487	0,0276	putative collagenase
ydgK	b1626	0,4982	0,0446	putative oxidoreductase
ydhF	b1647	2,1014	0,0131	putative oxidoreductase, NAD(P)-linked
ydiA	b1703	0,4022	0,0020	conserved protein
ydiH	b1685	0,0411	0,0002	hypothetical protein
ydiI	b1686	0,6335	0,0373	conserved hypothetical protein
ydiO	b1695	0,4899	0,0220	putative acyl-CoA dehydrogenase
ydiU	b1706	0,7123	0,0018	conserved protein
ydiY	b1722	0,2336	0,0097	conserved hypothetical protein
yeaC	b1777	0,2907	0,0234	conserved hypothetical protein
yeaD	b1780	0,8053	0,0485	conserved hypothetical protein
yeaK	b1787	0,4458	0,0020	conserved hypothetical protein
yeaL	b1789	0,4155	0,0189	hypothetical protein
yeaT	b1799	3,0720	0,0141	putative transcriptional regulator LYSR-type
yebE	b1846	0,6028	0,0479	conserved hypothetical protein
yebR	b1832	3,1582	0,0092	conserved hypothetical protein
yebU	b1835	0,5220	0,0183	hypothetical protein
yecN	b1869	0,3001	0,0013	putative membrane protein
yecP	b1871	0,4509	0,0069	putative enzyme
yedE	b1929	0,5180	0,0037	putative transport system permease protein
yedF	b1930	0,6433	0,0118	conserved hypothetical protein; might bind RNA
yedL	b1932	0,7679	0,0407	putative acyl-CoA N-acyltransferase
yeeZ	b2016	0,7112	0,0403	putative enzyme of sugar metabolism
yehU	b2126	1,3634	0,0204	putative 2-component sensor protein
yeiC	b2166	0,5199	0,0069	putative kinase
yeiH	b2158	0,5810	0,0329	putative membrane protein
yeiN	b2165	0,6223	0,0224	conserved protein
yeiP	b2171	0,4453	0,0110	putative elongation factor
yeiQ	b2172	1,6577	0,0089	putative oxidoreductase
yejE	b2179	1,2788	0,0062	YejA/YejB/YejE/YejF ABC transporter
yejM	b2188	0,6919	0,0221	putative sulfatase
yfbV	b2295	0,1983	0,0066	conserved hypothetical protein
yfeE	b2300	0,5028	0,0272	putative metallo-dependent phosphatase
yfeC	b2398	3,6524	0,0085	hypothetical protein
yfeD	b2399	4,6195	0,0073	hypothetical protein
yfeU	b2428	2,5545	0,0178	putative regulator
yfeZ	b2433	0,8288	0,0423	putative membrane protein
yfgD	b2495	1,3436	0,0280	putative oxidoreductase
yfhQ	b2532	0,7396	0,0351	putative ATP synthase beta subunit
yfiD	b2579	2,1520	0,0130	stress-induced alternate pyruvate formate-lyase subunit
yfiF	b2581	0,7263	0,0437	hypothetical protein
yfjD	b4461	0,6709	0,0382	putative membrane protein, hemolysin-like
yfjF	b2618	0,8164	0,0194	conserved hypothetical protein
yfjK	b2627	1,8469	0,0067	hypothetical protein
yfjW	b2642	2,9798	0,0025	hypothetical protein
ygaH	b2683	2,3469	0,0029	putative transport protein
ygaW	b2670	0,2097	0,0395	putative membrane protein
ygbT	b2755	1,5803	0,0209	conserved hypothetical protein
ygcE	b2776	0,6769	0,0395	putative kinase
ygcO	b2767	2,1793	0,0250	putative ferredoxin
ygeY	b2872	0,3333	0,0367	putative deacetylase
yggE	b2922	0,7072	0,0229	putative actin-like protein
yghU	b2989	0,6145	0,0305	glutathione transferase-like protein possibly involved in glutathionylspermidine metabolism
ygiR	b3015	0,1712	0,0020	conserved protein
yhaI	b3104	1,8901	0,0167	putative cytochrome
yhbG	b3201	0,7306	0,0489	YhbG/YhbN ABC transporter
yhbW	b3160	2,5842	0,0205	putative enzyme
yhcE	b3217	1,8476	0,0321	hypothetical protein
yhcH	b3221	1,4134	0,0166	conserved hypothetical protein; gene is in sialic acid catabolic operon
yhdE	b3248	1,4099	0,0332	conserved hypothetical protein
yhdN	b3293	0,3490	0,0092	conserved hypothetical protein
yhfG	b3362	2,0525	0,0319	conserved hypothetical protein
yhfT	b3377	0,5275	0,0096	putative transport protein
yhfX	b3381	0,8420	0,0430	conserved protein

gene	blattner	ratio A/B	p-value	function
yhjK	b3529	0,8141	0,0360	conserved protein
yhjR	b3535	3,3058	0,0027	hypothetical protein
yhjV	b3539	0,4101	0,0312	YhjV STP transporter
yiaJ	b3574	0,4842	0,0009	YiaJ transcriptional repressor
yibG	b3596	0,9825	0,0318	conserved hypothetical protein
yibI	b3598	1,7891	0,0258	hypothetical protein
yidI	b3677	3,0250	0,0389	hypothetical protein
yidZ	b3711	0,5369	0,0092	putative transcriptional regulator LysR-type
yifE	b3764	1,9633	0,0245	hypothetical protein
yifK	b3795	2,3518	0,0138	YifK APC transporter
yjcG	b4067	0,7076	0,0091	YjcG SSS transporter
yjcZ	b4110	1,5987	0,0010	hypothetical protein
yjdF	b4121	1,6223	0,0050	putative membrane protein
yjeI	b4144	1,6231	0,0306	conserved protein
yjeO	b4158	0,7234	0,0164	conserved hypothetical protein
yjgM	b4256	1,3106	0,0028	putative acyltransferase
yjhB	b4279	0,2981	0,0096	YjhB MFS transporter
yjhC	b4280	0,3673	0,0052	KpLE2 phage-like element; putative NAD(P)-binding dehydrogenase
yjhP	b4306	0,6759	0,0413	putative methyltransferase
yjHT	b4310	0,4662	0,0446	putative enzyme contains galactose oxidase-like domain
yjiA	b4352	1,7339	0,0199	P-loop guanosine triphosphatase
yjiG	b4329	0,5318	0,0394	putative membrane protein
yjiT	b4342	10,7703	0,0111	conserved protein
yjiX	b4353	1,7994	0,0423	hypothetical protein
yjiY	b4354	15,2032	0,0105	putative carbon starvation protein
yjiI	b4380	1,3283	0,0003	conserved hypothetical protein
yjiK	b4391	0,6653	0,0186	YjiK
yjiM	b4357	2,3936	0,0179	hypothetical protein
ykiA	b0392	1,7064	0,0390	hypothetical protein
yliA	b0457	1,5530	0,0301	conserved protein
yliC	b0831	1,4983	0,0007	YliA/YliB/YliC/YliD ABC transporter
yliH	b0836	0,1439	0,0035	putative receptor; induced in stationary phase
ymcD	b0987	1,7643	0,0439	hypothetical protein
ymfE	b1138	0,1571	0,0060	hypothetical protein
ymgA	b1165	0,1361	0,0148	hypothetical protein
ymjA	b1295	0,5853	0,0312	hypothetical protein
yoaA	b1808	0,6334	0,0318	putative enzyme
yoaB	b1809	0,5757	0,0165	conserved protein
yoaG	b1796	2,4294	0,0346	hypothetical protein
ypfJ	b2475	1,4938	0,0049	conserved protein
yphF	b2548	0,4557	0,0415	YphD/YphE/YphF ABC transporter
yqaB	b2690	0,6835	0,0377	putative phosphoglucomutase that contains a phosphatase-like domain
yqcD	b2794	0,6211	0,0481	conserved hypothetical protein
yqeH	b2846	0,8070	0,0380	conserved protein
yqgE	b2948	0,6944	0,0062	conserved protein
yqiI	b3048	0,9092	0,0276	conserved protein
yraN	b3148	0,6869	0,0193	conserved hypothetical protein
yrbA	b3190	0,6820	0,0270	hypothetical protein
yrfG	b3399	0,4865	0,0216	putative hydrolase with a phosphatase-like domain
ytfL	b4218	0,4845	0,0258	putative transport protein
ytfN	b4221	0,7948	0,0361	conserved protein
ytjB	b4387	0,7147	0,0043	membrane protein
zwf	b1852	1,3295	0,0490	glucose 6-phosphate-1-dehydrogenase
	b3837	0,6879	0,0253	
	b0322	0,8183	0,0423	
	b2391	0,5201	0,0434	
	b3948	0,7383	0,0244	

CSH50 (A) CSH50fs (B) in Transition to Stationary

aat	b0885	1,5610	0,0387	leucyl, phenylalanyl-tRNA-protein transferase
abrB	b0715	0,4795	0,0092	putative transport protein; mutation affects aidB expression
ampH	b0376	0,6790	0,0417	putative enzyme
aphA	b4055	0,4046	0,0303	acid phosphatase/phosphotransferase
apt	b0469	0,8461	0,0496	adenine phosphoribosyltransferase
arcA	b4401	1,1326	0,0030	ArcA-Phosphorylated transcriptional dual regulator
argB	b3959	0,7534	0,0093	N-acetylglutamate kinase
asr	b1597	0,6179	0,0119	acid shock protein
astD	b1746	0,7371	0,0469	succinylglutamic semialdehyde dehydrogenase
btuF	b0158	0,5590	0,0133	periplasmic vitamin B12 binding protein

gene	blattner	ratio A/B	p-value	function
chaA	b1216	1,5703	0,0273	ChaA calcium CaCA transporter
cls	b1249	1,8397	0,0135	cardiolipin synthase
csgF	b1038	2,6963	0,0232	curli assembly component
csiD	b2659	0,7824	0,0300	hypothetical protein; gene expression is induced by carbon starvation
cyaY	b3807	1,1582	0,0458	iron-binding frataxin homolog
dctR	b3507	3,5342	0,0231	protein involved in metabolism of C4-dicarboxylates
ddlA	b0381	1,3455	0,0452	D-alanine-D-alanine ligase A
ddpB	b1486	0,7867	0,0321	YddR
dicA	b1570	1,5452	0,0082	DicA transcriptional regulator
dmsA	b0894	1,3291	0,0290	dimethyl sulfoxide reductase, chain A
dnaQ	b0215	1,5304	0,0205	DNA polymerase III, epsilon subunit
dpiA	b0620	0,7592	0,0156	CitB transcriptional regulator
dsbA	b3860	1,3750	0,0408	disulfide oxidoreductase
dusB	b3260	0,3858	0,0382	tRNA dihydrouridine synthase
entA	b0596	4,4954	0,0362	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
envY	b0566	1,7235	0,0175	EnvY transcriptional activator
eutL	b2439	0,6545	0,0455	hypothetical protein
eutM	b2457	0,6548	0,0414	putative detox protein, ethanolamine utilization
exuT	b3093	0,7604	0,0156	ExuT hexuronate MFS transporter
fliK	b1943	0,7529	0,0246	flagellar hook-length control protein FliK
frlC	b3372	1,6858	0,0348	fructoselysine and psicoselysine degradation
fruB	b2169	3,2743	0,0351	EIIIFru
fruK	b2168	1,4091	0,0251	1-phosphofructokinase monomer
fsaA	b0825	1,2606	0,0464	Fsa
gadC	b1492	22,0335	0,0374	XasA GABA APC transporter
gadE	b3512	14,1482	0,0012	GadE transcriptional activator
gadW	b3515	5,4482	0,0241	GadWtranscriptional repressor
gatR_1	b2087	1,2194	0,0338	negative DNA-binding transcriptional regulator of galactitol metabolism, subunit of GatR transcriptional repressor
glpF	b3927	0,4719	0,0301	GlpF - glycerol MIP channel
hchA	b1967	1,3473	0,0385	heat shock protein (Hsp) 31
hdeD	b3511	8,1344	0,0428	protein involved in acid resistance
hemY	b3802	0,6097	0,0422	a late step of protoheme IX synthesis
hisC	b2021	0,3625	0,0199	histidine-phosphate aminotransferase
hisD	b2020	0,6774	0,0110	histidinal dehydrogenase / histidinol dehydrogenase
htrA	b0161	0,3838	0,0164	DegP
hyi	b0508	0,5405	0,0469	hydroxypyruvate isomerase
hypB	b2727	1,4330	0,0072	guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3
inaA	b2237	1,1707	0,0448	pH-inducible protein involved in stress response
lplA	b4386	0,5894	0,0042	lipoyl-protein ligase A
mcrB	b4346	3,7015	0,0154	MrcB subunit of 5-methylcytosine restriction system
mdtG	b1053	2,7845	0,0406	YceE drug MFS transporter
mraZ	b0081	0,6347	0,0132	protein encoded by an operon involved in formation of the cell envelope and cell division
mtlA	b3599	1,6503	0,0315	EIIMtl
nanA	b3225	1,2989	0,0251	N-acetylneuraminate lyase
nikD	b3479	1,4297	0,0492	nickel ABC transporter
norR	b2709	1,2152	0,0376	transcriptional regulator of the anaerobic response to reactive nitrogen species
nudE	b3397	1,3014	0,0258	ADP-ribose diphosphatase
obgE	b3183	0,6501	0,0090	GTPase involved in chromosomal partitioning
ogrK	b2082	1,3568	0,0499	OgrK transcriptional regulator
ompF	b0929	0,4480	0,0442	outer membrane porin OmpF
orn	b4162	1,8637	0,0289	oligoribonuclease monomer
pdhR	b0113	0,7167	0,0089	PdhR-pyruvate
polB	b0060	1,7041	0,0257	DNA polymerase II
proW	b2678	0,8448	0,0427	proline ABC transporter
prpD	b0334	0,4135	0,0183	2-methylcitrate dehydratase
purC	b2476	1,4330	0,0212	phosphoribosylaminoimidazole-succinocarboxamide synthase
purH	b4006	1,1431	0,0481	AICAR transformylase / IMP cyclohydrolase
puuA	b1297	3,7881	0,0276	putative glutamine synthetase (EC 6.3.1.2)
qor	b4051	1,4220	0,0378	quinone oxidoreductase
qseB	b3025	0,6844	0,0099	putative 2-component transcriptional regulator
rbsA	b3749	0,3311	0,0281	ribose ABC transporter
rbsC	b3750	0,2093	0,0265	ribose ABC transporter
rbsD	b3748	0,2205	0,0061	D-ribose utilization
rem	b1561	1,8185	0,0457	hypothetical protein
rhaS	b3905	0,7904	0,0441	RhaS transcriptional activator
rhaT	b3907	1,2690	0,0108	rhamnose RhaT transporter
rihB	b2162	1,7911	0,0339	ribonucleoside hydrolase 2 (pyrimidine-specific)
rof	b0189	1,8022	0,0294	Rho-binding antiterminator
rplT	b1716	1,7302	0,0078	50S ribosomal subunit protein L20, and regulator

gene	blattner	ratio A/B	p-value	function
rpsQ	b3311	0,5968	0,0243	30S ribosomal subunit protein S17
rrmA	b1822	1,4094	0,0108	23S rRNA m1G745 methyltransferase
rseA	b2572	0,5825	0,0476	anti-sigma factor that inhibits sigmaE
rseB	b2571	0,6315	0,0494	negative regulator of sigmaE; interacts with RseA and stimulates binding of RseA to sigmaE
rseC	b2570	0,7732	0,0251	protein involved in reduction of the SoxR iron-sulfur cluster
ruvB	b1860	0,6261	0,0271	branch migration of Holliday structures; repair helicase
sapB	b1293	1,8571	0,0076	peptide uptake ABC transporter
setC	b3659	2,8429	0,0171	YicK MFS Transporter
slp	b3506	6,4852	0,0424	outer membrane protein induced after carbon starvation
sohB	b1272	1,1729	0,0025	putative protease
sufB	b1683	2,3472	0,0139	component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex
sufC	b1682	2,0037	0,0305	ATPase component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex
sufS	b1680	2,0407	0,0269	L-selenocysteine lyase (and L-cysteine desulfurase) monomer
subB	b2533	0,4978	0,0185	inositol monophosphatase
thiI	b0423	1,5919	0,0034	ThiI protein
thiL	b0417	1,2963	0,0475	thiamine phosphate kinase
trg	b1421	0,6236	0,0473	MCP-III
ugpE	b3451	1,9577	0,0269	glycerol-3-P ABC transporter / transport
upp	b2498	1,5767	0,0345	uracil phosphoribosyltransferase
uvrB	b0779	1,9383	0,0152	DNA repair; excision nuclease subunit B
uvrY	b1914	1,6618	0,0311	UvrY- Phosphorylated transcriptional regulator
xapR	b2405	1,7821	0,0157	XapR transcriptional activator
yafU	b0218	0,6355	0,0350	conserved hypothetical protein
ybaP	b0482	1,8267	0,0130	putative ligase
ybaT	b0486	2,9386	0,0011	YbaT APC transporter
ybbA	b0495	0,4183	0,0451	YbbA/YbbP ABC transporter
ybcH	b0567	1,8118	0,0067	conserved hypothetical protein
ybcM	b0546	1,8831	0,0318	putative ARAC-type regulatory protein
ybcN	b0547	0,6267	0,0456	hypothetical protein
ybeF	b0629	0,7562	0,0180	putative transcriptional regulator LYSR-type
ybgA	b0707	1,6805	0,0206	conserved protein
ybgH	b0709	0,5997	0,0112	YbgH peptide POT Transporter
ybhF	b0794	1,3972	0,0497	YbhF/YbhR/YbhS ABC transporter
ybiH	b0796	1,5534	0,0028	hypothetical protein
ycbB	b0925	1,9207	0,0065	putative amidase
yceP	b1060	2,1087	0,0460	conserved hypothetical protein
ycfR	b1112	1,2233	0,0181	conserved hypothetical protein
ycgJ	b1177	1,4740	0,0088	hypothetical protein
ycgX	b1161	1,4886	0,0341	hypothetical protein
ydeI	b1536	4,9897	0,0403	conserved hypothetical protein
ydeU	b1509	0,6562	0,0419	conserved protein
ydhS	b1668	2,5603	0,0370	putative oxidoreductase
ydjK	b1775	1,7556	0,0281	YdjK
yebW	b1837	1,9443	0,0270	hypothetical protein
yedR	b1963	1,6135	0,0135	hypothetical protein
yedW	b1969	2,2168	0,0108	putative 2-component transcriptional response regulator
yeeO	b1985	1,1961	0,0398	YeeO MATE Transporter
yfbN	b2273	0,5362	0,0182	conserved hypothetical protein
yfeC	b2398	1,9649	0,0396	hypothetical protein
yfgH	b2505	1,5726	0,0020	putative outer membrane lipoprotein
yfiE	b2577	1,2464	0,0464	putative transcriptional regulator LYSR-type
yfjP	b2632	0,7520	0,0345	putative GTP-binding protein
yfjS	b2636	1,7083	0,0099	inner membrane lipoprotein YfjS
ygcU	b2772	1,4215	0,0019	hypothetical protein
ygdQ	b2832	0,6766	0,0377	putative transport protein
ygiG	b3073	2,1750	0,0476	putrescine:2-oxoglutaric acid aminotransferase
yhdX	b3269	0,7823	0,0343	YhdW/YhdX/YhdY/YhdZ ABC transporter
yibA	b3594	5,6513	0,0212	putative lyase
yieP	b3755	1,9745	0,0106	hypothetical protein
yjgG	b4247	0,5699	0,0215	hypothetical protein
yjhE	b4282	1,3314	0,0382	KpLE2 phage-like element
yjhF	b4296	1,7197	0,0391	YjhF Gnt transporter
ykfB	b0250	0,5364	0,0047	hypothetical protein
ynaI	b1330	1,3820	0,0261	YnaI
yneE	b1520	2,2054	0,0150	conserved hypothetical protein
yneK	b1527	1,7412	0,0171	conserved protein
yphF	b2548	0,4656	0,0111	YphD/YphE/YphF ABC transporter
yqiJ	b3050	1,6472	0,0159	putative oxidoreductase
ytlL	b4218	0,6187	0,0431	putative transport protein

gene	blattner	ratio A/B	p-value	function
ytfM	b4220	0,6059	0,0406	hypothetical protein
CSH50 (A) & CSH50/fts (B) in Late Stationary				
aaeX	b3242	0,1162	0,0119	hypothetical protein
aceK	b4016	0,7802	0,0399	isocitrate dehydrogenase phosphatase / isocitrate dehydrogenase kinase
ada	b2213	0,5369	0,0145	Ada transcriptional dual regulator / O-6-methylguanine-DNA methyltransferase
alaS	b2697	0,7352	0,0016	alanyl-tRNA synthetase
alr	b4053	1,8816	0,0448	alanine racemase, minor
amiC	b2817	3,3668	0,0494	N-acetylmuramyl-L-alanine amidase
ampC	b4150	1,4236	0,0158	beta-lactamase; penicillin resistance
amtB	b0451	0,9258	0,0243	AmtB ammonium Amt transporter
araJ	b0396	0,5228	0,0297	AraJ MFS transporter
argG	b3172	0,5972	0,0146	argininosuccinate synthase
argH	b3960	3,5282	0,0064	argininosuccinate lyase
aroK	b3390	0,5174	0,0094	shikimate kinase I
asnA	b3744	0,8519	0,0127	aspartate-ammonia ligase
astC	b1748	9,1016	0,0329	acetylornithine transaminase, catabolic / succinylornithine transaminase
b1578	b1578	3,2990	0,0187	hypothetical protein
b2191	b2191	3,0472	0,0497	hypothetical protein
betA	b0311	0,6126	0,0046	choline dehydrogenase
betT	b0314	0,5842	0,0485	BefT choline BCCT transporter
borD	b0557	1,2137	0,0192	bacteriophage lambda Bor protein homolog
citT	b0612	1,4968	0,0388	CitT citrate DASS Transporter
clcA	b0155	2,5182	0,0325	EriC chloride ion ClC channel
clcB	b1592	0,7312	0,0360	YnfJ chloride ion ClC transporter
clpB	b2592	0,3280	0,0079	ClpB chaperone
cobS	b1992	0,7962	0,0307	cobalamin 5'-phosphate synthase / cobalamin synthase
codB	b0336	0,3742	0,0051	CodB cytosine NCS1 transporter
cpxP	b3913	0,2235	0,0170	regulator of the Cpx response and possible chaperone involved in resistance to extracytoplasmic stress
creB	b4398	0,4846	0,0434	CreB- Phosphorylated transcriptional regulator
creC	b4399	0,3937	0,0326	CreC-Phis
csdA	b2810	0,5874	0,0365	cysteine sulfinate desulfinate
csgC	b1043	1,2044	0,0112	putative curli production protein
cspD	b0880	16,0799	0,0280	DNA replication inhibitor
cspE	b0623	8,6680	0,0365	CspE transcriptional repressor
cspG	b0990	0,6140	0,0016	cold shock protein CspG
csrA	b2696	3,9886	0,0476	carbon storage regulator; controls glycogen synthesis, gluconeogenesis, cell size and surface properties
cusF	b0573	0,7829	0,0248	periplasmic copper-binding protein
cynS	b0340	0,3529	0,0120	cyanase monomer
cysW	b2423	0,6881	0,0280	sulfate ABC transporter
cysZ	b2413	0,4629	0,0035	required for sulfate transport
ddpX	b1488	0,5345	0,0362	D-Ala-D-Ala dipeptidase
deoC	b4381	9,0692	0,0321	deoxyribose-phosphate aldolase
dhaR	b1201	0,6436	0,0124	putative 2-component regulator
dksA	b0145	1,6863	0,0313	DksA
dnaE	b0184	0,5435	0,0106	DNA polymerase III, alpha subunit
dnaG	b3066	0,4222	0,0495	DNA biosynthesis; DNA primase
dppA	b3544	1,7303	0,0446	dipeptide ABC transporter
dsbA	b3860	1,1918	0,0084	disulfide oxidoreductase
ecpD	b0140	0,4814	0,0137	probable pilin chaperone similar to PapD
elbB	b3209	1,9231	0,0350	sigma cross-reacting protein 27A (SCRP-27A)
eutL	b2439	0,6724	0,0490	hypothetical protein
exuR	b3094	0,8492	0,0144	ExuR transcriptional repressor
fabF	b1095	0,6295	0,0460	beta-ketoacyl-ACP synthase II
fdrA	b0518	0,5497	0,0092	involved in protein transport; multicopy suppressor of dominant negative ftsH mutants
fecA	b4291	0,8222	0,0069	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fimC	b4316	0,4900	0,0315	periplasmic chaperone, required for type 1 fimbriae
flgB	b1073	0,5473	0,0051	flagellar basal-body rod protein FlgB
fliD	b1924	0,5664	0,0104	flagellar cap protein FliD; filament capping protein; enables filament assembly
fliK	b1943	2,0042	0,0318	flagellar hook-length control protein FliK
fliY	b1920	4,1059	0,0296	periplasmic cystine-binding protein; member of extracellular bacterial solute-binding protein family III
friC	b3372	1,1884	0,0410	fructoselysine and psicoselysine degradation
fruA	b2167	1,6009	0,0416	EIIIFru
frvX	b3898	0,6284	0,0373	frv operon protein
fsaB	b3946	0,5115	0,0025	fructose 6-phosphate aldolase 2
ftsW	b0089	1,6371	0,0330	essential cell division protein FtsW
fumB	b4122	1,4742	0,0092	fumarase B monomer
fumC	b1611	4,5730	0,0410	fumarase C monomer
fusA	b3340	7,4644	0,0072	elongation factor G

gene	blattner	ratio A/B	p-value	function
g30K	b1088	4,4609	0,0486	hypothetical protein
gatY	b2096	7,4188	0,0456	tagatose-1,6-bisphosphate aldolase 2
glgS	b3049	12,4340	0,0183	glycogen biosynthesis, rpoS dependent
glk	b2388	2,4011	0,0080	glucokinase
glnA	b3870	0,6508	0,0408	adenylyl-[glutamine synthetase]
gloB	b0212	0,7455	0,0328	glyoxalase II
glpA	b2241	1,8004	0,0339	glycerol-3-phosphate-dehydrogenase, anaerobic
gntU	b4476	0,6904	0,0450	GntU gluconate Gnt transporter
greA	b3181	0,5847	0,0466	transcription elongation factor; stimulates the mRNA cleavage activity of RNA polymerase
groL	b4143	0,1600	0,0302	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
grxB	b1064	3,0152	0,0423	oxidized glutaredoxin 2
gyrA	b2231	1,2523	0,0381	DNA gyrase, subunit A
hemC	b3805	0,7502	0,0425	hydroxymethylbilane synthase
hemH	b0475	1,2367	0,0211	ferrochelatase
hflX	b4173	1,1608	0,0414	putative GTPase; possible regulator of HflKC
htrA	b0161	0,3477	0,0251	DegP
htrL	b3618	0,4161	0,0089	involved in lipopolysaccharide biosynthesis
hyfI	b2489	0,6981	0,0143	hydrogenase 4, small subunit
ibpB	b3686	0,1277	0,0168	small heat shock protein IbpB
iscU	b2529	4,5133	0,0350	scaffold protein involved in iron-sulfur cluster assembly
kch	b1250	0,6951	0,0255	potassium VIC channel
kgtP	b2587	2,2993	0,0011	KgtP α-ketoglutarate MFS transporter
lpxC	b0096	2,7942	0,0029	UDP-3-O-acyl-N-acetylglucosamine deacetylase
lrhA	b2289	0,3796	0,0348	LrhA transcriptional repressor
lsrB	b1516	0,7399	0,0208	YneA
lysC	b4024	0,8123	0,0155	aspartate kinase III
lyxK	b3580	0,6681	0,0402	L-xylulose kinase
macB	b0879	0,1409	0,0120	MacAB macrolide efflux transporter complex
manZ	b1819	2,2877	0,0294	EIIMan
mdtA	b2074	1,2909	0,0336	MdtABC RND-type Drug Exporter
metI	b0198	0,8178	0,0151	L- and D-methionine uptake ABC permease
modF	b0760	0,8025	0,0038	ModF
mgo	b2210	0,6329	0,0302	malate dehydrogenase
mutT	b0099	0,7175	0,0241	dGTP pyrophosphohydrolase
mviM	b1068	2,0452	0,0053	putative virulence factor
napG	b2205	1,8609	0,0363	ferredoxin-type protein
narG	b1224	2,2871	0,0317	nitrate reductase A, α subunit
narJ	b1226	0,6000	0,0278	NarJ, private chaperone for NarG nitrate reductase subunit
nlpA	b3661	0,6811	0,0025	lipoprotein-28
nlpD	b2742	4,4441	0,0000	NlpD putative outer membrane lipoprotein
nrpI	b2674	0,5413	0,0160	stimulates ribonucleotide reduction
nuoE	b2285	0,9495	0,0379	NADH dehydrogenase I
nuoM	b2277	1,8342	0,0080	NADH dehydrogenase I
ompA	b0957	10,3993	0,0496	outer membrane protein 3a (II*;G;d)
osmY	b4376	4,2860	0,0255	hyperosmotically inducible periplasmic protein
pbpC	b2519	5,9984	0,0419	putative peptidoglycan enzyme
pckA	b3403	2,7797	0,0438	phosphoenolpyruvate carboxykinase (ATP)
pepD	b0237	0,5596	0,0476	peptidase D
pgaB	b1023	0,3651	0,0064	putative membrane protein
pgpA	b0418	0,3457	0,0195	phosphatidylglycerophosphatase A
pheT	b1713	16,3765	0,0495	phenylalanyl-tRNA synthetase β-chain
phnP	b4092	0,7634	0,0242	phosphonate metabolism
polB	b0060	0,6608	0,0120	DNA polymerase II
ppa	b4226	2,0727	0,0063	inorganic pyrophosphatase
proY	b0402	0,6754	0,0227	ProY cryptic proline APC transporter
pspA	b1304	0,3241	0,0349	negative transcriptional regulator of the psp operon
pstB	b3725	0,9267	0,0131	phosphate ABC transporter
ptsI	b2416	5,6371	0,0485	PTS enzyme I
pykA	b1854	0,8489	0,0169	pyruvate kinase II monomer
rfaI	b3627	0,4462	0,0388	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
rhsD	b0497	1,6558	0,0321	RhsD protein in rhs element
rhsE	b1456	1,1728	0,0329	RhsE protein in rhs element
ribD	b0414	0,6515	0,0084	pyrimidine reductase / pyrimidine deaminase
rimJ	b1066	1,7516	0,0255	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
rimM	b2608	3,7205	0,0153	protein required for wild-type 16S rRNA processing
rluA	b0058	0,4039	0,0494	23S rRNA and tRNA pseudouridine synthase
rmhB	b0183	0,4660	0,0478	RNase HII, degrades RNA of DNA-RNA hybrids
rplE	b3308	5,5781	0,0305	50S ribosomal subunit protein L5
rplI	b4203	2,4184	0,0300	50S ribosomal subunit protein L9

gene	blattner	ratio A/B	p-value	function
rplR	b3304	7,8773	0,0179	50S ribosomal subunit protein L18
rplX	b3309	3,5468	0,0478	50S ribosomal subunit protein L24
rpmA	b3185	0,4113	0,0210	50S ribosomal subunit protein L27
rpmI	b1717	6,8633	0,0383	50S ribosomal subunit protein A
rpoA	b3295	2,8507	0,0294	RNA polymerase, alpha subunit
rpsD	b3296	5,2826	0,0441	30S ribosomal subunit protein S4
rpsE	b3303	12,4222	0,0115	30S ribosomal subunit protein S5
rpsH	b3306	4,2597	0,0254	30S ribosomal subunit protein S8, and regulator
rpsN	b3307	6,6163	0,0259	30S ribosomal subunit protein S14
rpsR	b4202	1,8126	0,0017	30S ribosomal subunit protein S18
rsd	b3995	0,6020	0,0268	regulator of sigma D
rseB	b2571	0,2066	0,0278	negative regulator of sigmaE; interacts with RseA and stimulates binding of RseA to sigmaE
rusA	b0550	0,6409	0,0385	endodeoxyribonuclease RUS (Holliday junction resolvase)
sdhB	b0724	1,7743	0,0237	succinate dehydrogenase iron-sulfur protein
sfsA	b0146	3,3885	0,0017	SfsA
sgrR	b0069	0,5711	0,0195	SgrR transcriptional regulator
slp	b3506	1,8331	0,0144	outer membrane protein induced after carbon starvation
slyA	b1642	4,5810	0,0274	SlyA transcriptional activator
smf	b4473	1,0372	0,0064	hypothetical protein
sohB	b1272	0,5393	0,0272	putative protease
somA	b0877	0,7299	0,0121	putative enzyme
speD	b0120	0,5703	0,0350	adenosylmethionine decarboxylase, proenzyme
speE	b0121	1,3579	0,0421	spermidine synthase
speG	b1584	0,4922	0,0388	spermidine acetyltransferase
spoT	b3650	0,4810	0,0407	GDP diphosphokinase / guanosine-3',5'-bis(diphosphate) 3'-diphosphatase
sucA	b0726	8,0970	0,0066	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
surE	b2744	1,5675	0,0023	phosphatase with broad substrate specificity / 3'-nucleotidase / 5'-nucleotidase
talA	b2464	7,9764	0,0051	transaldolase A
tauA	b0365	1,1408	0,0442	TauA/TauB/TauC ABC transporter
tfaQ	b1546	4,3804	0,0443	hypothetical protein
trkA	b3290	0,8203	0,0039	TrkA
trmD	b2607	8,9475	0,0351	tRNA (guanine-1-)-methyltransferase
trmU	b1133	0,5271	0,0381	catalyzes 2-thiouridine modification of tRNA
ttk	b3641	3,3439	0,0494	Ttk transcriptional regulator
ubiE	b3833	0,8435	0,0494	S-adenosylmethionine:2-DMK methyltransferase / 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase
upp	b2498	0,5649	0,0007	uracil phosphoribosyltransferase
uspG	b0607	2,9614	0,0340	universal stress protein of the UspA family
uxuA	b4322	0,8406	0,0459	mannonate dehydratase
uxuR	b4324	0,7367	0,0352	UxuR transcriptional regulator
wrbA	b1004	4,9428	0,0377	WrbA
xapA	b2407	0,7936	0,0468	xanthosine phosphorylase
xylA	b3565	2,0099	0,0081	xylose isomerase
xylB	b3564	0,5746	0,0049	xylulokinase
xylF	b3566	0,7195	0,0419	xylose ABC transporter
yaaH	b0010	0,6869	0,0271	putative transport protein
yabI	b0065	1,8964	0,0149	putative integral membrane protein
yadH	b0128	3,3596	0,0418	YadG/YadH ABC transporter
yadR	b0156	2,8838	0,0285	conserved hypothetical protein
yafS	b0213	0,6999	0,0147	putative methyltransferase
yahC	b0317	0,8078	0,0212	putative membrane protein
yahK	b0325	1,3928	0,0045	putative oxidoreductase
ybbP	b0496	0,7792	0,0036	YbbA/YbbP ABC transporter
ybcO	b0549	0,6231	0,0253	hypothetical protein
ybdL	b0600	0,4618	0,0229	methionine aminotransferase
ybeB	b0637	1,7480	0,0389	conserved hypothetical protein
ybeR	b0645	0,5813	0,0326	conserved hypothetical protein
ybhA	b0766	0,7300	0,0055	putative phosphatase
ybhL	b0786	2,1462	0,0351	putative transport protein
ybhN	b0788	0,7033	0,0260	hypothetical protein
ycbU	b0942	0,7402	0,0421	putative fimbrial-like protein
yccJ	b1003	5,6972	0,0370	hypothetical protein
ycdF	b1005	3,8775	0,0307	hypothetical protein
ycdJ	b1009	2,2829	0,0227	putative acetyltransferase
ycdN	b1016	1,7264	0,0325	hypothetical protein of the OFeT transport family
yceK	b1050	0,9386	0,0468	hypothetical protein
ycjF	b1322	2,8255	0,0176	putative membrane protein
ycjO	b1311	0,5416	0,0001	YcjN/YcjO/YcjP ABC transporter
yddL	b1472	0,6258	0,0181	putative outer membrane porin protein
ydeI	b1536	3,2270	0,0014	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ydfJ	b1543	0,2900	0,0231	YdfJ
yeaK	b1787	1,5080	0,0319	conserved hypothetical protein
yebQ	b1828	0,8734	0,0441	YebQ
yebS	b1833	0,8160	0,0391	putative membrane protein
yecC	b1917	0,7788	0,0141	putative ATP-binding component of a transport system
yeeA	b2008	0,6257	0,0087	putative membrane protein, transport
yeeL_2	b1979	0,6176	0,0176	putative transport protein
yeeO	b1985	0,5128	0,0485	YeeO MATE Transporter
yeeT	b2003	0,5966	0,0348	hypothetical protein
yejB	b2178	1,2896	0,0364	YejA/YejB/YejE/YejF ABC transporter
yfbE	b2253	0,5801	0,0012	UDP-L-Ara4O C-4" transaminase
yfeC	b2398	0,3352	0,0137	hypothetical protein
yfeK	b2419	0,6148	0,0371	conserved protein
yfgM	b2513	0,4685	0,0406	conserved protein
yfhG	b2555	0,9007	0,0264	conserved protein
yfhR	b2534	0,8297	0,0101	putative methylase or hydrolase
yfiP	b2583	1,7964	0,0494	conserved hypothetical protein
yfjX	b2643	0,7308	0,0082	hypothetical protein
ygdQ	b2832	0,6379	0,0085	putative transport protein
ygeF	b2850	0,8063	0,0120	conserved hypothetical protein
yggC	b2928	6,2501	0,0187	putative kinase
yggN	b2958	0,7475	0,0321	conserved hypothetical protein
yghJ	b2974	1,1108	0,0216	predicted inner membrane lipoprotein
yghU	b2989	1,1448	0,0338	glutathione transferase-like protein possibly involved in glutathionylspermidine metabolism
ygiH	b3059	0,6438	0,0454	putative membrane protein
ygiU	b3022	3,8905	0,0267	putative cyanide hydratase
ygjJ	b3079	0,9097	0,0041	hypothetical protein
yhaK	b3106	2,4963	0,0437	conserved hypothetical protein
yhbN	b3200	0,6192	0,0050	YhbG/YhbN ABC transporter
yhfX	b3381	1,2679	0,0037	conserved protein
yhhX	b3440	0,7634	0,0300	putative galactose 1-dehydrogenase
yhjD	b3522	2,7084	0,0452	putative membrane protein
yiaD	b3552	2,3769	0,0160	putative outer membrane protein
yiaV	b3586	0,5516	0,0468	putative membrane protein
yicH	b3655	1,5065	0,0436	conserved protein
yifN	b3777	0,5132	0,0378	conserved hypothetical protein
yigF	b3817	0,4341	0,0171	conserved hypothetical protein
yiiX	b3937	0,6653	0,0054	conserved hypothetical protein of the NlpC/P60 peptidase superfamily
yjdK	b4128	0,6048	0,0143	hypothetical protein
yjeQ	b4161	0,9234	0,0275	GTPase and putative translation factor / GTPase
yjgR	b4263	0,7614	0,0369	putative enzyme with P-loop containing nucleotide triphosphate hydrolase domain
yjhB	b4279	4,7570	0,0247	YjhB MFS transporter
yjhT	b4310	0,8659	0,0460	putative enzyme contains galactose oxidase-like domain
ykgJ	b0288	0,5411	0,0198	putative ferredoxin
ymgA	b1165	1,8693	0,0273	hypothetical protein
ymgC	b1167	13,1366	0,0366	hypothetical protein
ymgD	b1171	0,3867	0,0100	hypothetical protein
ynaA	b1368	0,9570	0,0079	putative alpha helix protein
yncA	b1448	1,1679	0,0391	putative N-acetyltransferase
yneG	b1523	1,1135	0,0464	conserved hypothetical protein
ynfA	b1582	5,9471	0,0110	inner membrane protein
yniB	b1726	3,4656	0,0443	hypothetical protein
yoaG	b1796	0,5357	0,0394	hypothetical protein
yobB	b1843	0,7096	0,0410	conserved hypothetical protein
yohC	b2135	3,0037	0,0304	putative transport protein
yohD	b2136	0,6268	0,0385	hypothetical protein
yohJ	b2141	0,8408	0,0481	putative transmembrane protein
yphA	b2543	2,8374	0,0476	hypothetical protein
yqjE	b3099	1,9245	0,0368	conserved protein
yraM	b3147	0,8763	0,0122	putative glycosylase
yrbD	b3193	1,2481	0,0359	YrbD
yrdA	b3279	0,4732	0,0240	putative transferase
yrfG	b3399	0,5282	0,0267	putative hydrolase with a phosphatase-like domain
ytfF	b4210	0,4613	0,0484	putative transmembrane subunit
ytfK	b4217	11,1610	0,0296	hypothetical protein
ytjB	b4387	0,5306	0,0382	membrane protein
znuA	b1857	0,4613	0,0187	ZnuA/ZnuB/ZnuC ABC transporter
zraP	b4002	0,2157	0,0093	zinc homeostasis protein
	b0395	2,2058	0,0439	

gene	blattner	ratio A/B	p-value	function
	b0322	1,4431	0,0208	
	b3948	0,7342	0,0285	

CSH50 (A) & CSH50*hns* (B) in Mid-Exponential

acrE	b3265	0,4232	0,0319	transmembrane protein affects septum formation and cell membrane permeability
ade	b3665	0,0880	0,0027	cryptic adenine deaminase monomer
agaB	b3138	0,5821	0,0060	EIIAga
agaC	b3139	0,5600	0,0258	EIIAga
allD	b0517	0,3467	0,0295	ureidoglycolate dehydrogenase
alsA	b4087	1,4648	0,0056	YjcW
alsK	b4084	1,6686	0,0186	putative D-allose kinase
aniC	b4115	0,1952	0,0013	AdiC Arginine:Agmatine Antiporter
artJ	b0860	1,3014	0,0092	arginine ABC transporter
asnA	b3744	4,5645	0,0110	aspartate-ammonia ligase
azoR	b1412	1,7670	0,0328	acyl carrier protein phosphodiesterase
b0501	b0501	0,3204	0,0148	hypothetical protein
b1172	b1172	0,3230	0,0046	conserved hypothetical protein
b1364	b1364	1,7953	0,0104	hypothetical protein
b1437	b1437	2,0579	0,0149	hypothetical protein
b2084	b2084	0,2573	0,0018	hypothetical protein
b2680	b2680	0,2973	0,0151	YgaY MFS transporter
b4283	b4283	0,7779	0,0431	IS911 protein
basR	b4113	0,5152	0,0269	BasR-Phosphorylated transcriptional regulator
bcsE	b3536	0,7416	0,0435	putative protease
bglG	b3723	0,3084	0,0458	BglG monomer
bioF	b0776	0,5910	0,0182	8-amino-7-oxononanoate synthase
cadA	b4131	0,4186	0,0251	lysine decarboxylase
cfa	b1661	1,7766	0,0466	cyclopropane fatty acid synthase
chaC	b1218	0,6361	0,0124	cation transport regulator
chbB	b1738	0,7761	0,0260	EIIChb
chbR	b1735	0,6426	0,0292	ChbR transcriptional regulator
citC	b0618	0,4542	0,0028	citrate lyase ligase
citD	b0617	0,4617	0,0403	subunit of acyl carrier protein
clpA	b0882	2,1712	0,0279	ATP-binding component of serine protease
clpB	b2592	1,8746	0,0335	ClpB chaperone
copA	b0484	2,0211	0,0020	YbaR
csgA	b1042	0,3262	0,0123	curlin, major subunit
csgB	b1041	0,3223	0,0205	curlin, minor subunit precursor
csgD	b1040	0,2580	0,0060	CsgD transcriptional activator
csgF	b1038	0,3660	0,0143	curli assembly component
csiE	b2535	2,3439	0,0459	hypothetical protein
cspC	b1823	0,5094	0,0463	cold shock protein CspC
cspI	b1552	0,1583	0,0104	cold shock protein CspI
cutC	b1874	0,6803	0,0402	copper homeostasis protein
cysH	b2762	1,3960	0,0442	3'-phospho-adenylsulfate reductase
cysP	b2425	1,7696	0,0110	thiosulfate ABC transporter
dcrB	b3472	1,7334	0,0438	conserved protein involved in bacteriophage adsorption
dctR	b3507	0,4226	0,0328	protein involved in metabolism of C4-dicarboxylates
dcuS	b4125	1,6044	0,0224	DcuS-Phis349
ddpC	b1485	1,3826	0,0444	YddQ
dgoR	b3694	1,6453	0,0106	regulator protein for dgo operon
djlC	b0649	0,6688	0,0445	Hsc56; a DnaJ-like protein that activates ATPase activity of Hsc62
dmsB	b0895	1,5182	0,0340	dimethyl sulfoxide reductase, chain B
dmsC	b0896	1,4176	0,0279	dimethyl sulfoxide reductase, chain C
dmsD	b1591	1,3281	0,0123	DMS reductase maturation protein
dpiA	b0620	0,2993	0,0020	CitB transcriptional regulator
dpiB	b0619	0,2370	0,0054	DpiB
dsbC	b2893	0,3743	0,0137	DsbC_{oxidized}
elaD	b2269	0,7119	0,0344	putative sulfatase / phosphatase
entA	b0596	1,8924	0,0444	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
exbB	b3006	3,9960	0,0236	ExbB protein; uptake of enterochelin; tonB-dependent uptake of B colicins
exbD	b3005	3,9950	0,0076	ExbD uptake of enterochelin; tonB-dependent uptake of B colicins
fdoG	b3894	1,9381	0,0090	formate dehydrogenase-O, α subunit
fecR	b4292	3,3052	0,0019	regulator for fec operon, periplasmic
feoB	b3409	8,1963	0,0108	FeoB ferrous iron transporter
fepC	b0588	2,0669	0,0123	Ferric Enterobactin Transport System
fhuA	b0150	3,0188	0,0173	FhuA outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuB	b0153	1,7527	0,0468	ferrichrome uptake system
fhuC	b0151	2,1582	0,0127	ferrichrome uptake system

gene	blattner	ratio A/B	p-value	function
fic	b3361	1,3570	0,0403	stationary-phase protein with possible role in p-aminobenzoate or folate biosynthesis
fimB	b4312	0,1579	0,0019	regulator for fimA
fimC	b4316	0,2925	0,0204	periplasmic chaperone, required for type 1 fimbriae
fimD	b4317	0,2625	0,0115	outer membrane protein; export and assembly of type 1 fimbriae, interrupted
fimE	b4313	0,4518	0,0341	regulator for fimA
fimF	b4318	0,1795	0,0195	fimbrial morphology
fimG	b4319	0,3289	0,0425	fimbrial morphology
fimH	b4320	0,3630	0,0420	minor fimbrial subunit, D-mannose specific adhesin
fixA	b0041	0,2419	0,0368	probable flavoprotein subunit required for anaerobic carnitine metabolism
flgA	b1072	5,3030	0,0410	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgC	b1074	13,7652	0,0406	flagellar basal-body rod protein FlgC
flgD	b1075	11,0115	0,0367	flagellar biosynthesis, initiation of hook assembly
flgG	b1078	5,4828	0,0333	flagellar basal-body rod protein FlgG
flgI	b1080	2,4887	0,0470	flagellar P-ring protein FlgI
fliE	b1937	1,6564	0,0329	flagellar basal-body protein FliE
fliH	b1940	1,5432	0,0196	flagellar biosynthesis protein FliH
fliL	b1944	5,3308	0,0268	flagellar biosynthesis
fliN	b1946	4,7917	0,0295	flagellar motor switch protein FliN; component of motor switch and energizing, enabling rotation and determining its direction
fliZ	b1921	4,2696	0,0330	possible cell-density responsive regulator of sigmaF
folC	b2315	0,7311	0,0443	folylpoly-γ-glutamate synthetase / dihydrofolate synthetase
fpr	b3924	2,5348	0,0149	flavodoxin NADP+ reductase
frdD	b4151	1,6186	0,0382	fumarate reductase membrane protein
frlB	b3371	2,2009	0,0184	fructoselysine 6-phosphate deglycase monomer
fruB	b2169	0,3434	0,0332	EIIIFru
fruK	b2168	0,4896	0,0376	1-phosphofructokinase monomer
fsaA	b0825	7,7628	0,0036	Fsa
ftnA	b1905	0,5763	0,0388	cytoplasmic ferritin, an iron storage protein)
gadA	b3517	0,0773	0,0039	glutamate decarboxylase A subunit
gadC	b1492	0,1005	0,0061	XasA GABA APC transporter
gadE	b3512	0,1805	0,0075	GadE transcriptional activator
gadW	b3515	0,2415	0,0112	GadWtranscriptional repressor
gadX	b3516	0,2187	0,0018	GadX transcriptional activator
gcl	b0507	1,3668	0,0281	glyoxylate carboligase
glf	b2036	0,8672	0,0128	UDP-galactopyranose mutase
glk	b2388	1,8333	0,0429	glucokinase
glnB	b2553	1,3692	0,0068	PII-UMP
glnQ	b0809	1,7145	0,0305	glutamine ABC transporter
glpK	b3926	1,4158	0,0147	glycerol kinase
gltF	b3214	0,3892	0,0017	regulator of gltBDF operon, induction of Ntr enzymes
gltJ	b0654	1,5962	0,0062	glutamate ABC transporter
gor	b3500	1,5677	0,0412	glutathione reductase (NADPH)
groE	b4142	1,7003	0,0104	GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity
groL	b4143	1,6506	0,0412	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
grpE	b2614	2,1870	0,0236	phage lambda replication; host DNA synthesis; heat shock protein; protein repair
hdeD	b3511	0,1890	0,0048	protein involved in acid resistance
hemA	b1210	0,5195	0,0126	glutamyl-tRNA reductase
hlyE	b1182	0,1049	0,0060	hemolysin E
hofB	b0107	1,8089	0,0424	protein involved in plasmid replication
hsdS	b4348	1,3534	0,0115	specificity determinant for hsdM and hsdR
htrL	b3618	0,3544	0,0428	involved in lipopolysaccharide biosynthesis
hycF	b2720	1,3712	0,0000	formate hydrogenlyase complex
hyfA	b2481	1,4088	0,0450	hydrogenase 4, component A
hyfI	b2489	1,2438	0,0144	hydrogenase 4, small subunit
hypB	b2727	1,7286	0,0223	guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3
iaaA	b0828	1,6736	0,0020	beta cleavage product of IaaA
idnD	b4267	0,5169	0,0436	L-idonate 5-dehydrogenase
idnR	b4264	1,1480	0,0279	IdnR-5-ketogluconate
ilvC	b3774	1,6530	0,0410	acetohydroxy acid isomeroeductase
ilvY	b3773	1,7029	0,0090	IlvY transcriptional dual regulator
infB	b3168	0,8211	0,0337	protein chain initiation factor IF-2
intG	b1936	0,3431	0,0453	hypothetical protein
katG	b3942	1,3880	0,0202	hydroperoxidase I
kdsB	b0918	1,5677	0,0297	3-deoxy-D-manno-octulosonate-cytidylyltransferase
ldhA	b1380	2,9107	0,0129	D-lactate dehydrogenase
lrhA	b2289	0,4409	0,0449	LrhA transcriptional repressor
mak	b0394	1,4938	0,0390	manno(fructo)kinase
malQ	b3416	1,2649	0,0206	maltose degrading enzyme 2 / maltose degrading enzyme / amylomaltase
map	b0168	2,1116	0,0092	methionine aminopeptidase
mcrC	b4345	0,7384	0,0462	MrcC subunit of 5-methylcytosine restriction system

gene	blattner	ratio A/B	p-value	function
mdtC	b2076	0,7845	0,0383	MdtABC RND-type Drug Exporter
mdtF	b3514	0,4998	0,0195	YhiV
mdtM	b4337	0,6514	0,0140	YjiO drug MFS transporter
menF	b2265	0,6845	0,0468	isochorismate synthase, menaquinone-specific
menG	b3929	1,4163	0,0172	inhibitor of ribonuclease E (RNase E) activity
mfd	b1114	1,2470	0,0009	transcription-repair coupling factor; mutation frequency decline
mntH	b2392	2,1445	0,0446	MntH manganese ion NRAMP transporter
mobA	b3857	2,0022	0,0164	molybdopterin guanine dinucleotide synthase
molR_1	b2115	0,5716	0,0391	molybdate metabolism regulator, interrupted
mppA	b1329	0,3284	0,0002	periplasmic murein tripeptide binding protein
msbA	b0914	0,7297	0,0302	ATP-binding transport protein; multicopy suppressor of htrB
mtlA	b3599	1,2772	0,0244	EIIMtl
murA	b3189	0,6703	0,0265	UDP-N-acetylglucosamine enolpyruvyl transferase
mutS	b2733	0,7424	0,0275	MutHLS complex, methyl-directed mismatch repair
nrdH	b2673	4,4358	0,0460	glutaredoxin-like protein; hydrogen donor
nrdI	b2674	2,8928	0,0050	stimulates ribonucleotide reduction
nuoB	b2287	1,3211	0,0440	NADH dehydrogenase I
ompF	b0929	2,0493	0,0041	outer membrane porin OmpF
ompR	b3405	1,5638	0,0031	OmpR transcriptional dual regulator
ompW	b1256	1,5536	0,0299	OmpW, outer membrane protein
osmC	b1482	0,3366	0,0477	osmotically inducible peroxidase OsmC
paaH	b1395	1,6745	0,0471	putative 3-hydroxy-acyl-CoA dehydrogenase of phenylacetate degradation
paaI	b1396	1,5659	0,0497	hypothetical protein with some similarity to thioesterases
pagP	b0622	0,2030	0,0037	PagP monomer
pfkA	b3916	2,4655	0,0114	6-phosphofructokinase-1 monomer / putative NAD+ kinase
pflB	b0903	2,0318	0,0371	pyruvate formate-lyase (inactive)
pflD	b3951	1,4252	0,0361	formate acetyltransferase 2
pflE	b0824	4,1008	0,0376	putative pyruvate formate-lyase 2 activating enzyme
pgaA	b1024	1,9171	0,0243	putative outer membrane protein
pgaB	b1023	0,5469	0,0305	putative membrane protein
pgk	b2926	1,3537	0,0305	phosphoglycerate kinase
pinR	b1374	0,2637	0,0145	putative transposon resolvase
pmrF	b2254	0,3626	0,0319	undecaprenyl phosphate-L-Ara4FN transferase
pptA	b1461	0,5373	0,0206	probable 4-oxalocrotonate tautomerase (4-OT) monomer
prlC	b3498	1,6015	0,0034	oligopeptidase A
proV	b2677	0,1318	0,0010	proline ABC transporter
proW	b2678	0,1876	0,0048	proline ABC transporter
pspF	b1303	1,5821	0,0168	PspF transcriptional activator
pspG	b4050	0,7424	0,0314	phage shock protein PspG
pta	b2297	1,5264	0,0118	phosphate acetyltransferase
pyrB	b4245	2,0111	0,0261	aspartate carbamoyltransferase, PyrB subunit
rdgC	b0393	0,7189	0,0182	nonspecific DNA binding protein; nucleoid component
recA	b2699	0,7639	0,0133	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
recN	b2616	0,2723	0,0087	protein used in recombination and DNA repair
recX	b2698	0,4849	0,0425	inhibitor of RecA
relE	b1563	0,7927	0,0031	toxin of the RelE-RelB toxin-antitoxin system; cleaves mRNA in ribosome
rfaG	b3631	0,6527	0,0257	lipopolysaccharide core biosynthesis; glucosyltransferase I
rfaQ	b3632	0,5460	0,0077	lipopolysaccharide core biosynthesis
rhsA	b3593	0,4066	0,0429	RhsA protein in rhs element
rhsD	b0497	0,1528	0,0099	RhsD protein in rhs element
rihB	b2162	0,4066	0,0069	ribonucleoside hydrolase 2 (pyrimidine-specific)
rihC	b0030	2,2156	0,0351	ribonucleoside hydrolase 3
rna	b0611	1,9534	0,0081	RNase I, cleaves phosphodiester bond between any two nucleotides
rnhA	b0214	0,8180	0,0094	RNase HI, degrades RNA of DNA-RNA hybrids, participates in DNA replication
rpmH	b3703	0,5985	0,0307	50S ribosomal subunit protein L34
rsmC	b4371	0,6908	0,0180	putative enzyme
rsxB	b1628	0,4784	0,0272	member of SoxR-reducing complex
ruvA	b1861	0,5930	0,0118	branch migration of Holliday structures; repair
secA	b0098	1,7377	0,0270	Sec Protein Secretion Complex
selA	b3591	1,4733	0,0470	selenocysteine synthase monomer
sfmA	b0530	1,3127	0,0420	putative fimbrial-like protein
sgcR	b4300	1,3635	0,0167	SgcR transcriptional regulator
slp	b3506	0,2034	0,0108	outer membrane protein induced after carbon starvation
soxS	b4062	7,4619	0,0398	SoxS transcriptional activator
stpA	b2669	0,2808	0,0208	DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing?
sufA	b1684	2,0899	0,0341	scaffold protein for iron-sulfur cluster assembly
sufC	b1682	1,4335	0,0368	ATPase component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex
suhB	b2533	0,7121	0,0469	inositol monophosphatase
tdcR	b3119	1,3440	0,0327	TdcR transcriptional activator

gene	blattner	ratio A/B	p-value	function
tdk	b1238	0,2845	0,0028	thymidine kinase / deoxyuridine kinase
torT	b0994	1,5195	0,0473	TorT-unknown inducer
torZ	b1872	0,4520	0,0239	trimethylamine N-oxide reductase III, TorZ subunit
treB	b4240	1,3851	0,0394	EII _{Tre}
treC	b4239	1,5854	0,0202	trehalose-6-phosphate hydrolase
trpD	b1263	1,4240	0,0122	anthranilate synthase component II
trpE	b1264	1,3868	0,0296	anthranilate synthase component I
ubiD	b3843	1,3999	0,0173	3-octaprenyl-4-hydroxybenzoate decarboxylase monomer
ugd	b2028	0,5278	0,0277	UDP-glucose 6-dehydrogenase
ulaG	b4192	1,1945	0,0340	putative L-ascorbate 6-phosphate lactonase
uspA	b3495	2,2175	0,0364	universal stress protein; broad regulatory function?
wcaD	b2056	0,2374	0,0250	putative colanic acid polymerase
wzyE	b3793	1,4246	0,0304	4- α -fucosyltransferase
xapR	b2405	0,1865	0,0024	XapR transcriptional activator
xerC	b3811	1,3838	0,0440	site-specific recombinase, acts on cer sequence of CoIE1, effects chromosome segregation at cell division
yabP	b0056	0,4273	0,0003	conserved hypothetical protein
yacH	b0117	1,3658	0,0346	putative membrane protein
yadK	b0136	0,2247	0,0062	putative adhesin-like protein
yadL	b0137	0,4099	0,0151	putative adhesin-like protein
yafD	b0209	1,4773	0,0349	conserved hypothetical protein
yafW	b0246	1,8615	0,0241	antitoxin of the Ykfi-YafW toxin-antitoxin pair
yaiB	b0382	0,5256	0,0360	conserved hypothetical protein
yaiW	b0378	0,8394	0,0355	conserved hypothetical protein
yajD	b0410	1,3406	0,0194	conserved hypothetical protein
ybaD	b0413	1,5654	0,0479	conserved protein
ybaK	b0481	1,3718	0,0213	conserved hypothetical protein
ybaW	b0443	1,1589	0,0085	conserved hypothetical protein
ybbD	b0500	0,3702	0,0301	conserved hypothetical protein
ybcM	b0546	0,2015	0,0007	putative ARAC-type regulatory protein
ybdG	b0577	0,5999	0,0390	putative transport protein
ybhH	b0691	0,8192	0,0421	conserved hypothetical protein
ybgO	b0716	1,2872	0,0428	conserved hypothetical protein
ybiF	b0813	0,3984	0,0307	Threonine and Homoserine Exporter
ybiW	b0823	4,0177	0,0341	putative formate acetyltransferase
ybjL	b0847	0,7609	0,0095	putative transport protein
ycaK	b0901	0,6234	0,0102	YcaK
ycaL	b0909	1,2929	0,0439	putative heat shock protein
ycaM	b0899	0,3732	0,0035	YcaM APC amino acid transporter
ycbQ	b0938	0,2233	0,0046	putative fimbrial-like protein
ycbS	b0940	0,4473	0,0081	putative outer membrane protein
ycbT	b0941	0,5092	0,0133	homolog of Salmonella FimH protein
yccU	b0965	1,4442	0,0412	putative NAD(P)-binding enzyme
ycdN	b1016	1,2686	0,0288	hypothetical protein of the OFeT transport family
ycdU	b1029	0,3114	0,0236	putative enzyme
yceI	b1056	0,6004	0,0350	periplasmic protein; possibly secreted
ycfR	b1112	0,3049	0,0045	conserved hypothetical protein
ycgH_1	b1169	0,2603	0,0228	conserved protein; member of the Autotransporter family
ycgV	b1202	0,1758	0,0031	putative adhesion and penetration protein
yciE	b1257	0,5250	0,0110	conserved protein
ycjN	b1310	0,4274	0,0070	YcjN/YcjO/YcjP ABC transporter
ycjO	b1311	1,4055	0,0364	YcjN/YcjO/YcjP ABC transporter
ycjP	b1312	0,5766	0,0237	YcjN/YcjO/YcjP ABC transporter
ycjQ	b1313	0,5545	0,0251	putative oxidoreductase
ydbH	b1381	1,4568	0,0176	conserved protein
ydcA	b1419	0,7482	0,0460	hypothetical protein
yddJ	b1470	0,7674	0,0421	hypothetical protein
yddV	b1490	0,4204	0,0091	conserved protein
ydeH	b1535	0,2575	0,0002	hypothetical protein
ydeI	b1536	0,3455	0,0164	conserved hypothetical protein
ydeM	b1497	0,7525	0,0152	putative enzyme
ydeO	b1499	0,3105	0,0065	putative ARAC-type regulatory protein
ydeP	b1501	0,5015	0,0287	acid resistance protein
ydeS	b1504	0,4386	0,0418	putative fimbrial-like protein
ydeT	b1505	0,5607	0,0195	putative outer membrane protein
ydfJ	b1543	1,4099	0,0448	YdfJ
YdgE	b1599	0,1355	0,0016	YdgE SMR Protein
YdgF	b1600	0,0941	0,0008	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydgK	b1626	0,5783	0,0429	putative oxidoreductase
ydgT	b1625	0,3754	0,0341	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ydhT	b1669	0,6822	0,0135	conserved protein
ydhY	b1674	0,5117	0,0365	putative oxidoreductase, Fe-S subunit
ydiA	b1703	0,4514	0,0302	conserved protein
ydiT	b1700	0,5051	0,0079	putative ferredoxin
ydjI	b1773	0,5134	0,0380	putative aldolase
ydjJ	b1774	0,5684	0,0403	putative oxidoreductase
yeaD	b1780	2,3475	0,0375	conserved hypothetical protein
yeaJ	b1786	0,3536	0,0274	putative membrane protein
yeaU	b1800	0,6621	0,0455	putative tartrate dehydrogenase
yebN	b1821	0,3605	0,0299	putative membrane protein, terpenoid synthase-like
yecT	b1877	0,7868	0,0119	hypothetical protein
yedL	b1932	0,7234	0,0377	putative acyl-CoA N-acyltransferase
yedW	b1969	0,2224	0,0277	putative 2-component transcriptional response regulator
yeeP	b1999	1,5217	0,0256	putative histone
yeeR	b2001	3,3879	0,0270	hypothetical protein
yegI	b2070	0,5059	0,0139	putative chaperonin
yegJ	b2071	0,4400	0,0002	hypothetical protein
yegZ	b2083	0,4459	0,0458	hypothetical protein
yehD	b2111	1,2074	0,0153	putative fimbrial-like protein
yehZ	b2131	1,4371	0,0308	YehW/YehX/YehY/YehZ ABC transporter
yeiC	b2166	0,1058	0,0054	putative kinase
yeiL	b2163	0,2356	0,0045	yeiL transcriptional activator
yeiS	b2145	0,3579	0,0009	hypothetical protein
yfaO	b2251	0,6774	0,0483	putative enzyme (Nudix hydrolase)
yfbE	b2253	0,5011	0,0326	UDP-L-Ara4O C-4" transaminase
yfbT	b2293	1,7768	0,0251	putative phosphatase, contains a phosphatase-like domain
yfcV	b2339	0,2396	0,0363	putative fimbrial-like protein
yfcZ	b2343	1,9842	0,0309	conserved hypothetical protein
yfdY	b2377	1,9172	0,0152	hypothetical protein
yfeH	b2410	2,5659	0,0020	putative cytochrome oxidase
yfeO	b2389	1,3810	0,0219	hypothetical protein
yfgH	b2505	0,3998	0,0112	putative outer membrane lipoprotein
yfgI	b2506	0,3691	0,0138	putative membrane protein
yfiC	b2575	0,5114	0,0115	putative enzyme
yfiR	b2603	0,4214	0,0315	conserved protein
yfjT	b2637	1,2855	0,0166	hypothetical protein
ygaD	b2700	1,5905	0,0380	conserved protein
ygaQ	b2654	0,5771	0,0145	hypothetical protein
ygcG	b2778	0,5541	0,0426	putative membrane protein
ygcI	b2757	0,2705	0,0485	hypothetical protein
ygcK	b2759	0,1525	0,0146	hypothetical protein
ygeH	b2852	1,2703	0,0166	putative invasion protein
ygfJ	b2877	0,5915	0,0145	conserved protein
ygiD	b3039	1,7851	0,0438	putative enzyme with dioxygenase domain
ygiL	b3043	0,1979	0,0050	putative fimbrial-like protein
ygiP	b3060	0,3869	0,0138	putative transcriptional regulator LYSR-type
ygiG	b3073	0,7150	0,0032	putrescine:2-oxoglutaric acid aminotransferase
ygiR	b3087	1,7341	0,0151	putative NAD(P)-binding dehydrogenase
yhaC	b3121	0,7029	0,0259	conserved protein
yhaH	b3103	1,4810	0,0409	putative cytochrome
yheT	b3353	0,9395	0,0476	putative hydrolase with an alpha/beta-hydrolase domain
yhgG	b3410	8,7789	0,0083	putative transcriptional regulator
yhhS	b3473	1,9023	0,0214	YhhS MFS transporter
yhiM	b3491	0,3980	0,0150	conserved inner membrane protein
yhiS	b3504	0,4148	0,0135	conserved protein
yhjB	b3520	1,6281	0,0425	putative regulator
yhjD	b3522	1,3548	0,0218	putative membrane protein
yhjH	b3525	1,9821	0,0096	protein involved in flagellar function
yhjX	b3547	2,3356	0,0409	YhjX MFS transporter
yiaU	b3585	0,4160	0,0154	putative transcriptional regulator LYSR-type
yibA	b3594	0,2851	0,0477	putative lyase
yicO	b3664	0,2533	0,0165	putative membrane protein with possible relationship to novobiocin and deoxycholate resistance
yieI	b3716	1,7977	0,0144	putative membrane protein
yigF	b3817	0,4178	0,0439	conserved hypothetical protein
yigL	b3826	1,3312	0,0472	conserved protein with a phosphatase-like domain
yigZ	b3848	1,4946	0,0135	putative elongation factor
yihF	b3861	0,6315	0,0205	conserved protein
yjaG	b3999	1,5544	0,0152	conserved protein
yjbB	b4020	1,4828	0,0113	putative alpha helix protein

gene	blattner	ratio A/B	p-value	function
yjbM	b4048	0,5829	0,0309	conserved hypothetical protein
yjcZ	b4110	0,6510	0,0102	hypothetical protein
yjdA	b4109	0,3357	0,0151	hypothetical protein
yjdL	b4130	0,7255	0,0483	YjdL peptide POT transporter
yjeJ	b4145	0,5658	0,0365	conserved protein
yjeN	b4157	0,4976	0,0199	conserved hypothetical protein
yjeS	b4166	1,9051	0,0114	conserved ferredoxin-like protein
yjfM	b4185	1,4600	0,0495	conserved hypothetical protein
yjgK	b4252	1,5575	0,0381	conserved hypothetical protein
yjgN	b4257	0,6494	0,0031	putative membrane protein possible involved in transport
yjhE	b4282	0,6011	0,0270	KpLE2 phage-like element
yjhH	b4298	0,2791	0,0089	putative lyase/synthase
yjhI	b4299	0,3015	0,0021	putative regulator
yjiP	b4338	0,2074	0,0198	hypothetical protein
yjiW	b4347	0,3864	0,0124	hypothetical protein
yjiI	b4380	1,2300	0,0003	conserved hypothetical protein
yjiN	b4358	0,7146	0,0214	putative oxidoreductase
yliH	b0836	1,4511	0,0323	putative receptor; induced in stationary phase
ymdA	b1044	1,3743	0,0405	conserved hypothetical protein
ymdE	b1028	1,2439	0,0093	putative malonyl-CoA:Acyl carrier protein transacylase
yfmM	b1148	1,3536	0,0483	hypothetical protein
ymgD	b1171	0,4644	0,0021	hypothetical protein
ynaE	b1375	0,2665	0,0186	hypothetical protein
ynaI	b1330	0,5285	0,0218	YnaI
ynbD	b1411	1,4997	0,0330	putative enzyme
yncC	b1450	0,6862	0,0367	hypothetical protein
yncD	b1451	1,5934	0,0332	Probable TonB-dependent receptor
yncI	b1458	0,1672	0,0266	conserved protein
yneI	b1525	3,7228	0,0368	putative aldehyde dehydrogenase
yneK	b1527	0,9040	0,0285	conserved protein
ynfN	b1551	0,2403	0,0063	hypothetical protein
yohJ	b2141	2,9847	0,0353	putative transmembrane protein
yohN	b2107	0,6686	0,0265	hypothetical protein
ypfJ	b2475	1,4122	0,0100	conserved protein
ypjF	b2646	1,6516	0,0435	member of the YeeV, Ykfl, YpjF family of toxin proteins
yqaC	b2657	0,3850	0,0243	putative enzyme
yqcC	b2876	0,6850	0,0170	conserved protein
yqeI	b2847	0,3106	0,0215	putative sensory transducer
yqeJ	b2848	0,3761	0,0379	conserved hypothetical protein
yqgA	b2966	2,0839	0,0160	putative transport protein
yrhA	b3443	0,7276	0,0181	conserved hypothetical protein
ytfR	b4485	1,7393	0,0402	subunit of YtfQ/YtfR/YtfS/YtfT/YtfF ABC transporter
ytfT	b4230	1,5937	0,0012	YtfQ/YtfR/YtfS/YtfT/YtfF ABC transporter
zraS	b4003	2,0921	0,0305	ZraS-Phis

CSH50 (A) & CSH50*hms* (B) in Transition to Stationary

aaeB	b3240	1,1872	0,0075	hypothetical protein
aceE	b0114	0,2646	0,0654	subunit of E1p component of pyruvate dehydrogenase complex
acrD	b2470	1,3042	0,1589	AcrD
ade	b3665	0,0725	0,0088	cryptic adenine deaminase monomer
adiA	b4117	0,9019	0,0328	Adi
agaB	b3138	1,1736	0,1822	EIIAga
alsC	b4086	1,2567	0,1129	YjcV
ansB	b2957	0,2992	0,0537	asparaginase II
arpB_2	b1721	0,9159	0,1043	hypothetical protein
artJ	b0860	0,8070	0,0643	arginine ABC transporter
b1367	b1367	1,2731	0,0856	hypothetical protein
b1567	b1567	0,7688	0,1747	hypothetical protein
b3808	b3808	1,2642	0,0697	hypothetical protein
b4103	b4103	1,4344	0,0818	putative C terminus of split phnE gene product
betA	b0311	1,2923	0,0890	choline dehydrogenase
caiF	b0034	0,2262	0,0374	CaiF transcriptional activator
cheY	b1882	1,4371	0,1824	CheY-Pasp
csgD	b1040	0,6260	0,1715	CsgD transcriptional activator
cusB	b0574	1,8915	0,0232	membrane fusion protein of the CusCFBA copper efflux system
cydA	b0733	0,4010	0,0979	cytochrome bd-I terminal oxidase subunit I
cysS	b0526	0,8028	0,2224	cysteinyI-tRNA synthetase
dapB	b0031	0,5764	0,1246	dihydrodipicolinate reductase
degS	b3235	1,4438	0,2115	inner membrane serine protease required for the extracytoplasmic stress response mediated by sigmaE

gene	blattner	ratio A/B	p-value	function
ebgC	b3077	1,1456	0,1104	evolved beta-D-galactosidase, beta subunit; cryptic gene
entA	b0596	1,2670	0,1112	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
entC	b0593	0,7369	0,0692	isochorismate synthase, enterobactin specific
eutJ	b2454	0,8315	0,0043	putative ethanolamine utilization protein
fabB	b2323	0,4887	0,0554	beta-ketoacyl-ACP synthase I / malonyl-ACP decarboxylase
fadI	b2342	1,5169	0,2349	FadI monomer
fdrA	b0518	0,8147	0,1193	involved in protein transport; multicopy suppressor of dominant negative ftsH mutants
fhuB	b0153	1,3218	0,2319	ferrichrome uptake system
fimD	b4317	0,5627	0,2047	outer membrane protein; export and assembly of type 1 fimbriae, interrupted
fixA	b0041	0,0756	0,1450	probable flavoprotein subunit required for anaerobic carnitine metabolism
fixC	b0043	0,2155	0,2179	flavoprotein (electron transport), possibly involved in anaerobic carnitine metabolism
flgB	b1073	0,8033	0,0745	flagellar basal-body rod protein FlgB
folC	b2315	1,3627	0,0775	folylpoly-γ-glutamate synthetase / dihydrofolate synthetase
folP	b3177	1,2314	0,1694	dihydropteroate synthase
frlB	b3371	2,0432	0,0360	fructoselysine 6-phosphate deglycase monomer
frlC	b3372	1,2382	0,2287	fructoselysine and psicoselysine degradation
frmA	b0356	1,3302	0,0420	formaldehyde dehydrogenase, glutathione-dependent
fucA	b2800	0,2508	0,0258	L-fucose-phosphate aldolase
garD	b3128	0,3928	0,2088	galactarate dehydratase
gloA	b1651	1,3030	0,0348	glyoxalase I
gltJ	b0654	1,2726	0,0202	glutamate ABC transporter
gnd	b2029	0,2673	0,1255	6-phosphogluconate dehydrogenase (decarboxylating)
gspF	b3327	1,1553	0,2132	putative protein secretion protein for export
hemG	b3850	1,3439	0,1949	protoporphyrinogen oxidase
insB	b0264	1,2537	0,0298	IS1 protein InsB (B0264)
iscA	b2528	1,4368	0,0689	iron-sulfur cluster assembly protein
iscS	b2530	2,5506	0,1524	cysteine desulfurase monomer
kdsB	b0918	0,6326	0,0429	3-deoxy-D-manno-octulosonate-cytidyltransferase
kdtA	b3633	1,3532	0,1040	KDO transferase
kefG	b3351	1,3412	0,1984	KefG
lepB	b2568	1,1466	0,0947	leader peptidase (signal peptidase I)
mdtF	b3514	0,2922	0,2011	YhiV
menD	b2264	0,5481	0,0119	putative 2-hydroxyglutarate synthase / SHCHC synthase / 2-oxoglutarate decarboxylase
moaC	b0783	0,7275	0,0123	molybdopterin biosynthesis, protein C
nanA	b3225	1,7915	0,0363	N-acetylneuraminatase lyase
nfnB	b0578	0,6237	0,0070	dihydropteridine reductase
nrdH	b2673	1,4711	0,2098	glutaredoxin-like protein; hydrogen donor
ompF	b0929	1,7917	0,1439	outer membrane porin OmpF
oppF	b1247	0,8461	0,0600	oligopeptide ABC transporter
osmC	b1482	0,6061	0,1300	osmotically inducible peroxidase OsmC
paaE	b1392	1,6951	0,1043	putative oxygenase reductase of phenylacetate degradation
paaY	b1400	1,4811	0,0096	putative transferase
pgcA	b1022	0,6851	0,0781	predicted N-glycosyltransferase
potH	b0856	1,3620	0,0482	putrescine ABC transporter
ppsA	b1702	0,6429	0,1319	phosphoenolpyruvate synthase
proP	b4111	1,3631	0,1790	ProP proline/betaine MFS transporter
proV	b2677	0,4218	0,1799	proline ABC transporter
puuC	b1300	1,6935	0,1184	aldehyde dehydrogenase
pykA	b1854	0,7604	0,0838	pyruvate kinase II monomer
pyrB	b4245	1,1503	0,1874	aspartate carbamoyltransferase, PyrB subunit
rbsC	b3750	0,6695	0,0468	ribose ABC transporter
recA	b2699	0,3452	0,1832	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
relA	b2784	1,2742	0,1110	GDP pyrophosphokinase / GTP pyrophosphokinase
rfe	b3784	1,3370	0,2082	undecaprenyl-phosphate α-N-acetylglucosaminyl transferase
rluF	b4022	1,3140	0,1201	23S rRNA pseudouridine synthase
rusA	b0550	1,4113	0,1436	endodeoxyribonuclease RUS (Holliday junction resolvase)
serB	b4388	0,7904	0,0773	phosphoserine phosphatase
sieB	b1353	0,8383	0,1178	phage superinfection exclusion protein
slp	b3506	0,4025	0,1450	outer membrane protein induced after carbon starvation
sra	b1480	1,6764	0,1726	30S ribosomal subunit protein S22; sub-stoichiometric stationary phase ribosomal component
srlB	b2704	1,2552	0,1276	GutB
tdcD	b3115	0,1894	0,1458	propionate kinase / acetate kinase C
tfaS	b2353	1,2824	0,0709	hypothetical protein
thiC	b3994	0,9357	0,1591	thiC protein
thiE	b3993	1,2669	0,1306	thiamine phosphate synthase
thiL	b0417	1,2068	0,0179	thiamine phosphate kinase
torY	b1873	0,4910	0,1241	trimethylamine N-oxide reductase III, c-type cytochrome subunit
torZ	b1872	0,5350	0,0783	trimethylamine N-oxide reductase III, TorZ subunit
trmE	b3706	1,3641	0,0940	GTP-binding protein with a role in modification of tRNA

gene	blattner	ratio A/B	p-value	function
udk	b2066	1,1984	0,1082	uridine kinase / cytidine kinase
uppP	b3057	0,9220	0,0886	undecaprenyl diphosphatase; bacitracin resistance
uxuA	b4322	1,5879	0,1280	mannonate dehydratase
xapB	b2406	0,7826	0,0813	XapB xanthosine MFS transporter
xyIH	b3568	0,2488	0,1621	xylose ABC transporter
xyIR	b3569	0,5185	0,1010	XyIR-Xylose transcriptional activator
ybbV	b0510	0,8643	0,0029	hypothetical protein
ybgH	b0709	1,2353	0,1593	YbgH peptide POT Transporter
ycbY	b0948	1,4626	0,2285	putative methyltransferase
yccA	b0970	0,8900	0,1984	putative carrier/transport protein; substrate or modulator of FtsH-mediated proteolysis
yccU	b0965	1,6297	0,1818	putative NAD(P)-binding enzyme
yceH	b1067	0,7620	0,2327	conserved hypothetical protein
ycgH_1	b1169	0,3656	0,1003	conserved protein; member of the Autotransporter family
ycgV	b1202	0,5050	0,0863	putative adhesion and penetration protein
yciQ	b1268	1,0958	0,0693	putative membrane protein
ycjS	b1315	1,2033	0,2091	putative galactose 1-dehydrogenase
ycjX	b1321	0,8771	0,2180	putative EC 2.1 enzyme
ydaV	b1360	1,2315	0,1919	putative DNA replication factor
ydcF	b1414	1,3872	0,0086	conserved hypothetical protein
ydcL	b1431	1,3586	0,0134	conserved hypothetical protein
YdgF	b1600	0,4729	0,0174	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydgR	b1634	1,3701	0,0111	YdgR putative peptide POT Transporter
ydiQ	b1697	0,7378	0,0072	putative subunit of YdiQ-YdiR flavoprotein
ydiI	b1773	0,6874	0,0303	putative aldolase
yeaC	b1777	1,2788	0,0410	conserved hypothetical protein
yegK	b2072	0,7214	0,0032	conserved hypothetical protein
yegS	b2086	1,2631	0,0064	conserved protein
yeiC	b2166	0,3541	0,2324	putative kinase
yfdT	b2363	1,1129	0,0883	hypothetical protein
yfeX	b2431	0,7909	0,0108	conserved protein
yfiP	b2583	0,7684	0,0969	conserved hypothetical protein
yfiR	b2603	0,6636	0,1282	conserved protein
yfjP	b2632	1,3077	0,1930	putative GTP-binding protein
ygcB	b2761	0,4844	0,2032	putative enzyme
ygcI	b2757	0,2748	0,2013	hypothetical protein
ygcS	b2771	0,7026	0,1397	YgcS MFS transporter
ygcG	b2851	0,5939	0,1993	conserved hypothetical protein
yhbG	b3201	1,0641	0,0935	YhbG/YhbN ABC transporter
yhbW	b3160	1,4346	0,0533	putative enzyme
yhdX	b3269	0,8973	0,1366	YhdW/YhdX/YhdY/YhdZ ABC transporter
yhgE	b3402	1,3316	0,1019	putative transport
yhhA	b3448	1,3377	0,1710	conserved protein
yhhJ	b3485	1,1309	0,1809	YhiH/YhhJ ABC transporter
yhhW	b3439	1,1799	0,2435	conserved hypothetical protein
yhiM	b3491	0,1095	0,0552	conserved inner membrane protein
yhiP	b3496	1,1708	0,1262	YhiP peptide POT transporter
yhjD	b3522	1,4333	0,0321	putative membrane protein
yicI	b3656	1,8297	0,1437	putative alpha-xylosidase
yidC	b3705	1,4704	0,1123	inner-membrane protein insertion factor
yihW	b3884	0,8220	0,0407	putative DEOR-type transcriptional regulator
yjeM	b4156	0,7016	0,1081	YjeM APC transporter
yjhC	b4280	0,5790	0,1944	KpLE2 phage-like element; putative NAD(P)-binding dehydrogenase
yjhE	b4282	1,2886	0,0221	KpLE2 phage-like element
yjhI	b4299	0,5334	0,0761	putative regulator
yjhS	b4309	1,2490	0,1765	conserved protein
yjiP	b4338	0,2190	0,0587	hypothetical protein
ymfL	b1147	1,2231	0,1027	hypothetical protein
ynaI	b1330	0,3691	0,1029	YnaI
yneK	b1527	1,2307	0,0945	conserved protein
ynjH	b1760	1,2650	0,1545	conserved hypothetical protein
yphF	b2548	0,8131	0,1404	YphD/YphE/YphF ABC transporter
yqaA	b2689	1,5094	0,1026	putative integral membrane protein
yqcE	b2775	0,3813	0,0410	YqcE MFS transporter
yqeA	b2874	0,6119	0,2140	putative carbamate kinase
yqgF	b2949	1,1217	0,0662	possible Holliday junction resolvase
yraR	b3152	0,8804	0,0477	putative NADH dehydrogenase
yrbD	b3193	1,2804	0,0766	YrbD
yrhA	b3443	1,4004	0,1317	conserved hypothetical protein
ytfL	b4218	0,6807	0,0752	putative transport protein

gene	blattner	ratio A/B	p-value	function
CSH50 (A) & CSH50<i>hms</i> (B) in Late Stationary				
aas	b2836	0,8153	0,0200	2-acylglycerophosphoethanolamine acyltransferase / acyl-ACP synthetase
accA	b0185	0,6328	0,0126	acetyl CoA carboxylase
asnC	b3743	2,7539	0,0441	AsnC transcriptional dual regulator
astA	b1747	0,3481	0,0052	arginine succinyltransferase
astC	b1748	0,6661	0,0099	acetylornithine transaminase, catabolic / succinylornithine transaminase
b1567	b1567	0,7803	0,0356	hypothetical protein
b3975	b3975	1,3034	0,0341	hypothetical protein
bdm	b1481	0,2891	0,0268	hypothetical protein
ccmA	b2201	1,4349	0,0053	CcmABCDEFGH cytochrome c biogenesis system
clpS	b0881	1,4414	0,0407	specificity factor for ClpA-ClpP chaperone-protease complex
csgG	b1037	0,6187	0,0112	curli production component
cspI	b1552	0,2912	0,0302	cold shock protein CspI
cutC	b1874	0,7767	0,0309	copper homeostasis protein
dcm	b1961	0,6512	0,0238	DNA cytosine methylase
ddlA	b0381	0,7805	0,0467	D-alanine-D-alanine ligase A
degS	b3235	2,0142	0,0342	inner membrane serine protease required for the extracytoplasmic stress response mediated by sigmaE
dkgA	b3012	0,6653	0,0108	beta-keto ester reductase / 2,5-diketo-D-gluconate reductase A
ebgC	b3077	1,2066	0,0412	evolved beta-D-galactosidase, beta subunit; cryptic gene
essQ	b1556	1,3096	0,0194	hypothetical protein
fabZ	b0180	1,3977	0,0405	beta-hydroxyacyl-ACP dehydratase
fdnI	b1476	0,8282	0,0127	formate dehydrogenase N, γ subunit
fimI	b4315	0,6913	0,0188	fimbrial protein
fiu	b0805	0,7727	0,0214	putative outer membrane receptor for iron transport
fixX	b0044	0,8813	0,0500	putative ferredoxin possibly involved in anaerobic carnitine metabolism
folK	b0142	0,7003	0,0449	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase
fruR	b0080	1,5732	0,0110	FruR transcriptional dual regulator
frwD	b3953	1,3246	0,0112	PTS system fructose-like IIB component 2
gadA	b3517	0,1073	0,0024	glutamate decarboxylase A subunit
gadC	b1492	0,2366	0,0330	XasA GABA APC transporter
galU	b1236	0,5670	0,0482	UTP-glucose-1-phosphate uridylyltransferase
glgP	b3428	0,7249	0,0159	glycogen phosphorylase / glycogen-maltotetraose phosphorylase
gntX	b3413	1,4099	0,0310	gluconate periplasmic binding protein
grxA	b0849	0,5770	0,0229	oxidized glutaredoxin
hcaT	b2536	1,3120	0,0486	HcaT MFS transporter
hdeA	b3510	0,0575	0,0020	acid-resistance protein, possible chaperone
hdeB	b3509	0,0572	0,0013	10K-L protein, related to acid resistance protein of <i>Shigella flexneri</i>
hflC	b4175	1,6656	0,0464	regulator of FtsH protease
hlyE	b1182	0,4334	0,0228	hemolysin E
hpt	b0125	1,4604	0,0051	guanine phosphoribosyltransferase / hypoxanthine phosphoribosyltransferase
hybE	b2992	1,5741	0,0491	chaperone in Tat protein export
ibpA	b3687	4,8015	0,0454	small heat shock protein IbpA
ibpB	b3686	27,0211	0,0196	small heat shock protein IbpB
ilvG_1	b3767	0,6880	0,0458	IlvG_1
intB	b4271	1,1609	0,0338	prophage P4 integrase
intZ	b2442	0,6336	0,0499	putative prophage integrase
kefF	b0046	0,7476	0,0460	regulator of KefC-mediated potassium transport
lexA	b4043	1,2491	0,0064	LexA transcriptional repressor
mdtD	b2077	0,7885	0,0485	YegB
metR	b3828	1,2459	0,0091	MetR-Homocysteine transcriptional activator
mntH	b2392	1,3722	0,0434	MntH manganese ion NRAMP transporter
mtn	b0159	1,8303	0,0211	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase monomer
mviN	b1069	1,2873	0,0435	putative virulence factor
nudC	b3996	0,8052	0,0060	putative NAD ⁺ diphosphatase
osmC	b1482	0,7078	0,0028	osmotically inducible peroxidase OsmC
pdxB	b2320	1,2874	0,0306	erythronate-4-phosphate dehydrogenase
pepD	b0237	0,8060	0,0340	peptidase D
phnI	b4099	0,8943	0,0064	phosphonate metabolism
phoA	b0383	0,5971	0,0243	alkaline phosphatase
proY	b0402	0,7097	0,0303	ProY cryptic proline APC transporter
rcsA	b1951	0,6183	0,0022	positive DNA-binding transcriptional regulator of capsular polysaccharide synthesis, activates its own expression
rfaB	b2039	1,4182	0,0327	dTDP-glucose pyrophosphorylase
rhaD	b3902	1,1347	0,0373	rhamnulose-1-phosphate aldolase monomer
rsxG	b1631	1,0943	0,0407	member of SoxR-reducing complex
rzpD	b0556	1,2441	0,0411	bacteriophage lambda endopeptidase homolog
serB	b4388	0,6533	0,0326	phosphoserine phosphatase
srmB	b2576	0,6931	0,0163	SrmB, DEAD-box RNA helicase
sufB	b1683	0,7379	0,0307	component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex

gene	blattner	ratio A/B	p-value	function
tdcC	b3116	0,5550	0,0418	TdcC threonine STP transporter
thiQ	b0066	1,1434	0,0110	SfuC
trpS	b3384	0,7488	0,0006	tryptophanyl-tRNA synthetase
ubiG	b2232	0,7729	0,0299	3-demethylubiquinone 3-methyltransferase / 2-octaprenyl-6-hydroxyphenol methylase
ulaA	b4193	0,8742	0,0352	eiisga
wcaF	b2054	1,2259	0,0176	putative transferase
wza	b2062	0,7309	0,0460	Wza Outer Membrane Auxiliary (OMA) Protein, putative polysaccharide export protein
xapR	b2405	0,3692	0,0027	XapR transcriptional activator
xylA	b3565	0,8740	0,0471	xylose isomerase
yaiY	b0379	0,5364	0,0026	putative membrane protein
ybbJ	b0488	2,0666	0,0366	conserved protein
ybdJ	b0580	0,7815	0,0459	conserved hypothetical protein
ybdO	b0603	0,6554	0,0450	putative transcriptional regulator LYSR-type
ybfC	b0704	0,8179	0,0148	hypothetical protein
ybfD	b0706	0,4459	0,0407	conserved protein
ybfH	b0691	1,2496	0,0152	conserved hypothetical protein
ybhA	b0766	0,8134	0,0431	putative phosphatase
yccV	b0966	2,5767	0,0377	hemimethylated DNA-binding protein
ycfL	b1104	1,3666	0,0057	conserved hypothetical protein
ycfR	b1112	3,1414	0,0148	conserved hypothetical protein
ycfZ	b1121	0,6103	0,0092	homolog of virulence factor
ydcL	b1431	1,4454	0,0141	conserved hypothetical protein
ydcT	b1441	2,1704	0,0408	YdcS/YdcT/YdcV/YdcU ABC transporter
yddE	b1464	1,6330	0,0327	conserved protein
yddL	b1472	0,6888	0,0412	putative outer membrane porin protein
ydeI	b1536	0,2094	0,0105	conserved hypothetical protein
ydiE	b1705	1,3842	0,0087	conserved hypothetical protein
ydiN	b1691	0,7914	0,0208	YdiN MFS transporter
yeaU	b1800	0,8373	0,0483	putative tartrate dehydrogenase
yeaY	b1806	1,6602	0,0487	YeaY-outer membrane lipoprotein
yeiC	b2166	0,6387	0,0344	putative kinase
yeiN	b2165	0,7083	0,0244	conserved protein
yejH	b2184	0,6928	0,0353	putative ATP-dependent helicase
yfdM	b2356	0,8862	0,0233	hypothetical protein
yfdN	b2357	0,5394	0,0352	hypothetical protein
yfdP	b2359	0,8135	0,0108	hypothetical protein
ygaZ	b2682	1,2508	0,0420	hypothetical protein
ygbE	b2749	0,6796	0,0222	putative cytochrome oxidase subunit
ygdQ	b2832	0,6987	0,0374	putative transport protein
ygdR	b2833	1,8619	0,0313	conserved hypothetical protein
ygjJ	b3079	0,8702	0,0362	hypothetical protein
yhdX	b3269	0,8459	0,0481	YhdW/YhdX/YhdY/YhdZ ABC transporter
yhhH	b3483	1,2967	0,0413	hypothetical protein
yhhJ	b3485	1,4754	0,0452	YhiH/YhhJ ABC transporter
yhiK	b3489	0,7613	0,0013	hypothetical protein
yhiM	b3491	0,7525	0,0431	conserved inner membrane protein
yijP	b3955	0,8397	0,0421	hypothetical protein; related to invasion protein of pathogenic E. coli
yjjX	b4394	1,2584	0,0451	conserved hypothetical protein
ypfI	b2474	0,6593	0,0264	putative acyl-CoA N-acyltransferase
yqeA	b2874	0,6229	0,0368	putative carbamate kinase
yqiI	b3071	0,5697	0,0445	conserved hypothetical protein
ytfM	b4220	2,1209	0,0146	hypothetical protein
	b0671	1,2936	0,0166	

LZ41 (A) & LZ54 (B)

acrA	b0463	0,6308	0,0443	AcrA Membrane Fusion Protein
adiA	b4117	1,5642	0,0083	Adi
adk	b0474	0,5809	0,0178	adenylate kinase
agn43	b2000	1,4617	0,0017	outer membrane fluffing protein, sim. to adhesin
apaH	b0049	2,1825	0,0030	diadenosine tetraphosphatase
appC	b0978	1,6125	0,0146	cytochrome bd-II terminal oxidase subunit I
apt	b0469	0,3410	0,0071	adenine phosphoribosyltransferase
argO	b2923	0,5996	0,0187	arginine export protein
argR	b3237	0,8031	0,0265	ArgR transcriptional dual regulator
aroA	b0908	0,5593	0,0075	3-phosphoshikimate-1-carboxyvinyltransferase
aroH	b1704	0,3961	0,0044	2-dehydro-3-deoxyphosphoheptonate aldolase
aroK	b3390	0,7329	0,0170	shikimate kinase I
aroL	b0388	0,5122	0,0004	shikimate kinase II
arsR	b3501	1,5818	0,0001	ArsR transcriptional regulator

gene	blattner	ratio A/B	p-value	function
artQ	b0862	2,3631	0,0195	arginine ABC transporter
asd	b3433	0,4470	0,0376	aspartate semialdehyde dehydrogenase
asnC	b3743	2,1877	0,0338	AsnC transcriptional dual regulator
aspC	b0928	0,7245	0,0228	aspartate transaminase
aspS	b1866	1,7817	0,0499	aspartyl-tRNA synthetase
astD	b1746	1,3761	0,0106	succinylglutamic semialdehyde dehydrogenase
astE	b1744	1,5726	0,0411	succinylglutamate desuccinylase
atoA	b2222	1,7283	0,0293	AtoA / putative acetate CoA-transferase
atpC	b3731	1,4794	0,0280	ATP synthase, F1 complex, epsilon subunit
atpI	b3739	0,5296	0,0433	AtpI
b0165	b0165	0,5418	0,0021	hypothetical protein
b0373	b0373	0,5146	0,0463	hypothetical protein
b0501	b0501	1,1869	0,0303	hypothetical protein
b1354	b1354	1,2688	0,0397	hypothetical protein
b1402	b1402	0,4643	0,0317	IS22 protein
b1500	b1500	0,6253	0,0088	hypothetical protein; gene is in an operon associated with acid resistance
b1578	b1578	0,4580	0,0067	hypothetical protein
b2651	b2651	1,4453	0,0116	hypothetical protein
b3007	b3007	0,6589	0,0484	hypothetical protein
b3044	b3044	0,4584	0,0042	IS21 protein
basS	b4112	1,3828	0,0283	BasS-Phis
bcp	b2480	0,5107	0,0453	thiol peroxidase
bcsC	b3530	0,7130	0,0351	oxidase involved in cellulose synthesis
betI	b0313	0,5288	0,0174	BetI-choline
bglF	b3722	1,3763	0,0041	EIIBgl
bglH	b3720	1,9505	0,0053	putative receptor protein
caiE	b0035	1,6717	0,0488	caiE protein
carB	b0033	0,4703	0,0049	carbamoyl phosphate synthetase
ccmB	b2200	0,8787	0,0430	CcmABCDEFGH cytochrome c biogenesis system
cdd	b2143	1,7025	0,0128	cytidine deaminase
cheR	b1884	1,5095	0,0383	chemotaxis protein methyltransferase
cheW	b1887	1,5265	0,0097	MCP-II
cheY	b1882	1,5736	0,0050	CheY-Pasp
chiA	b3338	1,7647	0,0006	Endochitinase
citC	b0618	1,5867	0,0360	citrate lyase ligase
clcA	b0155	0,5353	0,0200	EriC chloride ion ClC channel
clpB	b2592	3,6839	0,0280	ClpB chaperone
cmr	b0842	0,3146	0,0056	MdfA/Cmr MFS multidrug transporter
coaE	b0103	0,4061	0,0235	dephospho-CoA kinase
cobS	b1992	0,7606	0,0094	cobalamin 5'-phosphate synthase / cobalamin synthase
codA	b0337	0,2755	0,0046	cytosine deaminase
codB	b0336	0,1651	0,0003	CodB cytosine NCS1 transporter
corA	b3816	0,2820	0,0025	CorA magnesium ion MIT transporter
cpdA	b3032	0,5229	0,0466	cAMP phosphodiesterase
creB	b4398	0,3404	0,0081	CreB- Phosphorylated transcriptional regulator
crl	b0240	0,3345	0,0017	Crl transcriptional regulator
crp	b2417	1,2769	0,0161	EIIBCrp
csgF	b1038	0,5393	0,0369	curli assembly component
cspB	b1557	0,2269	0,0473	cold shock protein CspB
cspF	b1558	0,2144	0,0418	cold shock protein CspF
cspG	b0990	0,0764	0,0004	cold shock protein CspG
cstA	b0598	0,5763	0,0340	peptide transporter induced by carbon starvation
cusC	b0572	1,5999	0,0057	outer membrane factor of the CusCFBA copper efflux system
cybB	b1418	0,4129	0,0035	cytochrome b561
cynR	b0338	1,4489	0,0241	CynR-Cyanate transcriptional activator
cysA	b2422	1,4211	0,0004	sulfate ABC transporter
cysG	b3368	1,5439	0,0416	uroporphyrinogen methyltransferase / 1,3-dimethyluroporphyrinogen III dehydrogenase / siroheme ferrochelatase
cysM	b2421	0,5164	0,0458	O-acetylserine (thiol)-lyase B
cysP	b2425	0,6509	0,0424	thiosulfate ABC transporter
cysS	b0526	0,5991	0,0153	cysteinyl-tRNA synthetase
cytR	b3934	0,5115	0,0315	CytR-cytidine
dapA	b2478	0,3715	0,0309	dihydrodipicolinate synthase
dapF	b3809	0,5113	0,0165	diaminopimelate epimerase
ddpX	b1488	1,7864	0,0151	D-Ala-D-Ala dipeptidase
deaD	b3162	0,4180	0,0153	CsdA, DEAD-box RNA helicase
degS	b3235	0,4224	0,0416	inner membrane serine protease required for the extracytoplasmic stress response mediated by sigmaE
deoA	b4382	2,2452	0,0294	thymidine phosphorylase / uracil phosphorylase
deoC	b4381	2,9812	0,0289	deoxyribose-phosphate aldolase
deoD	b4384	1,5761	0,0146	purine nucleoside phosphorylase / guanosine phosphorylase / deoxyguanosine phosphorylase / inosine phosphorylase / deoxyinosine phosphorylase / adenine phosphorylase / deoxyadenosine phosphorylase

gene	blattner	ratio A/B	p-value	function
dgkA	b4042	0,7702	0,0459	diacylglycerol kinase
dnaB	b4052	0,1732	0,0010	chromosome replication; chain elongation; part of primosome
dnaJ	b0015	2,4637	0,0141	chaperone with DnaK; heat shock protein
dnaK	b0014	2,8269	0,0266	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins
dpiB	b0619	0,6511	0,0237	DpiB
dsbC	b2893	0,4949	0,0056	DsbC_{oxidized}
dusA	b4049	0,4059	0,0115	tRNA dihydrouridine synthase
dusB	b3260	0,8122	0,0209	tRNA dihydrouridine synthase
dusC	b2140	0,5406	0,0092	tRNA dihydrouridine synthase
ecfB	b2969	0,7627	0,0191	putative protein exporter (General Secretory Pathway)
ecpD	b0140	2,2895	0,0056	probable pilin chaperone similar to PapD
edd	b1851	1,2374	0,0468	phosphogluconate dehydratase
elaC	b2268	0,5434	0,0212	binuclear zinc phosphodiesterase monomer
endA	b2945	1,2107	0,0482	DNA-specific endonuclease I
eno	b2779	1,5546	0,0318	enolase
entC	b0593	1,4434	0,0295	isochorismate synthase, enterobactin specific
entS	b0591	0,4444	0,0291	YbdA MFS transporter
era	b2566	0,4194	0,0021	GTP-binding protein
eutD	b2458	1,7723	0,0307	putative phosphate acetyltransferase, ethanolamine utilization
eutN	b2456	1,2249	0,0189	putative detox protein, ethanolamine utilization
evgA	b2369	2,8597	0,0440	EvgA-Phosphorylated transcriptional regulator
exbB	b3006	0,4761	0,0222	ExbB protein; uptake of enterochelin; tonB-dependent uptake of B colicins
exuR	b3094	0,5125	0,0127	ExuR transcriptional repressor
fabB	b2323	0,6336	0,0043	beta-ketoacyl-ACP synthase I / malonyl-ACP decarboxylase
fadA	b3845	1,7143	0,0296	3-ketoacyl-CoA thiolase
fbaA	b2925	1,6290	0,0164	fructose bisphosphate aldolase monomer
fdhE	b3891	0,5586	0,0161	protein that affects formate dehydrogenase-N activity
fdnG	b1474	1,3249	0,0138	formate dehydrogenase N, α subunit
fdnI	b1476	1,2886	0,0205	formate dehydrogenase N, γ subunit
fdx	b2525	1,7242	0,0044	oxidized ferredoxin
fecA	b4291	1,5609	0,0011	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fecB	b4290	1,3416	0,0287	ferric dicitrate uptake system
fecE	b4287	1,6438	0,0310	ferric dicitrate uptake system
ffh	b2610	1,2699	0,0362	protein component of the signal recognition particle (SRP)
fhuA	b0150	0,3657	0,0280	FhuA outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuE	b1102	1,2073	0,0239	outer membrane receptor for ferric iron uptake
fis	b3261	0,6869	0,0371	Fis transcriptional dual regulator
fixB	b0042	1,4473	0,0371	probable flavoprotein subunit required for anaerobic carnitine metabolism
fkpB	b0028	0,6004	0,0250	peptidylprolyl isomerase
fldA	b0684	1,4242	0,0442	oxidized flavodoxin I
flgA	b1072	4,8974	0,0024	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgB	b1073	3,8020	0,0007	flagellar basal-body rod protein FlgB
flgC	b1074	3,0031	0,0070	flagellar basal-body rod protein FlgC
flgD	b1075	2,2868	0,0061	flagellar biosynthesis, initiation of hook assembly
flgE	b1076	2,0251	0,0033	flagellar hook protein FlgE
flgF	b1077	3,8985	0,0053	flagellar basal-body rod protein FlgF
flgG	b1078	4,7678	0,0097	flagellar basal-body rod protein FlgG
flgH	b1079	4,1712	0,0007	flagellar L-ring protein FlgH; basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	b1080	3,1896	0,0062	flagellar P-ring protein FlgI
flgJ	b1081	2,6426	0,0051	FlgJ
flgM	b1071	3,2776	0,0167	anti-FliA (anti-sigma) factor; also known as RflB protein
flhD	b1892	0,3694	0,0068	FlhD transcriptional dual regulator
fliJ	b1942	3,5076	0,0196	flagellar biosynthesis protein FliJ
fliY	b1920	1,4499	0,0446	periplasmic cystine-binding protein; member of extracellular bacterial solute-binding protein family III
folA	b0048	0,2448	0,0312	dihydrofolate reductase, type I
folD	b0529	0,6301	0,0126	methyleneTHF enzyme / methenyltetrahydrofolate cyclohydrolase / methylenetetrahydrofolate dehydrogenase-(NADP+)
folE	b2153	0,7792	0,0323	GTP cyclohydrolase I
fre	b3844	1,6941	0,0218	FMN reductase
frlD	b3374	1,3997	0,0269	fructoselysine 6-kinase
frmA	b0356	1,4216	0,0269	formaldehyde dehydrogenase, glutathione-dependent
frsA	b0239	0,3476	0,0375	fermentation/respiration switch protein
fruA	b2167	1,9402	0,0169	EIIIFru
fruB	b2169	3,0732	0,0052	EIIIFru
fruK	b2168	2,8047	0,0036	1-phosphofructokinase monomer
frvA	b3900	1,6136	0,0067	EIIABC Fru
ftsL	b0083	0,6861	0,0288	essential cell division protein FtsL
ftsY	b3464	1,3341	0,0141	SRP receptor
ftsZ	b0095	1,2673	0,0362	essential cell division protein FtsZ
fumB	b4122	1,5703	0,0144	fumarase B monomer

gene	blattner	ratio A/B	p-value	function
fxsA	b4140	1,7993	0,0107	inner membrane protein; overproduction inhibits F exclusion of bacteriophage T7
gabT	b2662	1,3938	0,0210	4-aminobutyrate aminotransferase monomer
galM	b0756	0,4417	0,0141	aldose-1-epimerase
galU	b1236	0,9245	0,0435	UTP-glucose-1-phosphate uridylyltransferase
gapA	b1779	1,5277	0,0455	glyceraldehyde 3-phosphate dehydrogenase-A monomer
gapC_1	b1417	0,3207	0,0054	split glyceraldehyde 3-phosphate dehydrogenase C
gapC_2	b1416	0,3808	0,0072	glyceraldehyde 3-phosphate dehydrogenase C, interrupted
gatA	b2094	1,8580	0,0319	EIIIGat
gcvA	b2808	0,6508	0,0371	GcvA transcriptional dual regulator
gcvH	b2904	0,3188	0,0137	dihydrolipoyl-GcvH-protein
gcvR	b2479	0,2239	0,0056	GcvR-gly
gcvT	b2905	0,3352	0,0343	aminomethyltransferase
gidA	b3741	1,8465	0,0137	protein involved in a tRNA modification pathway
gidB	b3740	1,4613	0,0164	protein with a methyltransferase fold and a possible role in chromosome replication
glgS	b3049	1,4156	0,0496	glycogen biosynthesis, rpoS dependent
glmS	b3729	0,4371	0,0445	L-glutamine:D-fructose-6-phosphate aminotransferase
glmU	b3730	0,2036	0,0015	N-acetylglucosamine-1-phosphate uridylyltransferase / glucosamine-1-phosphate acetyltransferase
glnD	b0167	1,5034	0,0024	uridylyltransferase / uridylyl-removing enzyme
glnH	b0811	3,3975	0,0027	glutamine ABC transporter
glnL	b3869	0,6764	0,0331	NtrB
glnP	b0810	2,5879	0,0108	glutamine ABC transporter
glnQ	b0809	2,8329	0,0290	glutamine ABC transporter
glpD	b3426	0,5911	0,0107	glycerol 3-phosphate dehydrogenase, aerobic
glpG	b3424	0,4628	0,0143	inner membrane-associated protein of glp regulon
gltJ	b0654	1,6394	0,0293	glutamate ABC transporter
gltS	b3653	0,4306	0,0171	glutamate GltS transporter
glvB	b3682	0,6799	0,0498	subunit of EIIBCGLv
glyA	b2551	0,4848	0,0252	glycine hydroxymethyltransferase
gnd	b2029	1,3868	0,0122	6-phosphogluconate dehydrogenase (decarboxylating)
gntR	b3438	1,6774	0,0056	GntR-gluconate
gntY	b3414	2,1327	0,0397	predicted membrane-bound protein that is involved in high-affinity gluconate transport
gph	b3385	2,2255	0,0008	phosphoglycolate phosphatase
gpt	b0238	0,2560	0,0022	xanthine phosphoribosyltransferase / guanine phosphoribosyltransferase / hypoxanthine phosphoribosyltransferase
groL	b4143	4,0315	0,0048	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
grpE	b2614	2,5774	0,0005	phage lambda replication; host DNA synthesis; heat shock protein; protein repair
gshB	b2947	0,5455	0,0014	glutathione synthetase subunit
gspL	b3333	1,6779	0,0357	putative protein secretion protein for export
gssA	b2988	1,2719	0,0207	glutathionylspermidine synthetase / glutathionylspermidine amidase
guaB	b2508	0,4094	0,0161	IMP dehydrogenase
gutQ	b2708	0,8036	0,0386	protein with a sugar isomerase domain
gyrA	b2231	2,0736	0,0147	DNA gyrase, subunit A
gyrB	b3699	2,3694	0,0125	DNA gyrase, subunit B
hdeA	b3510	1,5879	0,0430	acid-resistance protein, possible chaperone
hdeB	b3509	1,4411	0,0245	10K-L protein, related to acid resistance protein of Shigella flexneri
hemC	b3805	0,2280	0,0041	hydroxymethylbilane synthase
hemD	b3804	0,3594	0,0026	uroporphyrinogen III synthase
hemN	b3867	0,5050	0,0222	coproporphyrinogen III oxidase, anaerobic
hisC	b2021	0,4224	0,0011	histidine-phosphate aminotransferase
hisD	b2020	0,2929	0,0068	histidinal dehydrogenase / histidinol dehydrogenase
hisS	b2514	0,4605	0,0043	histidyl-tRNA synthetase
holA	b0640	1,5856	0,0127	DNA polymerase III, delta subunit
holC	b4259	0,3684	0,0138	DNA polymerase III, chi subunit
holD	b4372	1,2748	0,0169	DNA polymerase III, psi subunit
holE	b1842	0,3028	0,0133	DNA polymerase III, theta subunit
hscA	b2526	1,3123	0,0271	chaperone, member of Hsp70 protein family
hslO	b3401	2,2344	0,0459	molecular chaperone Hsp33
hslR	b3400	2,1711	0,0238	heat shock protein Hsp15
hslU	b3931	2,3896	0,0292	ATPase component of the HslVU protease
htrA	b0161	1,4630	0,0500	DegP
htrL	b3618	6,3708	0,0079	involved in lipopolysaccharide biosynthesis
hupA	b4000	1,7633	0,0170	DNA-binding protein HU-alpha (HU-2)
hyaA	b0972	3,0036	0,0427	hydrogenase I, HyaA subunit
hycC	b2723	1,5122	0,0284	HycC
hypF	b2712	1,3499	0,0196	hydrogenase maturation protein
ibpA	b3687	2,4960	0,0181	small heat shock protein IbpA
icdA	b1136	0,4590	0,0372	Icd
ilvB	b3671	0,2982	0,0162	IlvB / putative 2-hydroxyglutarate synthase
ilvD	b3771	0,4038	0,0384	dihydroxy-acid dehydratase
ilvE	b3770	0,6301	0,0172	branched chain amino acid aminotransferase

gene	blattner	ratio A/B	p-value	function
ilvG_1	b3767	0,1723	0,0016	IlvG_1
ilvM	b3769	0,2445	0,0021	acetohydroxybutanoate synthase II / acetolactate synthase II
imp	b0054	0,4662	0,0012	organic solvent tolerance
inaA	b2237	0,3959	0,0046	pH-inducible protein involved in stress response
intR	b1345	0,2726	0,0058	putative transposase
iscA	b2528	1,4419	0,0027	iron-sulfur cluster assembly protein
iscR	b2531	1,4496	0,0114	IscR transcriptional regulator
iscS	b2530	1,4231	0,0277	cysteine desulfurase monomer
iscX	b2524	1,5162	0,0325	protein with possible role in iron-sulfur cluster biogenesis
ispA	b0421	0,1884	0,0089	geranyl diphosphate synthase / farnesyl diphosphate synthase
ispB	b3187	0,5571	0,0115	octaprenyl diphosphate synthase
ispD	b2747	0,5815	0,0136	4-diphosphocytidyl-2C-methyl-D-erythritol synthetase monomer
ispG	b2515	0,3474	0,0431	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
kdgT	b3909	0,3451	0,0140	KdgT 2-keto-3-deoxygluconate transporter
kdpA	b0698	1,6937	0,0216	potassium ion P-type ATPase transporter
kdpB	b0697	0,8031	0,0119	potassium ion P-type ATPase transporter
kdpD	b0695	1,5142	0,0271	KdpD-Phis
kdsC	b3198	0,4227	0,0092	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase monomer
kdtA	b3633	0,4096	0,0361	KDO transferase
lamB	b4036	2,1449	0,0483	phage lambda receptor protein; maltose high-affinity receptor
ldcA	b1192	0,6533	0,0323	L,D-carboxypeptidase A
lepA	b2569	0,3884	0,0089	GTP-binding elongation factor, may be inner membrane protein
leuA	b0074	0,5502	0,0232	2-isopropylmalate synthase
leuD	b0071	0,8324	0,0343	isopropylmalate isomerase
leuO	b0076	0,4671	0,0383	LeuO transcriptional activator
ligT	b0147	0,3612	0,0043	hypothetical protein
lipB	b0630	1,8242	0,0342	lipoyl-protein ligase
lolB	b1209	0,4537	0,0046	outer membrane lipoprotein, localization of lipoproteins in the outer membrane
lolC	b1116	0,4315	0,0356	LolCDE ABC lipoprotein transporter
lolD	b1117	0,6023	0,0038	LolCDE ABC lipoprotein transporter
lolE	b1118	0,4199	0,0393	LolCDE ABC lipoprotein transporter
lon	b0439	2,0180	0,0071	DNA-binding, ATP-dependent protease La
lpcA	b0222	0,3721	0,0282	lipopolysaccharide core biosynthesis; phosphoheptose isomerase
lpxK	b0915	1,3126	0,0035	tetraacyldisaccharide 4'-kinase
lrhA	b2289	0,7251	0,0129	LrhA transcriptional repressor
lspA	b0027	0,5579	0,0203	prolipoprotein signal peptidase (SPase II)
maa	b0459	0,6307	0,0483	maltose acetyltransferase
macB	b0879	1,5831	0,0121	MacAB macrolide efflux transporter complex
manA	b1613	0,5844	0,0131	mannose-6-phosphate isomerase
mdtK	b1663	0,4735	0,0183	NorE multidrug efflux MATE transporter
menD	b2264	0,4174	0,0067	putative 2-hydroxyglutarate synthase / SHCHC synthase / 2-oxoglutarate decarboxylase
menF	b2265	0,2973	0,0031	isochorismate synthase, menaquinone-specific
mepA	b2328	1,3493	0,0164	murein DD-endopeptidase, penicillin-insensitive
metB	b3939	0,4626	0,0078	O-succinylhomoserine lyase / O-succinylhomoserine(thiol)-lyase
metL	b3940	1,7369	0,0443	aspartate kinase II / homoserine dehydrogenase II
mfd	b1114	0,8365	0,0468	transcription-repair coupling factor; mutation frequency decline
mhpD	b0350	1,8046	0,0472	2-keto-4-pentenoate hydratase
mhpE	b0352	1,4561	0,0483	4-hydroxy-2-ketovaleate aldolase
miaA	b4171	0,7647	0,0368	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase
minC	b1176	0,2576	0,0099	cell division inhibitor of the MinC-MinD-MinE and DicB-MinC systems that regulate septum placement
minD	b1175	0,3669	0,0070	membrane ATPase of the MinC-MinD-MinE system that regulates septum placement
minE	b1174	0,3218	0,0180	cell division topological specificity factor and inhibitory component of the MinC-MinD-MinE system that regulates septum placement
mioC	b3742	2,8032	0,0061	flavoprotein involved in biotin synthesis
mltC	b2963	0,3174	0,0208	membrane-bound lytic murein transglycosylase C
mngB	b0732	1,4808	0,0136	alpha-mannosidase
moaA	b0781	0,3113	0,0250	molybdopterin biosynthesis, protein A
modE	b0761	0,5883	0,0400	Molybdate-responsive transcription factor monomer
mokC	b0018	1,6023	0,0201	regulatory peptide whose translation enables hokC (gef) expression
mraW	b0082	0,6100	0,0309	S-adenosyl-dependent methyltransferase
mrdB	b0634	0,6931	0,0113	rod shape-determining membrane protein; sensitivity to radiation and drugs
mreB	b3251	0,4151	0,0130	rod shape-determining protein
mreC	b3250	0,5547	0,0187	rod shape-determining protein
mreD	b3249	0,4030	0,0041	rod shape-determining protein
msbB	b1855	0,2631	0,0138	myristoyl acyltransferase
mukE	b0923	0,2778	0,0005	protein involved in chromosome partitioning
mukF	b0922	0,2472	0,0062	Ca2+-binding protein involved in chromosome partitioning
mutY	b2961	0,2826	0,0046	adenine glycosylase; G.C --> T.A transversions
nadA	b0750	1,2867	0,0026	quinolinate synthetase A
nagZ	b1107	0,3709	0,0144	β-N-acetylglucosaminidase

gene	blattner	ratio A/B	p-value	function
nanR	b3226	0,6046	0,0191	NanR transcriptional regulator
narG	b1224	1,4419	0,0422	nitrate reductase A, α subunit
narP	b2193	0,4244	0,0046	NarP-Phosphorylated transcriptional regulator
ndh	b1109	0,2794	0,0021	NADH cupric reductase / NADH dehydrogenase II
ndk	b2518	0,5490	0,0297	nucleoside diphosphate kinase / UDP kinase / CDP kinase / dUDP kinase / dCDP kinase / dTDP kinase / dADP kinase / dGDP kinase / GDP kinase
nhaA	b0019	2,7531	0,0189	sodium/proton NhaA transporter
nhaR	b0020	1,8006	0,0051	NhaR-Na ⁺ transcriptional activator
nirD	b3366	1,2750	0,0385	nitrite reductase, small subunit
nlpB	b2477	0,3204	0,0188	lipoprotein-34
nlpC	b1708	0,8276	0,0132	NlpC-putative lipoprotein hydrolase
nlpD	b2742	0,4725	0,0091	NlpD putative outer membrane lipoprotein
npr	b3206	1,1115	0,0239	phosphocarrier protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I, Hpr
nth	b1633	2,1070	0,0198	endonuclease III; specific for apurinic and/or apyrimidinic sites
nudF	b3034	0,4112	0,0010	hypothetical protein
nudG	b1759	0,6794	0,0394	CTP pyrophosphohydrolase
nudH	b2830	0,4781	0,0025	putative invasion protein
nuoA	b2288	1,6603	0,0436	NADH dehydrogenase I
nuoB	b2287	2,1552	0,0017	NADH dehydrogenase I
nuoC	b2286	1,5429	0,0056	NADH dehydrogenase I
nuoE	b2285	1,4073	0,0195	NADH dehydrogenase I
nuoF	b2284	1,6783	0,0075	NADH dehydrogenase I
nusB	b0416	0,5649	0,0227	transcription termination; L factor
nusG	b3982	0,1716	0,0023	component in transcription antitermination
ogrK	b2082	1,8738	0,0121	OgrK transcriptional regulator
ompX	b0814	1,3900	0,0297	outer membrane protein X
osmB	b1283	1,9992	0,0416	OsmB osmotically inducible lipoprotein
oxyR	b3961	3,1506	0,0058	OxyR transcriptional dual regulator
paaJ	b1397	1,4298	0,0499	putative beta-keto-thiolase of phenylacetate degradation
pabA	b3360	1,4655	0,0359	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
pabC	b1096	0,3015	0,0413	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
pagP	b0622	2,7254	0,0221	PagP monomer
panB	b0134	0,5034	0,0001	3-methyl-2-oxobutanoate hydroxymethyltransferase monomer
panF	b3258	0,6070	0,0178	PanF sodium/pantothenate SSS transporter
parC	b3019	0,3991	0,0037	Topoisomerase IV subunit A
pcnB	b0143	0,5626	0,0040	poly(A) polymerase I
pdxH	b1638	0,5820	0,0297	pyridoxine 5'-phosphate oxidase / pyridoxamine 5'-phosphate oxidase
pepB	b2523	1,8383	0,0128	aminopeptidase (AP)
pepP	b2908	1,2182	0,0368	proline aminopeptidase P II
pepQ	b3847	2,4602	0,0335	proline dipeptidase
pfkB	b1723	1,4328	0,0085	6-phosphofructokinase-2 monomer
pflA	b0902	2,1225	0,0090	pyruvate formate-lyase activating enzyme
pgaC	b1022	1,4003	0,0250	predicted N-glycosyltransferase
pgi	b4025	0,7116	0,0462	phosphoglucose isomerase
pgpA	b0418	0,5727	0,0094	phosphatidylglycerophosphatase A
pheP	b0576	0,4252	0,0250	PheP phenylalanine APC transporter
phoE	b0241	1,3013	0,0094	PhoE
phoH	b1020	1,4888	0,0191	PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation
phoP	b1130	0,4417	0,0115	PhoP-Phosphorylated transcriptional dual regulator
phoQ	b1129	0,6685	0,0013	PhoQ-Phis
pitB	b2987	1,3798	0,0445	PitB
plsC	b3018	0,3763	0,0024	1-acylglycerol-3-phosphate acyltransferase
pmbA	b4235	0,5564	0,0213	protease involved in Microcin B17 maturation and in sensitivity to the DNA gyrase inhibitor LetD
pmrD	b2259	0,4652	0,0050	polymyxin resistance protein
pncB	b0931	0,2923	0,0110	nicotinate phosphoribosyltransferase
pnp	b3164	0,2968	0,0110	polynucleotide phosphorylase
polB	b0060	4,3621	0,0499	DNA polymerase II
potB	b1125	0,5130	0,0375	putrescine/spermidine ABC transporter
potC	b1124	0,5813	0,0046	putrescine/spermidine ABC transporter
poxA	b4155	0,5427	0,0338	putative regulator of pyruvate oxidase
ppiD	b0441	0,6513	0,0198	peptidyl-prolyl cis-trans isomerase
ppk	b2501	0,3301	0,0114	polyphosphate kinase
ppsA	b1702	0,7593	0,0328	phosphoenolpyruvate synthase
priC	b0467	0,5875	0,0232	primosomal replication protein N"
prmC	b1212	0,7663	0,0275	protein-(glutamine-N5) methyltransferase
proP	b4111	0,4204	0,0214	ProP proline/betaine MFS transporter
proQ	b1831	0,5181	0,0394	protein that affects osmoregulation of ProP transporter
proV	b2677	0,3005	0,0108	proline ABC transporter
proW	b2678	0,3934	0,0291	proline ABC transporter
psd	b4160	0,5710	0,0213	phosphatidylserine decarboxylase, proenzyme

gene	blattner	ratio A/B	p-value	function
pspB	b1305	1,6459	0,0420	stimulates PspC-mediated transcriptional activation of the psp operon; antitoxin of a PspC-PspB toxin-antitoxin pair
pssA	b2585	0,1873	0,0040	phosphatidylserine synthase
purA	b4177	0,5024	0,0178	adenylosuccinate synthase
purB	b1131	0,6679	0,0119	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase / adenylosuccinate lyase
purC	b2476	0,1510	0,0007	phosphoribosylaminoimidazole-succinocarboxamide synthase
purE	b0523	0,3132	0,0136	N5-carboxyaminoimidazole ribonucleotide mutase
purF	b2312	0,2208	0,0011	amidophosphoribosyl transferase
purK	b0522	0,2617	0,0039	N5-carboxyaminoimidazole ribonucleotide synthase monomer
purM	b2499	0,0976	0,0007	phosphoribosylformylglycinamide cyclo-ligase
purN	b2500	0,3565	0,0063	phosphoribosylglycinamide formyltransferase
purR	b1658	0,1999	0,0032	PurR transcriptional repressor
purT	b1849	0,5923	0,0436	GAR transformylase 2
purU	b1232	0,4050	0,0031	formyltetrahydrofolate deformylase
puuD	b1298	0,6547	0,0166	probable amidotransferase subunit
pyrB	b4245	0,4134	0,0108	aspartate carbamoyltransferase, PyrB subunit
pyrC	b1062	0,6009	0,0278	dihydroorotase
pyrD	b0945	0,3694	0,0012	dihydroorotate oxidase
radA	b4389	0,5088	0,0089	DNA recombination protein
rbfA	b3167	0,7704	0,0239	ribosome-binding factor A
rbsB	b3751	2,1321	0,0323	ribose ABC transporter
rscB	b2217	0,5589	0,0202	RcsB transcriptional activator
rscC	b2218	0,6588	0,0017	RcsC-Phis
rdgC	b0393	0,4658	0,0035	nonspecific DNA binding protein; nucleoid component
recA	b2699	6,1477	0,0006	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
recF	b3700	1,5026	0,0018	ssDNA and dsDNA binding, ATP binding
recN	b2616	5,2322	0,0003	protein used in recombination and DNA repair
recX	b2698	3,3785	0,0128	inhibitor of RecA
relA	b2784	0,6144	0,0009	GDP pyrophosphokinase / GTP pyrophosphokinase
rfaE	b3052	1,6731	0,0393	putative kinase
rfaH	b3842	0,6886	0,0257	RfaH transcriptional regulator
rfaI	b3627	3,7837	0,0015	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
rfaJ	b3626	3,0420	0,0174	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaK	b3623	3,1584	0,0170	lipopolysaccharide core biosynthesis; probably hexose transferase
rfaS	b3629	2,8794	0,0068	lipopolysaccharide core biosynthesis
rfaZ	b3624	3,4532	0,0385	protein involved in KdoIII attachment during lipopolysaccharide core biosynthesis
rfbB	b2041	0,7441	0,0376	RmlB
rhlB	b3780	0,5316	0,0049	ATP-dependent RNA helicase of the RNA degradosome
rhlE	b0797	0,2790	0,0010	DEAD-box-containing ATP-dependent RNA helicase family member
rhsD	b0497	0,5670	0,0166	RhsD protein in rhs element
ribB	b3041	0,4644	0,0229	3,4-dihydroxy-2-butanone 4-phosphate synthase
ribC	b1662	0,6318	0,0401	riboflavin synthase
ribF	b0025	0,1259	0,0103	riboflavin kinase / FMN adenylyltransferase
rihA	b0651	1,8484	0,0409	ribonucleoside hydrolase I (pyrimidine-specific)
rimJ	b1066	0,4103	0,0066	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
rluC	b1086	0,3153	0,0041	23S rRNA pseudouridine synthase
rluD	b2594	0,7043	0,0136	23S rRNA pseudouridine synthase
rluE	b1135	1,6545	0,0240	23S rRNA pseudouridine synthase
rnc	b2567	0,2112	0,0002	RNase III, ds RNA
rng	b3247	0,7647	0,0261	ribonuclease G (RNase G) monomer
rmhA	b0214	0,3725	0,0125	RNase HI, degrades RNA of DNA-RNA hybrids, participates in DNA replication
rnr	b4179	0,5088	0,0147	RNase R
rplY	b2185	1,4198	0,0156	50S ribosomal subunit protein L25
rpmE	b3936	1,9883	0,0287	50S ribosomal subunit protein L31
rpoA	b3295	1,7187	0,0281	RNA polymerase, alpha subunit
rpoH	b3461	1,5408	0,0047	sigma32 factor
rpsJ	b3321	1,7179	0,0451	30S ribosomal subunit protein S10
rpsL	b3342	1,3159	0,0319	30S ribosomal subunit protein S12
rpsU	b3065	2,0799	0,0248	30S ribosomal subunit protein S21
rspA	b1581	2,2521	0,0444	starvation sensing protein RspA
rspB	b1580	1,2583	0,0486	putative dehydrogenase RspB
rssA	b1234	0,2763	0,0088	hypothetical protein
rsuA	b2183	0,3324	0,0011	16S rRNA pseudouridine synthase
rsxE	b1632	1,6861	0,0192	integral membrane protein of SoxR-reducing complex
sdaC	b2796	0,5269	0,0174	SdaC serine STP transporter
sdhA	b0723	1,8472	0,0183	succinate dehydrogenase flavoprotein
sdhB	b0724	2,4021	0,0348	succinate dehydrogenase iron-sulfur protein
secE	b3981	0,1598	0,0033	Sec Protein Secretion Complex
secF	b0409	0,8540	0,0394	Sec Protein Secretion Complex
secG	b3175	0,3039	0,0132	Sec Protein Secretion Complex

gene	blattner	ratio A/B	p-value	function
selA	b3591	0,7449	0,0144	selenocysteine synthase monomer
sgbH	b3581	1,2423	0,0155	3-keto-L-gulonate 6-phosphate decarboxylase
sieB	b1353	0,8425	0,0185	phage superinfection exclusion protein
slt	b4392	0,6966	0,0171	soluble lytic murein transglycosylase
slyA	b1642	0,4284	0,0138	SlyA transcriptional activator
slyB	b1641	0,4100	0,0358	putative outer membrane protein
slyD	b3349	1,3580	0,0393	FKBP-type rotamase, peptidyl prolyl cis-trans isomerase
smf	b4473	0,6389	0,0144	hypothetical protein
smg	b3284	0,3104	0,0016	hypothetical protein
smpA	b2617	3,0746	0,0330	SmpA small membrane protein A
smtA	b0921	0,1732	0,0009	S-adenosylmethionine-dependent methyltransferase
speG	b1584	0,4151	0,0001	spermidine acetyltransferase
spr	b2175	0,1856	0,0008	putative lipoprotein
spy	b1743	1,8051	0,0064	periplasmic protein related to spheroblast formation
srnB	b2576	0,1828	0,0018	SrnB, DEAD-box RNA helicase
sscR	b2765	0,2846	0,0014	putative 6-pyruvoyl tetrahydrobiopterin synthase
sspA	b3229	1,7853	0,0360	regulator of transcription; stringent starvation protein A
sspB	b3228	1,6995	0,0121	SspB monomer
sthA	b3962	1,9483	0,0152	soluble pyridine nucleotide transhydrogenase
sucA	b0726	1,7723	0,0282	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
suhB	b2533	0,6030	0,0333	inositol monophosphatase
sulA	b0958	0,4776	0,0294	suppressor of lon; inhibits cell division and ftsZ ring formation
syd	b2793	0,7172	0,0401	interacts with secY
tdcD	b3115	1,3690	0,0028	propionate kinase / acetate kinase C
tdcE	b3114	1,8820	0,0225	2-ketobutyrate formate-lyase / pyruvate formate-lyase 4
tdh	b3616	1,6683	0,0198	threonine dehydrogenase
tesA	b0494	0,4861	0,0342	lysophospholipase L₁ / thioesterase I
thiI	b0423	0,3635	0,0002	ThiI protein
thyA	b2827	1,6662	0,0186	thymidylate synthase
tpiA	b3919	1,1555	0,0049	triose phosphate isomerase monomer
tra5-5	b2089	0,5946	0,0481	
treB	b4240	1,9360	0,0274	EII _{Tre}
treC	b4239	1,8400	0,0022	trehalose-6-phosphate hydrolase
trkA	b3290	1,6751	0,0358	TrkA
trkG	b1363	1,7115	0,0118	TrkG potassium ion Trk Transporter
trmD	b2607	1,4999	0,0322	tRNA (guanine-1-)-methyltransferase
trpB	b1261	0,8425	0,0438	tryptophan synthase, beta subunit
trpD	b1263	0,5060	0,0140	anthranilate synthase component II
trpE	b1264	0,4037	0,0115	anthranilate synthase component I
trpL	b1265	0,7864	0,0299	trp operon leader peptide
trpR	b4393	1,7569	0,0049	TrpR transcriptional repressor
trpS	b3384	2,1106	0,0124	tryptophanyl-tRNA synthetase
tsgA	b3364	0,6442	0,0017	YhfC MFS transporter
tsr	b4355	0,6068	0,0399	MCP-I
tsx	b0411	0,1946	0,0016	nucleoside channel; receptor of phage T6 and colicin K
ttk	b3641	0,4174	0,0019	Ttk transcriptional regulator
ubiC	b4039	0,2098	0,0001	chorismate pyruvate lyase
ubiF	b0662	1,5458	0,0334	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase
ubiG	b2232	0,7780	0,0016	3-demethylubiquinone 3-methyltransferase / 2-octaprenyl-6-hydroxyphenol methylase
uhpB	b3668	0,5983	0,0403	UhpB-Phis
uidA	b1617	1,2711	0,0362	beta-glucuronidase
ulaE	b4197	0,7571	0,0368	L-xylulose 5-phosphate 3-epimerase
ulaF	b4198	0,7998	0,0198	L-ribulose 5-phosphate 4-epimerase
ung	b2580	0,6029	0,0221	uracil-DNA-glycosylase
upp	b2498	0,4553	0,0208	uracil phosphoribosyltransferase
uvrB	b0779	1,9034	0,0153	DNA repair; excision nuclease subunit B
vacJ	b2346	0,6153	0,0168	putative lipoprotein
visC	b2906	1,7240	0,0071	hypothetical protein
waaP	b3630	1,9894	0,0370	lipopolysaccharide core biosynthesis; phosphorylation of core heptose
wbbI	b2034	1,6114	0,0023	hypothetical protein; not required for colanic acid biosynthesis
wbbK	b2032	1,3531	0,0045	putative transferase
wcaA	b2059	1,5321	0,0226	putative regulator
wcaB	b2058	1,4575	0,0374	putative transferase
wcaD	b2056	1,6890	0,0022	putative colanic acid polymerase
wcaJ	b2047	1,6790	0,0013	putative colanic acid biosynthesis UDP-glucose lipid carrier transferase
wza	b2062	1,3425	0,0424	Wza Outer Membrane Auxiliary (OMA) Protein, putative polysaccharide export protein
xapR	b2405	0,7902	0,0250	XapR transcriptional activator
xerD	b2894	0,4150	0,0016	site-specific recombinase
xseB	b0422	0,1805	0,0061	exonuclease VII, small subunit

gene	blattner	ratio A/B	p-value	function
xylR	b3569	0,5246	0,0295	XylR-Xylose transcriptional activator
yabP	b0056	0,4221	0,0292	conserved hypothetical protein
yafK	b0224	0,1376	0,0369	conserved protein; in enteroaggregative E. coli, YafK is required for development of biofilms
yagA	b0267	1,6600	0,0302	hypothetical protein
yagI	b0272	0,3762	0,0042	putative regulator
yagT	b0286	1,5660	0,0376	putative oxidoreductase, Fe-S subunit
yagU	b0287	1,2317	0,0268	conserved protein
ybaJ	b0461	0,2544	0,0048	conserved hypothetical protein
ybaN	b0468	0,3530	0,0019	hypothetical protein
ybaO	b0447	1,2709	0,0229	putative LRP-like transcriptional regulator
ybaV	b0442	0,5407	0,0434	conserved hypothetical protein
ybbO	b0493	0,6285	0,0137	putative oxidoreductase
ybcJ	b0528	0,5730	0,0490	putative RNA-binding protein
ybcK	b0544	1,1512	0,0052	hypothetical protein
ybeA	b0636	0,4138	0,0056	conserved hypothetical protein
ybeB	b0637	0,4743	0,0070	conserved hypothetical protein
ybeD	b0631	2,5488	0,0424	conserved hypothetical protein
ybeY	b0659	3,2204	0,0213	conserved hypothetical protein
ybeZ	b0660	3,8440	0,0151	putative ATP-binding protein
ybfF	b0686	0,4315	0,0108	putative enzyme
ybhK	b0780	0,2522	0,0010	putative structural protein
ybhO	b0789	1,6209	0,0479	cardiolipin synthase 2
ybiR	b0818	0,5665	0,0479	YbiR
ybjC	b0850	0,5750	0,0491	conserved hypothetical protein; gene is within soxRS regulon
ycaL	b0909	0,5299	0,0354	putative heat shock protein
ycbG	b0956	0,5827	0,0116	putative dehydrogenase
ycbK	b0926	0,4469	0,0152	conserved hypothetical protein
ycbQ	b0938	1,9263	0,0170	putative fimbrial-like protein
ycbR	b0939	1,8020	0,0084	putative chaperone
yccA	b0970	0,4983	0,0427	putative carrier/transport protein; substrate or modulator of FtsH-mediated proteolysis
yccF	b0961	0,5456	0,0466	conserved hypothetical protein
yccJ	b1003	1,1693	0,0345	hypothetical protein
yedF	b1005	0,5798	0,0023	hypothetical protein
yedZ	b1036	0,8246	0,0257	putative transport protein
yceB	b1063	1,4666	0,0413	conserved hypothetical protein
yceG	b1097	0,2704	0,0009	putative thymidylate kinase (EC 2.7.4.9)
yceH	b1067	0,4580	0,0122	conserved hypothetical protein
yceO	b1058	0,6506	0,0348	hypothetical protein
yefJ	b1110	0,4082	0,0338	hypothetical protein
yefP	b1108	0,4708	0,0147	putative hydrolase
yefR	b1112	0,3787	0,0147	conserved hypothetical protein
yefT	b1115	1,5947	0,0302	putative transport protein
yegH_2	b1170	1,9107	0,0317	conserved protein; member of the Autotransporter family
yegL	b1179	0,3430	0,0036	conserved hypothetical protein
yegM	b1180	0,4324	0,0364	putative isomerase
yegN	b1181	0,2587	0,0108	conserved hypothetical protein
yegR	b1194	1,3756	0,0420	protein involved in flagellar function
yegZ	b1164	0,4255	0,0168	hypothetical protein
yehF	b1203	1,6270	0,0442	putative GTP-binding protein
yehJ	b1233	0,3905	0,0170	conserved hypothetical protein
yehQ	b1213	0,6472	0,0161	hypothetical protein
yeiS	b1279	0,4349	0,0229	conserved hypothetical protein
ycjD	b1289	1,2011	0,0454	conserved hypothetical protein
ycjG	b1325	0,4835	0,0125	L-Ala-D/L-Glu epimerase, a muconate lactonizing enzyme
ycjR	b1314	1,8315	0,0473	putative epimerase/isomerase
ycjT	b1316	1,1203	0,0476	putative enzyme
ycjX	b1321	4,0841	0,0141	putative EC 2.1 enzyme
ydaO	b1344	0,2434	0,0148	conserved protein
ydbA_1	b1401	0,7691	0,0006	hypothetical protein product of fragment 1 of a split CDS
ydbA_2	b1405	0,7077	0,0491	hypothetical protein product of fragment 2 of a split CDS
ydcT	b1441	0,4358	0,0233	YdcS/YdcT/YdcV/YdcU ABC transporter
ydcX	b1445	2,3184	0,0377	hypothetical protein
yddE	b1464	0,7336	0,0245	conserved protein
ydeA	b1528	0,2041	0,0058	YdeA MFS transporter
ydeJ	b1537	1,4392	0,0057	conserved protein
ydeK	b1510	0,4875	0,0351	YdeK
ydfN	b1547	1,3671	0,0077	hypothetical protein
ydfT	b1559	1,3152	0,0336	hypothetical protein
ydfX	b1568	1,3846	0,0254	hypothetical protein

gene	blattner	ratio A/B	p-value	function
ydgH	b1604	0,4280	0,0237	conserved hypothetical protein
ydgT	b1625	0,1702	0,0097	conserved hypothetical protein
ydhA	b1639	0,6550	0,0304	conserved hypothetical protein
ydhH	b1640	0,4726	0,0304	conserved hypothetical protein
ydhI	b1643	0,3978	0,0137	hypothetical protein
ydiA	b1703	0,3178	0,0056	conserved protein
ydiO	b1695	1,6655	0,0206	putative acyl-CoA dehydrogenase
ydiR	b1698	1,8979	0,0320	putative subunit of YdiQ-YdiR flavoprotein
ydjG	b1771	1,3397	0,0169	putative oxidoreductase
yeaD	b1780	1,7584	0,0268	conserved hypothetical protein
yeaE	b1781	0,4205	0,0018	putative oxidoreductase, NAD(P)-linked
yeaZ	b1807	0,4660	0,0019	hypothetical protein
yebC	b1864	1,6986	0,0245	conserved protein
yebF	b1847	2,0516	0,0108	conserved hypothetical protein
yebG	b1848	2,3442	0,0088	hypothetical protein; gene is part of SOS regulon
yebK	b1853	0,5355	0,0044	hypothetical protein
yebN	b1821	0,4945	0,0468	putative membrane protein, terpenoid synthase-like
yebR	b1832	0,2435	0,0027	conserved hypothetical protein
yebY	b1839	0,4488	0,0070	conserved hypothetical protein
yebZ	b1840	0,5229	0,0048	putative resistance protein
yecD	b1867	0,4582	0,0236	putative enzyme
yecN	b1869	0,1959	0,0051	putative membrane protein
yecO	b1870	0,2973	0,0060	putative methyltransferase
yecP	b1871	0,4271	0,0274	putative enzyme
yedF	b1930	1,6425	0,0395	conserved hypothetical protein; might bind RNA
yedI	b1958	0,5069	0,0041	hypothetical protein
yedK	b1931	1,5169	0,0377	conserved hypothetical protein
yedR	b1963	0,5416	0,0326	hypothetical protein
yedS_2	b1965	1,4927	0,0201	putative outer membrane protein
yeeE	b2013	0,2863	0,0317	putative transport system permease protein
yeeN	b1983	9,6166	0,0005	conserved protein
yeeP	b1999	0,6937	0,0431	putative histone
yeeT	b2003	1,9457	0,0049	hypothetical protein
yeeZ	b2016	0,8883	0,0272	putative enzyme of sugar metabolism
yegD	b2069	0,2637	0,0019	actin family protein
yegR	b2085	1,5686	0,0058	hypothetical protein
yegW	b2101	0,6534	0,0191	putative transcriptional regulator
yegX	b2102	0,4954	0,0096	putative hydrolase
yegZ	b2083	1,3932	0,0173	hypothetical protein
yehM	b2120	1,2804	0,0220	conserved hypothetical protein
yeiG	b2154	1,0945	0,0217	putative esterase (EC 3.1.1.-).
yeiR	b2173	0,5560	0,0087	putative enzyme
yeiU	b2174	0,2626	0,0007	putative permease
yfaD	b2244	1,4122	0,0462	hypothetical protein
yfaH	b2238	1,2445	0,0457	hypothetical protein
yfaV	b2246	1,1332	0,0162	YfaV
yfbP	b2275	1,5584	0,0337	hypothetical protein
yfcE	b2300	1,5089	0,0198	putative metallo-dependent phosphatase
yfcF	b2301	1,2969	0,0213	putative glutathione S-transferase
yfdK	b2354	1,7437	0,0090	hypothetical protein
yfdS	b2362	1,4456	0,0350	hypothetical protein
yfeA	b2395	0,4562	0,0281	putative membrane protein
yfeR	b2409	0,9066	0,0367	putative transcriptional regulator LYSR-type
yfgA	b2516	0,3313	0,0004	putative membrane protein
yfgB	b2517	0,5090	0,0150	putative pyruvate formate lyase activating enzyme 2
yfgM	b2513	0,5801	0,0186	conserved protein
yfhG	b2555	0,2721	0,0038	conserved protein
yfhL	b2562	0,2394	0,0380	putative ferredoxin
yfiC	b2575	0,0971	0,0043	putative enzyme
yfiF	b2581	0,3560	0,0086	hypothetical protein
yfiH	b2593	0,6179	0,0045	conserved hypothetical protein
yfjG	b2619	1,8649	0,0277	toxin of a putative toxin-antitoxin pair
yfjH	b2623	0,8041	0,0238	putative histone
yfjM	b2629	0,7850	0,0144	hypothetical protein
ygaH	b2683	0,2149	0,0002	putative transport protein
ygaZ	b2682	0,2232	0,0059	hypothetical protein
ygcG	b2778	1,3701	0,0023	putative membrane protein
ygcL	b2760	1,1770	0,0296	hypothetical protein with possible relationship to novobiocin and deoxycholate resistance
ygdD	b2807	0,3655	0,0005	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ygdK	b2811	0,5579	0,0386	conserved hypothetical protein
ygeA	b2840	0,6668	0,0082	putative resistance protein
ygeW	b2870	1,5976	0,0306	putative carbamoyl transferase
ygfS	b2886	1,6634	0,0453	putative oxidoreductase, Fe-S subunit
ygfZ	b2898	0,4766	0,0063	conserved protein
yggD	b2929	0,6247	0,0483	putative transcriptional regulator
yggH	b2960	0,3658	0,0154	tRNA (m7G46) methyltransferase
yggJ	b2946	0,5829	0,0022	conserved hypothetical protein
yggL	b2959	0,3754	0,0018	conserved hypothetical protein
yggN	b2958	0,4816	0,0155	conserved hypothetical protein
yggR	b2950	1,3249	0,0011	putative protein transport
yggT	b2952	0,6371	0,0193	putative resistance protein
yggU	b2953	0,6630	0,0123	conserved hypothetical protein
yggX	b2962	0,2253	0,0002	conserved hypothetical protein with role in oxidation-resistance of iron-sulfur clusters
yghQ	b2983	1,1911	0,0240	putative serine protease
ygiD	b3039	1,3052	0,0295	putative enzyme with dioxygenase domain
ygiR	b3015	0,5716	0,0207	
ygiD	b3064	0,5170	0,0195	putative O-sialoglycoprotein endopeptidase
ygiK	b3080	1,6347	0,0393	putative isomerase
ygiO	b3084	0,2990	0,0067	hypothetical methyltransferase
ygiR	b3087	0,7899	0,0217	putative NAD(P)-binding dehydrogenase
yhaC	b3121	1,3252	0,0082	conserved protein
yhaL	b3107	1,5740	0,0103	hypothetical protein
yhbY	b3180	1,3778	0,0003	possible RNA-binding protein
yhcB	b3233	0,3045	0,0076	conserved hypothetical protein
yhcD	b3216	1,2268	0,0167	putative outer membrane protein
yhcM	b3232	0,5048	0,0277	hypothetical protein
yhdA	b3252	0,2359	0,0129	conserved protein
yhdJ	b3262	1,4149	0,0321	cell cycle-regulated methyltransferase
yheN	b3345	0,7700	0,0372	conserved hypothetical protein
yheO	b3346	0,6517	0,0156	hypothetical protein
yhfK	b3358	1,2451	0,0042	hypothetical protein
yhfP	b3372	1,6321	0,0166	
yhfY	b3382	1,4063	0,0453	conserved protein
yhhF	b3465	0,5337	0,0473	putative methyltransferase
yhhQ	b3471	0,5279	0,0413	hypothetical protein; gene is a predicted member of the purine regulon
yhhW	b3439	1,2975	0,0352	conserved hypothetical protein
yhiQ	b3497	1,2301	0,0328	putative methyltransferase
yhjE	b3523	1,3547	0,0178	YhjE MFS transporter
yhjW	b3546	0,4600	0,0499	putative transmembrane protein
yhjY	b3548	1,4042	0,0366	putative lipase
viaU	b3585	1,7518	0,0059	putative transcriptional regulator LYSR-type
yibJ	b3595	1,6482	0,0413	hypothetical protein
yibK	b3606	0,6207	0,0426	hypothetical protein
yicE	b3654	0,1109	0,0096	YicE NCS2 transporter
yidB	b3698	0,6946	0,0443	conserved hypothetical protein
yieG	b3714	0,1975	0,0106	putative membrane / transport protein
yieH	b3715	0,3625	0,0303	putative enzyme with a phosphatase-like domain
yieK	b3718	1,6885	0,0200	putative 6-phosphogluconolactonase
yifK	b3795	0,5430	0,0211	YifK APC transporter
yihI	b3866	0,2921	0,0024	conserved protein
yihL	b3872	1,4923	0,0255	YihL transcriptional regulator
yihO	b3876	1,6352	0,0233	YihO GPH transporter
yihU	b3882	1,3139	0,0204	putative dehydrogenase
yjaH	b4001	0,7337	0,0240	conserved protein
yjbE	b4026	1,7450	0,0047	conserved hypothetical protein
yjdA	b4109	0,1906	0,0022	hypothetical protein
yjeB	b4178	0,2074	0,0020	conserved protein with a Winged helix domain
yjeH	b4141	0,5607	0,0389	YjeH APC transporter
yjeK	b4146	0,3898	0,0150	hypothetical protein
yjgA	b4234	0,4405	0,0253	putative transport protein (ABC superfamily, atp_bind)
yjgP	b4261	0,3739	0,0266	putative transmembrane protein possibly involved in transport
yjiA	b4352	1,5128	0,0062	P-loop guanosine triphosphatase
yjjW	b4379	1,3791	0,0400	putative activating enzyme
ykfG	b0247	1,6946	0,0353	putative DNA repair protein
ykgE	b0306	0,7957	0,0470	putative dehydrogenase subunit
ykgH	b0310	1,6076	0,0086	conserved protein
ylaC	b0458	3,0304	0,0296	putative membrane protein
ylbE	b0519	1,2920	0,0327	conserved protein

gene	blattner	ratio A/B	p-value	function
yliI	b0837	1,4805	0,0023	putative dehydrogenase
ymcD	b0987	1,4309	0,0262	hypothetical protein
ymjA	b1295	0,3256	0,0039	hypothetical protein
yncD	b1451	1,8939	0,0328	Probable TonB-dependent receptor
yneG	b1523	1,1789	0,0050	conserved hypothetical protein
ynfB	b1583	0,3934	0,0061	conserved hypothetical protein
ynfD	b1586	2,2054	0,0346	conserved hypothetical protein
ynfN	b1551	0,8465	0,0196	hypothetical protein
ynhG	b1678	1,3503	0,0343	putative ATP synthase subunit
yoaB	b1809	0,6240	0,0129	conserved protein
yobA	b1841	0,3019	0,0058	hypothetical protein
yobF	b1824	2,0754	0,0274	hypothetical protein
ypdF	b2385	1,4856	0,0415	putative peptidase
ypfI	b2475	0,2824	0,0036	conserved protein
ypjC	b2650	1,8240	0,0458	hypothetical protein
ypjE	b2613	1,5857	0,0110	
yqaA	b2689	0,4979	0,0431	putative integral membrane protein
yqaB	b2690	0,4069	0,0160	putative phosphoglucomutase that contains a phosphatase-like domain
yqcD	b2794	0,6900	0,0288	conserved hypothetical protein
yqfA	b2899	0,6159	0,0239	putative oxidoreductase
yqfB	b2900	0,4738	0,0088	conserved hypothetical protein
yqiA	b3031	0,5976	0,0359	putative hydrolase
yqiB	b3033	0,4189	0,0462	putative enzyme
yqiH	b3047	2,4661	0,0276	putative membrane protein
yqjC	b3097	1,5209	0,0227	conserved protein
yqjD	b3098	1,5220	0,0102	conserved hypothetical protein
yraI	b3143	1,3222	0,0262	putative chaperone
yraM	b3147	0,5303	0,0388	putative glycosylase
yrbH	b3197	0,5469	0,0155	arabinose 5-phosphate isomerase monomer
yrbL	b3207	0,2776	0,0169	conserved hypothetical protein; transcription is regulated by Mg ²⁺
yrdD	b3283	0,4003	0,0038	putative DNA topoisomerase
ytfK	b4217	0,6795	0,0081	hypothetical protein
zipA	b2412	0,3991	0,0357	essential cell division protein ZipA
zitB	b0752	1,9751	0,0090	ZitB zinc CDF transporter
znuA	b1857	0,5007	0,0149	ZnuA/ZnuB/ZnuC ABC transporter
znuC	b1858	1,5621	0,0156	ZnuA/ZnuB/ZnuC ABC transporter

LZ41_{fis} (A) & LZ54_{fis} (B)

aaeB	b3240	1,2701	0,0129	hypothetical protein
adk	b0474	0,5852	0,0267	adenylate kinase
adrA	b0385	1,5751	0,0281	putative membrane protein
agaB	b3138	1,6067	0,0201	EIIAga
agaD	b3140	2,4760	0,0490	EIIAga
agn43	b2000	1,9466	0,0365	outer membrane fluffing protein, sim. to adhesin
allC	b0516	2,6899	0,0373	allantoate amidohydrolase
alpA	b2624	0,5764	0,0288	AlpA transcriptional activator
alr	b4053	0,2726	0,0082	alanine racemase, minor
alsK	b4084	1,8614	0,0254	putative D-allose kinase
apaH	b0049	1,3196	0,0053	diadenosine tetraphosphatase
appC	b0978	1,8506	0,0232	cytochrome bd-II terminal oxidase subunit I
aqpZ	b0875	0,4831	0,0077	AqpZ - water MIP channel
aroA	b0908	0,6666	0,0280	3-phosphoshikimate-1-carboxyvinyltransferase
aroB	b3389	0,6970	0,0352	3-dehydroquinate synthase
arsR	b3501	2,0062	0,0043	ArsR transcriptional regulator
artI	b0863	2,0420	0,0102	arginine ABC transporter
artP	b0864	1,6630	0,0391	arginine ABC transporter
ascB	b2716	0,4567	0,0314	6-phospho-beta-glucosidase; cryptic
ascF	b2715	0,3701	0,0083	EIIAsc
ascG	b2714	0,2203	0,0292	AscG transcriptional regulator
asd	b3433	0,3109	0,0249	aspartate semialdehyde dehydrogenase
astE	b1744	1,9337	0,0209	succinylglutamate desuccinylase
atpB	b3738	0,5641	0,0218	ATP synthase, F0 complex, a subunit
atpC	b3731	1,8372	0,0366	ATP synthase, F1 complex, epsilon subunit
atpI	b3739	0,5233	0,0310	AtpI
b0165	b0165	0,4909	0,0269	hypothetical protein
b0255	b0255	0,3208	0,0410	hypothetical protein
b1172	b1172	2,5087	0,0177	conserved hypothetical protein
b1364	b1364	1,8486	0,0389	hypothetical protein
b1402	b1402	0,6370	0,0207	IS22 protein

gene	blattner	ratio A/B	p-value	function
b2084	b2084	2,3089	0,0387	hypothetical protein
b2680	b2680	0,6069	0,0111	YgaY MFS transporter
b3808	b3808	0,4513	0,0034	hypothetical protein
b4283	b4283	0,3477	0,0343	IS911 protein
b4339	b4339	0,4301	0,0234	hypothetical protein
bax	b3570	0,4668	0,0105	putative ATP-binding protein
bcp	b2480	0,3972	0,0258	thiol peroxidase
bcsG	b3538	1,5125	0,0251	putative membrane protein
bdm	b1481	0,4571	0,0254	hypothetical protein
betI	b0313	0,4422	0,0145	BetI-choline
bglF	b3722	2,3222	0,0326	EIIBgl
btuD	b1709	0,4855	0,0190	vitamin B12 transport system
caiC	b0037	2,6932	0,0083	carnitine-CoA ligase / crotonobetaine-CoA ligase
caiT	b0040	1,9407	0,0255	CaiT carnitine BCCT transporter
carA	b0032	0,1987	0,0003	carbamoyl phosphate synthetase
carB	b0033	0,5195	0,0297	carbamoyl phosphate synthetase
cbpM	b0999	0,7011	0,0474	chaperone-modulator protein CbpM
cdaR	b0162	0,2974	0,0285	SdaR transcriptional regulator
chaA	b1216	1,8253	0,0435	ChaA calcium CaCA transporter
cheW	b1887	1,4429	0,0031	MCP-II
cheY	b1882	1,4736	0,0153	CheY-Pasp
citD	b0617	2,1690	0,0098	subunit of acyl carrier protein
citE	b0616	1,3927	0,0367	subunit of citryl-ACP lyase
citF	b0615	1,5300	0,0418	subunit of citrate-ACP transferase
clcA	b0155	0,5515	0,0298	EriC chloride ion ClC channel
clpB	b2592	1,6744	0,0098	ClpB chaperone
clpS	b0881	0,5757	0,0045	specificity factor for ClpA-ClpP chaperone-protease complex
cmr	b0842	0,3828	0,0352	MdfA/Cmr MFS multidrug transporter
coaA	b3974	0,2063	0,0077	pantothenate kinase monomer
cobC	b0638	2,5183	0,0233	alpha-ribazole-5'-P phosphatase
cobT	b1991	0,6766	0,0163	dimethylbenzimidazole phosphoribosyltransferase
cpsG	b2048	1,7548	0,0421	phosphomannomutase
cpxR	b3912	0,3442	0,0296	CpxR-Phosphorylated transcriptional dual regulator
creA	b4397	0,2676	0,0054	hypothetical protein
creB	b4398	0,1607	0,0018	CreB- Phosphorylated transcriptional regulator
creC	b4399	0,4234	0,0038	CreC-Phis
crl	b0240	0,2018	0,0046	Crl transcriptional regulator
csgA	b1042	1,4150	0,0203	curlin, major subunit
csgC	b1043	0,4527	0,0035	putative curli production protein
csgD	b1040	0,5255	0,0417	CsgD transcriptional activator
csiE	b2535	0,1601	0,0201	hypothetical protein
cspA	b3556	0,1189	0,0043	cold shock protein CspA
cspB	b1557	0,0902	0,0121	cold shock protein CspB
cspF	b1558	0,0878	0,0007	cold shock protein CspF
cspG	b0990	0,1566	0,0211	cold shock protein CspG
cusR	b0571	0,2240	0,0067	CusR transcriptional activator
cusS	b0570	0,3579	0,0313	putative 2-component sensor protein
cutE	b0657	2,6030	0,0037	apolipoprotein N-acyltransferase
cvpA	b2313	0,1480	0,0030	membrane protein required for colicin V production
cyaY	b3807	0,6324	0,0031	iron-binding frataxin homolog
cysE	b3607	0,5219	0,0143	cysteine synthase
cysM	b2421	0,3365	0,0109	O-acetylserine (thiol)-lyase B
cytR	b3934	0,2132	0,0070	CytR-cytidine
dam	b3387	1,5263	0,0296	DNA adenine methylase
dapF	b3809	0,3456	0,0309	diaminopimelate epimerase
dcm	b1961	0,3666	0,0421	DNA cytosine methylase
dcuS	b4125	0,5027	0,0194	DcuS-Phis349
degQ	b3234	0,4658	0,0158	serine endoprotease
degS	b3235	0,3105	0,0028	inner membrane serine protease required for the extracytoplasmic stress response mediated by sigmaE
deoR	b0840	0,2578	0,0132	DeoR transcriptional repressor
dgkA	b4042	0,4758	0,0169	diacylglycerol kinase
dgoA	b3692	1,8315	0,0260	dgoA 3871635-3871018 : '2-dehydro-3-deoxyphosphogalactonate aldolase / dgoD 3871021-3869873 : galactonate dehydratase
dgt	b0160	0,1774	0,0119	deoxyguanosinetriphosphate triphosphohydrolase
dhaK	b1200	0,4352	0,0455	dihydroxyacetone kinase subunit K
dhaR	b1201	0,2678	0,0011	putative 2-component regulator
diaA	b3149	0,2334	0,0190	DiaA protein
dinB	b0231	1,7171	0,0272	DNA polymerase IV (Y-family DNA polymerase; translesion DNA synthesis)
dmsA	b0894	2,2635	0,0076	dimethyl sulfoxide reductase, chain A
dnaB	b4052	0,1982	0,0057	chromosome replication; chain elongation; part of primosome

gene	blattner	ratio A/B	p-value	function
dnaG	b3066	2,1643	0,0067	DNA biosynthesis; DNA primase
dnaJ	b0015	2,9351	0,0192	chaperone with DnaK; heat shock protein
dsbC	b2893	0,4666	0,0342	DsbC_{oxidized}
dusB	b3260	0,2969	0,0469	tRNA dihydrouridine synthase
dxr	b0173	1,4221	0,0086	DXP reductoisomerase
dxs	b0420	0,3652	0,0190	1-deoxyxylulose-5-phosphate synthase
ecfB	b2969	0,5313	0,0451	putative protein exporter (General Secretory Pathway)
ecfI	b3688	0,3510	0,0497	conserved hypothetical protein with possible extracytoplasmic function
eda	b1850	1,7908	0,0038	oxaloacetate decarboxylase / 2-keto-3-deoxy-6-phosphogluconate aldolase / 2-keto-4-hydroxyglutarate aldolase
elaC	b2268	0,6163	0,0010	binuclear zinc phosphodiesterase monomer
emrE	b0543	1,6186	0,0068	EmrE SMR transporter
epd	b2927	0,5294	0,0315	erythrose 4-phosphate dehydrogenase
eutB	b2441	1,2809	0,0329	ethanolamine ammonia-lyase, probable regulatory subunit
eutH	b2452	1,4972	0,0336	putative transport protein, ethanolamine utilization
eutT	b2459	1,3095	0,0136	putative cobalamine adenosyltransferase, ethanolamine utilization
evgA	b2369	0,3168	0,0144	EvgA-Phosphorylated transcriptional regulator
exoX	b1844	0,5678	0,0038	exonuclease X
exuR	b3094	0,3228	0,0132	ExuR transcriptional repressor
fabI	b1288	1,6863	0,0303	enoyl-ACP reductase (NAD[P]H) / enoyl-ACP reductase (NADPH) / enoyl-ACP reductase (NADH)
fadJ	b2341	0,3121	0,0367	FadJ monomer
fdnI	b1476	1,7767	0,0053	formate dehydrogenase N, γ subunit
fhiA	b0229	1,5449	0,0317	flagellar biosynthesis
fhuB	b0153	2,1649	0,0409	ferrichrome uptake system
fhuF	b4367	1,7515	0,0482	acts in reduction of ferrioxamine B iron
fic	b3361	1,4568	0,0439	stationary-phase protein with possible role in p-aminobenzoate or folate biosynthesis
fimE	b4313	1,7756	0,0279	regulator for fimA
fixB	b0042	2,0297	0,0368	probable flavoprotein subunit required for anaerobic carnitine metabolism
flgF	b1077	2,2351	0,0239	flagellar basal-body rod protein FlgF
flgG	b1078	1,9647	0,0136	flagellar basal-body rod protein FlgG
flgI	b1080	1,7273	0,0119	flagellar P-ring protein FlgI
flgJ	b1081	2,1703	0,0020	FlgJ
flgN	b1070	2,3245	0,0287	flagellar biosynthesis protein FlgN
flhB	b1880	1,8348	0,0063	flagellar biosynthesis protein FlhB
flhC	b1891	0,1181	0,0079	FlhC transcriptional regulator
flhD	b1892	0,0774	0,0260	FlhD transcriptional dual regulator
fliC	b1923	0,5536	0,0223	flagellar biosynthesis; flagellin, filament structural protein
fliD	b1924	0,3745	0,0118	flagellar cap protein FliD; filament capping protein; enables filament assembly
fliG	b1939	1,9682	0,0326	flagellar motor switch protein FliG; component of motor switching and energizing, enabling rotation and determining its direction
fliI	b1941	2,4306	0,0107	flagellum-specific ATP synthase FliI
fliK	b1943	2,1579	0,0307	flagellar hook-length control protein FliK
fliR	b1950	5,8099	0,0221	flagellar biosynthesis protein FliR
fliS	b1925	0,5073	0,0341	flagellar biosynthesis protein FliS
fnr	b1334	3,9209	0,0118	FNR transcriptional dual regulator
focA	b0904	0,6551	0,0243	FocA formate FNT transporter
focB	b2492	0,2494	0,0129	FocB formate FNT transporter
folA	b0048	0,2106	0,0098	dihydrofolate reductase, type I
frdD	b4151	2,4605	0,0058	fumarate reductase membrane protein
frlA	b3370	1,6878	0,0011	YhfM methionine APC transporter
frlB	b3371	1,7603	0,0228	fructoselysine 6-phosphate deglycase monomer
frlR	b3375	0,5910	0,0107	putative transcriptional regulator
frmA	b0356	1,7397	0,0295	formaldehyde dehydrogenase, glutathione-dependent
frmB	b0355	2,7771	0,0194	putative S-formylglutathione hydrolase
frsA	b0239	0,3854	0,0052	fermentation/respiration switch protein
fruR	b0080	0,2985	0,0085	FruR transcriptional dual regulator
frwD	b3953	1,4822	0,0450	PTS system fructose-like IIB component 2
fryA	b2383	1,3141	0,0080	putative PTS system enzyme IIA component, enzyme I
fsaB	b3946	1,4734	0,0059	fructose 6-phosphate aldolase 2
ftsB	b2748	0,2075	0,0061	essential cell division protein FtsB
ftsQ	b0093	1,2917	0,0493	essential cell division protein FtsQ
ftsW	b0089	1,9956	0,0151	essential cell division protein FtsW
fxsA	b4140	1,9361	0,0366	inner membrane protein; overproduction inhibits F exclusion of bacteriophage T7
gadE	b3512	1,2316	0,0070	GadE transcriptional activator
gadW	b3515	1,9617	0,0376	GadWtranscriptional repressor
gadX	b3516	2,3498	0,0110	GadX transcriptional activator
galE	b0759	1,3965	0,0349	UDP-glucose 4-epimerase monomer
galM	b0756	0,5556	0,0412	aldose-1-epimerase
galR	b2837	0,3381	0,0120	GalR-galactose
gatY	b2096	0,2247	0,0190	tagatose-1,6-bisphosphate aldolase 2
gcvH	b2904	0,1838	0,0232	dihydrolipoyl-GcvH-protein

gene	blattner	ratio A/B	p-value	function
gcvR	b2479	0,2803	0,0150	GcvR-gly
gcvT	b2905	0,1397	0,0379	aminomethyltransferase
glcD	b2979	1,4604	0,0131	glycolate oxidase subunit D
glf	b2036	1,4061	0,0231	UDP-galactopyranose mutase
glgA	b3429	2,0868	0,0462	glycogen synthase
glmS	b3729	0,6548	0,0257	L-glutamine:D-fructose-6-phosphate aminotransferase
glnD	b0167	1,4223	0,0065	uridylyltransferase / uridylyl-removing enzyme
glnE	b3053	0,7644	0,0097	glutamine synthetase adenylyltransferase / glutamine synthetase deadenylylating enzyme
gloA	b1651	1,7203	0,0236	glyoxalase I
glpD	b3426	0,6000	0,0106	glycerol 3-phosphate dehydrogenase, aerobic
glpE	b3425	0,3290	0,0046	thiosulfate sulfurtransferase
glpF	b3927	0,5645	0,0474	GlpF - glycerol MIP channel
glpG	b3424	0,2077	0,0184	inner membrane-associated protein of glp regulon
gltF	b3214	1,8806	0,0235	regulator of gltBDF operon, induction of Ntr enzymes
gltL	b0652	1,8842	0,0056	glutamate ABC transporter
gltP	b4077	0,7136	0,0418	GltP glutamate/aspartate DAACS transporter
glyA	b2551	0,3875	0,0034	glycine hydroxymethyltransferase
gntY	b3414	2,7979	0,0384	predicted membrane-bound protein that is involved in high-affinity gluconate transport
gpp	b3779	0,4360	0,0260	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase
groL	b4143	2,3507	0,0471	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
grpE	b2614	2,3641	0,0303	phage lambda replication; host DNA synthesis; heat shock protein; protein repair
grxC	b3610	0,4843	0,0071	oxidized glutaredoxin 3
gshB	b2947	0,5134	0,0198	glutathione synthetase subunit
gspE	b3326	1,8012	0,0127	putative protein secretion protein for export
gspH	b3329	1,2960	0,0067	putative protein secretion protein for export
gspI	b3330	1,3340	0,0008	putative protein secretion protein for export
gspJ	b3331	2,1075	0,0087	putative protein secretion protein for export
gssA	b2988	1,7232	0,0036	glutathionylspermidine synthetase / glutathionylspermidine amidase
guaA	b2507	0,7222	0,0199	GMP synthase / GMP synthase (ammonia dependent)
gyrB	b3699	2,5880	0,0017	DNA gyrase, subunit B
hcaB	b2541	1,2806	0,0246	3-phenylpropionate-2',3'-dihydrodiol dehydrogenase
hcaD	b2542	1,6383	0,0207	ferredoxin NAD ⁺ reductase
hcaE	b2538	0,5174	0,0278	3-phenylpropionate dioxygenase, alpha subunit
hcr	b0872	2,8116	0,0329	NADH oxidoreductase
hdeD	b3511	2,0630	0,0226	protein involved in acid resistance
hdfR	b4480	0,3225	0,0184	transcriptional regulator
hemC	b3805	0,4388	0,0311	hydroxymethylbilane synthase
hemG	b3850	0,4767	0,0075	protoporphyrinogen oxidase
hemH	b0475	1,6086	0,0151	ferrochelataase
hemN	b3867	0,4698	0,0211	coproporphyrinogen III oxidase, anaerobic
hflD	b1132	0,4773	0,0130	membrane protein in operon with purB
hha	b0460	0,3786	0,0126	haemolysin expression modulating protein
hipB	b1508	0,0870	0,0061	HipB transcriptional activator
hmp	b2552	1,8564	0,0046	nitric oxide dioxygenase / dihydropteridine reductase 2
hofN	b3394	0,3123	0,0307	conserved protein
holA	b0640	2,0348	0,0021	DNA polymerase III, delta subunit
holB	b1099	1,5205	0,0029	DNA polymerase III, delta prime subunit
holC	b4259	0,5840	0,0321	DNA polymerase III, chi subunit
holE	b1842	0,2431	0,0003	DNA polymerase III, theta subunit
hscC	b0650	1,6203	0,0217	Hsc62; an Hsp70-family ATPase that negatively regulates sigma70 / non-chaperonin molecular chaperone ATPase
hslU	b3931	4,1300	0,0123	ATPase component of the HslVU protease
htpG	b0473	1,8306	0,0130	HtpG monomer
htrL	b3618	6,9782	0,0063	involved in lipopolysaccharide biosynthesis
hyaA	b0972	2,2684	0,0027	hydrogenase I, HyaA subunit
hybF	b2991	1,6921	0,0285	protein involved with the maturation of hydrogenases 1 and 2
hycE	b2721	2,0488	0,0454	formate hydrogenlyase complex
iaaA	b0828	0,1133	0,0019	beta cleavage product of IaaA
ibpA	b3687	4,2244	0,0016	small heat shock protein IbpA
ibpB	b3686	7,6875	0,0014	small heat shock protein IbpB
icdA	b1136	0,3462	0,0100	Icd
iclR	b4018	0,2325	0,0125	IclR-PEP
idnR	b4264	0,2909	0,0338	IdnR-5-ketogluconate
idnT	b4265	0,3169	0,0249	IdnT idonate Gnt transporter
ihfB	b0912	1,9863	0,0061	IHF transcriptional dual regulator
ilvA	b3772	0,4362	0,0424	threonine dehydratase (biosynthetic)
inaA	b2237	0,2907	0,0071	pH-inducible protein involved in stress response
insA_5	b1894	0,3935	0,0446	insA_5 1977239-1976964 : IS1 protein InsA / insA_1 20508-20233 : IS1 protein InsA / insA_6 3581506-3581781 : IS1 protein InsA
intR	b1345	0,2551	0,0239	putative transposase
intS	b2349	1,9457	0,0169	putative prophage Sf6-like integrase

gene	blattner	ratio A/B	p-value	function
iscU	b2529	1,8083	0,0053	scaffold protein involved in iron-sulfur cluster assembly
ispA	b0421	0,1813	0,0151	geranyl diphosphate synthase / farnesyl diphosphate synthase
ispD	b2747	0,4908	0,0411	4-diphosphocytidyl-2C-methyl-D-erythritol synthetase monomer
katE	b1732	1,7021	0,0305	hydroperoxidase II
kdtA	b3633	0,3601	0,0028	KDO transferase
kduD	b2842	1,5255	0,0331	2-deoxy-D-gluconate 3-dehydrogenase
kefG	b3351	1,3584	0,0057	KefG
ldcA	b1192	1,7002	0,0372	L,D-carboxypeptidase A
leuB	b0073	1,7972	0,0055	3-isopropylmalate dehydrogenase
leuC	b0072	1,6773	0,0000	isopropylmalate isomerase
leuD	b0071	2,0207	0,0112	isopropylmalate isomerase
ligT	b0147	0,1852	0,0026	hypothetical protein
lipB	b0630	2,1877	0,0000	lipoyl-protein ligase
livH	b3457	1,9033	0,0131	leucine ABC transporter
livM	b3456	1,6094	0,0498	leucine ABC transporter
lolA	b0891	0,7885	0,0361	periplasmic chaperone, effects translocation of lipoproteins from inner membrane to outer
lolB	b1209	0,4806	0,0227	outer membrane lipoprotein, localization of lipoproteins in the outer membrane
lolE	b1118	0,4575	0,0420	LolCDE ABC lipoprotein transporter
lon	b0439	2,6981	0,0091	DNA-binding, ATP-dependent protease La
lpcA	b0222	0,2400	0,0125	lipopolysaccharide core biosynthesis; phosphoheptose isomerase
lrp	b0889	0,4179	0,0402	Lrp-Leucine transcriptional activator
lsrG	b1518	1,4543	0,0022	conserved hypothetical protein
lysA	b2838	1,7920	0,0487	diaminopimelate decarboxylase
macB	b0879	2,0724	0,0127	MacAB macrolide efflux transporter complex
malT	b3418	0,1905	0,0107	MalT-MalK
malY	b1622	0,4203	0,0185	bifunctional: repressor of maltose regulon / cystathionine beta-lyase
mdl	b0449	2,7100	0,0423	MdlB
mdoC	b1047	0,1432	0,0145	protein required for succinyl modification of osmoregulated periplasmic glucans
mdoH	b1049	1,6043	0,0230	membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO)
mdtF	b3514	1,8716	0,0244	YhiV
mdtN	b4082	2,2488	0,0020	putative membrane protein
mdtO	b4081	1,5951	0,0435	YjcQ
menD	b2264	0,3726	0,0138	putative 2-hydroxyglutarate synthase / SHCHC synthase / 2-oxoglutarate decarboxylase
menF	b2265	0,3477	0,0276	isochorismate synthase, menaquinone-specific
mfd	b1114	0,5650	0,0126	transcription-repair coupling factor; mutation frequency decline
mhpF	b0351	1,8446	0,0238	acetaldehyde dehydrogenase 2
minC	b1176	0,2414	0,0115	cell division inhibitor of the MinC-MinD-MinE and DicB-MinC systems that regulate septum placement
minD	b1175	0,4152	0,0065	membrane ATPase of the MinC-MinD-MinE system that regulates septum placement
minE	b1174	0,3703	0,0160	cell division topological specificity factor and inhibitory component of the MinC-MinD-MinE system that regulates septum placement
mioC	b3742	1,6938	0,0341	flavoprotein involved in biotin synthesis
mliC	b2963	0,4421	0,0091	membrane-bound lytic murein transglycosylase C
mmuP	b0260	0,3741	0,0038	MmuP APC transporter
mnmC	b2324	0,5136	0,0357	bifunctional enzyme catalyzing the formation of mnm5s2U in tRNA
mntH	b2392	0,3161	0,0066	MntH manganese ion NRAMP transporter
moaA	b0781	0,2797	0,0039	molybdopterin biosynthesis, protein A
mobA	b3857	0,2268	0,0063	molybdopterin guanine dinucleotide synthase
mobB	b3856	0,7633	0,0125	molybdopterin-guanine dinucleotide biosynthesis protein B
modE	b0761	0,3788	0,0052	Molybdate-responsive transcription factor monomer
moeB	b0826	2,0014	0,0025	molybdopterin biosynthesis
mpaA	b1326	0,4207	0,0207	murein peptide amidase A
mrr	b4351	0,4108	0,0084	restriction of methylated adenine
msbB	b1855	0,2154	0,0023	myristoyl acyltransferase
mtlD	b3600	0,3066	0,0272	mannitol-1-phosphate 5-dehydrogenase
mukE	b0923	0,3600	0,0166	protein involved in chromosome partitioning
mukF	b0922	0,2126	0,0048	Ca ²⁺ -binding protein involved in chromosome partitioning
murI	b3967	2,6898	0,0094	glutamate racemase
murP	b2429	0,3862	0,0083	MurP
mutY	b2961	0,3526	0,0252	adenine glycosylase; G.C --> T.A transversions
mviM	b1068	0,7293	0,0284	putative virulence factor
nadD	b0639	2,8386	0,0006	nicotinate-mononucleotide adenyllyltransferase
nadR	b4390	0,5652	0,0094	NadR transcriptional repressor / NMN adenyllyltransferase
nanR	b3226	0,2529	0,0184	NanR transcriptional regulator
narQ	b2469	1,8665	0,0482	NarQ-Phis
narV	b1465	1,9002	0,0087	nitrate reductase Z, γ subunit
nfnB	b0578	0,7030	0,0451	dihydropteridine reductase
nfrB	b0569	0,4153	0,0012	bacteriophage N4 receptor, outer membrane protein
nhaA	b0019	1,9281	0,0447	sodium/proton NhaA transporter
nhaR	b0020	2,4259	0,0270	NhaR-Na ⁺ transcriptional activator
nikA	b3476	2,3805	0,0063	nickel ABC transporter

gene	blattner	ratio A/B	p-value	function
nikR	b3481	1,4287	0,0386	NikR-Ni
nirB	b3365	1,6021	0,0034	nitrite reductase, large subunit
nth	b1633	2,2184	0,0022	endonuclease III; specific for apurinic and/or apyrimidinic sites
nudD	b2051	1,8515	0,0395	GDP-mannose mannosyl hydrolase
nudF	b3034	0,3009	0,0092	hypothetical protein
nuoL	b2278	2,3112	0,0467	NADH dehydrogenase I
osmC	b1482	1,9756	0,0398	osmotically inducible peroxidase OsmC
osmE	b1739	1,3600	0,0369	OsmE-osmotically inducible protein
pabB	b1812	0,1391	0,0082	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
panE	b0425	0,4718	0,0353	2-dehydropanoate reductase
parC	b3019	0,5366	0,0439	Topoisomerase IV subunit A
pbpG	b2134	0,2733	0,0252	penicillin-binding protein 7
pepB	b2523	2,0445	0,0308	aminopeptidase (AP)
pflA	b0902	2,2414	0,0213	pyruvate formate-lyase activating enzyme
pgsA	b1912	0,5084	0,0407	phosphatidylglycerophosphate synthase
phnE	b4104	1,3120	0,0044	alkylphosphonate ABC transporter
phnG	b4101	2,1147	0,0227	phosphonate metabolism
phnK	b4097	1,6222	0,0319	PhnK
phoH	b1020	1,3684	0,0361	PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation
pitA	b3493	0,6222	0,0296	PitA
pitB	b2987	1,2746	0,0137	PitB
plsB	b4041	1,6234	0,0168	glycerol-3-phosphate acyltransferase
plsC	b3018	0,3811	0,0229	1-acylglycerol-3-phosphate acyltransferase
plsX	b1090	0,3719	0,0337	glycerolphosphate auxotrophy in plsB background
pmrF	b2254	1,6010	0,0321	undecaprenyl phosphate-L-Ara4FN transferase
pncB	b0931	0,2520	0,0142	nicotinate phosphoribosyltransferase
polB	b0060	3,1483	0,0221	DNA polymerase II
ppk	b2501	0,2034	0,0093	polyphosphate kinase
prmC	b1212	1,4586	0,0477	protein-(glutamine-N5) methyltransferase
proS	b0194	1,7249	0,0261	prolyl-tRNA synthetase
proV	b2677	0,4042	0,0250	proline ABC transporter
pspF	b1303	0,1755	0,0002	PspF transcriptional activator
pstB	b3725	0,6518	0,0392	phosphate ABC transporter
ptsA	b3947	1,8352	0,0003	PEP-protein phosphotransferase system enzyme I
purB	b1131	0,7366	0,0390	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase / adenylosuccinate lyase
purC	b2476	0,2064	0,0057	phosphoribosylaminoimidazole-succinocarboxamide synthase
purE	b0523	0,1169	0,0008	N5-carboxyaminoimidazole ribonucleotide mutase
purF	b2312	0,1474	0,0009	amidophosphoribosyl transferase
purH	b4006	0,4496	0,0475	AICAR transformylase / IMP cyclohydrolase
purK	b0522	0,1805	0,0075	N5-carboxyaminoimidazole ribonucleotide synthase monomer
purM	b2499	0,2023	0,0208	phosphoribosylformylglycinamide cyclo-ligase
purN	b2500	0,3009	0,0412	phosphoribosylglycinamide formyltransferase
purR	b1658	0,2390	0,0090	PurR transcriptional repressor
purT	b1849	0,1801	0,0082	GAR transformylase 2
puuA	b1297	0,1427	0,0155	putative glutamine synthetase (EC 6.3.1.2)
pykA	b1854	1,4726	0,0128	pyruvate kinase II monomer
pykF	b1676	1,2394	0,0301	pyruvate kinase I monomer
pyrB	b4245	0,4807	0,0207	aspartate carbamoyltransferase, PyrB subunit
pyrI	b4244	0,6993	0,0415	aspartate carbamoyltransferase, PyrI subunit
qseB	b3025	0,2860	0,0050	putative 2-component transcriptional regulator
racR	b1356	0,3752	0,0040	hypothetical protein
rbsK	b3752	0,7165	0,0029	ribokinase
rcsA	b1951	3,6667	0,0186	positive DNA-binding transcriptional regulator of capsular polysaccharide synthesis, activates its own expression
rcsD	b2216	0,4726	0,0181	putative 2-component sensor protein
rdoA	b3859	0,5228	0,0406	cytoplasmic protein of low abundance
recA	b2699	3,2066	0,0263	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
recD	b2819	2,0842	0,0351	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recE	b1350	1,9766	0,0078	exonuclease VIII, ds DNA exonuclease, 5' --> 3' specific
recN	b2616	5,3559	0,0008	protein used in recombination and DNA repair
recT	b1349	1,3586	0,0348	recombinase, DNA renaturation
rfaB	b3628	2,5413	0,0011	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase
rfaG	b3631	3,0643	0,0002	lipopolysaccharide core biosynthesis; glucosyltransferase I
rfaI	b3627	4,1170	0,0163	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
rfaJ	b3626	4,3983	0,0081	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaK	b3623	3,1484	0,0132	lipopolysaccharide core biosynthesis; probably hexose transferase
rfaQ	b3632	2,4984	0,0107	lipopolysaccharide core biosynthesis
rfaS	b3629	3,0101	0,0025	lipopolysaccharide core biosynthesis
rfaY	b3625	4,7308	0,0194	lipopolysaccharide core biosynthesis
rfaZ	b3624	4,3286	0,0096	protein involved in KdoIII attachment during lipopolysaccharide core biosynthesis

gene	blattner	ratio A/B	p-value	function
rfc	b2035	1,8291	0,0009	O-antigen polymerase
rfe	b3784	0,2683	0,0097	undecaprenyl-phosphate α-N-acetylglucosaminyl transferase
rffA	b3791	1,6016	0,0227	TDP-4-oxo-6-deoxy-D-glucose transaminase
rffT	b3792.1	2,4442	0,0046	4-acetamido-4,6-dideoxy-D-galactose transferase
rhaA	b3903	2,4561	0,0417	L-rhamnose isomerase / L-lyxose isomerase
rho	b3783	0,5828	0,0440	transcription termination factor Rho monomer; polarity suppressor
rhsD	b0497	0,1966	0,0113	RhsD protein in rhs element
rhtC	b3823	0,4390	0,0253	RhtC threonine Rht Transporter
ribB	b3041	0,6220	0,0498	3,4-dihydroxy-2-butanone 4-phosphate synthase
ribF	b0025	0,1784	0,0073	riboflavin kinase / FMN adenyltransferase
rimJ	b1066	0,4039	0,0138	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
rimK	b0852	1,5209	0,0253	ribosomal protein S6 modification protein
rimL	b1427	0,5475	0,0053	acetylation of N-terminal serine of 30S ribosomal subunit protein L7; acetyl transferase
rlmB	b4180	1,7133	0,0062	23S rRNA methyltransferase monomer
rlpB	b0641	1,9134	0,0175	rare lipoprotein RlpB
rmuC	b3832	0,4993	0,0038	conserved protein
rph	b3643	1,1124	0,0148	RNase PH monomer
rplS	b2606	2,4571	0,0178	50S ribosomal subunit protein L19
rplT	b1716	2,5117	0,0282	50S ribosomal subunit protein L20, and regulator
rpoD	b3067	3,0416	0,0132	sigma70 factor
rpoE	b2573	0,6493	0,0378	sigmaE
rpoZ	b3649	0,5481	0,0118	RNA polymerase, omega subunit
rpsQ	b3311	1,9759	0,0388	30S ribosomal subunit protein S17
rrmJ	b3179	1,3369	0,0240	23S rRNA m2U2552 methyltransferase
rseA	b2572	0,3836	0,0167	anti-sigma factor that inhibits sigmaE
rseB	b2571	0,5258	0,0112	negative regulator of sigmaE; interacts with RseA and stimulates binding of RseA to sigmaE
rseC	b2570	0,4367	0,0061	protein involved in reduction of the SoxR iron-sulfur cluster
rspA	b1581	1,7883	0,0421	starvation sensing protein RspA
rspB	b1580	1,8606	0,0395	putative dehydrogenase RspB
rsxD	b1630	1,4943	0,0285	integral membrane protein of SoxR-reducing complex
rsxE	b1632	2,6850	0,0103	integral membrane protein of SoxR-reducing complex
rsxG	b1631	3,0731	0,0067	member of SoxR-reducing complex
sapB	b1293	1,7823	0,0146	peptide uptake ABC transporter
secG	b3175	0,5156	0,0209	Sec Protein Secretion Complex
seqA	b0687	0,3340	0,0283	SeqA, negative modulator of initiation of replication
serB	b4388	0,3970	0,0271	phosphoserine phosphatase
setC	b3659	1,3102	0,0144	YicK MFS Transporter
sfmC	b0531	2,1401	0,0045	putative chaperone
sgcE	b4301	1,6837	0,0317	putative epimerase
sgcX	b4305	0,3168	0,0116	SgcB
slt	b4392	0,5759	0,0147	soluble lytic murein transglycosylase
slyA	b1642	0,4451	0,0416	SlyA transcriptional activator
smf	b4473	0,3130	0,0254	hypothetical protein
smg	b3284	0,1539	0,0006	hypothetical protein
smpA	b2617	1,8755	0,0132	SmpA small membrane protein A
smtA	b0921	0,1256	0,0007	S-adenosylmethionine-dependent methyltransferase
sohB	b1272	1,8038	0,0119	putative protease
speA	b2938	2,2897	0,0138	arginine decarboxylase, biosynthetic
speD	b0120	1,2622	0,0360	adenosylmethionine decarboxylase, proenzyme
spr	b2175	0,1527	0,0041	putative lipoprotein
spy	b1743	1,6568	0,0122	periplasmic protein related to spheroblast formation
srnB	b2576	0,3930	0,0324	SrmB, DEAD-box RNA helicase
sscR	b2765	0,3470	0,0259	putative 6-pyruvoyl tetrahydrobiopterin synthase
sspA	b3229	1,7662	0,0298	regulator of transcription; stringent starvation protein A
ssuD	b0935	2,1101	0,0410	alkanesulfonate monooxygenase
sucB	b0727	1,7606	0,0413	SucB-lipoate
sucD	b0729	2,0786	0,0326	succinyl-CoA synthetase, alpha subunit
sufE	b1679	1,4500	0,0180	sulfur acceptor that activates SufS cysteine desulfurase
sufS	b1680	1,9117	0,0189	L-selenocysteine lyase (and L-cysteine desulfurase) monomer
sulA	b0958	0,4846	0,0244	suppressor of lon; inhibits cell division and ftsZ ring formation
surE	b2744	0,6982	0,0147	phosphatase with broad substrate specificity / 3'-nucleotidase / 5'-nucleotidase
talB	b0008	0,7356	0,0361	transaldolase B
tatE	b0627	1,3041	0,0170	TatABCE protein export complex
tdcF	b3113	2,0890	0,0324	hypothetical protein
thyA	b2827	1,5495	0,0232	thymidylate synthase
tolC	b3035	0,4953	0,0287	TolC outer membrane channel
torZ	b1872	0,5113	0,0085	trimethylamine N-oxide reductase III, TorZ subunit
trmE	b3706	1,6715	0,0450	GTP-binding protein with a role in modification of tRNA
trpE	b1264	0,2196	0,0041	anthranilate synthase component I

gene	blattner	ratio A/B	p-value	function
trpH	b1266	1,2995	0,0096	putative enzyme
trpR	b4393	1,8827	0,0116	TrpR transcriptional repressor
truD	b2745	0,5425	0,0108	tRNA pseudouridine 13 synthase
trxA	b3781	0,6949	0,0406	oxidized thioredoxin
ubiC	b4039	0,1951	0,0166	chorismate pyruvate lyase
ugpC	b3450	1,3303	0,0342	glycerol-3-P ABC transporter / transport
ulaB	b4194	1,8991	0,0096	eisga
umuC	b1184	1,4019	0,0198	SOS mutagenesis and repair
uup	b0949	1,5046	0,0356	Uup
uvrA	b4058	3,2580	0,0017	excision nuclease subunit A
uvrB	b0779	1,5440	0,0191	DNA repair; excision nuclease subunit B
valS	b4258	1,3789	0,0229	valyl-tRNA synthetase
vsr	b1960	0,4472	0,0407	DNA mismatch endonuclease of the very short patch (VSP) mismatch repair pathway
waaP	b3630	2,8880	0,0034	lipopolysaccharide core biosynthesis; phosphorylation of core heptose
wbbI	b2034	2,0928	0,0325	hypothetical protein; not required for colanic acid biosynthesis
wbbK	b2032	1,5888	0,0445	putative transferase
wcaI	b2050	1,4786	0,0422	putative colanic biosynthesis glycosyl transferase
wecB	b3786	1,9582	0,0212	UDP-N-acetylglucosamine-2-epimerase
xerD	b2894	0,2913	0,0334	site-specific recombinase
xseB	b0422	0,1745	0,0055	exonuclease VII, small subunit
yabP	b0056	0,5265	0,0390	conserved hypothetical protein
yacC	b0122	0,1421	0,0092	conserved hypothetical protein
yadE	b0130	1,9353	0,0038	conserved hypothetical protein
yadF	b0126	0,5334	0,0299	carbonic anhydrase
yadH	b0128	0,5583	0,0088	YadG/YadH ABC transporter
yadL	b0137	2,6672	0,0200	putative adhesin-like protein
yaeI	b0164	1,6713	0,0162	conserved protein
yaeR	b0187	0,3976	0,0325	putative enzyme
yafJ	b0223	0,1911	0,0015	putative amidotransferase
yafK	b0224	0,2183	0,0034	conserved protein; in enteroaggregative E. coli, YafK is required for development of biofilms
yafQ	b0225	0,3068	0,0158	conserved hypothetical protein
yafS	b0213	1,5738	0,0014	putative methyltransferase
yagB	b0266	0,1046	0,0003	hypothetical protein
yagN	b0280	0,2692	0,0237	hypothetical protein
yahF	b0320	1,8661	0,0118	putative oxidoreductase subunit
yahJ	b0324	1,4514	0,0167	putative deaminase
yajC	b0407	0,5517	0,0123	Sec Protein Secretion Complex
yajI	b0412	0,6979	0,0356	conserved hypothetical protein
ybaJ	b0461	0,1803	0,0125	conserved hypothetical protein
ybaK	b0481	1,4925	0,0073	conserved hypothetical protein
ybaN	b0468	0,4393	0,0017	hypothetical protein
ybaQ	b0483	0,1888	0,0099	conserved protein with a DNA-binding domain
ybaY	b0453	2,1228	0,0458	glycoprotein/polysaccharide metabolism
ybbB	b0503	0,6974	0,0351	tRNA 2-selenouridine synthase
ybdJ	b0580	0,3651	0,0026	conserved hypothetical protein
ybeD	b0631	3,2155	0,0247	conserved hypothetical protein
ybeX	b0658	2,4451	0,0016	putative transport protein
ybeY	b0659	3,1107	0,0068	conserved hypothetical protein
ybeZ	b0660	3,0813	0,0018	putative ATP-binding protein
ybfF	b0686	0,4851	0,0234	putative enzyme
ybfH	b0691	2,0652	0,0161	conserved hypothetical protein
ybgA	b0707	1,5050	0,0370	conserved protein
ybgC	b0736	0,5182	0,0269	Tol-Pal Cell Envelope Complex
ybgI	b0710	0,5520	0,0236	conserved protein, putative hydrolase-oxidase monomer
ybgS	b0753	1,6386	0,0415	putative homeobox protein
ybhI	b0770	1,6162	0,0084	YbhI DASS Transporter
ybiF	b0813	0,4910	0,0351	Threonine and Homoserine Exporter
ybiH	b0796	0,1350	0,0012	hypothetical protein
ybjJ	b0845	1,8338	0,0024	putative DEOR-type transcriptional regulator
ybjN	b0853	0,4973	0,0357	putative sensory transduction regulator
ybjO	b0858	0,7793	0,0239	putative membrane protein
ybjS	b0868	0,5267	0,0068	putative nucleotide di-P-sugar epimerase or dehydratase
ycaK	b0901	2,4091	0,0338	YcaK
ycaL	b0909	0,4133	0,0127	putative heat shock protein
ycbB	b0925	0,4752	0,0426	putative amidase
ycbK	b0926	0,2670	0,0090	conserved hypothetical protein
ycbQ	b0938	1,6913	0,0497	putative fimbrial-like protein
ycbW	b0946	0,8124	0,0000	conserved hypothetical protein
yccM	b0992	1,6258	0,0274	hypothetical protein

gene	blattner	ratio A/B	p-value	function
yccR	b0959	0,4415	0,0330	conserved protein
yccV	b0966	1,9670	0,0301	hemimethylated DNA-binding protein
yceA	b1055	0,5663	0,0415	hypothetical protein
yceH	b1067	0,5404	0,0358	conserved hypothetical protein
ycfH	b1100	2,0582	0,0168	putative hydrolase
ycfJ	b1110	0,6676	0,0447	hypothetical protein
ycfP	b1108	0,5438	0,0176	putative hydrolase
ycfQ	b1111	2,2543	0,0293	hypothetical protein
ycfX	b1119	0,5776	0,0347	putative sugar kinase, ROK family protein
yegG	b1168	2,7312	0,0499	conserved protein
yegL	b1179	0,3957	0,0211	conserved hypothetical protein
yegM	b1180	0,3111	0,0120	putative isomerase
yegN	b1181	0,2615	0,0009	conserved hypothetical protein
yegZ	b1164	0,3437	0,0011	hypothetical protein
yehH	b1205	0,3360	0,0075	conserved hypothetical protein
yeiI	b1251	1,8595	0,0266	conserved hypothetical protein
yeiQ	b1268	2,0023	0,0382	putative membrane protein
yejD	b1289	1,8598	0,0220	conserved hypothetical protein
yejF	b1322	4,5462	0,0002	putative membrane protein
yejR	b1314	2,8426	0,0026	putative epimerase/isomerase
yejX	b1321	5,2223	0,0078	putative EC 2.1 enzyme
yejZ	b1328	0,3330	0,0288	putative transcriptional regulator LYSR-type
ydaC	b1347	2,1926	0,0196	hypothetical protein
ydaL	b1340	0,4087	0,0084	hypothetical protein
ydaO	b1344	0,3090	0,0329	conserved protein
ydbK	b1378	1,5381	0,0088	putative pyruvate synthase
ydcD	b1457	0,2425	0,0233	hypothetical protein
ydcF	b1414	0,3249	0,0248	conserved hypothetical protein
ydcP	b1435	0,5182	0,0437	putative collagenase
ydcQ	b1438	0,6588	0,0380	hypothetical protein
ydcV	b1443	2,3103	0,0430	YdcS/YdcT/YdcV/YdcU ABC transporter
ydcX	b1445	1,7926	0,0407	hypothetical protein
ydcZ	b1447	0,6629	0,0339	putative transport protein
ydeI	b1536	1,4337	0,0167	conserved hypothetical protein
ydeK	b1510	0,5430	0,0356	YdeK
ydeP	b1501	1,2063	0,0190	acid resistance protein
ydfH	b1540	0,4468	0,0056	hypothetical protein
ydfX	b1568	1,9527	0,0006	hypothetical protein
ydgK	b1626	0,2396	0,0104	putative oxidoreductase
ydgT	b1625	0,1619	0,0070	conserved hypothetical protein
ydhA	b1639	0,3471	0,0143	conserved hypothetical protein
ydhC	b1660	0,5332	0,0469	YdhC drug MFS transporter
ydhF	b1647	0,6866	0,0318	putative oxidoreductase, NAD(P)-linked
ydhH	b1640	0,5178	0,0331	conserved hypothetical protein
ydhI	b1643	0,3395	0,0016	hypothetical protein
ydhX	b1671	1,4069	0,0177	putative oxidoreductase, Fe-S subunit
ydiA	b1703	0,4230	0,0097	conserved protein
ydiF	b1694	2,3786	0,0350	putative enzyme / putative acetate CoA-transferase
ydiU	b1706	0,3937	0,0051	conserved protein
ydjA	b1765	0,2828	0,0032	conserved protein
ydjE	b1769	1,5337	0,0078	YdjE MFS transporter
ydjG	b1771	1,5063	0,0105	putative oxidoreductase
ydjI	b1773	1,8655	0,0163	putative aldolase
yeaB	b1813	0,3894	0,0148	conserved hypothetical protein, MutT-like
yeaD	b1780	1,6695	0,0155	conserved hypothetical protein
yeaN	b1791	1,5049	0,0207	YeaN
yeaQ	b1795	2,2111	0,0082	conserved hypothetical protein
yebF	b1847	1,6698	0,0283	conserved hypothetical protein
yebK	b1853	0,2495	0,0033	hypothetical protein
yebQ	b1828	1,8190	0,0400	YebQ
yebR	b1832	0,3530	0,0270	conserved hypothetical protein
yebW	b1837	0,4682	0,0099	hypothetical protein
yecD	b1867	0,2234	0,0222	putative enzyme
yecN	b1869	0,3102	0,0188	putative membrane protein
yecP	b1871	0,3399	0,0218	putative enzyme
yecT	b1877	1,0931	0,0431	hypothetical protein
yedA	b1959	0,5288	0,0316	putative transmembrane subunit
yedR	b1963	1,5955	0,0146	hypothetical protein
yedS_1	b1964	2,2882	0,0042	putative outer membrane protein

gene	blattner	ratio A/B	p-value	function
yedS_2	b1965	1,7587	0,0236	putative outer membrane protein
yedV	b1968	1,8495	0,0385	putative 2-component sensor protein
yeeI	b1976	0,0966	0,0010	conserved hypothetical protein
yeeN	b1983	4,9594	0,0148	conserved protein
yeeR	b2001	2,6686	0,0487	hypothetical protein
yeeT	b2003	2,3201	0,0034	hypothetical protein
yeeV	b2005	1,3165	0,0457	toxin of the YeeV-YeeU toxin-antitoxin pair
yegK	b2072	1,7271	0,0442	conserved hypothetical protein
yegS	b2086	2,0901	0,0070	conserved protein
yegZ	b2083	2,2403	0,0450	hypothetical protein
yeiB	b2152	0,3697	0,0315	putative flavoprotein
yeiE	b2157	0,3697	0,0245	LYSR-type transcriptional regulator
yeiH	b2158	0,4992	0,0227	putative membrane protein
yeiS	b2145	0,4582	0,0020	hypothetical protein
yeiU	b2174	0,4647	0,0046	putative permease
yejO	b2190	0,7784	0,0168	putative outer membrane protein
yfbE	b2253	2,0569	0,0265	UDP-L-Ara4O C-4" transaminase
yfbN	b2273	2,3173	0,0063	conserved hypothetical protein
yfbP	b2275	1,8398	0,0323	hypothetical protein
yfbS	b2292	1,5779	0,0333	putative transport protein
yfdG	b2350	0,2271	0,0070	hypothetical protein
yfdT	b2363	1,6042	0,0163	hypothetical protein
yfdY	b2377	0,3177	0,0340	hypothetical protein
yfdZ	b2379	0,4370	0,0356	putative aminotransferase
yfeT	b2427	0,3878	0,0370	conserved protein
yffP	b2447	0,5387	0,0462	hypothetical protein
yfgA	b2516	0,3806	0,0060	putative membrane protein
yfgB	b2517	0,5726	0,0383	putative pyruvate formate lyase activating enzyme 2
yfgC	b2494	0,5296	0,0021	conserved protein
yfgJ	b2510	2,4079	0,0095	putative cytochrome
yfhG	b2555	0,2458	0,0032	conserved protein
yfhL	b2562	0,2615	0,0411	putative ferredoxin
yfhR	b2534	1,6968	0,0195	putative methylase or hydrolase
yfiC	b2575	0,1195	0,0045	putative enzyme
yfiR	b2603	0,4114	0,0278	conserved protein
yfjD	b4461	1,6322	0,0139	putative membrane protein, hemolysin-like
yfjG	b2619	1,8502	0,0087	toxin of a putative toxin-antitoxin pair
yfjL	b2628	0,1625	0,0098	hypothetical protein
yfjO	b2631	0,5072	0,0379	hypothetical protein
yfjS	b2636	1,9190	0,0123	inner membrane lipoprotein YfjS
yfjU	b2638	0,5267	0,0020	hypothetical protein
ygaD	b2700	0,4320	0,0264	conserved protein
ygaH	b2683	0,4552	0,0216	putative transport protein
ygbE	b2749	0,1583	0,0105	putative cytochrome oxidase subunit
ygcF	b2777	2,5383	0,0021	hypothetical protein
ygdI	b2809	2,2634	0,0305	hypothetical protein
ygdK	b2811	0,3282	0,0174	conserved hypothetical protein
ygdR	b2833	0,4614	0,0075	conserved hypothetical protein
ygeG	b2851	1,7509	0,0180	conserved hypothetical protein
ygeK	b2855	2,0910	0,0188	putative 2-component transcriptional regulator
ygeW	b2870	1,8672	0,0031	putative carbamoyl transferase
ygfH	b2920	1,5120	0,0087	propionyl-CoA:succinate CoA transferase
ygfS	b2886	1,9879	0,0229	putative oxidoreductase, Fe-S subunit
yggH	b2960	0,4393	0,0186	tRNA (m7G46) methyltransferase
yggJ	b2946	0,5103	0,0052	conserved hypothetical protein
yggX	b2962	0,2130	0,0026	conserved hypothetical protein with role in oxidation-resistance of iron-sulfur clusters
yghQ	b2983	1,5927	0,0325	putative serine protease
yghS	b2985	2,5090	0,0044	conserved protein
ygiA	b3036	0,4378	0,0239	hypothetical protein
ygiF	b3054	0,4550	0,0096	conserved hypothetical protein
ygiH	b3059	0,3702	0,0081	putative membrane protein
ygiU	b3022	0,2603	0,0069	putative cyanide hydratase
ygiG	b3073	1,9440	0,0152	putrescine:2-oxoglutaric acid aminotransferase
ygiN	b3083	0,4759	0,0137	conserved hypothetical protein
ygiR	b3087	0,4817	0,0398	putative NAD(P)-binding dehydrogenase
yhaK	b3106	0,6327	0,0013	conserved hypothetical protein
yhbP	b3154	0,2861	0,0046	conserved protein
yhcA	b3215	1,7828	0,0096	putative chaperone
yhcB	b3233	0,4240	0,0252	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
yhcD	b3216	2,5320	0,0410	putative outer membrane protein
yhcM	b3232	0,2725	0,0003	hypothetical protein
yhdA	b3252	0,1678	0,0074	conserved protein
yhdJ	b3262	1,4106	0,0325	cell cycle-regulated methyltransferase
yheN	b3345	0,6302	0,0272	conserved hypothetical protein
yheO	b3346	0,5020	0,0092	hypothetical protein
yhfG	b3362	1,9518	0,0284	conserved hypothetical protein
yhfX	b3381	1,9848	0,0205	conserved protein
yhhK	b3459	0,4123	0,0018	putative acyltransferase
yhhM	b3467	0,3265	0,0159	putative receptor
yhhN	b3468	0,4588	0,0073	putative enzyme
yhhS	b3473	0,3667	0,0188	YhhS MFS transporter
yhhT	b3474	0,5527	0,0461	hypothetical protein
yhiL	b3490	2,2476	0,0051	hypothetical protein
yhiP	b3496	1,3365	0,0190	YhiP peptide POT transporter
yhiS	b3504	1,6910	0,0222	conserved protein
yhjA	b3518	2,6298	0,0076	putative cytochrome C peroxidase (EC 1.11.1)
yhjC	b3521	0,2139	0,0092	putative transcriptional regulator LYSR-type
yhjR	b3535	0,2767	0,0243	hypothetical protein
yiaJ	b3574	0,3464	0,0228	YiaJ transcriptional repressor
yiaV	b3586	2,4422	0,0226	putative membrane protein
yibA	b3594	2,4261	0,0343	putative lyase
yicE	b3654	0,0934	0,0007	YicE NCS2 transporter
yidI	b3677	0,5721	0,0151	hypothetical protein
yieO	b3754	0,5670	0,0417	YieO drug MFS transporter
yifE	b3764	1,7605	0,0381	hypothetical protein
yigA	b3810	0,4061	0,0291	conserved hypothetical protein
yigL	b3826	1,9789	0,0325	conserved protein with a phosphatase-like domain
yihI	b3866	0,3969	0,0382	conserved protein
yihN	b3874	1,3163	0,0362	YihN MFS transporter
yihW	b3884	0,5544	0,0009	putative DEOR-type transcriptional regulator
yihX	b3885	0,1479	0,0070	putative phosphatase
yjbE	b4026	2,1742	0,0103	conserved hypothetical protein
yjbJ	b4045	0,8546	0,0153	highly abundant nonessential protein
yjbQ	b4056	0,3680	0,0272	conserved hypothetical protein
yjdA	b4109	0,1308	0,0055	hypothetical protein
yjeB	b4178	0,1691	0,0045	conserved protein with a Winged helix domain
yjeK	b4146	0,2195	0,0017	hypothetical protein
yjeS	b4166	5,5584	0,0055	conserved ferredoxin-like protein
yjfY	b4199	2,3690	0,0232	conserved hypothetical protein
yjfZ	b4204	1,7639	0,0428	hypothetical protein
yjgK	b4252	0,7295	0,0143	conserved hypothetical protein
yjhQ	b4307	1,4246	0,0099	hypothetical protein
yjiP	b4338	2,4980	0,0122	hypothetical protein
yjjK	b4391	1,7150	0,0293	YjjK
yjjV	b4378	0,5588	0,0453	putative hydrolase
ykfA	b0253	0,6499	0,0241	putative GTP-binding protein
ykfl	b0245	1,4478	0,0135	toxin of the Ykfl-YafW toxin-antitoxin pair
ymdB	b1045	0,3716	0,0228	conserved protein
ymfE	b1138	0,3125	0,0102	hypothetical protein
ymfL	b1147	2,2281	0,0426	hypothetical protein
ymjA	b1295	0,2117	0,0004	hypothetical protein
ynaE	b1375	0,3494	0,0151	hypothetical protein
ynaI	b1330	2,3789	0,0357	YnaI
yncA	b1448	0,2369	0,0176	putative N-acetyltransferase
yncI	b1458	0,3663	0,0269	conserved protein
yncE	b1520	0,3459	0,0204	conserved hypothetical protein
yncH	b1524	0,2425	0,0072	putative glutaminase
yoaB	b1809	0,7879	0,0038	conserved protein
yoaG	b1796	1,8050	0,0152	hypothetical protein
yoaH	b1811	0,4847	0,0212	conserved hypothetical protein
yobA	b1841	0,4374	0,0151	hypothetical protein
yodA	b1973	1,4017	0,0256	cadmium-induced metal binding protein
ypdA	b2380	0,4128	0,0202	putative sensor protein
yphA	b2543	0,5045	0,0317	hypothetical protein
ypjA	b2647	1,4597	0,0449	putative outer membrane protein
ypjF	b2646	2,1806	0,0102	member of the YeeV, Ykfl, YpjF family of toxin proteins
yqaA	b2689	0,3480	0,0062	putative integral membrane protein
yqeI	b2847	0,2786	0,0052	putative sensory transducer

gene	blattner	ratio A/B	p-value	function
yqgE	b2948	0,4450	0,0370	conserved protein
yqgF	b2949	0,3997	0,0078	possible Holliday junction resolvase
yqiA	b3031	0,4262	0,0079	putative hydrolase
yqiB	b3033	0,3117	0,0078	putative enzyme
yqiJ	b3050	1,4637	0,0242	putative oxidoreductase
yqjC	b3097	1,4751	0,0229	conserved protein
yqjK	b3100	1,6055	0,0133	conserved hypothetical protein
yraM	b3147	0,3549	0,0084	putative glycosylase
yraN	b3148	0,3605	0,0169	conserved hypothetical protein
yrbL	b3207	0,3337	0,0259	conserved hypothetical protein; transcription is regulated by Mg ²⁺
yrdD	b3283	0,1449	0,0047	putative DNA topoisomerase
ytfA	b4205	0,8018	0,0308	hypothetical protein
ytfG	b4211	1,9267	0,0219	putative oxidoreductase
ytfN	b4221	0,6361	0,0427	conserved protein
ytfP	b4222	0,5980	0,0212	conserved hypothetical protein
ytjB	b4387	0,5868	0,0341	membrane protein
zapA	b2910	0,1619	0,0022	ZapA protein, localizes to the cytokinetic ring
zipA	b2412	0,2297	0,0272	essential cell division protein ZipA
zitB	b0752	2,0419	0,0407	ZitB zinc CDF transporter
znuA	b1857	0,4717	0,0485	ZnuA/ZnuB/ZnuC ABC transporter
zur	b4046	0,3387	0,0049	Zur transcriptional regulator

LZ41hns (A) & LZ54hns (B)

acpS	b2563	1,5407	0,0218	holo-[acyl-carrier-protein] synthase
acrE	b3265	0,1990	0,0005	transmembrane protein affects septum formation and cell membrane permeability
acrF	b3266	0,4401	0,0079	AcrEF-TolC Drug Efflux Transport System
ade	b3665	0,4857	0,0346	cryptic adenine deaminase monomer
agaA	b3135	1,3368	0,0175	AgaA
agp	b1002	1,7053	0,0169	3-phytase / glucose-1-phosphatase
allD	b0517	0,8448	0,0140	ureidoglycolate dehydrogenase
alsK	b4084	2,0491	0,0034	putative D-allose kinase
amn	b1982	0,6066	0,0233	AMP nucleosidase
ampH	b0376	0,6290	0,0473	putative enzyme
apt	b0469	0,4031	0,0012	adenine phosphoribosyltransferase
arcB	b3210	1,3746	0,0005	ArcB-Phis292
argE	b3957	0,4469	0,0206	acetylornithine deacetylase
argP	b2916	1,8354	0,0114	ArgP transcriptional activator
argR	b3237	0,8272	0,0077	ArgR transcriptional dual regulator
aroG	b0754	0,4066	0,0018	2-dehydro-3-deoxyphosphoheptonate aldolase
aroL	b0388	0,6991	0,0407	shikimate kinase II
aroM	b0390	1,2587	0,0066	protein of aro operon, regulated by aroR
arsR	b3501	2,1332	0,0342	ArsR transcriptional regulator
artJ	b0860	1,4705	0,0115	arginine ABC transporter
ascF	b2715	0,6756	0,0021	EIIAsc
asd	b3433	0,3715	0,0107	aspartate semialdehyde dehydrogenase
asr	b1597	1,4676	0,0477	acid shock protein
atoC	b2220	1,4762	0,0173	AtoC-Pasp
b0165	b0165	0,5609	0,0062	hypothetical protein
b0255	b0255	0,4577	0,0292	hypothetical protein
b0501	b0501	1,7323	0,0252	hypothetical protein
b0582	b0582	1,6254	0,0305	IS186 protein
b0609	b0609	1,7352	0,0238	hypothetical protein
b1052	b1052	0,6634	0,0425	hypothetical protein
b1144	b1144	2,3356	0,0306	hypothetical protein
b1371	b1371	1,3289	0,0228	hypothetical protein
b1402	b1402	0,5199	0,0099	IS22 protein
b1578	b1578	0,3596	0,0018	hypothetical protein
b3004	b3004	1,5667	0,0459	hypothetical protein
b3044	b3044	0,4341	0,0020	IS21 protein
b3975	b3975	0,6083	0,0012	hypothetical protein
bcp	b2480	0,4248	0,0031	thiol peroxidase
bcsB	b3532	1,3097	0,0175	cellulose biosynthesis protein
bcsZ	b3531	1,5108	0,0233	endo-1,4-D-glucanase
bfd	b3337	1,5485	0,0247	bacterioferritin-associated ferredoxin
bglJ	b4366	0,6250	0,0347	BglJ transcriptional regulator
bisC	b3551	0,7735	0,0310	biotin sulfoxide reductase / methionine-S-sulfoxide reductase
bolA	b0435	1,2797	0,0184	BolA transcriptional regulator
borD	b0557	0,3304	0,0257	bacteriophage lambda Bor protein homolog
btuB	b3966	2,9792	0,0085	outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23

gene	blattner	ratio A/B	p-value	function
btuF	b0158	1,6355	0,0409	periplasmic vitamin B12 binding protein
cadA	b4131	1,5715	0,0317	lysine decarboxylase
caiD	b0036	1,4534	0,0482	crotonobetainyl-CoA hydratase / carnitine racemase
carA	b0032	0,2101	0,0070	carbamoyl phosphate synthetase
ccmA	b2201	1,6431	0,0142	CcmABCDEFGH cytochrome c biogenesis system
cfa	b1661	0,6266	0,0211	cyclopropane fatty acid synthase
cheY	b1882	1,3741	0,0165	CheY-Pasp
citX	b0614	1,6215	0,0232	holo-ACP synthase
clpA	b0882	1,3076	0,0196	ATP-binding component of serine protease
clpB	b2592	1,7953	0,0255	ClpB chaperone
cmr	b0842	0,6968	0,0355	MdfA/Cmr MFS multidrug transporter
cobC	b0638	2,3925	0,0065	alpha-ribazole-5'-P phosphatase
codA	b0337	0,3324	0,0112	cytosine deaminase
codB	b0336	0,3778	0,0284	CodB cytosine NCS1 transporter
corA	b3816	0,6187	0,0409	CorA magnesium ion MIT transporter
cpdA	b3032	0,6411	0,0141	cAMP phosphodiesterase
cpsB	b2049	4,1414	0,0042	mannose-1-phosphate guanylyltransferase-(GDP)
cpsG	b2048	3,9546	0,0014	phosphomannomutase
cpxP	b3913	2,3448	0,0199	regulator of the Cpx response and possible chaperone involved in resistance to extracytoplasmic stress
creB	b4398	0,3912	0,0063	CreB- Phosphorylated transcriptional regulator
crl	b0240	0,3398	0,0058	Crl transcriptional regulator
csgA	b1042	1,1757	0,0491	curlin, major subunit
csgD	b1040	0,3335	0,0298	CsgD transcriptional activator
csgE	b1039	0,3294	0,0116	curli production assembly/transport component
csgG	b1037	0,6373	0,0467	curli production component
cspA	b3556	0,1595	0,0272	cold shock protein CspA
cspB	b1557	0,0804	0,0020	cold shock protein CspB
cspF	b1558	0,1563	0,0010	cold shock protein CspF
cspI	b1552	0,4222	0,0364	cold shock protein CspI
cvpA	b2313	0,4563	0,0323	membrane protein required for colicin V production
cyaY	b3807	0,7207	0,0274	iron-binding frataxin homolog
cybB	b1418	0,4149	0,0121	cytochrome b561
cybC	b4236	0,5877	0,0172	cytochrome b562 (soluble)
cynR	b0338	1,4730	0,0246	CynR-Cyanate transcriptional activator
cyoA	b0432	1,6203	0,0356	cytochrome bo terminal oxidase subunit II
cyoD	b0429	1,2541	0,0388	cytochrome bo terminal oxidase subunit IV
cyoE	b0428	1,7729	0,0214	heme O synthase
cysJ	b2764	0,8120	0,0324	sulfite reductase flavoprotein subunit
cysM	b2421	0,7167	0,0338	O-acetylserine (thiol)-lyase B
cytR	b3934	0,3074	0,0076	CytR-cytidine
dapA	b2478	0,5629	0,0328	dihydrodipicolinate synthase
dapF	b3809	0,5061	0,0428	diaminopimelate epimerase
dcm	b1961	0,8273	0,0436	DNA cytosine methylase
dcrB	b3472	2,0849	0,0233	conserved protein involved in bacteriophage adsorption
ddpA	b1487	1,5696	0,0361	YddS
ddpC	b1485	2,0675	0,0310	YddQ
degS	b3235	0,4723	0,0130	inner membrane serine protease required for the extracytoplasmic stress response mediated by sigmaE
dfp	b3639	0,4912	0,0038	P-pantothenate cysteine ligase / P-pantothenoylcysteine decarboxylase
dnaB	b4052	0,2288	0,0030	chromosome replication; chain elongation; part of primosome
dnaG	b3066	2,0680	0,0024	DNA biosynthesis; DNA primase
dppC	b3542	1,7014	0,0194	dipeptide ABC transporter
dppF	b3540	1,6050	0,0225	dipeptide ABC transporter
dsbB	b1185	0,7021	0,0043	dsbB protein
dsbC	b2893	0,5304	0,0070	DsbC_{oxidized}
dtl	b3887	0,6855	0,0317	D-Tyr-tRNATyr deacylase
dxr	b0173	1,5005	0,0195	DXP reductoisomerase
eda	b1850	1,6768	0,0060	oxaloacetate decarboxylase / 2-keto-3-deoxy-6-phosphogluconate aldolase / 2-keto-4-hydroxyglutarate aldolase
elaA	b2267	0,7645	0,0471	hypothetical protein
elaC	b2268	0,6841	0,0220	binuclear zinc phosphodiesterase monomer
emrE	b0543	1,4396	0,0395	EmrE SMR transporter
entD	b0583	0,7069	0,0132	phosphopantetheinyl transferase
entE	b0594	0,5193	0,0155	enterobactin synthase multienzyme complex
envR	b3264	0,6510	0,0447	EnvR transcriptional regulator
epd	b2927	0,4460	0,0015	erythrose 4-phosphate dehydrogenase
eutN	b2456	1,0929	0,0134	putative detox protein, ethanolamine utilization
fabA	b0954	1,3210	0,0488	beta-hydroxyacyl-ACP dehydrase / beta-hydroxydecanoyl-ACP dehydrase / trans-2-decenoyl-ACP isomerase
fabB	b2323	0,5971	0,0302	beta-ketoacyl-ACP synthase I / malonyl-ACP decarboxylase
fadE	b0221	1,6673	0,0495	acyl-CoA dehydrogenase
fdnI	b1476	1,9523	0,0061	formate dehydrogenase N, γ subunit

gene	blattner	ratio A/B	p-value	function
fdrA	b0518	1,2709	0,0284	involved in protein transport; multicopy suppressor of dominant negative ftsH mutants
fecA	b4291	1,7276	0,0273	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fecI	b4293	3,0790	0,0101	sigma19 factor
fhuC	b0151	0,5705	0,0007	ferrichrome uptake system
fldA	b0684	1,1793	0,0126	oxidized flavodoxin 1
flgJ	b1081	1,5509	0,0122	FlgJ
flhD	b1892	0,3498	0,0204	FlhD transcriptional dual regulator
fliK	b1943	1,5668	0,0293	flagellar hook-length control protein FliK
fliY	b1920	0,5595	0,0124	periplasmic cystine-binding protein; member of extracellular bacterial solute-binding protein family III
fmt	b3288	1,4785	0,0271	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase
fnr	b1334	2,6607	0,0164	FNR transcriptional dual regulator
folB	b3058	0,5634	0,0051	dihydroneopterin aldolase
folD	b0529	0,6659	0,0470	methyleneTHF enzyme / methenyltetrahydrofolate cyclohydrolase / methylenetetrahydrofolate dehydrogenase-(NADP+)
fre	b3844	1,6805	0,0020	FMN reductase
frlR	b3375	0,7577	0,0058	putative transcriptional regulator
frmA	b0356	1,5071	0,0219	formaldehyde dehydrogenase, glutathione-dependent
frsA	b0239	0,4360	0,0232	fermentation/respiration switch protein
fruR	b0080	0,6025	0,0156	FruR transcriptional dual regulator
frvA	b3900	1,5012	0,0441	EIIABC _{Frv}
frwB	b3950	2,0264	0,0163	EIIBC _{Frw}
frwC	b3949	1,7660	0,0430	EIIBC _{Frw}
ftsB	b2748	0,3995	0,0032	essential cell division protein FtsB
fumB	b4122	1,5288	0,0433	fumarase B monomer
fur	b0683	1,5727	0,0358	Fur transcriptional dual regulator
gadX	b3516	0,5996	0,0010	GadX transcriptional activator
galT	b0758	1,5496	0,0183	UDP-glucose-hexose-1-phosphate uridylyltransferase / galactose-1-phosphate uridylyltransferase
galU	b1236	1,1283	0,0373	UTP-glucose-1-phosphate uridylyltransferase
gapC_1	b1417	0,6328	0,0268	split glyceraldehyde 3-phosphate dehydrogenase C
gapC_2	b1416	0,7832	0,0228	glyceraldehyde 3-phosphate dehydrogenase C, interrupted
gatC	b2092	0,5533	0,0229	EII _{Gat}
gatD	b2091	0,5303	0,0482	galactitol-1-phosphate dehydrogenase
gatY	b2096	0,2303	0,0083	tagatose-1,6-bisphosphate aldolase 2
gatZ	b2095	0,3772	0,0024	tagatose-1,6-bisphosphate aldolase 2
gcvH	b2904	0,1767	0,0186	dihydrolipoyl-GcvH-protein
gcvR	b2479	0,2386	0,0003	GcvR-gly
glcA	b2975	1,2470	0,0468	YghK transporter
glf	b2036	1,4291	0,0266	UDP-galactopyranose mutase
glmU	b3730	0,2684	0,0006	N-acetylglucosamine-1-phosphate uridylyltransferase / glucosamine-1-phosphate acetyltransferase
glnD	b0167	1,5254	0,0066	uridylyltransferase / uridylyl-removing enzyme
glpB	b2242	1,6094	0,0343	glycerol-3-phosphate-dehydrogenase, anaerobic
glpD	b3426	0,6947	0,0391	glycerol 3-phosphate dehydrogenase, aerobic
gltI	b0655	2,1460	0,0238	putative periplasmic binding transport protein
gltJ	b0654	1,8439	0,0084	glutamate ABC transporter
gltL	b0652	2,3251	0,0499	glutamate ABC transporter
glyA	b2551	0,6522	0,0151	glycine hydroxymethyltransferase
glyQ	b3560	0,7048	0,0451	glycine-tRNA synthetase, alpha subunit
gntU	b4476	1,5662	0,0354	GntU gluconate Gnt transporter
gntY	b3414	2,5638	0,0235	predicted membrane-bound protein that is involved in high-affinity gluconate transport
gpt	b0238	0,6101	0,0011	xanthine phosphoribosyltransferase / guanine phosphoribosyltransferase / hypoxanthine phosphoribosyltransferase
greA	b3181	2,0067	0,0017	transcription elongation factor; stimulates the mRNA cleavage activity of RNA polymerase
grxA	b0849	1,5161	0,0008	oxidized glutaredoxin
grxB	b1064	0,6716	0,0024	oxidized glutaredoxin 2
gspC	b3324	0,6446	0,0495	putative protein secretion protein for export
gspD	b3325	0,6169	0,0078	putative protein secretion protein for export
gspG	b3328	1,3373	0,0380	putative protein secretion protein for export
gspJ	b3331	1,5637	0,0307	putative protein secretion protein for export
gspM	b3334	1,6029	0,0266	putative protein secretion protein
gst	b1635	0,4622	0,0007	glutathione transferase
guaB	b2508	0,4105	0,0135	IMP dehydrogenase
gudX	b2788	2,0225	0,0315	putative glucarate dehydratase
gyrB	b3699	2,0935	0,0014	DNA gyrase, subunit B
hcaC	b2540	0,6918	0,0184	ferredoxin, 3-phenylpropionate dioxygenase system
hcaT	b2536	0,7188	0,0131	HcaT MFS transporter
hcr	b0872	1,7460	0,0357	NADH oxidoreductase
hdeA	b3510	0,6336	0,0024	acid-resistance protein, possible chaperone
hdfr	b4480	0,5965	0,0480	transcriptional regulator
hemA	b1210	2,4332	0,0162	glutamyl-tRNA reductase
hemC	b3805	0,3060	0,0013	hydroxymethylbilane synthase
hemD	b3804	0,4619	0,0020	uroporphyrinogen III synthase

gene	blattner	ratio A/B	p-value	function
hemG	b3850	0,6070	0,0126	protoporphyrinogen oxidase
hemH	b0475	1,6618	0,0431	ferrochelatase
hflD	b1132	0,5428	0,0224	membrane protein in operon with purB
hflX	b4173	0,6818	0,0118	putative GTPase; possible regulator of HflKC
hfq	b4172	0,5741	0,0397	RNA-binding protein that affects many cellular processes; homolog of mammalian Sm/Sm-like proteins
hha	b0460	0,3066	0,0051	haemolysin expression modulating protein
hisC	b2021	0,5274	0,0366	histidine-phosphate aminotransferase
hisD	b2020	0,4683	0,0485	histidinal dehydrogenase / histidinol dehydrogenase
hisF	b2025	0,8078	0,0189	imidazole glycerol phosphate synthase, HisF subunit
hisS	b2514	0,6173	0,0477	histidyl-tRNA synthetase
hns	b1237	0,5055	0,0012	H-NS transcriptional dual regulator
hofO	b3393	2,0366	0,0008	conserved hypothetical protein
holA	b0640	1,8168	0,0002	DNA polymerase III, delta subunit
holC	b4259	0,2779	0,0200	DNA polymerase III, chi subunit
holE	b1842	0,2376	0,0017	DNA polymerase III, theta subunit
hslR	b3400	1,6952	0,0251	heat shock protein Hsp15
htrA	b0161	1,3676	0,0489	DegP
htrL	b3618	3,3010	0,0333	involved in lipopolysaccharide biosynthesis
hycH	b2718	1,3428	0,0378	processing of large subunit (HycE) of hydrogenase 3 (part of the FHL complex)
hypF	b2712	1,5597	0,0001	hydrogenase maturation protein
ibpA	b3687	1,9972	0,0407	small heat shock protein IbpA
iclR	b4018	0,3761	0,0272	IclR-PEP
idnD	b4267	0,6061	0,0334	L-idonate 5-dehydrogenase
idnO	b4266	0,6120	0,0319	5-keto-D-gluconate 5-reductase / putative acetoin dehydrogenase
ilvG_1	b3767	0,3376	0,0394	IlvG_1
ilvM	b3769	0,3697	0,0001	acetoxybutanoate synthase II / acetolactate synthase II
imp	b0054	0,6460	0,0370	organic solvent tolerance
infA	b0884	1,9363	0,0438	protein chain initiation factor IF-1
intR	b1345	0,5249	0,0341	putative transposase
intZ	b2442	0,7707	0,0220	putative prophage integrase
iscR	b2531	3,2160	0,0490	IscR transcriptional regulator
iscU	b2529	2,3333	0,0037	scaffold protein involved in iron-sulfur cluster assembly
iscX	b2524	1,9429	0,0374	protein with possible role in iron-sulfur cluster biogenesis
ispA	b0421	0,2156	0,0032	geranyl diphosphate synthase / farnesyl diphosphate synthase
ispG	b2515	0,4793	0,0372	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
kdpA	b0698	1,4635	0,0082	potassium ion P-type ATPase transporter
kdtA	b3633	0,5128	0,0192	KDO transferase
kefC	b0047	1,4900	0,0328	KefC potassium CPA2 transporter
lctD	b3605	1,5950	0,0088	L-Lactate:Quinone Oxidoreductase
leuA	b0074	0,5604	0,0386	2-isopropylmalate synthase
leuO	b0076	0,4172	0,0372	LeuO transcriptional activator
ligT	b0147	0,3631	0,0028	hypothetical protein
lipB	b0630	1,7073	0,0027	lipoyl-protein ligase
lolB	b1209	0,5077	0,0232	outer membrane lipoprotein, localization of lipoproteins in the outer membrane
lon	b0439	1,7720	0,0416	DNA-binding, ATP-dependent protease La
lpcA	b0222	0,5206	0,0283	lipopolysaccharide core biosynthesis; phosphoheptose isomerase
lpxP	b2378	1,5961	0,0222	palmitoleoyl acyltransferase
maa	b0459	0,4667	0,0368	maltose acetyltransferase
malP	b3417	1,6906	0,0124	maltodextrin phosphorylase monomer
malT	b3418	0,4985	0,0239	MalT-MalK
marA	b1531	0,5442	0,0225	MarA transcriptional activator
mazE	b2783	0,8900	0,0434	antitoxin of the MazEF "addiction module"
mcrA	b1159	0,4973	0,0172	restriction of DNA at 5-methylcytosine residues
mcrB	b4346	1,3712	0,0144	MrcB subunit of 5-methylcytosine restriction system
mdaB	b3028	0,5909	0,0179	NADPH quinone reductase
mdoG	b1048	1,3670	0,0155	periplasmic glucan (MDO) biosynthesis protein
mdtF	b3514	2,2727	0,0041	YhiV
mdtK	b1663	0,4631	0,0216	NorE multidrug efflux MATE transporter
mdtN	b4082	1,4199	0,0116	putative membrane protein
menF	b2265	0,3329	0,0082	isochorismate synthase, menaquinone-specific
metC	b3008	1,3616	0,0383	L-cysteine desulfhydrase / cystathionine-beta-lyase
mgrB	b1826	0,6490	0,0364	hypothetical protein; product of a gene induced by low magnesium
minC	b1176	0,1945	0,0010	cell division inhibitor of the MinC-MinD-MinE and DicB-MinC systems that regulate septum placement
minD	b1175	0,3435	0,0101	membrane ATPase of the MinC-MinD-MinE system that regulates septum placement
minE	b1174	0,3672	0,0145	cell division topological specificity factor and inhibitory component of the MinC-MinD-MinE system that regulates septum placement
mltC	b2963	0,5062	0,0384	membrane-bound lytic murein transglycosylase C
mnmC	b2324	0,5470	0,0326	bifunctional enzyme catalyzing the formation of mnm5s2U in tRNA
mobA	b3857	0,6706	0,0302	molybdopterin guanine dinucleotide synthase
motB	b1889	0,7051	0,0060	MotB protein, enables flagellar motor rotation, linking torque machinery to cell wall

gene	blattner	ratio A/B	p-value	function
mreB	b3251	0,5301	0,0235	rod shape-determining protein
msbB	b1855	0,3370	0,0177	myristoyl acyltransferase
msrB	b1778	1,0943	0,0060	methionine sulfoxide reductase B / protein-methionine-S-oxide reductase / methionine sulfoxide reductase
mtlD	b3600	0,4275	0,0087	mannitol-1-phosphate 5-dehydrogenase
mukE	b0923	0,4201	0,0052	protein involved in chromosome partitioning
mukF	b0922	0,2947	0,0054	Ca ²⁺ -binding protein involved in chromosome partitioning
murC	b0091	1,5288	0,0169	UDP-N-acetylmuramate-alanine ligase
murI	b3967	2,4431	0,0020	glutamate racemase
mutM	b3635	1,4678	0,0408	formamidopyrimidine DNA glycosylase
mutY	b2961	0,3818	0,0326	adenine glycosylase; G.C --> T.A transversions
nadD	b0639	2,2259	0,0009	nicotinate-mononucleotide adenylyltransferase
nadE	b1740	0,7970	0,0374	NAD ⁺ synthase, glutamine dependent / NAD ⁺ synthase, NH ₃ -dependent
nadK	b2615	1,2935	0,0461	NAD kinase monomer
nagZ	b1107	0,5177	0,0214	β-N-acetylglucosaminidase
nanR	b3226	0,3753	0,0253	NanR transcriptional regulator
napC	b2202	1,5349	0,0131	cytochrome c protein
narI	b1227	1,4294	0,0314	nitrate reductase A, γ subunit
narP	b2193	0,5047	0,0363	NarP-Phosphorylated transcriptional regulator
narX	b1222	0,7241	0,0227	NarX-Phis
ndh	b1109	0,3534	0,0481	NADH cupric reductase / NADH dehydrogenase II
nfo	b2159	0,7313	0,0447	endonuclease IV
nhaA	b0019	1,6748	0,0323	sodium/proton NhaA transporter
nhaB	b1186	0,7111	0,0329	NhaB sodium/proton transporter
nhaR	b0020	1,5626	0,0364	NhaR-Na ⁺ transcriptional activator
nirD	b3366	1,2931	0,0487	nitrite reductase, small subunit
nlpB	b2477	0,4282	0,0017	lipoprotein-34
nlpD	b2742	0,5889	0,0384	NlpD putative outer membrane lipoprotein
nmpC	b0553	0,2798	0,0066	outer membrane porin protein; locus of qsr prophage
nrdH	b2673	1,5595	0,0197	glutaredoxin-like protein; hydrogen donor
nrfB	b4071	1,4551	0,0140	nitrite reductase complex
nrfG	b4076	0,7857	0,0445	maturation of formate-dependent nitrite reductase complex
nth	b1633	2,1800	0,0177	endonuclease III; specific for apurinic and/or apyrimidinic sites
nudF	b3034	0,5025	0,0228	hypothetical protein
nudH	b2830	0,4636	0,0223	putative invasion protein
nuoA	b2288	1,6995	0,0472	NADH dehydrogenase I
nuoB	b2287	1,5197	0,0379	NADH dehydrogenase I
nuoE	b2285	1,4198	0,0304	NADH dehydrogenase I
nuoF	b2284	1,4220	0,0317	NADH dehydrogenase I
nusG	b3982	0,2852	0,0347	component in transcription antitermination
ompX	b0814	1,4445	0,0493	outer membrane protein X
osmB	b1283	3,4496	0,0098	OsmB osmotically inducible lipoprotein
pabA	b3360	1,6781	0,0002	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
pabB	b1812	0,5495	0,0354	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
pabC	b1096	0,3442	0,0019	para-aminobenzoate synthase multi-enzyme complex / para-aminobenzoate synthase
panB	b0134	0,7353	0,0027	3-methyl-2-oxobutanoate hydroxymethyltransferase monomer
panE	b0425	0,5460	0,0418	2-dehydropanoate reductase
parC	b3019	0,4320	0,0075	Topoisomerase IV subunit A
pcnB	b0143	0,6795	0,0070	poly(A) polymerase I
pdxA	b0052	1,3711	0,0238	PdxA dehydrogenase/decarboxylase
pdxK	b2418	1,2254	0,0374	pyridoxamine kinase / hydroxymethylpyrimidine kinase / pyridoxal kinase
pepA	b4260	0,3097	0,0122	aminopeptidase A/I
pepB	b2523	2,2644	0,0239	aminopeptidase (AP)
pepP	b2908	1,3593	0,0065	proline aminopeptidase P II
pepT	b1127	0,6833	0,0395	peptidase T
pgm	b0688	1,5303	0,0417	phosphoglucomutase
pgpB	b1278	0,4697	0,0419	phosphatidylglycerophosphatase B
pheA	b2599	0,6656	0,0384	chorismate mutase / prephenate dehydratase
pheT	b1713	0,7457	0,0492	phenylalanyl-tRNA synthetase β-chain
phoP	b1130	0,6028	0,0020	PhoP-Phosphorylated transcriptional dual regulator
pitB	b2987	0,4848	0,0403	PitB
plsC	b3018	0,4674	0,0213	1-acylglycerol-3-phosphate acyltransferase
pmbA	b4235	0,4596	0,0021	protease involved in Microcin B17 maturation and in sensitivity to the DNA gyrase inhibitor LetD
pmrF	b2254	0,5087	0,0075	undecaprenyl phosphate-L-Ara4FN transferase
pncA	b1768	1,5147	0,0154	pyrazinamidase / nicotinamidase
polB	b0060	3,0331	0,0022	DNA polymerase II
poxA	b4155	0,4978	0,0301	putative regulator of pyruvate oxidase
pphB	b2734	1,5408	0,0047	protein phosphatase 2 / protein-tyrosine-phosphatase / phosphoprotein phosphatase
ppk	b2501	0,3409	0,0076	polyphosphate kinase
pppA	b2972	0,8174	0,0270	prepilin peptidase

gene	blattner	ratio A/B	p-value	function
pqqL	b1494	2,4892	0,0097	putative zinc peptidase
prkB	b3355	0,6558	0,0194	probable phosphoribulokinase
prmA	b3259	1,1549	0,0237	methylation of 50S ribosomal subunit protein L11
proB	b0242	0,4436	0,0305	gamma-glutamyl kinase-GP-reductase multienzyme complex
proQ	b1831	0,4270	0,0085	protein that affects osmoregulation of ProP transporter
prpR	b0330	1,3979	0,0217	PrpR transcriptional regulator
pspE	b1308	1,3420	0,0120	thiosulfate sulfurtransferase
pssA	b2585	0,3090	0,0108	phosphatidylserine synthase
ptsA	b3947	1,4554	0,0198	PEP-protein phosphotransferase system enzyme I
purA	b4177	0,5294	0,0086	adenylosuccinate synthase
purC	b2476	0,1639	0,0003	phosphoribosylaminoimidazole-succinocarboxamide synthase
purE	b0523	0,2509	0,0013	N5-carboxyaminoimidazole ribonucleotide mutase
purF	b2312	0,2414	0,0192	amidophosphoribosyl transferase
purM	b2499	0,1577	0,0004	phosphoribosylformylglycinamide cyclo-ligase
purN	b2500	0,5155	0,0120	phosphoribosylglycinamide formyltransferase
purR	b1658	0,3655	0,0001	PurR transcriptional repressor
purT	b1849	0,6975	0,0250	GAR transformylase 2
purU	b1232	0,4724	0,0343	formyltetrahydrofolate deformylase
puuC	b1300	1,2759	0,0124	aldehyde dehydrogenase
pykA	b1854	1,2788	0,0072	pyruvate kinase II monomer
pykF	b1676	0,6019	0,0200	pyruvate kinase I monomer
pyrC	b1062	0,5738	0,0154	dihydroorotase
pyrF	b1281	0,3505	0,0074	orotidine-5'-phosphate-decarboxylase
qseB	b3025	0,5963	0,0366	putative 2-component transcriptional regulator
radC	b3638	0,7993	0,0107	hypothetical protein
rarA	b0892	1,3775	0,0153	recombination factor
rbsA	b3749	1,3686	0,0067	ribose ABC transporter
rdoA	b3859	0,3650	0,0037	cytoplasmic protein of low abundance
recB	b2820	1,3049	0,0003	RecB; DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recF	b3700	1,8782	0,0203	ssDNA and dsDNA binding, ATP binding
recN	b2616	3,2489	0,0013	protein used in recombination and DNA repair
rfaJ	b3626	2,9390	0,0359	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
rfaK	b3623	2,5429	0,0162	lipopolysaccharide core biosynthesis; probably hexose transferase
rfaS	b3629	2,4712	0,0160	lipopolysaccharide core biosynthesis
rfaY	b3625	2,7443	0,0257	lipopolysaccharide core biosynthesis
rfaZ	b3624	2,8758	0,0135	protein involved in KdoIII attachment during lipopolysaccharide core biosynthesis
rfbX	b2037	1,5328	0,0192	RfbX lipopolysaccharide PST transporter
rfc	b2035	2,1537	0,0085	O-antigen polymerase
rfe	b3784	0,2504	0,0025	undecaprenyl-phosphate α-N-acetylglucosaminyl transferase
rffC	b3790	1,8384	0,0174	TDP-fucosamine acetyltransferase
rhaR	b3906	1,5371	0,0023	RhaR-L-rhamnose transcriptional activator
rhIE	b0797	0,5998	0,0306	DEAD-box-containing ATP-dependent RNA helicase family member
rhsD	b0497	0,3038	0,0094	RhsD protein in rhs element
ribB	b3041	0,4756	0,0036	3,4-dihydroxy-2-butanone 4-phosphate synthase
ribC	b1662	0,6034	0,0484	riboflavin synthase
ribF	b0025	0,2311	0,0048	riboflavin kinase / FMN adenylyltransferase
rimI	b4373	1,2616	0,0232	acetylates N-terminal alanine of 30S ribosomal subunit protein S18 / ribosomal-protein-alanine N-acetyltransferase
rimJ	b1066	0,3654	0,0033	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
rluE	b1135	1,5925	0,0139	23S rRNA pseudouridine synthase
rnC	b2567	0,3545	0,0116	RNase III, ds RNA
rpmA	b3185	1,2009	0,0086	50S ribosomal subunit protein L27
rpmB	b3637	0,7069	0,0448	50S ribosomal subunit protein L28
rpmF	b1089	1,3157	0,0137	50S ribosomal subunit protein L32
rpoD	b3067	2,3387	0,0271	sigma70 factor
rpoE	b2573	0,6299	0,0405	sigmaE
rpoH	b3461	1,4151	0,0363	sigma32 factor
rseA	b2572	0,4158	0,0006	anti-sigma factor that inhibits sigmaE
rseB	b2571	0,5185	0,0085	negative regulator of sigmaE; interacts with RseA and stimulates binding of RseA to sigmaE
rssA	b1234	0,5582	0,0116	hypothetical protein
rssB	b1235	0,6895	0,0442	RssB-P
rsxA	b1627	1,9291	0,0099	integral membrane protein of SoxR-reducing complex
rsxB	b1628	1,6538	0,0104	member of SoxR-reducing complex
rsxC	b1629	2,0272	0,0303	member of SoxR-reducing complex
rsxD	b1630	1,5930	0,0439	integral membrane protein of SoxR-reducing complex
rsxE	b1632	2,2544	0,0002	integral membrane protein of SoxR-reducing complex
rsxG	b1631	2,4324	0,0084	member of SoxR-reducing complex
rtn	b2176	1,1293	0,0298	hypothetical protein
sanA	b2144	0,4376	0,0187	vancomycin sensitivity
sbcD	b0398	1,3094	0,0159	ATP-dependent dsDNA exonuclease

gene	blattner	ratio A/B	p-value	function
sdaB	b2797	1,2729	0,0279	L-threonine deaminase II / L-serine deaminase 2
sdhA	b0723	2,4428	0,0087	succinate dehydrogenase flavoprotein
sdhB	b0724	1,8201	0,0024	succinate dehydrogenase iron-sulfur protein
sdhC	b0721	2,3445	0,0253	succinate dehydrogenase membrane protein
sdhD	b0722	1,9449	0,0060	succinate dehydrogenase membrane protein
sdiA	b1916	0,5260	0,0202	SdiA transcriptional activator
secE	b3981	0,2013	0,0210	Sec Protein Secretion Complex
secG	b3175	0,5355	0,0233	Sec Protein Secretion Complex
sfsB	b3188	1,4450	0,0295	Nlp transcriptional regulator
shiA	b1981	0,3314	0,0445	ShiA shikimate MFS transporter
skp	b0178	1,3482	0,0022	periplasmic chaperone
smg	b3284	0,4759	0,0018	hypothetical protein
smpA	b2617	2,0368	0,0327	SmpA small membrane protein A
smtA	b0921	0,1981	0,0013	S-adenosylmethionine-dependent methyltransferase
sodC	b1646	0,5884	0,0295	superoxide dismutase precursor (Cu-Zn)
speC	b2965	1,1224	0,0484	ornithine decarboxylase, biosynthetic
speG	b1584	0,4098	0,0187	spermidine acetyltransferase
spr	b2175	0,3174	0,0244	putative lipoprotein
spy	b1743	1,6823	0,0465	periplasmic protein related to spheroblast formation
sra	b1480	0,5126	0,0007	30S ribosomal subunit protein S22; sub-stoichiometric stationary phase ribosomal component
srlR	b2707	0,4372	0,0018	GutR-sorbitol
srnB	b2576	0,2487	0,0347	SrnB, DEAD-box RNA helicase
sscR	b2765	0,5881	0,0085	putative 6-pyruvoyl tetrahydrobiopterin synthase
sspA	b3229	1,4235	0,0255	regulator of transcription; stringent starvation protein A
sthA	b3962	1,4674	0,0398	soluble pyridine nucleotide transhydrogenase
sucA	b0726	1,7215	0,0420	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
sufS	b1680	1,4919	0,0303	L-selenocysteine lyase (and L-cysteine desulfurase) monomer
sulA	b0958	0,3282	0,0018	suppressor of Ion; inhibits cell division and ftsZ ring formation
tam	b1519	1,3876	0,0359	trans-aconitate methyltransferase
tap	b1885	2,0690	0,0425	MCP-IV
tatB	b3838	1,3899	0,0436	TatABCE protein export complex
tatC	b3839	1,3590	0,0079	TatABCE protein export complex
tdcB	b3117	1,5829	0,0012	threonine dehydratase (catabolic)
tdcC	b3116	0,6742	0,0130	TdcC threonine STP transporter
tesA	b0494	0,4687	0,0017	lysophospholipase L₁ / thioesterase I
thyA	b2827	2,4688	0,0437	thymidylate synthase
tktA	b2935	0,7435	0,0147	transketolase I
tolC	b3035	0,6930	0,0345	TolC outer membrane channel
torS	b0993	0,8969	0,0128	TorS-Phis850
torY	b1873	0,3115	0,0139	trimethylamine N-oxide reductase III, c-type cytochrome subunit
torZ	b1872	0,7072	0,0237	trimethylamine N-oxide reductase III, TorZ subunit
trkH	b3849	0,6885	0,0381	TrkH potassium ion Trk Transporter
trmH	b3651	1,8914	0,0192	tRNA (Gm18) 2'-O-methyltransferase
trpE	b1264	0,3805	0,0021	anthranilate synthase component I
trxB	b0888	2,0565	0,0480	thioredoxin reductase monomer
tsx	b0411	0,2461	0,0277	nucleoside channel; receptor of phage T6 and colicin K
ttk	b3641	0,6729	0,0216	Ttk transcriptional regulator
tufA	b3339	0,7291	0,0156	elongation factor Tu
tyrR	b1323	0,7217	0,0246	TyrR-Phenylalanine transcriptional repressor
ubiC	b4039	0,2269	0,0075	chorismate pyruvate lyase
udk	b2066	1,5831	0,0047	uridine kinase / cytidine kinase
ugpB	b3453	1,9109	0,0225	glycerol-3-P ABC transporter / transport
ulaG	b4192	1,5035	0,0480	putative L-ascorbate 6-phosphate lactonase
uppS	b0174	0,6969	0,0442	subunit of undecaprenyl diphosphate synthase
uspF	b1376	0,5835	0,0176	nucleotide binding protein
uvrB	b0779	1,7413	0,0390	DNA repair; excision nuclease subunit B
uvrY	b1914	0,5143	0,0135	UvrY- Phosphorylated transcriptional regulator
vsr	b1960	0,6583	0,0004	DNA mismatch endonuclease of the very short patch (VSP) mismatch repair pathway
wbbI	b2034	1,8917	0,0454	hypothetical protein; not required for colanic acid biosynthesis
wcaB	b2058	3,4010	0,0356	putative transferase
wcaC	b2057	3,4672	0,0035	putative glycosyl transferase
wcaE	b2055	2,1253	0,0353	putative colanic acid biosynthesis glycosyl transferase
wcaF	b2054	2,3400	0,0172	putative transferase
wcaJ	b2047	3,5268	0,0124	putative colanic acid biosynthesis UDP-glucose lipid carrier transferase
wcaK	b2045	3,6607	0,0020	putative galactokinase (EC 2.7.1.6).
wcaL	b2044	3,4923	0,0027	putative colanic acid biosynthesis glycosyl transferase
wcaM	b2043	3,6739	0,0018	hypothetical protein
wzc	b2060	2,2224	0,0433	tyrosine kinase involved in colanic acid biosynthesis
wzxC	b2046	3,2937	0,0149	WzxC

gene	blattner	ratio A/B	p-value	function
wzxE	b3792	1,7476	0,0290	metabolism; biosynthesis of macromolecules (cellular constituents); enterobacterial common antigen (surface glycolipid) transport
wzzE	b3785	0,5895	0,0452	putative transport protein
xapR	b2405	0,3135	0,0382	XapR transcriptional activator
xdhB	b2867	1,1750	0,0243	putative xanthine dehydrogenase subunit, FAD-binding domain
xdhD	b2881	1,6833	0,0105	putative oxidoreductase; possible component of selenate reductase with possible role in purine salvage
xerD	b2894	0,4958	0,0395	site-specific recombinase
xseB	b0422	0,1694	0,0020	exonuclease VII, small subunit
xylA	b3565	0,4106	0,0021	xylose isomerase
xylG	b3567	0,8076	0,0315	xylose ABC transporter
xylR	b3569	0,5108	0,0188	XylR-Xylose transcriptional activator
yabP	b0056	0,5438	0,0159	conserved hypothetical protein
yadL	b0137	0,6723	0,0395	putative adhesin-like protein
yaeB	b0195	1,4683	0,0342	hypothetical protein
yaeF	b0193	1,3932	0,0097	putative synthase of the YaeF/YiiX family
yaeH	b0163	0,7470	0,0373	putative structural protein
yafK	b0224	0,3497	0,0087	conserved protein; in enteroaggregative E. coli, YafK is required for development of biofilms
yagA	b0267	1,6510	0,0239	hypothetical protein
yagK	b0277	1,2809	0,0271	hypothetical protein
yagL	b0278	2,0628	0,0124	DNA-binding protein
yagN	b0280	0,4906	0,0152	hypothetical protein
yagU	b0287	0,5401	0,0210	conserved protein
yagZ	b0293	1,5683	0,0418	conserved hypothetical protein
yahA	b0315	0,3553	0,0092	hypothetical protein
yahG	b0321	1,5771	0,0398	conserved protein
yahJ	b0324	1,6920	0,0040	putative deaminase
yaiB	b0382	0,2451	0,0009	conserved hypothetical protein
yajR	b0427	1,2541	0,0397	YajR MFS transporter
ybaJ	b0461	0,2101	0,0016	conserved hypothetical protein
ybaN	b0468	0,4651	0,0207	hypothetical protein
ybaP	b0482	0,4012	0,0131	putative ligase
ybbK	b0489	1,2971	0,0106	putative protease
ybbW	b0511	1,7524	0,0306	YbbW NCS1 Transporter
ybcK	b0544	2,1084	0,0046	hypothetical protein
ybdM	b0601	1,5187	0,0100	conserved protein
ybeD	b0631	2,1582	0,0344	conserved hypothetical protein
ybeY	b0659	2,4213	0,0071	conserved hypothetical protein
ybeZ	b0660	2,9088	0,0292	putative ATP-binding protein
ybfE	b0685	1,8437	0,0015	hypothetical protein, transcriptionally regulated by LexA
ybgA	b0707	1,5859	0,0393	conserved protein
ybgD	b0719	0,5899	0,0284	putative fimbrial-like protein
ybhC	b0772	0,4417	0,0083	putative pectinesterase
ybiN	b0807	0,6910	0,0207	putative methyltransferase
ybjC	b0850	0,5669	0,0359	conserved hypothetical protein; gene is within soxRS regulon
ybjK	b0846	1,7319	0,0164	putative DEOR-type transcriptional regulator
ybjP	b0865	1,4541	0,0338	putative enzyme
ycaL	b0909	0,4083	0,0132	putative heat shock protein
ycbB	b0925	0,6763	0,0145	putative amidase
ycdO	b1018	1,6105	0,0013	conserved hypothetical protein
yceJ	b1057	1,4910	0,0123	putative cytochrome
ycfM	b1105	0,5966	0,0118	putative fibronectin-binding protein
ycfQ	b1111	2,1759	0,0130	hypothetical protein
ycgE	b1162	0,4795	0,0012	putative transcriptional regulator
ycgH_1	b1169	1,8719	0,0154	conserved protein; member of the Autotransporter family
ycgJ	b1177	0,7096	0,0429	hypothetical protein
ycgL	b1179	0,3597	0,0007	conserved hypothetical protein
ycgN	b1181	0,2099	0,0018	conserved hypothetical protein
ychF	b1203	1,8344	0,0127	putative GTP-binding protein
ychJ	b1233	0,4063	0,0421	conserved hypothetical protein
yciK	b1271	0,5205	0,0025	putative oxidoreductase
yciO	b1267	1,3356	0,0473	conserved protein
yciS	b1279	0,6049	0,0052	conserved hypothetical protein
ycjG	b1325	0,4886	0,0004	L-Ala-D/L-Glu epimerase, a muconate lactonizing enzyme
ycjZ	b1328	0,3753	0,0083	putative transcriptional regulator LYSR-type
ydaO	b1344	0,4843	0,0448	conserved protein
ydaT	b1358	1,2401	0,0281	hypothetical protein
ydbK	b1378	1,3365	0,0031	putative pyruvate synthase
ydcD	b1457	0,4394	0,0073	hypothetical protein
ydcV	b1443	1,5826	0,0274	YdcS/YdcT/YdcV/YdcU ABC transporter
ydeH	b1535	0,6334	0,0003	hypothetical protein

gene	blattner	ratio A/B	p-value	function
ydeI	b1536	0,7006	0,0434	conserved hypothetical protein
ydeO	b1499	1,8404	0,0071	putative ARAC-type regulatory protein
ydeP	b1501	1,8515	0,0329	acid resistance protein
ydeQ	b1502	1,5966	0,0329	putative adhesin; similar to FimH protein
ydeS	b1504	2,0807	0,0078	putative fimbrial-like protein
ydfH	b1540	0,6051	0,0014	hypothetical protein
ydfT	b1559	1,2620	0,0433	hypothetical protein
YdgE	b1599	0,5062	0,0374	YdgE SMR Protein
ydgI	b1605	1,2957	0,0413	ArcD APC transporter
ydgT	b1625	0,2841	0,0002	conserved hypothetical protein
ydhF	b1647	0,5142	0,0040	putative oxidoreductase, NAD(P)-linked
ydhH	b1640	0,5712	0,0220	conserved hypothetical protein
ydhK	b1645	0,7743	0,0177	putative membrane protein
ydhR	b1667	0,5054	0,0468	conserved hypothetical protein
ydiA	b1703	0,3698	0,0021	conserved protein
ydiO	b1695	1,7686	0,0429	putative acyl-CoA dehydrogenase
ydjF	b1770	0,6322	0,0205	putative DEOR-type transcriptional regulator
ydjG	b1771	1,1870	0,0339	putative oxidoreductase
ydjJ	b1774	0,7716	0,0258	putative oxidoreductase
ydjO	b1730	0,7452	0,0045	putative enzyme
yeaK	b1787	0,5384	0,0111	conserved hypothetical protein
yeaL	b1789	0,5540	0,0222	hypothetical protein
yeaO	b1792	0,7835	0,0264	conserved hypothetical protein
yeaS	b1798	1,1343	0,0208	hypothetical protein
yebC	b1864	1,9628	0,0112	conserved protein
yebE	b1846	1,4183	0,0339	conserved hypothetical protein
yebF	b1847	1,6011	0,0157	conserved hypothetical protein
yebG	b1848	2,0455	0,0150	hypothetical protein; gene is part of SOS regulon
yebK	b1853	0,6198	0,0144	hypothetical protein
yebN	b1821	0,1208	0,0031	putative membrane protein, terpenoid synthase-like
yebQ	b1828	1,7129	0,0232	YebQ
yebR	b1832	0,2946	0,0066	conserved hypothetical protein
yebY	b1839	0,3459	0,0078	conserved hypothetical protein
yebZ	b1840	0,5397	0,0052	putative resistance protein
yecN	b1869	0,4794	0,0004	putative membrane protein
yecO	b1870	0,6886	0,0159	putative methyltransferase
yedI	b1958	0,7429	0,0417	hypothetical protein
yedL	b1932	0,8697	0,0339	putative acyl-CoA N-acyltransferase
yedS_1	b1964	0,5165	0,0447	putative outer membrane protein
yedS_3	b1966	0,5465	0,0327	putative outer membrane protein
yedW	b1969	0,2470	0,0035	putative 2-component transcriptional response regulator
yeeN	b1983	7,1154	0,0127	conserved protein
yeeT	b2003	1,3786	0,0008	hypothetical protein
yeeU	b2004	2,0721	0,0304	antitoxin of the YeeV-YeeU toxin-antitoxin pair
yefM	b2017	1,3962	0,0282	antitoxin of the YoeB-YefM toxin-antitoxin pair
yegE	b2067	1,7115	0,0038	putative sensor-type protein
yegI	b2070	0,5358	0,0484	putative chaperonin
yegS	b2086	3,9159	0,0491	conserved protein
yehD	b2111	2,1221	0,0057	putative fimbrial-like protein
yeiE	b2157	0,6563	0,0387	LYSR-type transcriptional regulator
yejE	b2179	1,5636	0,0046	YejA/YejB/YejE/YejF ABC transporter
yejG	b2181	1,5816	0,0091	conserved hypothetical protein
yfaE	b2236	1,4667	0,0481	conserved hypothetical protein, 2Fe-2S ferredoxin-related
yfbE	b2253	0,3390	0,0015	UDP-L-Ara4O C-4" transaminase
yfbN	b2273	0,6296	0,0373	conserved hypothetical protein
yfcL	b2325	1,4297	0,0332	conserved hypothetical protein
yfcR	b2335	1,6257	0,0449	putative fimbrial protein
yfdK	b2354	0,8266	0,0174	hypothetical protein
yfdO	b2358	1,7079	0,0258	hypothetical protein
yfdP	b2359	1,3431	0,0013	hypothetical protein
yfgA	b2516	0,3616	0,0096	putative membrane protein
yfhG	b2555	0,4592	0,0050	conserved protein
yfiB	b2605	0,6708	0,0141	putative outer membrane protein
yfiF	b2581	0,4349	0,0213	hypothetical protein
yfjD	b4461	1,1920	0,0274	putative membrane protein, hemolysin-like
yfjG	b2619	1,8537	0,0213	toxin of a putative toxin-antitoxin pair
yfjJ	b2626	1,4374	0,0028	hypothetical protein
ygaH	b2683	0,3070	0,0005	putative transport protein
ygaZ	b2682	0,2806	0,0339	hypothetical protein

gene	blattner	ratio A/B	p-value	function
ygcH	b2756	1,5103	0,0470	hypothetical protein
ygcK	b2759	0,5237	0,0303	hypothetical protein
ygcL	b2760	0,4734	0,0068	hypothetical protein with possible relationship to novobiocin and deoxycholate resistance
ygcT	b2773	1,3680	0,0295	hypothetical protein
ygdR	b2833	2,0681	0,0458	conserved hypothetical protein
ygeO	b2857	1,4246	0,0028	hypothetical protein
ygfB	b2909	0,6455	0,0197	conserved hypothetical protein
ygfM	b2880	1,8759	0,0385	putative oxidoreductase with a FAD-binding domain; possible component of selenate reductase
ygfZ	b2898	0,6440	0,0118	conserved protein
yggG	b2936	1,3788	0,0242	conserved protein
yggH	b2960	0,3883	0,0278	tRNA (m7G46) methyltransferase
yggJ	b2946	0,4258	0,0253	conserved hypothetical protein
yggL	b2959	0,4522	0,0265	conserved hypothetical protein
yggN	b2958	0,5163	0,0247	conserved hypothetical protein
yggX	b2962	0,3380	0,0026	conserved hypothetical protein with role in oxidation-resistance of iron-sulfur clusters
yghO	b2981	1,4352	0,0178	putative acyltransferase
ygiA	b3036	0,6569	0,0453	hypothetical protein
ygiD	b3039	1,2199	0,0229	putative enzyme with dioxygenase domain
ygiF	b3054	0,4578	0,0171	conserved hypothetical protein
ygiL	b3043	0,4481	0,0024	putative fimbrial-like protein
ygiU	b3022	0,5823	0,0419	putative cyanide hydratase
ygiD	b3064	0,5001	0,0291	putative O-sialoglycoprotein endopeptidase
yhbY	b3180	2,4069	0,0493	possible RNA-binding protein
yhcE	b3217	1,6908	0,0322	hypothetical protein
yhdA	b3252	0,4853	0,0034	conserved protein
yhdN	b3293	2,2147	0,0304	conserved hypothetical protein
yheN	b3345	0,7236	0,0466	conserved hypothetical protein
yheO	b3346	0,6587	0,0186	hypothetical protein
yhfA	b3356	0,4740	0,0196	conserved hypothetical protein
yhfG	b3362	1,5910	0,0072	conserved hypothetical protein
yhfL	b3369	0,7399	0,0465	hypothetical protein
yhfU	b3378	1,5087	0,0383	hypothetical protein
yhfX	b3381	1,4728	0,0231	conserved protein
yhhH	b3483	0,7173	0,0406	hypothetical protein
yhhJ	b3485	1,2472	0,0276	YhiH/YhhJ ABC transporter
yhhS	b3473	0,5354	0,0441	YhhS MFS transporter
yhhZ	b3442	1,5149	0,0020	conserved protein
yhiS	b3504	1,7373	0,0348	conserved protein
yhjA	b3518	1,6786	0,0050	putative cytochrome C peroxidase (EC 1.11.1)
yhjR	b3535	0,3739	0,0105	hypothetical protein
yhjY	b3548	1,6225	0,0111	putative lipase
yi5A	b3557	0,5204	0,0060	IS5 protein
yiaA	b3562	0,3268	0,0239	hypothetical protein
yiaB	b3563	0,2619	0,0011	inner membrane protein
yiaN	b3578	0,5853	0,0361	YiaMNO Binding Protein-dependent Secondary (TRAP) Transporter
yiaW	b3587	0,4349	0,0065	hypothetical protein
yibD	b3615	2,3369	0,0409	putative glycosyltransferase
yibJ	b3595	1,4681	0,0140	hypothetical protein
yicE	b3654	0,2155	0,0218	YicE NCS2 transporter
yicL	b3660	0,5423	0,0107	inhibitor of heme biosynthesis
yicN	b3663	0,7539	0,0488	conserved hypothetical protein
yidF	b3674	1,4127	0,0375	putative transcriptional regulator
yidP	b3684	1,4297	0,0316	putative transcriptional regulator
yieG	b3714	0,5508	0,0395	putative membrane / transport protein
yieH	b3715	0,4511	0,0214	putative enzyme with a phosphatase-like domain
yieN	b3746	1,6277	0,0158	putative 2-component regulator
yihF	b3861	0,7083	0,0087	conserved protein
yihI	b3866	0,6516	0,0111	conserved protein
yihP	b3877	1,3286	0,0172	YihP GPH transporter
yihS	b3880	1,5315	0,0430	conserved hypothetical protein
yihT	b3881	1,5667	0,0274	putative aldolase
yihW	b3884	0,5351	0,0149	putative DEOR-type transcriptional regulator
yihX	b3885	0,5078	0,0280	putative phosphatase
yiiR	b3921	0,7676	0,0009	putative membrane protein
yjbE	b4026	2,5798	0,0431	conserved hypothetical protein
yjbQ	b4056	0,5074	0,0444	conserved hypothetical protein
yjdA	b4109	0,2889	0,0378	hypothetical protein
yjeB	b4178	0,3239	0,0058	conserved protein with a Winged helix domain
yjeF	b4167	0,6840	0,0052	putative kinase

gene	blattner	ratio A/B	p-value	function
yjeM	b4156	0,5081	0,0299	YjeM APC transporter
yjeQ	b4161	0,5621	0,0278	GTPase and putative translation factor / GTPase
yjfi	b4181	0,4271	0,0151	conserved hypothetical protein
yjfk	b4183	0,6194	0,0161	conserved hypothetical protein
yjgN	b4257	0,8020	0,0292	putative membrane protein possible involved in transport
yjgP	b4261	0,6738	0,0413	putative transmembrane protein possibly involved in transport
yjhB	b4279	1,8533	0,0006	YjhB MFS transporter
yjhH	b4298	0,5277	0,0150	putative lyase/synthase
yjiJ	b4332	0,6007	0,0492	putative transport protein
yjiP	b4338	1,2689	0,0190	hypothetical protein
yjiY	b4354	0,7537	0,0416	putative carbon starvation protein
yjjG	b4374	1,8650	0,0152	phosphatase
yjjN	b4358	1,3488	0,0441	putative oxidoreductase
yjjQ	b4365	0,5404	0,0231	putative regulator
yjjV	b4378	1,6584	0,0452	putative hydrolase
ykgC	b0304	0,4244	0,0245	putative oxidoreductase
ykgE	b0306	0,2061	0,0044	putative dehydrogenase subunit
ykgF	b0307	0,3156	0,0100	putative dehydrogenase
ylaB	b0457	1,6806	0,0383	conserved protein
yliI	b0837	2,0458	0,0402	putative dehydrogenase
ymbA	b0952	1,2388	0,0174	conserved protein
ymdA	b1044	1,4317	0,0156	conserved hypothetical protein
ymfM	b1148	1,7959	0,0269	hypothetical protein
ymfO	b1151	1,4852	0,0432	hypothetical protein
ymjA	b1295	0,4272	0,0063	hypothetical protein
ynaE	b1375	0,4467	0,0021	hypothetical protein
ynaK	b1365	0,5999	0,0473	hypothetical protein
yncA	b1448	0,6404	0,0336	putative N-acetyltransferase
yncI	b1458	2,0101	0,0095	conserved protein
yneH	b1524	0,6554	0,0043	putative glutaminase
ynfB	b1583	0,3413	0,0147	conserved hypothetical protein
ynfG	b1589	2,1065	0,0456	oxidoreductase, Fe-S subunit paralog of DmsB
ynfN	b1551	0,5507	0,0270	hypothetical protein
yoaH	b1811	0,7603	0,0410	conserved hypothetical protein
yobA	b1841	0,4646	0,0330	hypothetical protein
yobD	b1820	1,1210	0,0371	conserved protein
ypfI	b2475	0,4521	0,0132	conserved protein
yphF	b2548	1,2411	0,0065	YphD/YphE/YphF ABC transporter
ypjA	b2647	0,5454	0,0295	putative outer membrane protein
ypjC	b2650	1,9137	0,0202	hypothetical protein
ypjF	b2646	1,4842	0,0227	member of the YeeV, Ykfl, YpjF family of toxin proteins
yqaA	b2689	0,3779	0,0112	putative integral membrane protein
yqeF	b2844	1,4118	0,0054	putative acyltransferase
yqeI	b2847	0,4452	0,0151	putative sensory transducer
yqeJ	b2848	0,5502	0,0358	conserved hypothetical protein
yqiA	b3031	0,5500	0,0167	putative hydrolase
yqiJ	b3050	1,2244	0,0073	putative oxidoreductase
yqjI	b3071	1,2930	0,0385	conserved hypothetical protein
yraM	b3147	0,6143	0,0013	putative glycosylase
yrbK	b3199	0,5981	0,0347	conserved hypothetical protein
yrbL	b3207	0,4490	0,0310	conserved hypothetical protein; transcription is regulated by Mg ²⁺
yrdA	b3279	1,2726	0,0344	putative transferase
yrdD	b3283	0,4972	0,0020	putative DNA topoisomerase
yrfG	b3399	1,7111	0,0126	putative hydrolase with a phosphatase-like domain
ytfH	b4212	1,2193	0,0109	putative transcriptional regulator
ytfM	b4220	0,6790	0,0262	hypothetical protein
zapA	b2910	0,2597	0,0002	ZapA protein, localizes to the cytokinetic ring
zntR	b3292	2,0077	0,0173	ZntR transcriptional regulator
znuA	b1857	0,5075	0,0106	ZnuA/ZnuB/ZnuC ABC transporter
znuB	b1859	2,2343	0,0178	ZnuA/ZnuB/ZnuC ABC transporter
	b0332	1,2327	0,0317	
	b0395	0,7576	0,0331	

LZ41 (A) & LZ41fis (B)

aceB	b4014	0,4276	0,0445	malate synthase A
acrE	b3265	1,7547	0,0454	transmembrane protein affects septum formation and cell membrane permeability
add	b1623	0,8139	0,0457	deoxyadenosine deaminase / adenosine deaminase
adhE	b1241	0,5944	0,0064	PFL-deactivase / alcohol dehydrogenase / acetaldehyde dehydrogenase
adiA	b4117	0,7038	0,0075	Adi

gene	blattner	ratio A/B	p-value	function
adk	b0474	0,4914	0,0219	adenylate kinase
aer	b3072	0,3604	0,0182	aerotaxis sensor receptor, flavoprotein
afuB	b0263	0,6224	0,0389	AfuB
agn43	b2000	0,3450	0,0040	outer membrane fluffing protein, sim. to adhesin
ahpC	b0605	0,5014	0,0291	AhpC component
ahpF	b0606	0,5624	0,0434	AhpF component
aldA	b1415	0,7702	0,0392	putative succinate-semialdehyde dehydrogenase / aldehyde dehydrogenase
aldB	b3588	0,4765	0,0388	putative aminobutyraldehyde dehydrogenase / aldehyde dehydrogenase B
allR	b0506	0,3911	0,0082	AllR transcriptional regulator
amn	b1982	0,6432	0,0084	AMP nucleosidase
argO	b2923	1,8685	0,0322	arginine export protein
aroA	b0908	0,6815	0,0220	3-phosphoshikimate-1-carboxyvinyltransferase
aroB	b3389	1,7762	0,0173	3-dehydroquinate synthase
aroK	b3390	2,0007	0,0057	shikimate kinase I
arpA	b4017	0,7171	0,0434	regulator of acetyl CoA synthetase
artI	b0863	0,6821	0,0113	arginine ABC transporter
asnS	b0930	0,6778	0,0337	asparaginyI-tRNA synthetase
aspC	b0928	0,5126	0,0438	aspartate transaminase
aspS	b1866	0,5612	0,0181	aspartyl-tRNA synthetase
atpG	b3733	1,2411	0,0477	ATP synthase, F1 complex, gamma subunit
b0374	b0374	1,8747	0,0267	putative flagellin structural protein
b1364	b1364	1,9078	0,0056	hypothetical protein
bax	b3570	2,7324	0,0137	putative ATP-binding protein
bcsG	b3538	1,3907	0,0114	putative membrane protein
bioA	b0774	4,8174	0,0341	adenosylmethionine-8-amino-7-oxononanoate aminotransferase monomer
bioC	b0777	2,0996	0,0055	biotin biosynthesis; reaction prior to pimeloyl CoA
bioF	b0776	2,1697	0,0187	8-amino-7-oxononanoate synthase
btuE	b1710	0,4583	0,0002	vitamin B12 transport system
cdd	b2143	0,5184	0,0071	cytidine deaminase
cdsA	b0175	1,5062	0,0193	CDP-diglyceride synthetase
cld	b2027	1,6377	0,0049	regulator of length of O-antigen component of lipopolysaccharide chains
clpS	b0881	0,6844	0,0260	specificity factor for ClpA-ClpP chaperone-protease complex
cobC	b0638	1,5268	0,0269	alpha-ribazole-5'-P phosphatase
codA	b0337	0,5518	0,0394	cytosine deaminase
crl	b0240	0,5173	0,0122	Crl transcriptional regulator
crr	b2417	0,7022	0,0165	EIIBCMAIX
cspG	b0990	1,2495	0,0397	cold shock protein CspG
cybB	b1418	0,6780	0,0427	cytochrome b561
cyoB	b0431	1,4550	0,0005	cytochrome bo terminal oxidase subunit I
cyoD	b0429	1,8390	0,0014	cytochrome bo terminal oxidase subunit IV
cysE	b3607	1,3082	0,0119	cysteine synthase
cysZ	b2413	0,5453	0,0464	required for sulfate transport
cytR	b3934	0,6111	0,0078	CytR-cytidine
dadA	b1189	0,9183	0,0319	D-amino acid dehydrogenase, small subunit
dam	b3387	1,2185	0,0464	DNA adenine methylase
dapA	b2478	0,4234	0,0248	dihydrodipicolinate synthase
dapB	b0031	0,7373	0,0483	dihydrodipicolinate reductase
dcp	b1538	0,5793	0,0064	dipeptidyl carboxypeptidase II
def	b3287	2,0636	0,0181	peptide deformylase
degQ	b3234	1,3585	0,0176	serine endoprotease
dgoA	b3692	0,2418	0,0237	dgoA 3871635-3871018 : '2-dehydro-3-deoxyphosphogalactonate aldolase / dgoD 3871021-3869873 : galactonate dehydratase
dhaL	b1199	2,3586	0,0311	dihydroxyacetone kinase subunit L
dinB	b0231	0,3459	0,0147	DNA polymerase IV (Y-family DNA polymerase; translesion DNA synthesis)
dinD	b3645	0,3811	0,0274	DNA-damage-inducible protein
dld	b2133	0,2646	0,0007	D-lactate:Quinone Oxidoreductase
dnaE	b0184	2,0422	0,0092	DNA polymerase III, alpha subunit
dnaG	b3066	2,2790	0,0124	DNA biosynthesis; DNA primase
dnaK	b0014	0,6706	0,0044	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins
dps	b0812	0,6003	0,0129	stationary phase nucleoid protein that sequesters iron and protects DNA from damage
dsbA	b3860	0,4929	0,0066	disulfide oxidoreductase
dusB	b3260	3,5507	0,0209	tRNA dihydrouridine synthase
dxr	b0173	1,4993	0,0175	DXP reductoisomerase
ecfB	b2969	1,8193	0,0019	putative protein exporter (General Secretory Pathway)
ecfG	b3055	2,2413	0,0064	protein with possible extracytoplasmic function
ecfM	b3096	1,7005	0,0256	conserved hypothetical protein with possible extracytoplasmic function
eco	b2209	0,4839	0,0047	ecotin monomer; serine protease inhibitor
eda	b1850	0,6319	0,0048	oxaloacetate decarboxylase / 2-keto-3-deoxy-6-phosphogluconate aldolase / 2-keto-4-hydroxyglutarate aldolase
efp	b4147	1,3561	0,0306	elongation factor P (EF-P)
elaA	b2267	0,2865	0,0039	hypothetical protein

gene	blattner	ratio A/B	p-value	function
emrY	b2367	2,0045	0,0181	EmrY putative multidrug MFS transporter
eno	b2779	0,5823	0,0163	enolase
entA	b0596	4,0462	0,0315	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
entB	b0595	4,2178	0,0260	apo-EntB
essQ	b1556	2,3474	0,0281	hypothetical protein
evgA	b2369	2,3983	0,0080	EvgA-Phosphorylated transcriptional regulator
exbB	b3006	5,6978	0,0342	ExbB protein; uptake of enterochelin; tonB-dependent uptake of B colicins
exbD	b3005	7,3350	0,0026	ExbD uptake of enterochelin; tonB-dependent uptake of B colicins
fabB	b2323	1,1422	0,0378	beta-ketoacyl-ACP synthase I / malonyl-ACP decarboxylase
fadJ	b2341	0,6377	0,0434	FadJ monomer
fbaB	b2097	0,1525	0,0179	fructose bisphosphate aldolase monomer
fdx	b2525	1,5992	0,0271	oxidized ferredoxin
fecA	b4291	4,3615	0,0002	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fecB	b4290	11,8210	0,0049	ferric dicitrate uptake system
fecD	b4288	13,4703	0,0266	ferric dicitrate uptake system
fecI	b4293	2,5694	0,0143	sigma19 factor
fepA	b0584	2,2534	0,0377	FepA, outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D
fhuF	b4367	2,6792	0,0312	acts in reduction of ferrioxamine B iron
fimA	b4314	0,0452	0,0017	major type 1 subunit fimbrin (pilin)
fimI	b4315	0,2478	0,0086	fimbrial protein
fis	b3261	4,8968	0,0026	Fis transcriptional dual regulator
fixC	b0043	0,7563	0,0451	flavoprotein (electron transport), possibly involved in anaerobic carnitine metabolism
fkfB	b4207	0,4661	0,0011	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (a rotamase)
flgA	b1072	0,6317	0,0353	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgE	b1076	0,5821	0,0222	flagellar hook protein FlgE
flgH	b1079	1,4155	0,0024	flagellar L-ring protein FlgH; basal-body outer-membrane L (lipopolysaccharide layer) ring protein
fliC	b1923	0,7914	0,0186	flagellar biosynthesis; flagellin, filament structural protein
fliG	b1939	1,5644	0,0322	flagellar motor switch protein FliG; component of motor switching and energizing, enabling rotation and determining its direction
fliJ	b1942	1,5214	0,0394	flagellar biosynthesis protein FliJ
fliL	b1944	2,0419	0,0147	flagellar biosynthesis
fliM	b1945	2,0037	0,0079	flagellar motor switch protein FliM; component of motor switch and energizing, enabling rotation and determining its direction
fliN	b1946	1,5234	0,0159	flagellar motor switch protein FliN; component of motor switch and energizing, enabling rotation and determining its direction
fliP	b1948	1,8269	0,0083	flagellar biosynthesis protein FliP
fliQ	b1949	3,0840	0,0021	flagellar biosynthesis protein FliQ
fliR	b1950	7,4349	0,0077	flagellar biosynthesis protein FliR
flxA	b1566	0,4049	0,0066	hypothetical protein; gene is regulated by FliA
fmet	b3288	3,0666	0,0067	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase
folE	b2153	0,4596	0,0053	GTP cyclohydrolase I
folP	b3177	0,4636	0,0126	dihydropteroate synthase
frlA	b3370	0,7394	0,0427	YhfM methionine APC transporter
frr	b0172	0,7314	0,0363	ribosome recycling factor
fruL	b0079	1,7136	0,0205	fruR leader peptide
fruR	b0080	2,1871	0,0153	FruR transcriptional dual regulator
fryB	b2387	0,7759	0,0158	putative PTS system enzyme IIB component
ftnA	b1905	0,4482	0,0169	cytoplasmic ferritin, an iron storage protein)
ftsI	b0084	2,0097	0,0312	essential cell division protein FtsI; penicillin-binding protein 3
ftsK	b0890	1,3776	0,0159	essential cell division protein FtsK
ftsL	b0083	1,5537	0,0073	essential cell division protein FtsL
ftsQ	b0093	1,3855	0,0418	essential cell division protein FtsQ
ftsZ	b0095	0,8510	0,0421	essential cell division protein FtsZ
galF	b2042	1,2879	0,0298	homolog of Salmonella UTP--glucose-1-P uridylyltransferase, probably a UDP-gal transferase
galM	b0756	0,7402	0,0368	aldose-1-epimerase
gatC	b2092	0,5085	0,0245	EIIgGat
gatY	b2096	0,4530	0,0132	tagatose-1,6-bisphosphate aldolase 2
gcvA	b2808	2,3893	0,0386	GcvA transcriptional dual regulator
gcvR	b2479	0,5830	0,0331	GcvR-gly
ghrA	b1033	0,5389	0,0362	glyoxylate reductase
glcB	b2976	0,6074	0,0247	malate synthase G
glk	b2388	0,6440	0,0382	glucokinase
glmU	b3730	1,3338	0,0066	N-acetylglucosamine-1-phosphate uridylyltransferase / glucosamine-1-phosphate acetyltransferase
glnB	b2553	0,7567	0,0160	PII-UMP
glnH	b0811	1,3681	0,0225	glutamine ABC transporter
glnP	b0810	2,0480	0,0032	glutamine ABC transporter
glnQ	b0809	1,9701	0,0255	glutamine ABC transporter
gloB	b0212	1,6853	0,0005	glyoxalase II
glpD	b3426	1,5383	0,0086	glycerol 3-phosphate dehydrogenase, aerobic
glpE	b3425	1,5932	0,0002	thiosulfate sulfurtransferase
glpG	b3424	2,4244	0,0321	inner membrane-associated protein of glp regulon
glpQ	b2239	0,5777	0,0048	glycerophosphoryl diester phosphodiesterase, periplasmic

gene	blattner	ratio A/B	p-value	function
gltB	b3212	0,2558	0,0049	glutamate synthase (NADPH) large chain precursor
gltD	b3213	0,2960	0,0005	glutamate synthase (NADPH) small chain
gltF	b3214	2,1372	0,0310	regulator of gltBDF operon, induction of Ntr enzymes
gltX	b2400	0,6185	0,0045	glutamyl-tRNA synthetase
glyA	b2551	0,4249	0,0030	glycine hydroxymethyltransferase
gmd	b2053	0,3424	0,0173	GDP-mannose 4,6-dehydratase
gnd	b2029	0,7263	0,0098	6-phosphogluconate dehydrogenase (decarboxylating)
gpt	b0238	0,3020	0,0046	xanthine phosphoribosyltransferase / guanine phosphoribosyltransferase / hypoxanthine phosphoribosyltransferase
groE	b4142	0,7287	0,0389	GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity
grxB	b1064	0,5199	0,0055	oxidized glutaredoxin 2
gst	b1635	0,2880	0,0003	glutathione transferase
guaB	b2508	0,3418	0,0146	IMP dehydrogenase
hchA	b1967	0,3576	0,0101	heat shock protein (Hsp) 31
hdeA	b3510	0,5429	0,0329	acid-resistance protein, possible chaperone
hdhA	b1619	0,7009	0,0222	7-alpha-hydroxysteroid dehydrogenase
hemC	b3805	0,6080	0,0324	hydroxymethylbilane synthase
hemG	b3850	2,0623	0,0029	protoporphyrinogen oxidase
hemL	b0154	0,4775	0,0155	glutamate-1-semialdehyde aminotransferase
hepA	b0059	0,5983	0,0278	RNA Polymerase (RNAP)-binding ATPase and RNAP recycling factor
hflD	b1132	0,7830	0,0127	membrane protein in operon with purB
hipA	b1507	2,6139	0,0487	HipA transcriptional activator
hisC	b2021	0,4902	0,0017	histidine-phosphate aminotransferase
hisD	b2020	0,4810	0,0042	histidinal dehydrogenase / histidinol dehydrogenase
hisF	b2025	0,8798	0,0136	imidazole glycerol phosphate synthase, HisF subunit
hisH	b2023	0,6139	0,0394	imidazole glycerol phosphate synthase, HisH subunit
hisI	b2026	0,6499	0,0032	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphatase
hisJ	b2309	0,4481	0,0121	histidine ABC transporter
hofO	b3393	1,8479	0,0374	conserved hypothetical protein
hscA	b2526	1,6604	0,0128	chaperone, member of Hsp70 protein family
hsdR	b4350	2,3402	0,0036	host restriction; endonuclease R
hslO	b3401	2,0138	0,0492	molecular chaperone Hsp33
htrA	b0161	4,1874	0,0178	DegP
hycI	b2717	0,6596	0,0114	hydrogenase 3 maturation protease
ibpA	b3687	0,6656	0,0494	small heat shock protein IbpA
ilvY	b3773	2,5426	0,0045	IlvY transcriptional dual regulator
infA	b0884	1,2615	0,0395	protein chain initiation factor IF-1
infB	b3168	0,8553	0,0153	protein chain initiation factor IF-2
iscA	b2528	1,2803	0,0391	iron-sulfur cluster assembly protein
iscR	b2531	1,7491	0,0017	IscR transcriptional regulator
iscS	b2530	1,4813	0,0077	cysteine desulfurase monomer
iscX	b2524	1,6876	0,0213	protein with possible role in iron-sulfur cluster biogenesis
ispH	b0029	0,5317	0,0441	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase
kbl	b3617	0,7553	0,0413	2-amino-3-ketobutyrate CoA ligase
kdgR	b1827	0,6868	0,0412	putative ICLR-type transcriptional regulator
kdgT	b3909	1,6515	0,0454	KdgT 2-keto-3-deoxygluconate transporter
kduD	b2842	0,5804	0,0334	2-deoxy-D-gluconate 3-dehydrogenase
kduI	b2843	0,5660	0,0006	homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase
lctD	b3605	4,5610	0,0020	L-Lactate:Quinone Oxidoreductase
lepB	b2568	0,4975	0,0172	leader peptidase (signal peptidase I)
leuA	b0074	2,1920	0,0484	2-isopropylmalate synthase
lipB	b0630	0,5344	0,0060	lipoyl-protein ligase
lolB	b1209	0,7109	0,0354	outer membrane lipoprotein, localization of lipoproteins in the outer membrane
lpxB	b0182	2,4803	0,0069	lipid A disaccharide synthase
lpxD	b0179	1,9305	0,0077	UDP-3-O-[3-hydroxymyristoyl]glucosamine N-acetyltransferase
lysU	b4129	0,3741	0,0006	lysyl-tRNA synthetase (LysRSu), inducible
macB	b0879	0,7619	0,0000	MacAB macrolide efflux transporter complex
manY	b1818	0,5887	0,0161	EIIMan
map	b0168	1,6259	0,0237	methionine aminopeptidase
marA	b1531	2,1164	0,0161	MarA transcriptional activator
marR	b1530	1,7225	0,0168	MarR-salicylate
mdaB	b3028	1,6569	0,0030	NADPH quinone reductase
mdh	b3236	0,4517	0,0007	malate dehydrogenase
mdoC	b1047	6,6596	0,0265	protein required for succinyl modification of osmoregulated periplasmic glucans
mdoD	b1424	0,7811	0,0064	glucan biosynthesis protein D
menG	b3929	0,6569	0,0011	inhibitor of ribonuclease E (RNase E) activity
metB	b3939	0,5240	0,0189	O-succinylhomoserine lyase / O-succinylhomoserine(thiol)-lyase
metG	b2114	1,6218	0,0213	methionyl-tRNA synthetase
metK	b2942	1,3643	0,0040	MetK S-adenosylmethionine synthetase monomer
metN	b0199	3,0698	0,0232	L- and D-methionine uptake ABC permease

gene	blattner	ratio A/B	p-value	function
mgIB	b2150	0,4951	0,0238	galactose ABC transporter
mgsA	b0963	0,5158	0,0118	methylglyoxal synthase
miaB	b0661	0,5108	0,0076	hypothetical protein
mntR	b0817	1,3178	0,0124	putative toxin
moaE	b0785	0,5674	0,0315	molybdopterin synthase large subunit
moeB	b0826	0,5088	0,0285	molybdopterin biosynthesis
mog	b0009	0,6449	0,0095	required for the efficient incorporation of Mo into molybdoproteins
motB	b1889	0,7958	0,0468	MotB protein, enables flagellar motor rotation, linking torque machinery to cell wall
mraY	b0087	1,6065	0,0384	phospho-N-acetylmuramoyl-pentapeptide transferase
mraZ	b0081	2,0473	0,0380	protein encoded by an operon involved in formation of the cell envelope and cell division
mreB	b3251	0,7067	0,0373	rod shape-determining protein
mscL	b3291	0,5625	0,0188	MscL (Large Mechanosensitive Channel)
msrB	b1778	0,2242	0,0071	methionine sulfoxide reductase B / protein-methionine-S-oxide reductase / methionine sulfoxide reductase
mug	b3068	0,1598	0,0002	stationary phase mismatch/uracil DNA glycosylase
murB	b3972	0,6411	0,0055	UDP-N-acetylmuramate dehydrogenase
murG	b0090	1,8627	0,0219	N-acetylglucosaminyl transferase
mutM	b3635	0,5636	0,0298	formamidopyrimidine DNA glycosylase
nagB	b0678	0,6053	0,0321	glucosamine-6-phosphate deaminase
narL	b1221	0,3590	0,0003	NarL-Phosphorylated transcriptional dual regulator
narV	b1465	2,0037	0,0423	nitrate reductase Z, γ subunit
narX	b1222	0,4701	0,0282	NarX-Phis
nfnB	b0578	0,6965	0,0277	dihydropteridine reductase
nlpB	b2477	0,5501	0,0285	lipoprotein-34
nlpD	b2742	0,5577	0,0232	NlpD putative outer membrane lipoprotein
nrdA	b2234	2,5576	0,0170	ribonucleoside-diphosphate reductase / CDP reductase / UDP reductase / ADP reductase / GDP reductase
nrdB	b2235	1,5476	0,0143	ribonucleoside-diphosphate reductase / CDP reductase / UDP reductase / ADP reductase / GDP reductase
nudE	b3397	3,6839	0,0376	ADP-ribose diphosphatase
nupC	b2393	0,4373	0,0148	NupC nucleoside NUP transporter
nusB	b0416	0,6482	0,0130	transcription termination; L factor
ogrK	b2082	0,4525	0,0057	OgrK transcriptional regulator
ompA	b0957	0,6960	0,0393	outer membrane protein 3a (II*;G;d)
ompR	b3405	0,6561	0,0127	OmpR transcriptional dual regulator
oppA	b1243	0,5783	0,0065	OppA-oligopeptide ABC transporter substrate-binding
osmC	b1482	0,5889	0,0305	osmotically inducible peroxidase OsmC
oxyR	b3961	0,5975	0,0148	OxyR transcriptional dual regulator
paaX	b1399	0,6230	0,0285	PaaX transcriptional regulator
pal	b0741	0,5655	0,0097	Tol-Pal Cell Envelope Complex
panB	b0134	0,5737	0,0067	3-methyl-2-oxobutanoate hydroxymethyltransferase monomer
pckA	b3403	1,2819	0,0394	phosphoenolpyruvate carboxykinase (ATP)
pdxA	b0052	1,8798	0,0156	PdxA dehydrogenase/decarboxylase
pdxH	b1638	0,5634	0,0154	pyridoxine 5'-phosphate oxidase / pyridoxamine 5'-phosphate oxidase
pdxJ	b2564	0,5506	0,0132	pyridoxamine 5'-phosphate synthase monomer
pdxK	b2418	0,7062	0,0312	pyridoxamine kinase / hydroxymethylpyrimidine kinase / pyridoxal kinase
pepB	b2523	0,7989	0,0086	aminopeptidase (AP)
pepD	b0237	0,6038	0,0133	peptidase D
pepE	b4021	0,6872	0,0420	peptidase E, a dipeptidase where amino-terminal residue is aspartate
pepT	b1127	0,6315	0,0216	peptidase T
pfkA	b3916	0,4420	0,0165	6-phosphofructokinase-1 monomer / putative NAD+ kinase
pfkB	b1723	0,5181	0,0126	6-phosphofructokinase-2 monomer
pflA	b0902	0,4936	0,0038	pyruvate formate-lyase activating enzyme
pgpA	b0418	0,8301	0,0117	phosphatidylglycerophosphatase A
pgpB	b1278	0,7228	0,0332	phosphatidylglycerophosphatase B
pheS	b1714	1,6482	0,0332	phenylalanyl-tRNA synthetase α-chain
plsX	b1090	2,5029	0,0151	glycerolphosphate auxotrophy in plsB background
potC	b1124	0,7615	0,0005	putrescine/spermidine ABC transporter
potD	b1123	0,7572	0,0238	putrescine/spermidine ABC transporter
potI	b0857	0,7509	0,0248	putrescine ABC transporter
ppsA	b1702	0,3641	0,0451	phosphoenolpyruvate synthase
pptA	b1461	0,4533	0,0164	probable 4-oxalocrotonate tautomerase (4-OT) monomer
pqiB	b0951	0,6225	0,0116	paraquat-inducible protein B
prfA	b1211	2,6557	0,0311	peptide chain release factor RF-1
prfC	b4375	0,8757	0,0393	peptide chain release factor RF-3
prlC	b3498	1,4622	0,0107	oligopeptidase A
prmA	b3259	0,6684	0,0246	methylation of 50S ribosomal subunit protein L11
pspE	b1308	0,4076	0,0040	thiosulfate sulfurtransferase
pstC	b3727	1,5388	0,0331	phosphate ABC transporter
ptrA	b2821	0,4205	0,0083	protease III
ptsI	b2416	0,5853	0,0249	PTS enzyme I
purB	b1131	0,6886	0,0011	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase / adenylosuccinate lyase

gene	blattner	ratio A/B	p-value	function
purM	b2499	0,5518	0,0249	phosphoribosylformylglycinamide cyclo-ligase
purU	b1232	0,6528	0,0200	formyltetrahydrofolate deformylase
putA	b1014	0,4763	0,0210	PutA bifunctional enzyme and transcriptional regulator
puuR	b1299	2,5246	0,0286	putative oxidoreductase/putative regulator
pykA	b1854	0,5364	0,0003	pyruvate kinase II monomer
pyrD	b0945	0,6409	0,0178	dihydroorotate oxidase
qseB	b3025	1,3558	0,0154	putative 2-component transcriptional regulator
radC	b3638	1,5771	0,0440	hypothetical protein
rdoA	b3859	0,4925	0,0088	cytoplasmic protein of low abundance
recD	b2819	0,4467	0,0117	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recN	b2616	2,0533	0,0461	protein used in recombination and DNA repair
recO	b2565	0,5768	0,0062	protein interacts with RecR and possibly RecF proteins
recR	b0472	0,6890	0,0234	recombination and repair
relB	b1564	0,5403	0,0279	antitoxin of the RelE-RelB toxin-antitoxin system and transcriptional repressor of relBEF
relE	b1563	0,4842	0,0123	toxin of the RelE-RelB toxin-antitoxin system; cleaves mRNA in ribosome
rfaH	b3842	1,8283	0,0327	RfaH transcriptional regulator
rfaI	b3627	0,7426	0,0277	UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
rfaY	b3625	0,6530	0,0111	lipopolysaccharide core biosynthesis
rfaZ	b3624	0,6938	0,0035	protein involved in KdoIII attachment during lipopolysaccharide core biosynthesis
rfbB	b2041	1,5853	0,0067	RmlB
rhlE	b0797	1,1385	0,0098	DEAD-box-containing ATP-dependent RNA helicase family member
rhoL	b3782	1,7040	0,0054	rho operon leader peptide
rhsB	b3482	0,8055	0,0317	RhsB protein in rhs element
ribA	b1277	1,4064	0,0192	GTP cyclohydrolase II
rihA	b0651	0,3965	0,0007	ribonucleoside hydrolase I (pyrimidine-specific)
rimJ	b1066	0,6008	0,0050	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
mb	b1286	0,5168	0,0188	RNase II, mRNA degradation
rnxA	b3704	2,3870	0,0025	RNase P protein component; processes tRNA, 4.5S RNA
rph	b3643	0,3966	0,0020	RNase PH monomer
rplC	b3320	1,5214	0,0402	50S ribosomal subunit protein L3
rplD	b3319	1,4899	0,0297	50S ribosomal subunit protein L4, regulates expression of S10 operon
rplI	b4203	1,7848	0,0067	50S ribosomal subunit protein L9
rplK	b3983	1,4690	0,0323	50S ribosomal subunit protein L11
rplN	b3310	1,8011	0,0070	50S ribosomal subunit protein L14
rplQ	b3294	1,5026	0,0193	50S ribosomal subunit protein L17
rplS	b2606	1,8032	0,0386	50S ribosomal subunit protein L19
rpmH	b3703	2,4577	0,0050	50S ribosomal subunit protein L34
rpmI	b1717	1,6463	0,0100	50S ribosomal subunit protein A
rpoS	b2741	0,4760	0,0008	sigma38 factor
rpsI	b3230	1,5944	0,0225	30S ribosomal subunit protein S9
rpsJ	b3321	1,8766	0,0045	30S ribosomal subunit protein S10
rpsM	b3298	1,7120	0,0194	30S ribosomal subunit protein S13
rpsN	b3307	1,4824	0,0194	30S ribosomal subunit protein S14
rpsP	b2609	1,4326	0,0450	30S ribosomal subunit protein S16
rpsR	b4202	1,4594	0,0190	30S ribosomal subunit protein S18
rseA	b2572	1,2269	0,0063	anti-sigma factor that inhibits sigmaE
rseC	b2570	2,1501	0,0204	protein involved in reduction of the SoxR iron-sulfur cluster
rsmB	b3289	1,4365	0,0248	16S rRNA m5C967 methyltransferase
rspA	b1581	0,2047	0,0078	starvation sensing protein RspA
rsxB	b1628	2,6069	0,0042	member of SoxR-reducing complex
rsxC	b1629	2,5542	0,0057	member of SoxR-reducing complex
rumA	b2785	1,8745	0,0344	23S ribosomal RNA 5-methyluridine methyltransferase
rusA	b0550	2,0786	0,0385	endodeoxyribonuclease RUS (Holliday junction resolvase)
ruvA	b1861	0,4849	0,0298	branch migration of Holliday structures; repair
sdaB	b2797	0,6285	0,0002	L-threonine deaminase II / L-serine deaminase 2
sdaC	b2796	0,4271	0,0117	SdaC serine STP transporter
secM	b0097	1,3178	0,0023	secretion monitor that regulates SecA translation (General Secretory Pathway)
seqA	b0687	2,1946	0,0082	SeqA, negative modulator of initiation of replication
sfcA	b1479	0,8152	0,0181	MaeA
sfmF	b0534	1,6970	0,0472	putative fimbrial-like protein
sirA	b3470	0,6006	0,0488	possible RNA-binding protein required for wild-type FtsZ ring formation on rich media
slyB	b1641	0,4312	0,0113	putative outer membrane protein
slyD	b3349	0,6005	0,0258	FKBP-type rotamase, peptidyl prolyl cis-trans isomerase
smg	b3284	2,8745	0,0310	hypothetical protein
smpB	b2620	0,6515	0,0414	small protein B
sodB	b1656	0,5233	0,0110	superoxide dismutase (Fe)
sodC	b1646	0,4968	0,0252	superoxide dismutase precursor (Cu-Zn)
speB	b2937	0,6792	0,0484	agmatinase
speC	b2965	0,3877	0,0088	ornithine decarboxylase, biosynthetic

gene	blattner	ratio A/B	p-value	function
speD	b0120	0,3187	0,0009	adenosylmethionine decarboxylase, proenzyme
speE	b0121	0,4811	0,0061	spermidine synthase
spr	b2175	1,5236	0,0048	putative lipoprotein
sra	b1480	0,3080	0,0010	30S ribosomal subunit protein S22; sub-stoichiometric stationary phase ribosomal component
sscR	b2765	1,5203	0,0399	putative 6-pyruvoyl tetrahydrobiopterin synthase
sseA	b2521	0,5767	0,0312	3-mercaptopyruvate:cyanoide sulfurtransferase
sspA	b3229	1,2589	0,0498	regulator of transcription; stringent starvation protein A
sspB	b3228	1,8474	0,0062	SspB monomer
sstT	b3089	1,4008	0,0348	YgjU DAACS transporter
talA	b2464	0,6019	0,0196	transaldolase A
tar	b1886	0,6394	0,0421	MCP-II
tauD	b0368	1,2571	0,0377	taurine dioxygenase
tdcD	b3115	2,0221	0,0493	propionate kinase / acetate kinase C
tdh	b3616	0,6205	0,0168	threonine dehydrogenase
tdk	b1238	0,7191	0,0164	thymidine kinase / deoxyuridine kinase
tehB	b1430	0,6931	0,0312	tellurite resistance
tnaA	b3708	0,3883	0,0042	L-cysteine desulfhydrase / tryptophanase
tolA	b0739	1,8858	0,0200	Tol-Pal Cell Envelope Complex
tolB	b0740	0,6129	0,0276	Tol-Pal Cell Envelope Complex
tolC	b3035	1,8109	0,0166	TolC outer membrane channel
topB	b1763	1,9680	0,0432	DNA topoisomerase III
torZ	b1872	0,6633	0,0251	trimethylamine N-oxide reductase III, TorZ subunit
tpiA	b3919	0,5807	0,0093	triose phosphate isomerase monomer
tpx	b1324	0,4685	0,0031	thiol peroxidase 2
treB	b4240	0,7492	0,0204	EII _{Tre}
trg	b1421	0,3929	0,0362	MCP-III
trkH	b3849	2,8270	0,0037	TrkH potassium ion Trk Transporter
trpA	b1260	0,6073	0,0425	tryptophan synthase, alpha subunit / indoleglycerol phosphate aldolase
trpB	b1261	0,6074	0,0328	tryptophan synthase, beta subunit
trpH	b1266	0,7233	0,0438	putative enzyme
typA	b3871	0,6670	0,0187	protein possibly involved in LPS biosynthesis and host colonization
ubiB	b3835	1,7738	0,0367	2-octaprenylphenol hydroxylase
ubiC	b4039	0,4470	0,0135	chorismate pyruvate lyase
ubiF	b0662	0,4865	0,0324	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase
ubiG	b2232	0,5625	0,0002	3-demethylubiquinone 3-methyltransferase / 2-octaprenyl-6-hydroxyphenol methylase
ucpA	b2426	2,1286	0,0385	putative acetoin dehydrogenase
ulaE	b4197	0,5257	0,0078	L-xylulose 5-phosphate 3-epimerase
upp	b2498	0,5910	0,0244	uracil phosphoribosyltransferase
uvrA	b4058	0,5239	0,0019	excision nuclease subunit A
uvrD	b3813	0,8144	0,0346	DNA-dependent ATPase I and helicase II
wbbK	b2032	0,7715	0,0198	putative transferase
wcaI	b2050	0,6835	0,0103	putative colanic biosynthesis glycosyl transferase
wcaM	b2043	0,3200	0,0127	hypothetical protein
wzxC	b2046	0,7084	0,0032	WzxC
wzyE	b3793	1,9754	0,0268	4- α -fucosyltransferase
xthA	b1749	0,6059	0,0079	exonuclease III
xylF	b3566	1,8870	0,0111	xylose ABC transporter
xylH	b3568	2,3622	0,0026	xylose ABC transporter
yaaW	b0011	1,5008	0,0488	HtgA transcriptional regulator
yacH	b0117	1,3881	0,0384	putative membrane protein
yadK	b0136	1,6125	0,0421	putative adhesin-like protein
yaeB	b0195	1,3994	0,0117	hypothetical protein
yafL	b0227	1,2458	0,0276	putative lipoprotein
yafO	b0233	0,6314	0,0485	conserved protein with a possible role in spontaneous mutagenesis; toxin of a putative toxin-antitoxin pair
yafY	b0251	0,6373	0,0205	inner membrane lipoprotein YafY
yagM	b0279	1,3267	0,0037	hypothetical protein
yahO	b0329	0,7159	0,0211	conserved hypothetical protein
yaiP	b0363	2,5784	0,0399	polysaccharide metabolism
yaiY	b0379	1,3880	0,0403	putative membrane protein
yajG	b0434	2,1052	0,0002	putative polymerase/proteinase
yajL	b0424	0,6797	0,0397	YajL
ybaB	b0471	0,7466	0,0289	conserved hypothetical protein; tnscription is rpoE-dependent
ybaD	b0413	0,7223	0,0384	conserved protein
ybaK	b0481	0,4834	0,0267	conserved hypothetical protein
ybbN	b0492	0,4921	0,0481	putative thioredoxin-like protein
ybdB	b0597	6,2505	0,0061	conserved hypothetical protein
ybeB	b0637	0,7632	0,0489	conserved hypothetical protein
ybeD	b0631	0,3535	0,0003	conserved hypothetical protein
ybeL	b0643	0,4340	0,0165	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ybeZ	b0660	0,7738	0,0071	putative ATP-binding protein
ybfC	b0704	0,2580	0,0019	hypothetical protein
ybfD	b0706	0,2417	0,0088	conserved protein
ybfE	b0685	3,2986	0,0038	hypothetical protein, transcriptionally regulated by LexA
ybgA	b0707	0,5694	0,0092	conserved protein
ybgC	b0736	2,2715	0,0226	Tol-Pal Cell Envelope Complex
ybhL	b0786	0,4736	0,0364	putative transport protein
ybiB	b0800	0,5707	0,0300	putative enzyme
ybiC	b0801	0,2496	0,0064	putative dehydrogenase
ybiF	b0813	1,6029	0,0489	Threonine and Homoserine Exporter
ybiR	b0818	2,1306	0,0273	YbiR
ybjO	b0858	2,2594	0,0431	putative membrane protein
ycbL	b0927	0,6866	0,0197	putative enzyme
ycbQ	b0938	0,6103	0,0474	putative fimbrial-like protein
ycbR	b0939	0,6518	0,0108	putative chaperone
ycdN	b1016	0,7257	0,0321	hypothetical protein of the OFeT transport family
ycdX	b1034	0,6937	0,0343	putative DNA polymerase subunit
ycdY	b1035	0,4819	0,0151	putative oxidoreductase component
ycdZ	b1036	0,9178	0,0037	putative transport protein
yceK	b1050	1,6485	0,0298	hypothetical protein
yceP	b1060	1,2575	0,0186	conserved hypothetical protein
ycfF	b1103	0,5809	0,0081	hypothetical protein
ycfL	b1104	0,6008	0,0188	conserved hypothetical protein
ycfP	b1108	0,6776	0,0253	putative hydrolase
ycfQ	b1111	0,4481	0,0222	hypothetical protein
ycfX	b1119	0,6020	0,0137	putative sugar kinase, ROK family protein
yegH_1	b1169	2,6426	0,0080	conserved protein; member of the Autotransporter family
yegM	b1180	0,8640	0,0332	putative isomerase
yegR	b1194	0,5120	0,0005	protein involved in flagellar function
yegZ	b1164	0,1971	0,0013	hypothetical protein
yciA	b1253	2,3276	0,0365	putative enzyme
yciN	b1273	0,5538	0,0078	conserved hypothetical protein
yciS	b1279	0,5680	0,0114	conserved hypothetical protein
ycjO	b1311	2,7124	0,0316	YcjN/YcjO/YcjP ABC transporter
ycjP	b1312	0,7347	0,0241	YcjN/YcjO/YcjP ABC transporter
ycjX	b1321	0,6578	0,0175	putative EC 2.1 enzyme
ydcR	b1439	2,5283	0,0312	multi modular; putative transcriptional regulator ; also putative ATP-binding component of a transport system
ydcX	b1445	2,1871	0,0183	hypothetical protein
yddH	b1462	2,2272	0,0241	putative enzyme
ydeR	b1503	2,5428	0,0348	putative fimbrial-like protein
ydeS	b1504	0,5808	0,0291	putative fimbrial-like protein
ydfH	b1540	0,6839	0,0190	hypothetical protein
ydfJ	b1543	2,0107	0,0124	YdfJ
ydgA	b1614	0,6747	0,0482	conserved protein
YdgF	b1600	2,1962	0,0042	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydgR	b1634	1,2643	0,0005	YdgR putative peptide POT Transporter
ydhH	b1640	0,4079	0,0176	conserved hypothetical protein
ydhR	b1667	0,4304	0,0347	conserved hypothetical protein
ydhT	b1669	0,7874	0,0102	conserved protein
ydiA	b1703	0,2931	0,0113	conserved protein
ydiY	b1722	0,7966	0,0467	conserved hypothetical protein
ydiZ	b1724	0,3092	0,0002	conserved hypothetical protein
ydjA	b1765	0,6823	0,0153	conserved protein
ydjY	b1751	1,2582	0,0333	conserved protein, 4Fe-4S protein
yeaC	b1777	0,2726	0,0143	conserved hypothetical protein
yebF	b1847	1,2639	0,0016	conserved hypothetical protein
yebR	b1832	1,5900	0,0450	conserved hypothetical protein
yebV	b1836	0,7303	0,0472	hypothetical protein
yedF	b1930	0,5758	0,0367	conserved hypothetical protein; might bind RNA
yedI	b1958	0,6020	0,0091	hypothetical protein
yegD	b2069	0,1096	0,0022	actin family protein
yegP	b2080	0,7106	0,0331	conserved hypothetical protein
yegS	b2086	0,6537	0,0417	conserved protein
yegV	b2100	0,6305	0,0488	putative kinase
yejK	b2186	0,5169	0,0083	nucleoid component
yfaE	b2236	1,5204	0,0066	conserved hypothetical protein, 2Fe-2S ferredoxin-related
yfaY	b2249	0,6445	0,0134	putative competence-damage protein
yfbB	b2263	0,4472	0,0003	putative enzyme
yfcZ	b2343	0,5741	0,0249	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
yfdG	b2350	2,8866	0,0223	hypothetical protein
yfdH	b2351	4,5779	0,0047	putative glycan biosynthesis enzyme
yfdZ	b2379	0,4718	0,0255	putative aminotransferase
yfhA	b2554	0,6241	0,0138	putative 2-component transcriptional regulator
yfiF	b2581	0,3793	0,0154	hypothetical protein
yfiH	b2593	2,3518	0,0047	conserved hypothetical protein
yfiQ	b2584	0,6139	0,0054	putative NAD(P)-binding and ATP-binding acyl-CoA synthetase
ygaF	b2660	0,3095	0,0000	hypothetical protein
ygaZ	b2682	2,9721	0,0184	hypothetical protein
ygeL	b2760	0,7291	0,0047	hypothetical protein with possible relationship to novobiocin and deoxycholate resistance
ygeA	b2840	0,4954	0,0300	putative resistance protein
ygeO	b2857	1,8523	0,0339	hypothetical protein
ygfJ	b2877	0,6146	0,0146	conserved protein
ygfS	b2886	1,7328	0,0364	putative oxidoreductase, Fe-S subunit
yggJ	b2946	1,6239	0,0074	conserved hypothetical protein
yggL	b2959	0,6458	0,0023	conserved hypothetical protein
yggW	b2955	1,3703	0,0151	putative oxidase
yghB	b3009	0,7895	0,0308	putative integral membrane protein
yghU	b2989	0,2467	0,0025	glutathione transferase-like protein possibly involved in glutathionylspermidine metabolism
ygiA	b3036	1,6742	0,0177	hypothetical protein
yhaV	b3130	0,5692	0,0077	conserved hypothetical protein
yhcA	b3215	2,1510	0,0365	putative chaperone
yhdE	b3248	0,4955	0,0496	conserved hypothetical protein
yhdH	b3253	0,3436	0,0006	putative dehydrogenase
yheL	b3343	3,0897	0,0190	conserved hypothetical protein
yheM	b3344	4,4555	0,0202	conserved hypothetical protein
yheN	b3345	2,6968	0,0330	conserved hypothetical protein
yheO	b3346	2,2685	0,0223	hypothetical protein
yhfA	b3356	0,5425	0,0352	conserved hypothetical protein
yhhM	b3467	0,7356	0,0202	putative receptor
yhhT	b3474	1,3859	0,0171	hypothetical protein
yhiQ	b3497	1,6969	0,0181	putative methyltransferase
yhjK	b3529	1,4678	0,0029	conserved protein
yiaT	b3584	0,8971	0,0295	putative outer membrane protein
yibI	b3598	1,5584	0,0342	hypothetical protein
yicC	b3644	0,6226	0,0107	conserved protein
yifN	b3777	0,6923	0,0355	conserved hypothetical protein
yigZ	b3848	2,8187	0,0073	putative elongation factor
yiiR	b3921	0,6478	0,0117	putative membrane protein
yijP	b3955	0,4791	0,0024	hypothetical protein; related to invasion protein of pathogenic E. coli
yjbQ	b4056	0,2981	0,0075	conserved hypothetical protein
yjcZ	b4110	1,2700	0,0269	hypothetical protein
yjdM	b4108	0,3921	0,0080	hypothetical protein
yjgB	b4269	0,6383	0,0112	putative oxidoreductase
yjiG	b4329	0,6702	0,0021	putative membrane protein
yjjA	b4360	0,6315	0,0065	putative glycoprotein/receptor
yjjQ	b4365	1,8874	0,0056	putative regulator
ykfG	b0247	1,4225	0,0448	putative DNA repair protein
ykgB	b0301	0,2697	0,0126	putative membrane protein
ykgI	b0303	0,1371	0,0142	hypothetical protein
yliD	b0832	0,5942	0,0294	YliA/YliB/YliC/YliD ABC transporter
ymgA	b1165	0,1880	0,0008	hypothetical protein
ynaJ	b1332	0,6770	0,0219	conserved hypothetical protein
ynfD	b1586	0,4744	0,0302	conserved hypothetical protein
ynjH	b1760	0,1079	0,0001	conserved hypothetical protein
yoaB	b1809	0,4229	0,0064	conserved protein
yoaC	b1810	0,4432	0,0033	conserved hypothetical protein
yphC	b2545	0,7253	0,0435	predicted oxidoreductase
yqeG	b2845	2,3330	0,0145	YqeG STP transporter
yqfB	b2900	0,5018	0,0235	conserved hypothetical protein
yqiA	b3031	1,8528	0,0482	putative hydrolase
yqiI	b3048	1,5915	0,0251	conserved protein
yqiD	b3098	0,5135	0,0398	conserved hypothetical protein
yraM	b3147	0,6915	0,0206	putative glycosylase
yrbA	b3190	1,6358	0,0200	hypothetical protein
yrdC	b3282	1,9330	0,0102	RNA-binding protein with unique protein fold
yrdD	b3283	3,2410	0,0102	putative DNA topoisomerase
yrfF	b3398	3,1897	0,0119	putative dehydrogenase
ytfA	b4205	0,6230	0,0360	hypothetical protein

gene	blattner	ratio A/B	p-value	function
znuA	b1857	3,6361	0,0065	ZnuA/ZnuB/ZnuC ABC transporter
znuC	b1858	1,3426	0,0008	ZnuA/ZnuB/ZnuC ABC transporter
zraR	b4004	2,5337	0,0077	ZraR-Phosphorylated transcriptional activator
LZ54 (A) & LZ54fis (B)				
aaeX	b3242	0,3200	0,0268	hypothetical protein
abgB	b1337	0,4513	0,0162	hypothetical protein
aceF	b0115	1,4049	0,0029	AceF-lipoate
acs	b4069	0,0998	0,0401	putative hydroxycinnamate-CoA ligase / acetyl-CoA synthetase
adk	b0474	0,4908	0,0443	adenylate kinase
aegA	b2468	0,4339	0,0331	putative oxidoreductase, Fe-S subunit
ahpC	b0605	0,4949	0,0199	AhpC component
aldB	b3588	0,6066	0,0090	putative aminobutyraldehyde dehydrogenase / aldehyde dehydrogenase B
allR	b0506	0,3675	0,0004	AllR transcriptional regulator
amyA	b1927	1,4397	0,0367	alpha-amylase, cytoplasmic
aniC	b4115	0,9075	0,0200	AdiC Arginine:Agmatine Antiporter
argR	b3237	0,5889	0,0462	ArgR transcriptional dual regulator
aroA	b0908	0,7038	0,0037	3-phosphoshikimate-1-carboxyvinyltransferase
artQ	b0862	1,3759	0,0198	arginine ABC transporter
atpG	b3733	1,3528	0,0009	ATP synthase, F1 complex, gamma subunit
b0309	b0309	0,3686	0,0298	hypothetical protein
b0373	b0373	0,5710	0,0097	hypothetical protein
b1364	b1364	1,7894	0,0168	hypothetical protein
baeS	b2078	0,5383	0,0205	BaeS-Phis
bglG	b3723	1,2005	0,0036	BglG monomer
cbl	b1987	0,7237	0,0159	Cbl transcriptional activator
chbG	b1733	2,1422	0,0047	hypothetical protein, encoded by an operon required for growth on N,N'-diacetylchitobiose
cheB	b1883	2,0876	0,0004	CheB-Pasp / PGLuMase / protein-glutamine glutaminase
cheZ	b1881	1,3201	0,0444	CheZ
citE	b0616	2,1449	0,0394	subunit of citryl-ACP lyase
citX	b0614	0,4000	0,0370	holo-ACP synthase
clpA	b0882	0,7887	0,0340	ATP-binding component of serine protease
cpsB	b2049	0,3934	0,0301	mannose-1-phosphate guanylyltransferase-(GDP)
cpxP	b3913	2,7585	0,0052	regulator of the Cpx response and possible chaperone involved in resistance to extracytoplasmic stress
creA	b4397	0,6098	0,0489	hypothetical protein
csgA	b1042	0,5922	0,0165	curlin, major subunit
cydC	b0886	0,5727	0,0423	abc-6-cplx
dcd	b2065	0,5033	0,0057	dCTP deaminase
dcp	b1538	0,5735	0,0138	dipeptidyl carboxypeptidase II
deoB	b4383	2,8180	0,0292	phosphopentomutase
dgoR	b4479	0,3103	0,0080	regulator protein for dgo operon
dinB	b0231	0,5729	0,0144	DNA polymerase IV (Y-family DNA polymerase; translesion DNA synthesis)
dinD	b3645	0,5218	0,0499	DNA-damage-inducible protein
dld	b2133	0,3096	0,0065	D-lactate:Quinone Oxidoreductase
dnaG	b3066	2,8483	0,0412	DNA biosynthesis; DNA primase
dnaQ	b0215	0,4868	0,0086	DNA polymerase III, epsilon subunit
dppB	b3543	0,3745	0,0395	dipeptide ABC transporter
elaA	b2267	0,3654	0,0026	hypothetical protein
elbB	b3209	0,7262	0,0373	sigma cross-reacting protein 27A (SCR-27A)
emtA	b1193	0,5201	0,0102	murein transglycosylase E
entS	b0591	5,6019	0,0045	YbdA MFS transporter
erfK	b1990	0,4581	0,0299	hypothetical protein with similarity to universal stress protein
exbB	b3006	9,4812	0,0258	ExbB protein; uptake of enterochelin; tonB-dependent uptake of B colicins
exbD	b3005	4,8930	0,0016	ExbD uptake of enterochelin; tonB-dependent uptake of B colicins
fbaB	b2097	0,1818	0,0492	fructose bisphosphate aldolase monomer
fecA	b4291	3,3493	0,0110	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fecB	b4290	8,7354	0,0011	ferric dicitrate uptake system
feoA	b3408	1,5400	0,0067	ferrous iron transport protein A
fepA	b0584	3,0382	0,0381	FepA, outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D
fhuF	b4367	6,4472	0,0140	acts in reduction of ferrioxamine B iron
fimA	b4314	0,0474	0,0033	major type 1 subunit fimbrin (pilin)
fimI	b4315	0,1958	0,0097	fimbrial protein
fklB	b4207	0,6485	0,0088	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (a rotamase)
fkpA	b3347	0,6246	0,0037	peptidyl-prolyl cis-trans isomerase; in protein folding
flgJ	b1081	2,4784	0,0147	FlgJ
flgM	b1071	1,3378	0,0033	anti-FliA (anti-sigma) factor; also known as RflB protein
flgN	b1070	1,6620	0,0138	flagellar biosynthesis protein FlgN
flhB	b1880	1,7009	0,0337	flagellar biosynthesis protein FlhB
fliE	b1937	1,4750	0,0088	flagellar basal-body protein FliE

gene	blattner	ratio A/B	p-value	function
fliF	b1938	1,6666	0,0306	flagellar M-ring protein FliF; basal-body MS(membrane and supramembrane)-ring and collar protein
fliG	b1939	2,1045	0,0069	flagellar motor switch protein FliG; component of motor switching and energizing, enabling rotation and determining its direction
fliL	b1944	2,1945	0,0188	flagellar biosynthesis
fliM	b1945	2,0791	0,0003	flagellar motor switch protein FliM; component of motor switch and energizing, enabling rotation and determining its direction
fliP	b1948	1,9491	0,0114	flagellar biosynthesis protein FliP
fliQ	b1949	3,0936	0,0072	flagellar biosynthesis protein FliQ
fliZ	b1921	1,4597	0,0276	possible cell-density responsive regulator of sigmaF
flxA	b1566	1,6260	0,0119	hypothetical protein; gene is regulated by FliA
folE	b2153	0,6211	0,0207	GTP cyclohydrolase I
frmA	b0356	1,1962	0,0067	formaldehyde dehydrogenase, glutathione-dependent
ftnA	b1905	0,4044	0,0002	cytoplasmic ferritin, an iron storage protein)
ftsI	b0084	2,4213	0,0314	essential cell division protein FtsI; penicillin-binding protein 3
ftsL	b0083	1,7997	0,0053	essential cell division protein FtsL
galR	b2837	2,6916	0,0029	GalR-galactose
galT	b0758	0,6631	0,0384	UDP-glucose-hexose-1-phosphate uridylyltransferase / galactose-1-phosphate uridylyltransferase
galU	b1236	1,8258	0,0242	UTP-glucose-1-phosphate uridylyltransferase
garR	b3125	0,6022	0,0007	tartronate semialdehyde reductase
gcl	b0507	0,3585	0,0257	glyoxylate carboligase
ghrA	b1033	0,3564	0,0005	glyoxylate reductase
glmS	b3729	1,0956	0,0218	L-glutamine:D-fructose-6-phosphate aminotransferase
gloA	b1651	0,8364	0,0384	glyoxalase I
gltB	b3212	0,5950	0,0474	glutamate synthase (NADPH) large chain precursor
gltD	b3213	0,5153	0,0061	glutamate synthase (NADPH) small chain
glyA	b2551	0,5605	0,0266	glycine hydroxymethyltransferase
gmhB	b0200	0,6287	0,0027	GmhB
gpp	b3779	2,2141	0,0307	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase
grxB	b1064	0,4556	0,0213	oxidized glutaredoxin 2
gst	b1635	0,5631	0,0185	glutathione transferase
gutQ	b2708	0,7061	0,0173	protein with a sugar isomerase domain
hdeD	b3511	1,5185	0,0068	protein involved in acid resistance
hdR	b4480	0,6083	0,0428	transcriptional regulator
hemL	b0154	0,6270	0,0356	glutamate-1-semialdehyde aminotransferase
hepA	b0059	0,5258	0,0325	RNA Polymerase (RNAP)-binding ATPase and RNAP recycling factor
hflD	b1132	0,6486	0,0423	membrane protein in operon with purB
hipA	b1507	2,1862	0,0158	HipA transcriptional activator
hisI	b2026	0,7672	0,0436	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphatase
hisJ	b2309	0,5028	0,0038	histidine ABC transporter
hscA	b2526	1,7721	0,0266	chaperone, member of Hsp70 protein family
hsdM	b4349	0,7275	0,0448	host modification; DNA methylase M
hsdS	b4348	0,6614	0,0101	specificity determinant for hsdM and hsdR
htrA	b0161	2,8995	0,0097	DegP
hybD	b2993	0,4468	0,0191	hydrogenase 2 maturation endopeptidase
hydN	b2713	1,2745	0,0490	putative electron transport protein HydN
ibpA	b3687	2,0616	0,0065	small heat shock protein IbpA
inaA	b2237	1,3823	0,0226	pH-inducible protein involved in stress response
infC	b1718	1,3280	0,0197	protein chain initiation factor IF-3
iscA	b2528	1,4270	0,0242	iron-sulfur cluster assembly protein
iscS	b2530	1,4016	0,0167	cysteine desulfurase monomer
iscU	b2529	1,3576	0,0171	scaffold protein involved in iron-sulfur cluster assembly
iscX	b2524	1,8316	0,0294	protein with possible role in iron-sulfur cluster biogenesis
kdgT	b3909	2,3520	0,0274	KdgT 2-keto-3-deoxygluconate transporter
kduD	b2842	0,7186	0,0150	2-deoxy-D-gluconate 3-dehydrogenase
kduI	b2843	0,7822	0,0384	homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase
leuA	b0074	2,9952	0,0235	2-isopropylmalate synthase
lplA	b4386	0,6314	0,0266	lipoyl-protein ligase A
lysU	b4129	0,3830	0,0029	lysyl-tRNA synthetase (LysRSu), inducible
maa	b0459	0,6405	0,0004	maltose acetyltransferase
malX	b1621	0,5038	0,0496	EIIBCMalX
malY	b1622	0,7775	0,0304	bifunctional: repressor of maltose regulon / cystathionine beta-lyase
manA	b1613	0,5147	0,0334	mannose-6-phosphate isomerase
map	b0168	1,5951	0,0157	methionine aminopeptidase
marA	b1531	5,0995	0,0031	MarA transcriptional activator
marR	b1530	4,0195	0,0022	MarR-salicylate
mbhA	b0230	0,4200	0,0113	putative motility protein
mdaB	b3028	1,9345	0,0233	NADPH quinone reductase
mdoD	b1424	0,6780	0,0394	glucan biosynthesis protein D
mdtH	b1065	0,5184	0,0019	YceL MFS transporter
menG	b3929	0,7805	0,0366	inhibitor of ribonuclease E (RNase E) activity
mfd	b1114	0,5397	0,0158	transcription-repair coupling factor; mutation frequency decline

gene	blattner	ratio A/B	p-value	function
mglC	b2148	0,1817	0,0059	galactose ABC transporter
moeB	b0826	0,3297	0,0018	molybdopterin biosynthesis
mog	b0009	0,6094	0,0062	required for the efficient incorporation of Mo into molybdoproteins
motA	b1890	1,4410	0,0182	MotA protein, proton conductor component of motor; no effect on switching
mpaA	b1326	0,6680	0,0238	murein peptide amidase A
mraW	b0082	1,6512	0,0423	S-adenosyl-dependent methyltransferase
msrA	b4219	0,3359	0,0142	methionine sulfoxide reductase A / protein-methionine-S-oxide reductase / methionine sulfoxide reductase
mug	b3068	0,2422	0,0049	stationary phase mismatch/uracil DNA glycosylase
mukE	b0923	2,2877	0,0118	protein involved in chromosome partitioning
mukF	b0922	2,1539	0,0075	Ca ²⁺ -binding protein involved in chromosome partitioning
murC	b0091	1,3976	0,0217	UDP-N-acetylmuramate-alanine ligase
murD	b0088	1,1421	0,0308	UDP-N-acetylmuramoylalanine-D-glutamate ligase
mutH	b2831	0,4240	0,0337	MutHLS complex, methyl-directed mismatch repair
nadR	b4390	0,6257	0,0268	NadR transcriptional repressor / NMN adenyltransferase
nagA	b0677	0,5678	0,0282	N-acetylglucosamine-6-phosphate deacetylase
nagB	b0678	0,4101	0,0011	glucosamine-6-phosphate deaminase
narL	b1221	0,5206	0,0007	NarL-Phosphorylated transcriptional dual regulator
narX	b1222	0,4355	0,0202	NarX-Phis
nfi	b3998	0,6846	0,0473	endonuclease V (deoxyinosine 3'endoduclease)
nfnB	b0578	0,7962	0,0085	dihydropteridine reductase
nfrA	b0568	0,3236	0,0069	bacteriophage N4 receptor, outer membrane protein
nfsA	b0851	1,5581	0,0063	NADPH nitroreductase
nlpD	b2742	0,6439	0,0366	NlpD putative outer membrane lipoprotein
nudH	b2830	1,4474	0,0158	putative invasion protein
ompA	b0957	0,7281	0,0106	outer membrane protein 3a (II*;G;d)
ompC	b2215	2,0986	0,0040	outer membrane porin OmpC
ompX	b0814	0,6904	0,0223	outer membrane protein X
oxyR	b3961	0,6290	0,0201	OxyR transcriptional dual regulator
paaB	b1389	0,0991	0,0404	putative subunit of phenylacetate-CoA oxygenase
paaI	b1396	1,8933	0,0289	hypothetical protein with some similarity to thioesterases
pal	b0741	0,5468	0,0040	Tol-Pal Cell Envelope Complex
panF	b3258	0,7935	0,0164	PanF sodium/pantothenate SSS transporter
pepQ	b3847	1,5249	0,0184	proline dipeptidase
pfkA	b3916	0,5688	0,0041	6-phosphofructokinase-1 monomer / putative NAD ⁺ kinase
pfkB	b1723	0,4510	0,0068	6-phosphofructokinase-2 monomer
pgk	b2926	1,3521	0,0229	phosphoglycerate kinase
pheS	b1714	1,4275	0,0242	phenylalanyl-tRNA synthetase α-chain
phnI	b4099	2,1789	0,0451	phosphonate metabolism
plsX	b1090	2,1023	0,0467	glycerolphosphate auxotrophy in plsB background
pmbA	b4235	0,6317	0,0323	protease involved in Microcin B17 maturation and in sensitivity to the DNA gyrase inhibitor LetD
pnuC	b0751	1,2218	0,0260	PnuC NMN transporter
poxA	b4155	0,4524	0,0462	putative regulator of pyruvate oxidase
ppiD	b0441	0,7431	0,0500	peptidyl-prolyl cis-trans isomerase
prfA	b1211	2,0627	0,0070	peptide chain release factor RF-1
prfH	b0236	0,3770	0,0439	probable peptide chain release factor
prlC	b3498	0,5779	0,0203	oligopeptidase A
prmA	b3259	0,6861	0,0196	methylation of 50S ribosomal subunit protein L11
proA	b0243	0,8509	0,0152	gamma-glutamyl kinase-GP-reductase multienzyme complex
ptrA	b2821	0,2672	0,0247	protease III
purB	b1131	0,7424	0,0127	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase / adenylosuccinate lyase
purD	b4005	0,6497	0,0099	phosphoribosylamine-glycine ligase
purE	b0523	0,5049	0,0089	N5-carboxyaminoimidazole ribonucleotide mutase
purR	b1658	1,3164	0,0433	PurR transcriptional repressor
purT	b1849	0,4486	0,0494	GAR transformylase 2
puuA	b1297	0,4444	0,0002	putative glutamine synthetase (EC 6.3.1.2)
puuR	b1299	2,1380	0,0256	putative oxidoreductase/putative regulator
racR	b1356	1,7456	0,0218	hypothetical protein
rcsF	b0196	0,7467	0,0352	RcsF-P
recB	b2820	0,3206	0,0117	RecB; DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
recC	b2822	2,3410	0,0070	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
rep	b3778	0,5395	0,0242	rep helicase, a single-stranded DNA dependent ATPase
rffD	b3787	1,6810	0,0404	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
rffG	b3788	1,4341	0,0315	dTDP-glucose 4,6-dehydratase 2
rhcC_1	b0700	0,2172	0,0239	RhcC protein in rhs element, interrupted
rhtB	b3824	0,4705	0,0156	RhtB homoserine Rht Transporter
rimJ	b1066	0,6184	0,0212	acetylates N-terminal alanine of 30S ribosomal subunit protein S5 / ribosomal-protein-alanine N-acetyltransferase
rob	b4396	0,6252	0,0498	Rob transcriptional activator
rplD	b3319	1,8347	0,0070	50S ribosomal subunit protein L4, regulates expression of S10 operon
rplP	b3313	1,3529	0,0061	50S ribosomal subunit protein L16

gene	blattner	ratio A/B	p-value	function
rpmG	b3636	1,7607	0,0218	50S ribosomal subunit protein L33
rpsI	b3230	2,3038	0,0446	30S ribosomal subunit protein S9
ruvA	b1861	0,6819	0,0478	branch migration of Holliday structures; repair
sanA	b2144	3,4542	0,0022	vancomycin sensitivity
sapB	b1293	1,2822	0,0403	peptide uptake ABC transporter
sbcC	b0397	0,5204	0,0154	ATP-dependent dsDNA exonuclease
sbcD	b0398	0,5232	0,0154	ATP-dependent dsDNA exonuclease
secG	b3175	2,8489	0,0079	Sec Protein Secretion Complex
secY	b3300	1,6629	0,0061	Sec Protein Secretion Complex
setB	b2170	0,5873	0,0068	YeiO MFS transporter
slt	b4392	0,7163	0,0041	soluble lytic murein transglycosylase
smtA	b0921	2,2662	0,0008	S-adenosylmethionine-dependent methyltransferase
sodA	b3908	1,6251	0,0428	superoxide dismutase (Mn)
sodB	b1656	0,6871	0,0357	superoxide dismutase (Fe)
sohA	b3129	0,3949	0,0001	putative protease, affects protein secretion
soxS	b4062	0,7246	0,0408	SoxS transcriptional activator
speC	b2965	0,2278	0,0104	ornithine decarboxylase, biosynthetic
speD	b0120	0,4229	0,0032	adenosylmethionine decarboxylase, proenzyme
speE	b0121	0,3868	0,0023	spermidine synthase
spoT	b3650	2,1390	0,0249	GDP diphosphokinase / guanosine-3',5'-bis(diphosphate) 3'-diphosphatase
sspB	b3228	1,6238	0,0353	SspB monomer
stpA	b2669	0,6804	0,0362	DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing?
talA	b2464	0,5618	0,0078	transaldolase A
tauC	b0367	1,2163	0,0350	TauA/TauB/TauC ABC transporter
tdcA	b3118	0,7075	0,0382	TdcA transcriptional activator
tesB	b0452	0,5076	0,0130	thioesterase II
thrA	b0002	1,5206	0,0439	aspartate kinase I / homoserine dehydrogenase I
thrS	b1719	1,2919	0,0110	threonyl-tRNA synthetase
tnaB	b3709	0,3751	0,0371	TnaB tryptophan ArAAP transporter
tolB	b0740	0,6004	0,0079	Tol-Pal Cell Envelope Complex
tonB	b1252	4,8369	0,0178	TonB protein; energy transducer; uptake of iron, cyanocobalimin; sensitivity to phages, colicins
topB	b1763	2,2188	0,0171	DNA topoisomerase III
tpiA	b3919	0,5602	0,0113	triose phosphate isomerase monomer
tpx	b1324	0,5721	0,0037	thiol peroxidase 2
trkH	b3849	1,6425	0,0408	TrkH potassium ion Trk Transporter
trpA	b1260	0,6895	0,0091	tryptophan synthase, alpha subunit / indoleglycerol phosphate aldolase
ubiB	b3835	1,8429	0,0208	2-octaprenylphenol hydroxylase
ulaG	b4192	0,5353	0,0428	putative L-ascorbate 6-phosphate lactonase
ves	b1742	1,6031	0,0028	cold-induced member of the CspA family
wcaM	b2043	0,7903	0,0280	hypothetical protein
xdhD	b2881	0,4314	0,0203	putative oxidoreductase; possible component of selenate reductase with possible role in purine salvage
xseB	b0422	0,6395	0,0007	exonuclease VII, small subunit
xyIF	b3566	0,8595	0,0048	xylose ABC transporter
yaaA	b0006	0,6867	0,0434	putative membrane protein
yadI	b0129	0,6721	0,0176	EIIAga
yaeR	b0187	0,6633	0,0090	putative enzyme
yafK	b0224	0,5143	0,0141	conserved protein; in enteroaggregative E. coli, YafK is required for development of biofilms
yafL	b0227	0,6653	0,0187	putative lipoprotein
yagB	b0266	0,3543	0,0199	hypothetical protein
yahG	b0321	0,4435	0,0499	conserved protein
yajC	b0407	0,6234	0,0285	Sec Protein Secretion Complex
yajL	b0424	0,5924	0,0146	YajL
yajQ	b0426	0,7004	0,0019	nucleotide binding protein
ybbA	b0495	0,4961	0,0210	YbbA/YbbP ABC transporter
ybbN	b0492	0,5804	0,0095	putative thioredoxin-like protein
ybdB	b0597	1,8841	0,0034	conserved hypothetical protein
ybeD	b0631	0,5752	0,0204	conserved hypothetical protein
ybeF	b0629	0,5481	0,0405	putative transcriptional regulator LYSR-type
ybeL	b0643	0,5838	0,0267	conserved hypothetical protein
ybeR	b0645	0,6981	0,0297	conserved hypothetical protein
ybfC	b0704	0,4592	0,0473	hypothetical protein
ybgA	b0707	0,5380	0,0378	conserved protein
ybgF	b0742	0,7414	0,0495	Tol-Pal Cell Envelope Complex
ybhA	b0766	0,4283	0,0208	putative phosphatase
ybhL	b0786	0,4806	0,0166	putative transport protein
ybiC	b0801	0,2705	0,0026	putative dehydrogenase
ybjC	b0850	2,1246	0,0155	conserved hypothetical protein; gene is within soxRS regulon
ybjT	b0869	0,5382	0,0222	putative dTDP-glucose
ycaO	b0905	0,5635	0,0133	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ycaR	b0917	0,8119	0,0434	hypothetical protein
ycbK	b0926	0,4625	0,0396	conserved hypothetical protein
ycbQ	b0938	0,3915	0,0212	putative fimbrial-like protein
ycbW	b0946	0,4707	0,0294	conserved hypothetical protein
yedK	b1010	0,6659	0,0336	conserved protein
yedO	b1018	3,1170	0,0011	conserved hypothetical protein
yedX	b1034	0,6258	0,0106	putative DNA polymerase subunit
yedY	b1035	0,5220	0,0048	putative oxidoreductase component
yceP	b1060	3,0327	0,0061	conserved hypothetical protein
ycfF	b1103	0,7821	0,0425	hypothetical protein
ycfX	b1119	0,5588	0,0062	putative sugar kinase, ROK family protein
ycgF	b1163	0,4183	0,0033	conserved protein
ycgZ	b1164	0,2379	0,0051	hypothetical protein
yciA	b1253	2,1238	0,0447	putative enzyme
ycjO	b1311	2,0646	0,0042	YcjN/YcjO/YcjP ABC transporter
ycjZ	b1328	1,5357	0,0455	putative transcriptional regulator LYSR-type
ydcR	b1439	2,1811	0,0125	multi modular; putative transcriptional regulator ; also putative ATP-binding component of a transport system
ydcX	b1445	2,0821	0,0245	hypothetical protein
yddB	b1495	1,8931	0,0263	conserved protein
yddE	b1464	0,5672	0,0290	conserved protein
yddH	b1462	2,1448	0,0097	putative enzyme
ydeK	b1510	0,7567	0,0259	YdeK
ydeR	b1503	2,0061	0,0065	putative fimbrial-like protein
ydfD	b1576	1,1486	0,0464	hypothetical protein
ydfG	b1539	0,5150	0,0046	3-hydroxy acid dehydrogenase monomer
ydfJ	b1543	2,2617	0,0173	YdfJ
ydfR	b1555	1,4544	0,0272	hypothetical protein
YdgF	b1600	4,2412	0,0211	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydhH	b1640	0,4438	0,0035	conserved hypothetical protein
ydhO	b1655	1,6025	0,0127	putative lipoprotein
ydhR	b1667	2,0667	0,0134	conserved hypothetical protein
ydiA	b1703	0,5498	0,0081	conserved protein
ydiJ	b1687	0,6760	0,0039	putative oxidase
ydiZ	b1724	0,4478	0,0112	conserved hypothetical protein
ydjA	b1765	0,7449	0,0457	conserved protein
ydjJ	b1774	0,4478	0,0421	putative oxidoreductase
yecM	b1875	0,5730	0,0459	conserved hypothetical protein with structural similarity to metal binding isomerases and oxygenases
yecR	b1904	2,2905	0,0227	conserved hypothetical protein
yedA	b1959	0,3926	0,0268	putative transmembrane subunit
yedS_2	b1965	1,2318	0,0336	putative outer membrane protein
yedW	b1969	1,7473	0,0293	putative 2-component transcriptional response regulator
yeeV	b2005	2,3889	0,0447	toxin of the YeeV-YeeU toxin-antitoxin pair
yegD	b2069	0,4221	0,0152	actin family protein
yehS	b2124	1,5509	0,0010	conserved hypothetical protein
yfaY	b2249	0,6432	0,0439	putative competence-damage protein
yfcO	b2332	2,0298	0,0093	conserved hypothetical protein
yfdG	b2350	1,9660	0,0295	hypothetical protein
yfdH	b2351	2,2682	0,0127	putative glycan biosynthesis enzyme
yfdQ	b2360	0,7084	0,0485	hypothetical protein
yfdZ	b2379	0,4682	0,0142	putative aminotransferase
yfeA	b2395	3,1873	0,0153	putative membrane protein
yfgA	b2516	1,6228	0,0427	putative membrane protein
yfgG	b2504	1,9854	0,0010	hypothetical protein
yfiC	b2575	0,6816	0,0353	putative enzyme
ygaF	b2660	0,2733	0,0438	hypothetical protein
ygaH	b2683	4,1143	0,0001	putative transport protein
ygaZ	b2682	3,8502	0,0126	hypothetical protein
ygdR	b2833	0,7101	0,0443	conserved hypothetical protein
ygeA	b2840	0,7747	0,0342	putative resistance protein
yggG	b2936	0,5864	0,0044	conserved protein
yghU	b2989	0,2346	0,0021	glutathione transferase-like protein possibly involved in glutathionylspermidine metabolism
yghX	b2999	0,7351	0,0450	putative enzyme
ygiB	b3037	0,6675	0,0272	conserved hypothetical protein
ygiC	b3038	0,6545	0,0203	putative glutathione-like synthetase
ygiK	b3080	0,7192	0,0047	putative isomerase
yhaH	b3103	1,7228	0,0160	putative cytochrome
yhaO	b3110	0,4765	0,0045	YhaO STP transporter
yhaV	b3130	0,4633	0,0039	conserved hypothetical protein
yhdN	b3293	0,5429	0,0431	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
yhgA	b3411	0,8004	0,0317	hypothetical protein
yhhW	b3439	0,5175	0,0175	conserved hypothetical protein
yhhX	b3440	0,6329	0,0101	putative galactose 1-dehydrogenase
yicC	b3644	0,7406	0,0216	conserved protein
yidS	b3690	0,7631	0,0435	putative oxidoreductase with FAD/NAD(P)-binding domain
yidW	b3694	0,3773	0,0239	
yidZ	b3711	0,8211	0,0483	putative transcriptional regulator LysR-type
yifK	b3795	3,1137	0,0009	YifK APC transporter
yiiM	b3910	0,7020	0,0122	conserved hypothetical protein
yjdI	b4126	0,7375	0,0469	conserved hypothetical protein
yjdL	b4130	0,8934	0,0340	YjdL peptide POT transporter
yjeJ	b4145	1,3189	0,0227	conserved protein
yjhH	b4298	0,5714	0,0293	putative lyase/synthase
yjhQ	b4307	0,5879	0,0424	hypothetical protein
yjjQ	b4365	0,7703	0,0016	putative regulator
ykgB	b0301	0,1144	0,0233	putative membrane protein
ykgI	b0303	0,0811	0,0115	hypothetical protein
yliC	b0831	0,5742	0,0208	YliA/YliB/YliC/YliD ABC transporter
ymdB	b1045	0,4293	0,0044	conserved protein
ymfL	b1147	0,6034	0,0298	hypothetical protein
ymgA	b1165	0,2057	0,0011	hypothetical protein
ymgB	b1166	0,2193	0,0045	hypothetical protein
ynbB	b1409	1,8755	0,0346	putative phosphatidate cytidiltransferase
ynbD	b1411	2,0382	0,0189	putative enzyme
yncE	b1452	1,5010	0,0124	putative receptor
ynfA	b1582	0,5690	0,0326	inner membrane protein
ynfF	b1588	1,3945	0,0073	oxidoreductase subunit paralog of DmsA
ynfK	b1593	1,3710	0,0451	hypothetical protein
yoaB	b1809	0,6323	0,0226	conserved protein
yohK	b2142	0,6522	0,0298	putative transporter
yojI	b2211	4,8991	0,0006	YojI
ypfG	b2466	0,5804	0,0215	conserved hypothetical protein
ypjF	b2646	0,6684	0,0339	member of the YeeV, YkfI, YpjF family of toxin proteins
yqcD	b2794	0,5550	0,0359	conserved hypothetical protein
yqgF	b2949	0,5076	0,0306	possible Holliday junction resolvase
yqjE	b3099	0,5661	0,0492	conserved protein
yraR	b3152	0,6835	0,0499	putative NADH dehydrogenase
yrdA	b3279	0,3644	0,0141	putative transferase
yrdD	b3283	1,3095	0,0130	putative DNA topoisomerase
ytfN	b4221	0,7492	0,0064	conserved protein
zipA	b2412	2,6840	0,0155	essential cell division protein ZipA
znuA	b1857	2,8611	0,0069	ZnuA/ZnuB/ZnuC ABC transporter

LZ41 (A) LZ41hns (B)

aat	b0885	0,7595	0,0479	leucyl, phenylalanyl-tRNA-protein transferase
abgR	b1339	0,6195	0,0042	putative transcriptional regulator LYSR-type
acrA	b0463	4,5010	0,0065	AcrA Membrane Fusion Protein
acrE	b3265	0,1208	0,0044	transmembrane protein affects septum formation and cell membrane permeability
acrF	b3266	0,6175	0,0474	AcrEF-TolC Drug Efflux Transport System
ade	b3665	0,0536	0,0002	cryptic adenine deaminase monomer
agaA	b3135	0,5197	0,0250	AgaA
agaC	b3139	0,5391	0,0363	EIIAga
aldB	b3588	0,6583	0,0359	putative aminobutyraldehyde dehydrogenase / aldehyde dehydrogenase B
allA	b0505	0,6574	0,0061	ureidoglycolate hydrolase
allB	b0512	0,4423	0,0151	allantoinase
allC	b0516	0,4293	0,0117	allantoate amidohydrolase
allD	b0517	0,4905	0,0101	ureidoglycolate dehydrogenase
alsB	b4088	0,4271	0,0007	YjcX
aniC	b4115	0,4105	0,0212	AdiC Arginine:Agmatine Antiporter
araG	b1900	0,7483	0,0333	arabinose ABC transporter
araH	b4460	0,4566	0,0067	high-affinity L-arabinose transport protein (ABC superfamily, membrane)
arnT	b2257	0,2829	0,0208	4-amino-4-deoxy-L-arabinose (L-Ara4N) transferase
aroD	b1693	0,6190	0,0316	3-dehydroquinate dehydratase
aroH	b1704	0,5580	0,0038	2-dehydro-3-deoxyphosphoheptonate aldolase
asnS	b0930	1,7622	0,0368	asparaginyl-tRNA synthetase
astB	b1745	1,3454	0,0327	succinylarginine dihydrolase
atoA	b2222	2,3479	0,0324	AtoA / putative acetate CoA-transferase
b0501	b0501	0,1596	0,0008	hypothetical protein
b0816	b0816	0,4687	0,0373	hypothetical protein

gene	blattner	ratio A/B	p-value	function
b1172	b1172	0,1061	0,0001	conserved hypothetical protein
b1354	b1354	0,5533	0,0243	hypothetical protein
b1364	b1364	10,5092	0,0054	hypothetical protein
b1903	b1903	0,2168	0,0033	hypothetical protein
b2596	b2596	0,5031	0,0010	hypothetical protein
b2680	b2680	0,7122	0,0494	YgaY MFS transporter
b2856	b2856	0,6466	0,0035	hypothetical protein
bcsE	b3536	0,5509	0,0240	putative protease
bcsF	b3537	0,5029	0,0319	hypothetical protein
bcsZ	b3531	0,5272	0,0166	endo-1,4-D-glucanase
bdm	b1481	0,4413	0,0416	hypothetical protein
bioB	b0775	1,5107	0,0398	biotin synthase monomer
blc	b4149	0,6930	0,0385	Blc outer membrane lipoprotein (lipocalin)
bolA	b0435	0,5808	0,0485	BolA transcriptional regulator
borD	b0557	0,2028	0,0066	bacteriophage lambda Bor protein homolog
btuB	b3966	2,0282	0,0268	outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23
cadA	b4131	0,1817	0,0010	lysine decarboxylase
cadB	b4132	0,2314	0,0183	CadB cadaverine/lysine APC exchanger / Transporter
chaA	b1216	1,1728	0,0177	ChaA calcium CaCA transporter
chbF	b1734	0,4431	0,0084	6-phospho-beta-glucosidase; cryptic
chbG	b1733	0,5453	0,0153	hypothetical protein, encoded by an operon required for growth on N,N'-diacetylchitobiose
chbR	b1735	0,2703	0,0116	ChbR transcriptional regulator
cheY	b1882	3,2891	0,0487	CheY-Pasp
clpB	b2592	0,7053	0,0387	ClpB chaperone
cmr	b0842	0,4212	0,0345	MdfA/Cmr MFS multidrug transporter
codA	b0337	1,3776	0,0127	cytosine deaminase
cpsB	b2049	0,0143	0,0001	mannose-1-phosphate guanylyltransferase-(GDP)
cpsG	b2048	0,0793	0,0000	phosphomannomutase
csgA	b1042	0,1297	0,0015	curlin, major subunit
csgB	b1041	0,2784	0,0091	curlin, minor subunit precursor
csgD	b1040	0,2937	0,0139	CsgD transcriptional activator
csgE	b1039	0,4605	0,0168	curli production assembly/transport component
csgG	b1037	0,3495	0,0413	curli production component
cspA	b3556	2,1715	0,0311	cold shock protein CspA
cspB	b1557	0,3823	0,0091	cold shock protein CspB
cspC	b1823	0,2854	0,0008	cold shock protein CspC
cspG	b0990	0,2179	0,0008	cold shock protein CspG
cspI	b1552	0,1377	0,0009	cold shock protein CspI
cycA	b4208	0,7201	0,0338	CycA serine/alanine/glycine APC transporter
cyoC	b0430	0,6460	0,0438	cytochrome bo terminal oxidase subunit III
cysW	b2423	0,6811	0,0088	sulfate ABC transporter
dadX	b1190	0,5637	0,0240	alanine racemase, major
dctR	b3507	0,4508	0,0475	protein involved in metabolism of C4-dicarboxylates
dcuC	b0621	0,4523	0,0022	DcuC dicarboxylate transporter
dcyD	b1919	1,4064	0,0091	D-cysteine desulfhydrase monomer
degQ	b3234	1,3540	0,0123	serine endoprotease
deoD	b4384	1,5417	0,0073	purine nucleoside phosphorylase / guanosine phosphorylase / deoxyguanosine phosphorylase / inosine phosphorylase / deoxyinosine phosphorylase / adenine phosphorylase / deoxyadenosine phosphorylase
dgt	b0160	0,6156	0,0126	deoxyguanosinetriphosphate triphosphohydrolase
dmsC	b0896	1,2108	0,0248	dimethyl sulfoxide reductase, chain C
dnaA	b3702	1,5798	0,0490	DnaA-ATP transcriptional dual regulator
dnaG	b3066	1,3368	0,0473	DNA biosynthesis; DNA primase
dnaK	b0014	0,5937	0,0163	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins
dnaN	b3701	1,8832	0,0335	DNA polymerase III, beta-subunit
dnaX	b0470	1,3300	0,0296	DNA polymerase III, tau and gamma subunits; DNA elongation factor III
dpiB	b0619	0,4224	0,0076	DpiB
dppF	b3540	1,1825	0,0280	dipeptide ABC transporter
dps	b0812	0,5769	0,0236	stationary phase nucleoid protein that sequesters iron and protects DNA from damage
dsdX	b2365	0,3602	0,0190	DsdX Gnt transporter
dtd	b3887	1,2548	0,0380	D-Tyr-tRNATyr deacylase
elaC	b2268	0,6406	0,0465	binuclear zinc phosphodiesterase monomer
emrE	b0543	0,4603	0,0035	EmrE SMR transporter
emrK	b2368	0,5558	0,0366	EmrK putative membrane fusion protein
emrY	b2367	0,1336	0,0000	EmrY putative multidrug MFS transporter
envC	b3613	1,5602	0,0371	EnvC murein hydrolase
essQ	b1556	4,4414	0,0125	hypothetical protein
eutB	b2441	0,7106	0,0143	ethanolamine ammonia-lyase, probable regulatory subunit
eutD	b2458	0,4881	0,0053	putative phosphate acetyltransferase, ethanolamine utilization
eutN	b2456	0,5116	0,0035	putative detox protein, ethanolamine utilization
fcl	b2052	0,0327	0,0006	GDP-4-dehydro-6-deoxy-D-mannose epimerase / GDP-4-dehydro-6-L-deoxygalactose reductase

gene	blattner	ratio A/B	p-value	function
fecA	b4291	0,6549	0,0354	outer membrane receptor; citrate-dependent iron transport, outer membrane receptor
fecB	b4290	0,6183	0,0038	ferric dicitrate uptake system
fhlA	b2731	1,2443	0,0006	FhlA-Formate transcriptional activator
fhuC	b0151	2,0062	0,0140	ferrichrome uptake system
fic	b3361	1,3138	0,0372	stationary-phase protein with possible role in p-aminobenzoate or folate biosynthesis
fimA	b4314	0,0526	0,0007	major type 1 subunit fimbrin (pilin)
fimB	b4312	0,0776	0,0001	regulator for fimA
fimD	b4317	0,3019	0,0243	outer membrane protein; export and assembly of type 1 fimbriae, interrupted
fimE	b4313	0,0565	0,0001	regulator for fimA
fimG	b4319	0,5755	0,0041	fimbrial morphology
fimI	b4315	0,0712	0,0005	fimbrial protein
fixB	b0042	0,3451	0,0185	probable flavoprotein subunit required for anaerobic carnitine metabolism
fixC	b0043	0,4760	0,0273	flavoprotein (electron transport), possibly involved in anaerobic carnitine metabolism
flgA	b1072	27,1534	0,0010	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgB	b1073	24,5528	0,0038	flagellar basal-body rod protein FlgB
flgC	b1074	14,9393	0,0009	flagellar basal-body rod protein FlgC
flgD	b1075	16,5742	0,0019	flagellar biosynthesis, initiation of hook assembly
flgE	b1076	9,2717	0,0007	flagellar hook protein FlgE
flgF	b1077	6,1174	0,0007	flagellar basal-body rod protein FlgF
flgG	b1078	21,9901	0,0010	flagellar basal-body rod protein FlgG
flgH	b1079	9,7694	0,0040	flagellar L-ring protein FlgH; basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	b1080	15,6181	0,0055	flagellar P-ring protein FlgI
flgJ	b1081	6,3428	0,0005	FlgJ
flgK	b1082	4,5952	0,0289	flagellar biosynthesis, hook-filament junction protein 1
flgM	b1071	28,5501	0,0060	anti-FliA (anti-sigma) factor; also known as RflB protein
flgN	b1070	7,0812	0,0008	flagellar biosynthesis protein FlgN
flhA	b1879	2,5230	0,0463	flagellar biosynthesis protein FlhA
flhB	b1880	10,7222	0,0025	flagellar biosynthesis protein FlhB
flhE	b1878	1,3435	0,0065	flagellar protein
fliA	b1922	32,8560	0,0014	sigma28 factor
fliC	b1923	10,1921	0,0486	flagellar biosynthesis; flagellin, filament structural protein
fliD	b1924	12,4018	0,0338	flagellar cap protein FliD; filament capping protein; enables filament assembly
fliE	b1937	18,5368	0,0018	flagellar basal-body protein FliE
fliF	b1938	23,8464	0,0001	flagellar M-ring protein FliF; basal-body MS(membrane and supramembrane)-ring and collar protein
fliG	b1939	17,5399	0,0006	flagellar motor switch protein FliG; component of motor switching and energizing, enabling rotation and determining its direction
fliH	b1940	18,6885	0,0041	flagellar biosynthesis protein FliH
fliJ	b1942	14,2153	0,0015	flagellar biosynthesis protein FliJ
fliK	b1943	11,4774	0,0028	flagellar hook-length control protein FliK
fliL	b1944	21,9931	0,0024	flagellar biosynthesis
fliM	b1945	24,5354	0,0007	flagellar motor switch protein FliM; component of motor switch and energizing, enabling rotation and determining its direction
fliN	b1946	20,1390	0,0021	flagellar motor switch protein FliN; component of motor switch and energizing, enabling rotation and determining its direction
fliO	b1947	6,1100	0,0078	flagellar biosynthesis protein FliO
fliQ	b1949	16,8460	0,0006	flagellar biosynthesis protein FliQ
fliR	b1950	14,0112	0,0024	flagellar biosynthesis protein FliR
fliS	b1925	11,4258	0,0360	flagellar biosynthesis protein FliS
fliY	b1920	4,6961	0,0053	periplasmic cystine-binding protein; member of extracellular bacterial solute-binding protein family III
fliZ	b1921	11,3145	0,0013	possible cell-density responsive regulator of sigmaF
folX	b2303	0,7774	0,0119	dihydroneopterin triphosphate 2'-epimerase
frvR	b3897	1,5713	0,0220	FrvR predicted transcriptional regulator
frwC	b3949	1,2134	0,0259	EIIBCfrw
ftnA	b1905	0,2411	0,0207	cytoplasmic ferritin, an iron storage protein)
ftnB	b1902	0,2538	0,0225	hypothetical protein
ftsB	b2748	2,1787	0,0303	essential cell division protein FtsB
ftsK	b0890	0,8409	0,0222	essential cell division protein FtsK
ftsY	b3464	1,1435	0,0290	SRP receptor
fucI	b2802	0,7804	0,0498	L-fucose isomerase
fucU	b2804	0,5451	0,0123	cytoplasmic L-fucose binding protein
fumC	b1611	0,5797	0,0314	fumarase C monomer
fusA	b3340	1,6060	0,0216	elongation factor G
fxsA	b4140	0,5479	0,0484	inner membrane protein; overproduction inhibits F exclusion of bacteriophage T7
gadA	b3517	0,0922	0,0055	glutamate decarboxylase A subunit
gadC	b1492	0,1563	0,0066	XasA GABA APC transporter
gadE	b3512	0,1055	0,0047	GadE transcriptional activator
gadW	b3515	0,4779	0,0095	GadWtranscriptional repressor
galP	b2943	0,5043	0,0494	GalP - galactose MFS transporter
galS	b2151	0,7119	0,0404	GalS-galactose
garL	b3126	0,5428	0,0453	alpha-dehydro-beta-deoxy-D-glucarate aldolase
gatA	b2094	0,2319	0,0238	EIIgat
gatC	b2092	0,3166	0,0061	EIIgat

gene	blattner	ratio A/B	p-value	function
gatD	b2091	0,3602	0,0414	galactitol-1-phosphate dehydrogenase
gatR_1	b2087	0,6518	0,0330	negative DNA-binding transcriptional regulator of galactitol metabolism, subunit of GatR transcriptional repressor
glf	b2036	0,6716	0,0075	UDP-galactopyranose mutase
glgS	b3049	0,5189	0,0061	glycogen biosynthesis, rpoS dependent
glpG	b3424	1,5025	0,0339	inner membrane-associated protein of glp regulon
gltF	b3214	0,2557	0,0049	regulator of gltBDF operon, induction of Ntr enzymes
glxR	b0509	0,4957	0,0241	tartronate semialdehyde reductase 2
gmd	b2053	0,0770	0,0082	GDP-mannose 4,6-dehydratase
gmk	b3648	1,2627	0,0032	deoxyguanylate kinase / guanylate kinase
gmr	b1285	0,6330	0,0116	RNase II modulator
gnd	b2029	0,5770	0,0017	6-phosphogluconate dehydrogenase (decarboxylating)
gnsB	b1550	0,3110	0,0035	protein that affects unsaturated fatty acid abundance
gspD	b3325	0,5089	0,0206	putative protein secretion protein for export
gspE	b3326	0,6419	0,0197	putative protein secretion protein for export
gspG	b3328	0,6256	0,0416	putative protein secretion protein for export
gspH	b3329	0,1773	0,0015	putative protein secretion protein for export
hcaC	b2540	1,4004	0,0273	ferredoxin, 3-phenylpropionate dioxygenase system
hchA	b1967	0,4961	0,0197	heat shock protein (Hsp) 31
hcr	b0872	0,5809	0,0410	NADH oxidoreductase
hdeA	b3510	0,0218	0,0006	acid-resistance protein, possible chaperone
hdeB	b3509	0,0715	0,0064	10K-L protein, related to acid resistance protein of Shigella flexneri
hdhA	b1619	0,3868	0,0075	7-alpha-hydroxysteroid dehydrogenase
hemA	b1210	0,1261	0,0284	glutamyl-tRNA reductase
hha	b0460	0,3850	0,0259	haemolysin expression modulating protein
hipA	b1507	8,3272	0,0254	HipA transcriptional activator
hlyE	b1182	0,0720	0,0009	hemolysin E
hns	b1237	9,0470	0,0012	H-NS transcriptional dual regulator
holB	b1099	3,2529	0,0455	DNA polymerase III, delta prime subunit
hslR	b3400	0,8182	0,0329	heat shock protein Hsp15
htrA	b0161	0,3019	0,0256	DegP
htrL	b3618	0,3142	0,0055	involved in lipopolysaccharide biosynthesis
hybB	b2995	0,6320	0,0450	probable cytochrome Ni/Fe component of hydrogenase-2
icdA	b1136	0,6386	0,0068	Icd
idnK	b4268	0,6017	0,0247	gluconokinase II
idnO	b4266	0,5978	0,0248	5-keto-D-gluconate 5-reductase / putative acetoin dehydrogenase
inaA	b2237	2,1979	0,0462	pH-inducible protein involved in stress response
intF	b0281	1,8823	0,0476	putative phage integrase
intG	b1936	0,3321	0,0004	hypothetical protein
intR	b1345	0,5389	0,0226	putative transposase
katE	b1732	0,5629	0,0051	hydroperoxidase II
kbl	b3617	0,5504	0,0248	2-amino-3-ketobutyrate CoA ligase
kduD	b2842	1,1891	0,0386	2-deoxy-D-gluconate 3-dehydrogenase
kduI	b2843	0,6885	0,0274	homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase
leuO	b0076	0,3307	0,0226	LeuO transcriptional activator
lit	b1139	0,4834	0,0364	Lit, cell death peptidase; phage exclusion; e14 prophage
lon	b0439	0,6940	0,0326	DNA-binding, ATP-dependent protease La
lysS	b2890	1,2168	0,0189	lysyl tRNA synthetase (LysRSs), constitutive
maa	b0459	0,5169	0,0308	maltose acetyltransferase
malP	b3417	2,3538	0,0003	maltodextrin phosphorylase monomer
malZ	b0403	0,5110	0,0173	maltodextrin glucosidase
mcrA	b1159	0,6575	0,0372	restriction of DNA at 5-methylcytosine residues
mcrB	b4346	0,5308	0,0084	MrcB subunit of 5-methylcytosine restriction system
mcrC	b4345	0,4781	0,0069	MrcC subunit of 5-methylcytosine restriction system
mdoC	b1047	0,5105	0,0193	protein required for succinyl modification of osmoregulated periplasmic glucans
mdoG	b1048	0,6617	0,0179	periplasmic glucan (MDO) biosynthesis protein
mdtD	b2077	0,2947	0,0001	YegB
mdtM	b4337	0,2035	0,0056	YjiO drug MFS transporter
mdtP	b4080	0,6347	0,0466	putative enzyme
metE	b3829	0,7137	0,0147	Cobalamin-independent homocysteine transmethylase
mhpD	b0350	1,7196	0,0017	2-keto-4-pentenoate hydratase
moaE	b0785	1,1425	0,0282	molybdopterin synthase large subunit
mokC	b0018	0,5463	0,0278	regulatory peptide whose translation enables hokC (gef) expression
motB	b1889	31,7966	0,0090	MotB protein, enables flagellar motor rotation, linking torque machinery to cell wall
mqo	b2210	1,3940	0,0142	malate dehydrogenase
msbA	b0914	1,4206	0,0411	ATP-binding transport protein; multicopy suppressor of htrB
mtr	b3161	0,5406	0,0232	Mtr tryptophan ArAAP transporter
murB	b3972	1,3239	0,0246	UDP-N-acetylmuramate dehydrogenase
mutS	b2733	1,7394	0,0434	MutHLS complex, methyl-directed mismatch repair
mviN	b1069	6,8399	0,0383	putative virulence factor

gene	blattner	ratio A/B	p-value	function
nagA	b0677	1,4358	0,0326	N-acetylglucosamine-6-phosphate deacetylase
nanA	b3225	1,4721	0,0000	N-acetylneuraminate lyase
nanC	b4311	0,1875	0,0025	conserved hypothetical protein
narV	b1465	10,0792	0,0064	nitrate reductase Z, γ subunit
ndk	b2518	0,5474	0,0389	nucleoside diphosphate kinase / UDP kinase / CDP kinase / dUDP kinase / dCDP kinase / dTDP kinase / dADP kinase / dGDP kinase / GDP kinase
nmpC	b0553	0,1597	0,0178	outer membrane porin protein; locus of qsr prophage
nrpH	b2673	1,9330	0,0215	glutaredoxin-like protein; hydrogen donor
nrFB	b4071	0,7562	0,0150	nitrite reductase complex
nudD	b2051	0,0081	0,0000	GDP-mannose mannosyl hydrolase
ompF	b0929	4,4090	0,0048	outer membrane porin OmpF
ompL	b3875	0,4607	0,0424	OmpL
oppC	b1245	0,4030	0,0434	oligopeptide ABC transporter
osmB	b1283	0,1157	0,0062	OsmB osmotically inducible lipoprotein
osmC	b1482	0,2146	0,0012	osmotically inducible peroxidase OsmC
otsA	b1896	0,4210	0,0107	trehalose-6-phosphate synthase
paaB	b1389	0,4994	0,0344	putative subunit of phenylacetate-CoA oxygenase
paaI	b1396	8,7551	0,0044	hypothetical protein with some similarity to thioesterases
pagP	b0622	0,2253	0,0082	PagP monomer
parE	b3030	1,4510	0,0027	Topoisomerase IV subunit B
pdxA	b0052	0,8447	0,0010	PdxA dehydrogenase/decarboxylase
pflB	b0903	0,5179	0,0369	pyruvate formate-lyase (inactive)
pflD	b3951	0,7011	0,0477	formate acetyltransferase 2
pgaC	b1022	0,4106	0,0015	predicted N-glycosyltransferase
pgaD	b1021	0,3002	0,0038	putative inner membrane protein
pheM	b1715	0,5171	0,0303	phenylalanyl-tRNA synthetase (pheST) operon leader peptide
pinR	b1374	0,1294	0,0012	putative transposon resolvase
pitB	b2987	0,4130	0,0274	PitB
plsB	b4041	1,4149	0,0072	glycerol-3-phosphate acyltransferase
pmrF	b2254	0,1668	0,0000	undecaprenyl phosphate-L-Ara4FN transferase
polB	b0060	1,4392	0,0465	DNA polymerase II
potC	b1124	0,7024	0,0321	putrescine/spermidine ABC transporter
poxA	b4155	0,5601	0,0149	putative regulator of pyruvate oxidase
pphB	b2734	0,2574	0,0011	protein phosphatase 2 / protein-tyrosine-phosphatase / phosphoprotein phosphatase
pptA	b1461	0,4035	0,0291	probable 4-oxalocrotonate tautomerase (4-OT) monomer
pqqL	b1494	0,3738	0,0359	putative zinc peptidase
prfA	b1211	6,2321	0,0253	peptide chain release factor RF-1
prfH	b0236	0,4740	0,0086	probable peptide chain release factor
ptrB	b1845	0,6002	0,0443	protease II
purC	b2476	1,2969	0,0425	phosphoribosylaminoimidazole-succinocarboxamide synthase
puuR	b1299	8,2529	0,0016	putative oxidoreductase/putative regulator
pyrE	b3642	0,5836	0,0304	orotate phosphoribosyltransferase
rarD	b3819	0,3373	0,0007	hypothetical protein
rbfA	b3167	1,2320	0,0250	ribosome-binding factor A
rbsD	b3748	0,3624	0,0037	D-ribose utilization
rcsA	b1951	0,2865	0,0016	positive DNA-binding transcriptional regulator of capsular polysaccharide synthesis, activates its own expression
recT	b1349	0,2404	0,0026	recombinase, DNA renaturation
rfbA	b2039	0,6165	0,0268	dTDP-glucose pyrophosphorylase
rfbB	b2041	0,5623	0,0045	RmlB
rfbC	b2038	0,5770	0,0462	dTDP-4-dehydrorhamnose 3,5-epimerase
rfbX	b2037	0,5272	0,0173	RfbX lipopolysaccharide PST transporter
rfc	b2035	0,5906	0,0455	O-antigen polymerase
rhsA	b3593	0,4056	0,0183	RhsA protein in rhs element
rhsD	b0497	0,1818	0,0162	RhsD protein in rhs element
rihB	b2162	0,4616	0,0135	ribonucleoside hydrolase 2 (pyrimidine-specific)
rluC	b1086	0,7606	0,0060	23S rRNA pseudouridine synthase
rmuC	b3832	1,5317	0,0486	conserved protein
rplM	b3231	1,1735	0,0393	50S ribosomal subunit protein L13
rpmG	b3636	1,3762	0,0233	50S ribosomal subunit protein L33
rpoA	b3295	1,7007	0,0053	RNA polymerase, alpha subunit
rpsO	b3165	1,2800	0,0383	30S ribosomal subunit protein S15
rseA	b2572	0,6762	0,0264	anti-sigma factor that inhibits sigmaE
rseB	b2571	0,5923	0,0358	negative regulator of sigmaE; interacts with RseA and stimulates binding of RseA to sigmaE
rstA	b1608	0,4644	0,0241	RstA- Phosphorylated transcriptional regulator
rsxB	b1628	0,8140	0,0337	member of SoxR-reducing complex
rsxD	b1630	0,8446	0,0469	integral membrane protein of SoxR-reducing complex
ruvA	b1861	0,7247	0,0021	branch migration of Holliday structures; repair
sbmA	b0377	1,2804	0,0236	SbmA
sdhA	b0723	0,5308	0,0031	succinate dehydrogenase flavoprotein
sdhB	b0724	0,6045	0,0340	succinate dehydrogenase iron-sulfur protein

gene	blattner	ratio A/B	p-value	function
sfmC	b0531	0,6341	0,0140	putative chaperone
sfsA	b0146	0,7060	0,0346	SfsA
sgbU	b3582	0,3459	0,0092	probable 3-hexulose-6-phosphate isomerase
shiA	b1981	0,3567	0,0076	ShiA shikimate MFS transporter
skp	b0178	1,0703	0,0483	periplasmic chaperone
slp	b3506	0,4891	0,0409	outer membrane protein induced after carbon starvation
slyA	b1642	0,5661	0,0360	SlyA transcriptional activator
speD	b0120	0,6822	0,0032	adenosylmethionine decarboxylase, proenzyme
stpA	b2669	0,1356	0,0074	DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing?
tatA	b3836	1,3939	0,0306	TatA
tatD	b4483	1,7888	0,0417	magnesium-dependent DNase
tauA	b0365	0,5600	0,0404	TauA/TauB/TauC ABC transporter
tauB	b0366	0,6178	0,0194	TauA/TauB/TauC ABC transporter
tdcB	b3117	0,2584	0,0065	threonine dehydratase (catabolic)
tdcC	b3116	0,2341	0,0055	TdcC threonine STP transporter
tdcD	b3115	0,4677	0,0419	propionate kinase / acetate kinase C
tdcF	b3113	0,2775	0,0099	hypothetical protein
tdk	b1238	0,3639	0,0022	thymidine kinase / deoxyuridine kinase
tnaA	b3708	0,1418	0,0152	L-cysteine desulphydrase / tryptophanase
tolA	b0739	0,8478	0,0322	Tol-Pal Cell Envelope Complex
torS	b0993	2,0482	0,0380	TorS-Phis850
torY	b1873	0,2576	0,0198	trimethylamine N-oxide reductase III, c-type cytochrome subunit
torZ	b1872	0,3923	0,0120	trimethylamine N-oxide reductase III, TorZ subunit
treB	b4240	25,0943	0,0439	EII _{Tre}
treC	b4239	7,6034	0,0357	trehalose-6-phosphate hydrolase
trmA	b3965	1,5449	0,0177	tRNA (uracil-5-)-methyltransferase
trmH	b3651	1,5347	0,0249	tRNA (Gm18) 2'-O-methyltransferase
ubiG	b2232	1,1103	0,0475	3-demethylubiquinone 3-methyltransferase / 2-octaprenyl-6-hydroxyphenol methylase
ugd	b2028	0,0650	0,0009	UDP-glucose 6-dehydrogenase
ulaA	b4193	1,5705	0,0194	eii _{ga}
ulaR	b4191	0,7810	0,0103	putative DeoR-type transcriptional regulator
uppP	b3057	0,5663	0,0449	undecaprenyl diphosphatase; bacitracin resistance
uspD	b3923	0,4337	0,0346	stress protein involved in resistance to UV irradiation
uvrC	b1913	0,4947	0,0149	excinuclease ABC, subunit C; repair of UV damage to DNA
uxaA	b3091	0,7147	0,0481	altronate dehydratase
vsr	b1960	0,7256	0,0064	DNA mismatch endonuclease of the very short patch (VSP) mismatch repair pathway
wbbI	b2034	0,6317	0,0228	hypothetical protein; not required for colanic acid biosynthesis
wbbJ	b2033	0,6009	0,0130	putative transferase
wcaA	b2059	0,1328	0,0082	putative regulator
wcaB	b2058	0,0815	0,0015	putative transferase
wcaC	b2057	0,1000	0,0029	putative glycosyl transferase
wcaD	b2056	0,0149	0,0002	putative colanic acid polymerase
wcaE	b2055	0,0409	0,0011	putative colanic acid biosynthesis glycosyl transferase
wcaF	b2054	0,0262	0,0002	putative transferase
wcaI	b2050	0,3118	0,0133	putative colanic biosynthesis glycosyl transferase
wcaJ	b2047	0,1255	0,0000	putative colanic acid biosynthesis UDP-glucose lipid carrier transferase
wcaK	b2045	0,1130	0,0074	putative galactokinase (EC 2.7.1.6).
wcaL	b2044	0,0764	0,0036	putative colanic biosynthesis glycosyl transferase
wcaM	b2043	0,0293	0,0005	hypothetical protein
wza	b2062	0,1207	0,0140	Wza Outer Membrane Auxiliary (OMA) Protein, putative polysaccharide export protein
wzb	b2061	0,3249	0,0468	tyrosine phosphatase
wzc	b2060	0,1280	0,0091	tyrosine kinase involved in colanic acid biosynthesis
wzxC	b2046	0,2888	0,0079	Wzx _C
wzxE	b3792	1,5446	0,0476	metabolism; biosynthesis of macromolecules (cellular constituents); enterobacterial common antigen (surface glycolipid) transport
xapB	b2406	0,4569	0,0141	XapB xanthosine MFS transporter
xapR	b2405	0,3765	0,0027	XapR transcriptional activator
yaaW	b0011	3,2924	0,0115	HtgA transcriptional regulator
yacH	b0117	0,8161	0,0238	putative membrane protein
yadC	b0135	0,4099	0,0206	putative fimbrial-like protein
yadL	b0137	0,2631	0,0178	putative adhesin-like protein
yadN	b0141	0,6154	0,0468	putative fimbrial-like protein
yafT	b0217	0,2068	0,0031	putative aminopeptidase
yagL	b0278	0,0609	0,0012	DNA-binding protein
yagM	b0279	0,3618	0,0281	hypothetical protein
yagU	b0287	0,5429	0,0268	conserved protein
yagW	b0290	0,1221	0,0006	putative receptor
yagX	b0291	0,1265	0,0029	putative enzyme
yagZ	b0293	0,0142	0,0005	conserved hypothetical protein
yahA	b0315	0,3523	0,0129	hypothetical protein

gene	blattner	ratio A/B	p-value	function
yahB	b0316	0,6555	0,0219	putative transcriptional regulator LYSR-type
yahI	b0323	0,5829	0,0393	putative carbamate kinase
yaiB	b0382	0,4839	0,0452	conserved hypothetical protein
yaiP	b0363	0,2167	0,0005	polysaccharide metabolism
ybaJ	b0461	0,2263	0,0008	conserved hypothetical protein
ybaT	b0486	1,5467	0,0361	YbaT APC transporter
ybaX	b0444	1,3088	0,0297	hypothetical protein with similarity to the ALU1-P aluminum tolerance protein of <i>Arthrobacter viscosus</i>
ybbD	b0500	0,3711	0,0158	conserved hypothetical protein
ybbJ	b0488	0,4127	0,0062	conserved protein
ybbW	b0511	0,1329	0,0228	YbbW NCS1 Transporter
ybcC	b0539	0,6619	0,0153	putative exonuclease (EC 3.1.1.3) of lambda
ybcK	b0544	0,2294	0,0058	hypothetical protein
ybcL	b0545	0,2269	0,0037	possible kinase regulator
ybcM	b0546	0,1406	0,0048	putative ARAC-type regulatory protein
ybcW	b0559	0,4816	0,0023	hypothetical protein
ybdG	b0577	0,5895	0,0193	putative transport protein
ybdJ	b0580	0,5837	0,0492	conserved hypothetical protein
ybdM	b0601	0,8195	0,0493	conserved protein
ybdO	b0603	0,2801	0,0308	putative transcriptional regulator LYSR-type
ybcZ	b0660	0,6636	0,0464	putative ATP-binding protein
ybfD	b0706	0,1079	0,0006	conserved protein
ybfG	b0690	0,4707	0,0244	conserved hypothetical protein
ybfH	b0691	0,3421	0,0007	conserved hypothetical protein
ybhM	b0787	0,3888	0,0098	hypothetical protein
ybjC	b0850	0,7170	0,0462	conserved hypothetical protein; gene is within soxRS regulon
ybjG	b0841	0,2116	0,0107	putative permease
ybjJ	b0845	3,1930	0,0116	putative DEOR-type transcriptional regulator
ybjL	b0847	0,3923	0,0043	putative transport protein
ybjN	b0853	0,8482	0,0409	putative sensory transduction regulator
ycaN	b0900	0,5581	0,0284	putative transcriptional regulator LYSR-type
ycbQ	b0938	0,0713	0,0025	putative fimbrial-like protein
ycbR	b0939	0,1824	0,0184	putative chaperone
ycbS	b0940	0,1652	0,0073	putative outer membrane protein
yccE	b1001	0,4529	0,0130	putative hemoglobin-binding protein
yccM	b0992	0,6335	0,0164	hypothetical protein
ycdN	b1016	1,6654	0,0122	hypothetical protein of the OFeT transport family
ycdU	b1029	0,1999	0,0116	putative enzyme
yceI	b1056	0,2268	0,0001	periplasmic protein; possibly secreted
yceJ	b1057	0,1945	0,0009	putative cytochrome
yceP	b1060	0,3901	0,0267	conserved hypothetical protein
ycgH_1	b1169	0,1993	0,0039	conserved protein; member of the Autotransporter family
ycgH_2	b1170	0,4386	0,0046	conserved protein; member of the Autotransporter family
ycgV	b1202	0,3109	0,0415	putative adhesion and penetration protein
ycgX	b1161	0,7611	0,0359	hypothetical protein
ycgZ	b1164	0,5664	0,0112	hypothetical protein
yciA	b1253	11,0540	0,0002	putative enzyme
yciE	b1257	0,3808	0,0301	conserved protein
yciF	b1258	0,1428	0,0003	conserved protein
yciQ	b1268	5,5117	0,0014	putative membrane protein
ycjO	b1311	8,6194	0,0110	YcjN/YcjO/YcjP ABC transporter
ycjQ	b1313	0,2968	0,0286	putative oxidoreductase
ydaL	b1340	0,6179	0,0096	hypothetical protein
ydaT	b1358	0,7086	0,0152	hypothetical protein
ydaY	b1366	0,4876	0,0346	hypothetical protein
ydbA_2	b1405	0,4749	0,0312	hypothetical protein product of fragment 2 of a split CDS
ydcC	b1460	0,1497	0,0021	conserved protein, similar to H-repeat associated proteins
ydcD	b1457	0,5139	0,0497	hypothetical protein
ydcR	b1439	5,6513	0,0349	multi modular; putative transcriptional regulator ; also putative ATP-binding component of a transport system
ydcX	b1445	3,8934	0,0011	hypothetical protein
yddB	b1495	7,9254	0,0046	conserved protein
yddH	b1462	11,8388	0,0095	putative enzyme
yddJ	b1470	1,7194	0,0428	hypothetical protein
yddK	b1471	0,7743	0,0210	putative glycoprotein
yddV	b1490	0,4278	0,0017	conserved protein
ydeH	b1535	0,3768	0,0061	hypothetical protein
ydeI	b1536	0,0747	0,0002	conserved hypothetical protein
ydeK	b1510	0,4789	0,0370	YdeK
ydeO	b1499	0,0998	0,0062	putative ARAC-type regulatory protein
ydeP	b1501	0,1115	0,0201	acid resistance protein

gene	blattner	ratio A/B	p-value	function
ydeQ	b1502	0,2304	0,0123	putative adhesin; similar to FimH protein
ydeR	b1503	7,3709	0,0202	putative fimbrial-like protein
ydeS	b1504	0,3919	0,0199	putative fimbrial-like protein
ydfJ	b1543	42,4461	0,0301	YdfJ
ydfO	b1549	0,5234	0,0174	hypothetical protein
ydfV	b1565	0,7286	0,0417	hypothetical protein
YdgE	b1599	0,2334	0,0201	YdgE SMR Protein
YdgF	b1600	0,0826	0,0007	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydiA	b1703	0,2332	0,0171	conserved protein
ydiB	b1692	0,4286	0,0109	shikimate dehydrogenase
ydiF	b1694	0,3148	0,0286	putative enzyme / putative acetate CoA-transferase
ydiO	b1695	0,4529	0,0403	putative acyl-CoA dehydrogenase
ydiR	b1698	1,8775	0,0115	putative subunit of YdiQ-YdiR flavoprotein
ydjH	b1772	0,4958	0,0014	putative kinase
ydjI	b1773	0,2754	0,0004	putative aldolase
ydjJ	b1774	0,1765	0,0009	putative oxidoreductase
yeaE	b1781	0,4708	0,0318	putative oxidoreductase, NAD(P)-linked
yeaJ	b1786	0,4275	0,0188	putative membrane protein
yebN	b1821	0,3622	0,0207	putative membrane protein, terpenoid synthase-like
yebQ	b1828	3,1669	0,0052	YebQ
yecD	b1867	0,4967	0,0298	putative enzyme
yecR	b1904	18,6699	0,0070	conserved hypothetical protein
yecT	b1877	0,3511	0,0159	hypothetical protein
yedK	b1931	1,3670	0,0277	conserved hypothetical protein
yedM	b1935	2,1595	0,0289	hypothetical protein
yedN_2	b1933	0,5833	0,0372	hypothetical protein
yedS_1	b1964	0,4832	0,0090	putative outer membrane protein
yedS_2	b1965	0,1868	0,0002	putative outer membrane protein
yedS_3	b1966	0,0869	0,0022	putative outer membrane protein
yedV	b1968	0,3589	0,0025	putative 2-component sensor protein
yedW	b1969	0,3706	0,0275	putative 2-component transcriptional response regulator
yeeE	b2013	0,7926	0,0476	putative transport system permease protein
yeeN	b1983	0,5430	0,0021	conserved protein
yeeW	b2006	0,7709	0,0145	hypothetical protein
yegI	b2070	0,3095	0,0072	putative chaperonin
yegJ	b2071	0,2268	0,0018	hypothetical protein
yegR	b2085	0,1713	0,0037	hypothetical protein
yegS	b2086	0,2875	0,0021	conserved protein
yegW	b2101	0,7504	0,0332	putative transcriptional regulator
yegZ	b2083	0,2051	0,0136	hypothetical protein
yehL	b2119	0,1192	0,0005	putative transport protein (ABC superfamily, atp_bind)
yehM	b2120	0,2962	0,0436	conserved hypothetical protein
yehX	b2129	1,5433	0,0241	YehW/YehX/YehY/YehZ ABC transporter
yeiG	b2154	0,6806	0,0088	putative esterase (EC 3.1.1.-).
yeiH	b2158	0,6070	0,0478	putative membrane protein
yeiT	b2146	0,5692	0,0283	putative dihydrothymine dehydrogenase
yfaO	b2251	0,3555	0,0129	putative enzyme (Nudix hydrolase)
yfaQ	b2226	0,6289	0,0473	conserved protein
yfaS_1	b2228	0,4905	0,0091	putative membrane protein
yfaU	b2245	0,3551	0,0071	protein with similarity to HHED aldolases
yfbB	b2263	1,5292	0,0311	putative enzyme
yfbE	b2253	0,4484	0,0060	UDP-L-Ara4O C-4" transaminase
yfbP	b2275	0,5151	0,0301	hypothetical protein
yfdP	b2359	0,5750	0,0474	hypothetical protein
yfdU	b2373	0,4607	0,0057	putative enzyme
yffb	b2471	0,3324	0,0071	conserved thioredoxin-like protein
yfgH	b2505	0,4115	0,0103	putative outer membrane lipoprotein
yfhK	b2556	1,8314	0,0452	putative 2-component sensor protein
yfiB	b2605	0,6217	0,0406	putative outer membrane protein
yfiC	b2575	0,7187	0,0190	putative enzyme
yfiP	b2583	1,3837	0,0071	conserved hypothetical protein
yfiR	b2603	0,3222	0,0010	conserved protein
yfjK	b2627	0,3419	0,0029	hypothetical protein
yfjL	b2628	0,3105	0,0061	hypothetical protein
yfjO	b2631	0,3841	0,0077	hypothetical protein
ygbT	b2755	0,1586	0,0012	conserved hypothetical protein
ygcG	b2778	0,4150	0,0418	putative membrane protein
ygcI	b2757	0,0266	0,0000	hypothetical protein
ygcJ	b2758	0,4687	0,0197	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
ygcK	b2759	0,0180	0,0001	hypothetical protein
ygcL	b2760	0,1023	0,0021	hypothetical protein with possible relationship to novobiocin and deoxycholate resistance
ygdR	b2833	0,4092	0,0084	conserved hypothetical protein
ygeQ	b2863	0,6468	0,0449	hypothetical protein
ygeW	b2870	0,5789	0,0021	putative carbamoyl transferase
yghJ	b2973	0,4626	0,0310	predicted inner membrane lipoprotein
yghR	b2984	1,2529	0,0320	conserved protein
ygiL	b3043	0,0354	0,0001	putative fimbrial-like protein
ygiD	b3064	1,4330	0,0151	putative O-sialoglycoprotein endopeptidase
yhaB	b3120	0,6588	0,0079	conserved protein
yhcH	b3221	1,4678	0,0226	conserved hypothetical protein; gene is in sialic acid catabolic operon
yhdH	b3253	1,5233	0,0446	putative dehydrogenase
yhfK	b3358	0,7711	0,0070	hypothetical protein
yhlL	b3369	0,1799	0,0003	hypothetical protein
yhhI	b3484	0,1140	0,0042	conserved protein similar to H-repeat-associated proteins
yhiK	b3489	0,5909	0,0164	hypothetical protein
yhjB	b3520	0,6632	0,0240	putative regulator
yhjH	b3525	15,5314	0,0446	protein involved in flagellar function
yhjR	b3535	0,3106	0,0149	hypothetical protein
yiaA	b3562	0,3589	0,0101	hypothetical protein
yiaJ	b3574	1,4560	0,0188	YiaJ transcriptional repressor
yiaN	b3578	0,5883	0,0029	YiaMNO Binding Protein-dependent Secondary (TRAP) Transporter
yiaT	b3584	0,3441	0,0061	putative outer membrane protein
yiaU	b3585	0,3785	0,0049	putative transcriptional regulator LYSR-type
yiaV	b3586	0,5890	0,0043	putative membrane protein
yiaW	b3587	0,2799	0,0038	hypothetical protein
yibA	b3594	0,1903	0,0047	putative lyase
yibJ	b3595	0,2186	0,0238	hypothetical protein
yieL	b3719	0,5420	0,0231	putative xylanase
yigF	b3817	0,2284	0,0094	conserved hypothetical protein
yigZ	b3848	1,3342	0,0497	putative elongation factor
yihN	b3874	0,4333	0,0156	YihN MFS transporter
yihO	b3876	0,6279	0,0411	YihO GPH transporter
yihQ	b3878	0,6251	0,0380	putative glycosidase
yiiG	b3896	0,2402	0,0073	conserved protein
yiiS	b3922	0,2364	0,0157	conserved hypothetical protein
yiiU	b3928	1,3852	0,0299	conserved hypothetical protein
yjbE	b4026	0,0840	0,0029	conserved hypothetical protein
yjbM	b4048	0,4310	0,0137	conserved hypothetical protein
yjeB	b4178	1,6962	0,0415	conserved protein with a Winged helix domain
yjeJ	b4145	0,3840	0,0307	conserved protein
yjeM	b4156	0,2229	0,0057	YjeM APC transporter
yjeN	b4157	0,3408	0,0038	conserved hypothetical protein
yjfJ	b4182	0,6175	0,0334	conserved protein
yjfK	b4183	0,4529	0,0043	conserved hypothetical protein
yjfL	b4184	0,5766	0,0073	hypothetical protein
yjfN	b4188	1,3712	0,0202	conserved hypothetical protein
yjfZ	b4204	0,3394	0,0322	hypothetical protein
yjgM	b4256	0,4628	0,0240	putative acyltransferase
yjgN	b4257	0,5071	0,0145	putative membrane protein possible involved in transport
yjhB	b4279	0,3122	0,0246	YjhB MFS transporter
yjhC	b4280	0,3612	0,0064	KpLE2 phage-like element; putative NAD(P)-binding dehydrogenase
yjhF	b4296	0,1057	0,0123	YjhF Gnt transporter
yjhG	b4297	0,3226	0,0116	putative dehydratase
yjhH	b4298	0,0468	0,0002	putative lyase/synthase
yjhI	b4299	0,1141	0,0053	putative regulator
yjhP	b4306	0,5874	0,0178	putative methyltransferase
yjiW	b4347	0,2530	0,0215	hypothetical protein
ykgA	b0300	0,5109	0,0205	putative ARAC-type regulatory protein
ykgB	b0301	0,2477	0,0014	putative membrane protein
ykgF	b0307	0,2214	0,0430	putative dehydrogenase
ykgH	b0310	0,3306	0,0076	conserved protein
ykgI	b0303	0,0848	0,0003	hypothetical protein
ykiA	b0392	0,3451	0,0025	hypothetical protein
ylbA	b0515	0,4807	0,0467	conserved hypothetical protein
yliF	b0834	0,7291	0,0466	conserved protein
ymcC	b0986	0,5145	0,0239	putative synthetase, lipoprotein, and/or outer membrane porin
ymfE	b1138	0,1606	0,0015	hypothetical protein
ymfK	b1145	1,3071	0,0271	putative phage repressor

gene	blattner	ratio A/B	p-value	function
ymgA	b1165	0,3510	0,0002	hypothetical protein
ymgB	b1166	0,2729	0,0002	hypothetical protein
ymgD	b1171	0,1185	0,0000	hypothetical protein
ynaE	b1375	0,1056	0,0000	hypothetical protein
ynaI	b1330	0,5331	0,0212	YnaI
ynaK	b1365	0,2104	0,0022	hypothetical protein
ynbB	b1409	9,4657	0,0003	putative phosphatidate cytidiltransferase
ynbD	b1411	8,0957	0,0101	putative enzyme
yncD	b1451	7,7140	0,0189	Probable TonB-dependent receptor
yncH	b1455	0,6158	0,0168	hypothetical protein
yncI	b1458	0,0504	0,0048	conserved protein
yneG	b1523	1,4493	0,0097	conserved hypothetical protein
yneK	b1527	0,7595	0,0440	conserved protein
ynfC	b1585	0,6339	0,0385	YnfC lipoprotein
ynfN	b1551	0,1481	0,0169	hypothetical protein
ynjI	b1762	0,5647	0,0434	conserved protein
yoaC	b1810	0,5527	0,0163	conserved hypothetical protein
yobF	b1824	0,2638	0,0011	hypothetical protein
yodA	b1973	0,4038	0,0074	cadmium-induced metal binding protein
yodB	b1974	0,6011	0,0076	putative cytochrome
ypdE	b2384	0,1729	0,0092	putative endoglucanase
yphE	b2547	0,7172	0,0119	YphD/YphE/YphF ABC transporter
yqeA	b2874	0,7065	0,0379	putative carbamate kinase
yqeI	b2847	0,5345	0,0347	putative sensory transducer
yqeJ	b2848	0,5636	0,0205	conserved hypothetical protein
yqgF	b2949	2,0009	0,0211	possible Holliday junction resolvase
yqiH	b3047	0,4868	0,0245	putative membrane protein
yqiJ	b3050	0,3830	0,0118	putative oxidoreductase
yqjK	b3100	0,7262	0,0339	conserved hypothetical protein
yraH	b3142	0,2087	0,0035	putative fimbrial-like protein
yraI	b3143	0,2992	0,0267	putative chaperone
ytfT	b4230	1,3375	0,0312	YtfQ/YtfR/YtfS/YtfT/YjfF ABC transporter
znuB	b1859	0,7309	0,0475	ZnuA/ZnuB/ZnuC ABC transporter
	b0322	0,7535	0,0039	

LZ54 (A) & LZ54hns (B)

acrA	b0463	8,3277	0,0131	AcrA Membrane Fusion Protein
acrE	b3265	0,1011	0,0148	transmembrane protein affects septum formation and cell membrane permeability
acrF	b3266	0,2552	0,0263	AcrEF-ToIC Drug Efflux Transport System
add	b1623	1,4042	0,0098	deoxyadenosine deaminase / adenosine deaminase
ade	b3665	0,0660	0,0072	cryptic adenine deaminase monomer
adiY	b4116	0,0713	0,0172	AdiY transcriptional activator
ais	b2252	0,1177	0,0011	protein induced by aluminum
allC	b0516	0,3939	0,0128	allantoate amidohydrolase
alsI	b4090	0,7750	0,0194	allose-6-phosphate isomerase / ribose-5-phosphate isomerase B
alsK	b4084	2,5002	0,0286	putative D-allose kinase
amiC	b2817	1,7337	0,0146	N-acetylmuramyl-L-alanine amidase
arsR	b3501	1,4310	0,0291	ArsR transcriptional regulator
atoS	b2219	0,6377	0,0248	AtoS-Phis
b0309	b0309	0,4289	0,0345	hypothetical protein
b0501	b0501	0,2721	0,0205	hypothetical protein
b1172	b1172	0,1161	0,0024	conserved hypothetical protein
b1354	b1354	0,2405	0,0296	hypothetical protein
b1578	b1578	0,6068	0,0497	hypothetical protein
b1903	b1903	0,3571	0,0463	hypothetical protein
b2084	b2084	0,2100	0,0429	hypothetical protein
b2680	b2680	1,5403	0,0320	YgaY MFS transporter
b3044	b3044	0,5660	0,0243	IS21 protein
basS	b4112	0,6845	0,0066	BasS-Phis
bcsF	b3537	0,4067	0,0472	hypothetical protein
bdm	b1481	0,1582	0,0096	hypothetical protein
betA	b0311	2,0313	0,0247	choline dehydrogenase
betB	b0312	2,1260	0,0391	betaine aldehyde dehydrogenase
betI	b0313	3,1436	0,0193	BetI-choline
bgIJ	b4366	0,3117	0,0457	BgIJ transcriptional regulator
borD	b0557	0,2556	0,0172	bacteriophage lambda Bor protein homolog
cadA	b4131	0,4549	0,0121	lysine decarboxylase
caiA	b0039	1,3966	0,0108	crotonobetaine reductase
cdd	b2143	0,6686	0,0274	cytidine deaminase

gene	blattner	ratio A/B	p-value	function
chbB	b1738	1,5210	0,0330	EIIChb
chbR	b1735	0,3341	0,0058	ChbR transcriptional regulator
chpB	b4225	0,7179	0,0459	ChpB transcriptional regulator
citE	b0616	1,9938	0,0234	subunit of citryl-ACP lyase
cmtA	b2933	0,4295	0,0164	EIIABCmt
cpsB	b2049	0,2756	0,0341	mannose-1-phosphate guanylyltransferase-(GDP)
creC	b4399	0,7339	0,0442	CreC-Phis
creD	b4400	0,6783	0,0283	tolerance to colicin E2
csgD	b1040	0,1783	0,0088	CsgD transcriptional activator
csgE	b1039	0,2969	0,0355	curli production assembly/transport component
cspA	b3556	1,4925	0,0396	cold shock protein CspA
cspC	b1823	0,3803	0,0208	cold shock protein CspC
cspI	b1552	0,1418	0,0099	cold shock protein CspI
cstA	b0598	1,7226	0,0068	peptide transporter induced by carbon starvation
cynT	b0339	1,4406	0,0420	carbonate dehydratase monomer
cytR	b3934	0,4811	0,0258	CytR-cytidine
dacA	b0632	1,4499	0,0371	D-alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5
damX	b3388	1,5321	0,0329	putative membrane protein
dapE	b2472	0,5982	0,0184	N-succinyl-L-diaminopimelate desuccinylase subunit
dcm	b1961	1,6163	0,0045	DNA cytosine methylase
dcuR	b4124	0,5341	0,0130	DcuR-Pasp56
dcuS	b4125	0,5773	0,0341	DcuS-Phis349
djlB	b0646	1,2276	0,0139	putative chaperone
dnaE	b0184	1,5214	0,0034	DNA polymerase III, alpha subunit
dnaK	b0014	0,4911	0,0367	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins
dpiB	b0619	0,4548	0,0076	DpiB
emrE	b0543	0,6713	0,0308	EmrE SMR transporter
emrY	b2367	0,2312	0,0466	EmrY putative multidrug MFS transporter
entA	b0596	2,3095	0,0058	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
envR	b3264	0,5029	0,0145	EnvR transcriptional regulator
essQ	b1556	4,5609	0,0352	hypothetical protein
eutN	b2456	0,6705	0,0289	putative detox protein, ethanolamine utilization
evgA	b2369	0,2767	0,0265	EvgA-Phosphorylated transcriptional regulator
evgS	b2370	0,4198	0,0441	EvgS-Phis
fabB	b2323	0,8572	0,0316	beta-ketoacyl-ACP synthase I / malonyl-ACP decarboxylase
fabR	b3963	1,6568	0,0385	FabR transcriptional repressor
fbp	b4232	0,7673	0,0093	fructose 1,6 bisphosphatase monomer
fecR	b4292	4,8729	0,0414	regulator for fec operon, periplasmic
fepE	b0587	0,2112	0,0281	ferric enterobactin (enterochelin) transport
fhuA	b0150	2,6610	0,0397	FhuA outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80
fhuC	b0151	2,1677	0,0270	ferrichrome uptake system
fimA	b4314	0,1075	0,0169	major type 1 subunit fimbrin (pilin)
fimB	b4312	0,0623	0,0004	regulator for fimA
fimD	b4317	0,6323	0,0042	outer membrane protein; export and assembly of type 1 fimbriae, interrupted
fimE	b4313	0,0983	0,0165	regulator for fimA
fimI	b4315	0,1498	0,0170	fimbrial protein
flgA	b1072	5,9250	0,0103	flagellar biosynthesis; assembly of basal-body periplasmic P ring
flgB	b1073	2,4622	0,0099	flagellar basal-body rod protein FlgB
flgC	b1074	5,0956	0,0165	flagellar basal-body rod protein FlgC
flgD	b1075	4,9964	0,0107	flagellar biosynthesis, initiation of hook assembly
flgE	b1076	5,2448	0,0144	flagellar hook protein FlgE
flgF	b1077	3,8916	0,0140	flagellar basal-body rod protein FlgF
flgG	b1078	6,8388	0,0172	flagellar basal-body rod protein FlgG
flgH	b1079	2,7794	0,0275	flagellar L-ring protein FlgH; basal-body outer-membrane L (lipopolysaccharide layer) ring protein
flgI	b1080	4,9957	0,0130	flagellar P-ring protein FlgI
flgJ	b1081	4,6874	0,0136	FlgJ
flgM	b1071	4,1452	0,0056	anti-FliA (anti-sigma) factor; also known as RflB protein
flgN	b1070	2,3884	0,0246	flagellar biosynthesis protein FlgN
flhB	b1880	3,0669	0,0156	flagellar biosynthesis protein FlhB
fliA	b1922	9,7781	0,0072	sigma28 factor
fliC	b1923	2,9614	0,0275	flagellar biosynthesis; flagellin, filament structural protein
fliD	b1924	3,9935	0,0464	flagellar cap protein FliD; filament capping protein; enables filament assembly
fliE	b1937	4,0249	0,0012	flagellar basal-body protein FliE
fliF	b1938	7,3494	0,0024	flagellar M-ring protein FliF; basal-body MS(membrane and supramembrane)-ring and collar protein
fliG	b1939	6,5031	0,0323	flagellar motor switch protein FliG; component of motor switching and energizing, enabling rotation and determining its direction
fliH	b1940	3,0144	0,0294	flagellar biosynthesis protein FliH
fliJ	b1942	4,6660	0,0065	flagellar biosynthesis protein FliJ
fliK	b1943	3,4194	0,0186	flagellar hook-length control protein FliK
fliL	b1944	7,1439	0,0097	flagellar biosynthesis

gene	blattner	ratio A/B	p-value	function
fliM	b1945	7,9995	0,0100	flagellar motor switch protein FliM; component of motor switch and energizing, enabling rotation and determining its direction
fliN	b1946	7,8012	0,0123	flagellar motor switch protein FliN; component of motor switch and energizing, enabling rotation and determining its direction
fliQ	b1949	3,9371	0,0296	flagellar biosynthesis protein FliQ
fliS	b1925	4,0888	0,0000	flagellar biosynthesis protein FliS
fliZ	b1921	4,4203	0,0056	possible cell-density responsive regulator of sigmaF
focA	b0904	0,3591	0,0199	FocA formate FNT transporter
frlA	b3370	0,6250	0,0009	YhfM methionine APC transporter
frmB	b0355	1,4987	0,0417	putative S-formylglutathione hydrolase
fsaB	b3946	1,6046	0,0285	fructose 6-phosphate aldolase 2
fxsA	b4140	0,5805	0,0376	inner membrane protein; overproduction inhibits F exclusion of bacteriophage T7
gadA	b3517	0,1582	0,0235	glutamate decarboxylase A subunit
gadC	b1492	0,2334	0,0316	XasA GABA APC transporter
gadE	b3512	0,1309	0,0490	GadE transcriptional activator
galE	b0759	1,2371	0,0142	UDP-glucose 4-epimerase monomer
gatD	b2091	0,2599	0,0438	galactitol-1-phosphate dehydrogenase
gatY	b2096	0,2067	0,0396	tagatose-1,6-bisphosphate aldolase 2
gatZ	b2095	0,1364	0,0278	tagatose-1,6-bisphosphate aldolase 2
ghrA	b1033	1,3218	0,0231	glyoxylate reductase
glf	b2036	0,7362	0,0107	UDP-galactopyranose mutase
glpF	b3927	0,6041	0,0017	GlpF - glycerol MIP channel
glpG	b3424	1,3109	0,0131	inner membrane-associated protein of glp regulon
gltD	b3213	1,3195	0,0434	glutamate synthase (NADPH) small chain
gltF	b3214	0,1336	0,0102	regulator of gltBDF operon, induction of Ntr enzymes
gltK	b0653	1,4577	0,0267	glutamate ABC transporter
gmd	b2053	0,3426	0,0190	GDP-mannose 4,6-dehydratase
gntX	b3413	1,8845	0,0301	gluconate periplasmic binding protein
gshA	b2688	1,5587	0,0456	glutamate-cysteine ligase
gspD	b3325	0,5645	0,0087	putative protein secretion protein for export
gspE	b3326	0,6429	0,0423	putative protein secretion protein for export
hdeA	b3510	0,0429	0,0068	acid-resistance protein, possible chaperone
hdeB	b3509	0,0449	0,0041	10K-L protein, related to acid resistance protein of Shigella flexneri
hdeD	b3511	0,3744	0,0297	protein involved in acid resistance
hdhA	b1619	0,3986	0,0141	7-alpha-hydroxysteroid dehydrogenase
hipA	b1507	4,0652	0,0109	HipA transcriptional activator
hisH	b2023	1,7301	0,0302	imidazole glycerol phosphate synthase, HisH subunit
hlyE	b1182	0,1729	0,0157	hemolysin E
hns	b1237	6,1952	0,0176	H-NS transcriptional dual regulator
hofM	b3395	1,4093	0,0034	conserved hypothetical protein
hscA	b2526	2,5483	0,0441	chaperone, member of Hsp70 protein family
hycI	b2717	1,2466	0,0014	hydrogenase 3 maturation protease
hypC	b2728	1,6554	0,0250	pleiotrophic effects on 3 hydrogenase isozymes
ibpA	b3687	0,6923	0,0383	small heat shock protein IbpA
idnK	b4268	0,4140	0,0285	gluconokinase II
ilvN	b3670	1,7883	0,0127	acetohydroxybutanoate synthase I / acetolactate synthase I
intZ	b2442	1,7292	0,0221	putative prophage integrase
ispB	b3187	1,2318	0,0439	octaprenyl diphosphate synthase
kbl	b3617	0,5690	0,0286	2-amino-3-ketobutyrate CoA ligase
kdpB	b0697	1,6697	0,0185	potassium ion P-type ATPase transporter
kdsB	b0918	1,7064	0,0110	3-deoxy-D-manno-octulosonate-cytidyltransferase
kefB	b3350	1,5528	0,0397	KefB potassium CPA2 transporter
lepA	b2569	1,9688	0,0349	GTP-binding elongation factor, may be inner membrane protein
lolD	b1117	1,2471	0,0101	LolCDE ABC lipoprotein transporter
lysP	b2156	2,0194	0,0452	LysP lysine APC transporter
maa	b0459	0,4245	0,0030	maltose acetyltransferase
mdtG	b1053	1,2882	0,0249	YceE drug MFS transporter
mdtL	b3710	0,7142	0,0215	YidY drug MFS transporter
metH	b4019	0,7227	0,0004	Cobalamin-dependent homocysteine transmethylase
metI	b0198	1,4979	0,0420	L- and D-methionine uptake ABC permease
metR	b3828	1,6070	0,0336	MetR-Homocysteine transcriptional activator
miaB	b0661	1,4769	0,0167	hypothetical protein
minC	b1176	0,5656	0,0077	cell division inhibitor of the MinC-MinD-MinE and DicB-MinC systems that regulate septum placement
mltB	b2701	1,6697	0,0259	membrane-bound lytic murein transglycosylase B
moaB	b0782	1,8201	0,0406	MoaB subunit
motB	b1889	8,5864	0,0015	MotB protein, enables flagellar motor rotation, linking torque machinery to cell wall
msbA	b0914	2,4362	0,0074	ATP-binding transport protein; multicopy suppressor of htrB
murP	b2429	0,3070	0,0310	MurP
nadC	b0109	1,2142	0,0267	quinolinate phosphoribosyltransferase (decarboxylating) monomer
nagA	b0677	1,3065	0,0297	N-acetylglucosamine-6-phosphate deacetylase
nanC	b4311	0,1870	0,0154	conserved hypothetical protein

gene	blattner	ratio A/B	p-value	function
nfnB	b0578	0,5525	0,0086	dihydropteridine reductase
nikC	b3478	1,8058	0,0147	nickel ABC transporter
nmpC	b0553	0,0693	0,0038	outer membrane porin protein; locus of qsr prophage
nrfD	b4073	0,4712	0,0109	nitrite reductase complex
nudD	b2051	0,0587	0,0129	GDP-mannose mannosyl hydrolase
nudE	b3397	1,8481	0,0487	ADP-ribose diphosphatase
ogrK	b2082	0,4983	0,0113	OgrK transcriptional regulator
ompC	b2215	0,6383	0,0480	outer membrane porin OmpC
ompF	b0929	2,5595	0,0108	outer membrane porin OmpF
osmB	b1283	0,2432	0,0020	OsmB osmotically inducible lipoprotein
osmC	b1482	0,4503	0,0263	osmotically inducible peroxidase OsmC
pagP	b0622	0,2419	0,0392	PagP monomer
parE	b3030	1,4390	0,0125	Topoisomerase IV subunit B
pflB	b0903	0,5987	0,0440	pyruvate formate-lyase (inactive)
pgaD	b1021	0,2752	0,0393	putative inner membrane protein
phoR	b0400	1,8038	0,0289	PhoR-Phis
pinR	b1374	0,1363	0,0086	putative transposon resolvase
pioO	b3322	0,5656	0,0226	calcium-binding protein required for initiation of chromosome replication
pitB	b2987	0,3142	0,0356	PitB
proB	b0242	0,5567	0,0474	gamma-glutamyl kinase-GP-reductase multienzyme complex
prpD	b0334	1,8705	0,0377	2-methylcitrate dehydratase
purL	b2557	1,1685	0,0423	phosphoribosylformylglycinamide synthase
puuP	b1296	1,5737	0,0077	YcjJ APC transporter
puuR	b1299	3,1778	0,0435	putative oxidoreductase/putative regulator
rbsC	b3750	0,3361	0,0271	ribose ABC transporter
rbsD	b3748	0,2044	0,0179	D-ribose utilization
rbsK	b3752	0,6382	0,0278	ribokinase
rcsA	b1951	0,0925	0,0303	positive DNA-binding transcriptional regulator of capsular polysaccharide synthesis, activates its own expression
rcsD	b2216	0,7698	0,0039	putative 2-component sensor protein
relA	b2784	1,3700	0,0315	GDP pyrophosphokinase / GTP pyrophosphokinase
rffD	b3787	2,2065	0,0462	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
rho	b3783	2,2388	0,0451	transcription termination factor Rho monomer; polarity suppressor
rhsA	b3593	0,4975	0,0344	RhsA protein in rhs element
rhsD	b0497	0,1777	0,0029	RhsD protein in rhs element
ribD	b0414	1,2103	0,0239	pyrimidine reductase / pyrimidine deaminase
rihC	b0030	2,3026	0,0130	ribonucleoside hydrolase 3
rng	b3247	1,6144	0,0451	ribonuclease G (RNase G) monomer
rplK	b3983	1,5386	0,0382	50S ribosomal subunit protein L11
rplL	b3986	1,6665	0,0070	50S ribosomal subunit protein L7/L12
rplU	b3186	1,8052	0,0302	50S ribosomal subunit protein L21
rpsC	b3314	1,5181	0,0057	30S ribosomal subunit protein S3
rpsJ	b3321	1,3506	0,0099	30S ribosomal subunit protein S10
rpsR	b4202	1,5535	0,0028	30S ribosomal subunit protein S18
rpsS	b3316	1,5309	0,0152	30S ribosomal subunit protein S19
rspB	b1580	0,2910	0,0312	putative dehydrogenase RspB
rumB	b0859	2,8430	0,0229	23S ribosomal RNA 5-methyluridine methyltransferase
rzpR	b1362	0,3718	0,0295	putative prophage lambda endopeptidase
serC	b0907	0,8655	0,0233	phosphohydroxythreonine transaminase / phosphoserine transaminase
sfmF	b0534	1,5761	0,0050	putative fimbrial-like protein
sfsB	b3188	0,6211	0,0341	Nlp transcriptional regulator
sgbU	b3582	0,4728	0,0465	probable 3-hexulose-6-phosphate isomerase
sgcR	b4300	0,7052	0,0469	SgcR transcriptional regulator
sieB	b1353	0,6826	0,0164	phage superinfection exclusion protein
slp	b3506	0,2794	0,0041	outer membrane protein induced after carbon starvation
sra	b1480	0,3405	0,0369	30S ribosomal subunit protein S22; sub-stoichiometric stationary phase ribosomal component
ssuC	b0934	1,3094	0,0450	YcbE/YcbM ABC transporter
stpA	b2669	0,2394	0,0352	DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing?
sufA	b1684	2,2615	0,0121	scaffold protein for iron-sulfur cluster assembly
sufC	b1682	2,6029	0,0111	ATPase component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex
tar	b1886	5,6716	0,0475	MCP-II
tatD	b4483	1,8518	0,0203	magnesium-dependent DNase
tauA	b0365	0,3175	0,0372	TauA/TauB/TauC ABC transporter
tdcC	b3116	0,1433	0,0075	TdcC threonine STP transporter
tdcD	b3115	0,4925	0,0458	propionate kinase / acetate kinase C
tgt	b0406	0,7951	0,0462	tRNA-guanine transglycosylase monomer
thiD	b2103	0,7993	0,0109	hydroxymethylpyrimidine kinase 2 / HMP-P kinase
tnaA	b3708	0,0673	0,0163	L-cysteine desulfhydrase / tryptophanase
tolB	b0740	1,3875	0,0321	Tol-Pal Cell Envelope Complex
trpD	b1263	1,2758	0,0363	anthranilate synthase component II

gene	blattner	ratio A/B	p-value	function
tsr	b4355	2,6861	0,0245	MCP-I
ttdB	b3062	0,7602	0,0085	L-tartrate dehydratase, beta subunit
ubiC	b4039	1,5219	0,0401	chorismate pyruvate lyase
ugd	b2028	0,1087	0,0032	UDP-glucose 6-dehydrogenase
ung	b2580	1,1711	0,0157	uracil-DNA-glycosylase
uvrB	b0779	1,5839	0,0266	DNA repair; excision nuclease subunit B
uvrC	b1913	0,6579	0,0189	excinuclease ABC, subunit C; repair of UV damage to DNA
uvrY	b1914	0,5041	0,0474	UvrY- Phosphorylated transcriptional regulator
wcaA	b2059	0,5870	0,0415	putative regulator
wcaC	b2057	0,5717	0,0358	putative glycosyl transferase
wcaD	b2056	0,0530	0,0169	putative colanic acid polymerase
wcaE	b2055	0,1901	0,0098	putative colanic acid biosynthesis glycosyl transferase
wcaF	b2054	0,1153	0,0195	putative transferase
wcaM	b2043	0,3407	0,0472	hypothetical protein
wzc	b2060	0,3446	0,0355	tyrosine kinase involved in colanic acid biosynthesis
wzxE	b3792	1,8477	0,0010	metabolism; biosynthesis of macromolecules (cellular constituents); enterobacterial common antigen (surface glycolipid) transport
wzyE	b3793	1,4866	0,0048	4- α -fucosyltransferase
xapR	b2405	0,1931	0,0064	XapR transcriptional activator
xerC	b3811	1,4882	0,0457	site-specific recombinase, acts on cer sequence of ColE1, effects chromosome segregation at cell division
xseA	b2509	1,6165	0,0433	exonuclease VII, large subunit
xyIB	b3564	0,4772	0,0249	xylulokinase
xyIF	b3566	0,5971	0,0345	xylose ABC transporter
yaaY	b0024	2,2168	0,0034	hypothetical protein
yabP	b0056	0,6871	0,0260	conserved hypothetical protein
yadD	b0132	1,2444	0,0248	hypothetical protein
yadL	b0137	0,2804	0,0369	putative adhesin-like protein
yafD	b0209	1,4135	0,0200	conserved hypothetical protein
yafJ	b0223	0,6082	0,0284	putative amidotransferase
yafS	b0213	1,4431	0,0410	putative methyltransferase
yagG	b0270	0,5001	0,0099	YagG GPH Transporter
yagT	b0286	0,6949	0,0498	putative oxidoreductase, Fe-S subunit
yagX	b0291	0,3706	0,0491	putative enzyme
yagZ	b0293	0,0536	0,0008	conserved hypothetical protein
yahA	b0315	0,3956	0,0385	hypothetical protein
ybaJ	b0461	0,2760	0,0119	conserved hypothetical protein
ybbD	b0500	0,3847	0,0090	conserved hypothetical protein
ybbL	b0490	0,7678	0,0092	YbbL
ybcJ	b0528	1,3234	0,0305	putative RNA-binding protein
ybcW	b0559	0,4321	0,0311	hypothetical protein
ybdB	b0597	1,9962	0,0233	conserved hypothetical protein
ybfD	b0706	0,2376	0,0116	conserved protein
ybfF	b0686	1,5949	0,0464	putative enzyme
ybgD	b0719	0,5377	0,0327	putative fimbrial-like protein
ybgS	b0753	1,8287	0,0028	putative homeobox protein
ybhM	b0787	0,4738	0,0397	hypothetical protein
ybiB	b0800	1,3766	0,0189	putative enzyme
ybiU	b0821	0,8261	0,0211	conserved hypothetical protein
ybjD	b0876	0,5663	0,0278	conserved protein with a nucleotide triphosphate hydrolase domain
ybjL	b0847	0,5150	0,0010	putative transport protein
ycbQ	b0938	0,1147	0,0155	putative fimbrial-like protein
ycdJ	b1009	1,6640	0,0210	putative acetyltransferase
ycdL	b1011	2,0719	0,0001	putative synthetase
yceG	b1097	2,3657	0,0237	putative thymidylate kinase (EC 2.7.4.9)
yceI	b1056	0,3488	0,0018	periplasmic protein; possibly secreted
yceJ	b1057	0,3421	0,0458	putative cytochrome
ycfH	b1100	2,0979	0,0027	putative hydrolase
ycfR	b1112	5,2716	0,0014	conserved hypothetical protein
ycgE	b1162	0,6911	0,0063	putative transcriptional regulator
ycgV	b1202	0,2423	0,0354	putative adhesion and penetration protein
ycgX	b1161	0,4727	0,0469	hypothetical protein
ychJ	b1233	1,3522	0,0498	conserved hypothetical protein
ychQ	b1213	1,7261	0,0345	hypothetical protein
yciA	b1253	2,8879	0,0202	putative enzyme
yciF	b1258	0,3526	0,0266	conserved protein
ycjN	b1310	0,3041	0,0419	YcjN/YcjO/YcjP ABC transporter
ycjO	b1311	2,4268	0,0369	YcjN/YcjO/YcjP ABC transporter
ycjT	b1316	0,7525	0,0127	putative enzyme
ydbA_1	b1401	0,7593	0,0356	hypothetical protein product of fragment 1 of a split CDS
ydcC	b1460	0,2272	0,0112	conserved protein, similar to H-repeat associated proteins

gene	blattner	ratio A/B	p-value	function
ydcL	b1431	0,6791	0,0441	conserved hypothetical protein
ydcR	b1439	4,0253	0,0261	multi modular; putative transcriptional regulator ; also putative ATP-binding component of a transport system
ydeA	b1528	2,7790	0,0432	YdeA MFS transporter
ydeI	b1536	0,1821	0,0253	conserved hypothetical protein
ydeK	b1510	0,6187	0,0071	YdeK
ydeP	b1501	0,1915	0,0184	acid resistance protein
ydeS	b1504	0,4539	0,0400	putative fimbrial-like protein
ydfB	b1572	1,6584	0,0428	hypothetical protein
ydfE	b1577	0,6538	0,0130	hypothetical protein
ydfJ	b1543	3,1165	0,0181	YdfJ
YdgE	b1599	0,2358	0,0111	YdgE SMR Protein
YdgF	b1600	0,1460	0,0053	YdgF SMR protein; toxin of a putative toxin-antitoxin pair
ydgR	b1634	2,3865	0,0058	YdgR putative peptide POT Transporter
ydiA	b1703	0,3853	0,0309	conserved protein
ydjG	b1771	0,6625	0,0268	putative oxidoreductase
ydjI	b1773	0,3205	0,0299	putative aldolase
ydjJ	b1774	0,3084	0,0391	putative oxidoreductase
ydjL	b1776	0,6122	0,0341	putative oxidoreductase
yeaG	b1783	0,4721	0,0039	conserved protein
yeaJ	b1786	0,4354	0,0260	putative membrane protein
yebN	b1821	0,2184	0,0221	putative membrane protein, terpenoid synthase-like
yebW	b1837	1,6464	0,0240	hypothetical protein
yecR	b1904	3,4357	0,0288	conserved hypothetical protein
yedS_2	b1965	0,2584	0,0387	putative outer membrane protein
yedS_3	b1966	0,2391	0,0482	putative outer membrane protein
yedV	b1968	0,1575	0,0161	putative 2-component sensor protein
yeeE	b2013	1,3107	0,0382	putative transport system permease protein
yeeN	b1983	0,3367	0,0153	conserved protein
yegJ	b2071	0,2035	0,0169	hypothetical protein
yehT	b2125	0,5225	0,0364	two-component response regulator
yeiS	b2145	0,4474	0,0138	hypothetical protein
yfaL	b2233	1,3955	0,0170	potential adhesin
yfaO	b2251	0,4117	0,0366	putative enzyme (Nudix hydrolase)
yfbE	b2253	0,2945	0,0149	UDP-L-Ara4O C-4" transaminase
yfbN	b2273	0,1982	0,0195	conserved hypothetical protein
yfcI	b2305	0,5760	0,0448	hypothetical protein
yfcV	b2339	0,1962	0,0324	putative fimbrial-like protein
yfdP	b2359	0,7302	0,0446	hypothetical protein
yfdZ	b2379	1,3458	0,0451	putative aminotransferase
yfeD	b2399	0,6741	0,0159	hypothetical protein
yfeX	b2431	1,2507	0,0360	conserved protein
yffb	b2471	0,3893	0,0112	conserved thioredoxin-like protein
yfgH	b2505	0,1761	0,0294	putative outer membrane lipoprotein
yfiR	b2603	0,5716	0,0344	conserved protein
yfjH	b2623	0,5403	0,0467	putative histone
yfjK	b2627	0,5869	0,0193	hypothetical protein
ygbE	b2749	2,2898	0,0383	putative cytochrome oxidase subunit
ygbT	b2755	0,3143	0,0043	conserved hypothetical protein
ygcF	b2777	0,4973	0,0417	hypothetical protein
ygcI	b2757	0,0520	0,0045	hypothetical protein
ygcJ	b2758	0,4560	0,0338	conserved hypothetical protein
ygcK	b2759	0,0541	0,0086	hypothetical protein
ygcL	b2760	0,0966	0,0050	hypothetical protein with possible relationship to novobiocin and deoxycholate resistance
ygdI	b2809	1,7669	0,0042	hypothetical protein
ygdL	b2812	1,7338	0,0474	putative enzyme
ygeO	b2859	0,7191	0,0320	conserved protein
yggP	b2931	0,4937	0,0082	putative NAD(P)-binding dehydrogenase (B2931)
yghQ	b2983	1,6030	0,0092	putative serine protease
yghS	b2985	0,3944	0,0088	conserved protein
ygiL	b3043	0,0454	0,0037	putative fimbrial-like protein
ygiR	b3015	2,2378	0,0114	
ygiU	b3022	1,4623	0,0263	putative cyanide hydratase
yhbW	b3160	1,3420	0,0364	putative enzyme
yhcA	b3215	0,4083	0,0170	putative chaperone
yhdX	b3269	0,4868	0,0189	YhdW/YhdX/YhdY/YhdZ ABC transporter
yhlL	b3369	0,2237	0,0277	hypothetical protein
yhhH	b3483	0,5665	0,0435	hypothetical protein
yhhI	b3484	0,2639	0,0294	conserved protein similar to H-repeat-associated proteins
yhiP	b3496	1,4822	0,0076	YhiP peptide POT transporter

gene	blattner	ratio A/B	p-value	function
yhjB	b3520	0,5360	0,0254	putative regulator
yhjR	b3535	0,3791	0,0427	hypothetical protein
yhjX	b3547	0,4577	0,0155	YhjX MFS transporter
yiaA	b3562	0,2225	0,0295	hypothetical protein
yiaN	b3578	0,3218	0,0405	YiaMNO Binding Protein-dependent Secondary (TRAP) Transporter
yiaT	b3584	0,3228	0,0018	putative outer membrane protein
yiaU	b3585	0,2708	0,0129	putative transcriptional regulator LYSR-type
yiaV	b3586	0,6530	0,0169	putative membrane protein
yiaW	b3587	0,1805	0,0226	hypothetical protein
yibA	b3594	0,2554	0,0369	putative lyase
yibI	b3598	1,5678	0,0042	hypothetical protein
yibJ	b3595	0,4409	0,0364	hypothetical protein
yifK	b3795	1,6627	0,0041	YifK APC transporter
yiiS	b3922	0,2877	0,0426	conserved hypothetical protein
yjbE	b4026	0,2320	0,0056	conserved hypothetical protein
yjdI	b4126	0,3844	0,0223	conserved hypothetical protein
yjeJ	b4145	0,1947	0,0001	conserved protein
yjfJ	b4182	0,4165	0,0368	conserved protein
yjfO	b4189	0,6287	0,0167	conserved protein
yjgA	b4234	1,4336	0,0306	putative transport protein (ABC superfamily, atp_bind)
yjgM	b4256	0,3526	0,0092	putative acyltransferase
yjhF	b4296	0,3026	0,0290	YjhF Gnt transporter
yjhG	b4297	0,3862	0,0320	putative dehydratase
yjhH	b4298	0,1447	0,0289	putative lyase/synthase
yjhI	b4299	0,1010	0,0196	putative regulator
yjiW	b4347	0,3016	0,0341	hypothetical protein
yjjQ	b4365	0,5375	0,0405	putative regulator
yjjY	b4402	1,8482	0,0252	hypothetical protein
ykfF	b0249	1,4653	0,0173	hypothetical protein
ykgA	b0300	0,3332	0,0455	putative ARAC-type regulatory protein
ykgB	b0301	0,4130	0,0197	putative membrane protein
ykgF	b0307	0,0923	0,0096	putative dehydrogenase
ykgI	b0303	0,1914	0,0271	hypothetical protein
ykgK	b0294	0,3670	0,0464	putative regulator
ykiA	b0392	0,4606	0,0100	hypothetical protein
yliF	b0834	0,5389	0,0387	conserved protein
ymgD	b1171	0,2996	0,0307	hypothetical protein
ynaE	b1375	0,1454	0,0051	hypothetical protein
ynaI	b1330	0,4059	0,0015	YnaI
ynaK	b1365	0,2128	0,0235	hypothetical protein
yncC	b1450	0,7923	0,0469	hypothetical protein
yncD	b1451	4,6042	0,0276	Probable TonB-dependent receptor
yncI	b1458	0,2616	0,0295	conserved protein
ynfN	b1551	0,1250	0,0013	hypothetical protein
ynjF	b1758	1,9527	0,0260	putative cytochrome oxidase
ynjI	b1762	0,6095	0,0436	conserved protein
yoaC	b1810	0,5329	0,0343	conserved hypothetical protein
yobF	b1824	0,2197	0,0180	hypothetical protein
yodA	b1973	0,3883	0,0353	cadmium-induced metal binding protein
yohL	b2105	0,8820	0,0341	conserved hypothetical protein
yojI	b2211	2,6739	0,0227	YojI
ypfJ	b2475	1,7103	0,0293	conserved protein
ypjF	b2646	1,7408	0,0282	member of the YeeV, Ykfl, YpjF family of toxin proteins
yqcC	b2792	1,1876	0,0346	conserved hypothetical protein
yqeI	b2847	0,3092	0,0385	putative sensory transducer
yqhC	b3010	1,5425	0,0156	putative ARAC-type regulatory protein
yqjF	b3101	1,9399	0,0112	putative membrane protein
yraH	b3142	0,4222	0,0010	putative fimbrial-like protein
yraQ	b3151	1,7555	0,0334	putative membrane protein
yrdD	b3283	0,8037	0,0413	putative DNA topoisomerase
yrfF	b3398	1,2449	0,0097	putative dehydrogenase
ysgA	b3830	1,9227	0,0146	putative enzyme
ytfA	b4205	0,5673	0,0178	hypothetical protein
ytfT	b4230	1,5645	0,0022	YtfQ/YtfR/YtfS/YtfT/YjfF ABC transporter
ytjB	b4387	1,3640	0,0001	membrane protein

Table II Real-Time PCR results for selected genes shown in Figure 2 of the paper.

QuantiTect® SYBR® Green one-step RT-PCR reactions (QIAGEN) were performed in triplicates following the manual of manufacturer using a Mx3000P™ Real-time cycler (Stratagene®). Mean ratios of Real-Time-PCR and microarray data are indicated. All obtained ratios are significant ($p < 0.05$).

Gene	LZ41/LZ54		LZ41 <i>fis</i> /LZ54 <i>fis</i>		LZ41 <i>hns</i> /LZ54 <i>hns</i>		Function
	QPCR	array	QPCR	array	QPCR	array	
<i>aceB</i>	0,29				0,18		malate synthase A
<i>glcB</i>	0,75		0,79		0,81		malate synthase G
<i>purC</i>	0,07	0,15	0,06	0,20	0,06	0,16	phosphoribosylaminoimidazole-succinocarboxamide synthase
<i>purF</i>	0,24	0,22	0,07	0,15	0,25	0,24	amidophosphoribosyl transferase
<i>purK</i>	0,06	0,26	0,02	0,18	0,08		N5-carboxyaminoimidazole ribonucleotide synthase monomer
<i>sdhD</i>	1,64		1,85		1,33	1,94	succinate dehydrogenase membrane protein
<i>sucC</i>	1,89		1,41		1,43		succinyl-CoA synthetase, beta subunit

Table III Distribution analyses of the growth phase-dependent (set A) supercoiling-associated (set B) and the mapped genes

Set A (CSH50)

	total	total unique	more in CSH50	more in CSH50 mut
<i>fis</i> experiment	888	819	389	499
<i>hns</i> experiment	669	610	305	364

Set B (LZ)

	Single-coded			
	Rel	Hyp	Act	Rep
wt experiment	322	419		
<i>fis</i> experiment	345	400	322	477
<i>hns</i> experiment	332	400	288	555
total unique	778	818		
common wt, <i>fis</i> & <i>hns</i>	41	104		

	Double-coded			
	Rel/Act	Rel/Rep	Hyp/Act	Hyp/Rep
wt & <i>fis</i> experiment	55	68	73	106
wt & <i>hns</i> experiment	45	118	45	111

Sets A & B (mapped genes)

	total mapped	Single-coded				Double-coded			
		Rel	Hyp	Act	Rep	Rel/Act	Rel/Rep	Hyp/Act	Hyp/Rep
<i>fis</i> experiment									
more in CSH50	175	62	69	38	38	6	5	12	8
more in CSH50 <i>fis</i>	239	74	94	35	95	11	13	9	24
total unique	397	129	158	71	125	16	17	21	29
<i>hns</i> experiment									
more in CSH50	123	42	33	55	18	12	5	6	2
more in CSH50 <i>hns</i>	210	48	68	15	148	1	25	4	38
total unique	329	89	100	68	165	13	30	9	40