Table 2. Gene expression ratios for the Δ*yceP* biofilm relative to the wild-type biofilm in LB glu. Only genes consistently expressed more than 2-fold in both data sets are shown. AI-2, stress, and stationary phase signal (indole) related gene references are shown.

Gene	**b-no**	**fold change #1**	**fold change #2**	**Product**	**AI-2**	**Stress**	**indole**
Information storage and processing							
Translation							
aspV	*b0216*	-3.48	-2.64	tRNAaspV			
leuS	*b0642*	-2.30	-2.30	leucine tRNA synthetase			
rpsA	*b0911*	-2.14	-2.83	30S ribosomal subunit protein S1			
rnpB	*b3123*	-2.64	-3.73	RnpB RNA, catalytic subunit of RNAse P			
metY	*b3171*	-2.30	-3.25	tRNAmetY			
rplU	*b3186*	-4.29	-2.46	50S ribosomal subunit protein L21			
rplM	*b3231*	-2.46	-2.64	50S ribosomal subunit protein L13			
thrV	*b3273*	-2.30	-2.14	tRNAthrV			
alaU	*b3276*	-2.30	-2.83	tRNAalaU			
rplQ	*b3294*	-3.03	-2.83	50S ribosomal subunit protein L17			
rpsD	*b3296*	-3.73	-2.64	30S ribosomal subunit protein S4			
rpsK	*b3297*	-3.03	-2.64	30S ribosomal subunit protein S11	(7)		
rpsM	*b3298*	-2.83	-3.03	30S ribosomal subunit protein S13			
rpmJ	*b3299*	-3.48	-3.48	50S ribosomal subunit protein L36			
rplO	*b3301*	-3.48	-3.48	50S ribosomal subunit protein L15			
rpmD	*b3302*	-3.03	-3.48	50S ribosomal subunit protein L30			
rpsE	*b3303*	-3.25	-2.46	30S ribosomal subunit protein S5			
rplR	*b3304*	-3.03	-2.83	50S ribosomal subunit protein L18	(7)		
rplF	*b3305*	-2.64	-2.83	50S ribosomal subunit protein L6			
rpsH	*b3306*	-2.30	-3.03	30S ribosomal subunit protein S8, and regulator			
rpsN	*b3307*	-2.30	-3.25	30S ribosomal subunit protein S14			
rplX	*b3309*	-2.46	-3.03	50S ribosomal subunit protein L24	(7)		
rplN	*b3310*	-2.14	-3.03	50S ribosomal subunit protein L14	(7)		
rpmC	*b3312*	-3.25	-2.30	50S ribosomal subunit protein L29			
tufA	*b3339*	-2.14	-2.64	protein chain elongation factor EF-Tu			
fusA	*b3340*	-2.46	-2.30	GTP-binding protein chain elongation factor EF-G			
rpmG	*b3636*	-2.30	-2.64	50S ribosomal subunit protein L33			
rpmB	*b3637*	-2.30	-2.64	50S ribosomal subunit protein L28			
thrU	*b3976*	-3.48	-2.30	tRNAthrU			
tufB	*b3980*	-2.64	-3.03	protein chain elongation factor EF-Tu			
rplJ	*b3985*	-3.25	-2.64	50S ribosomal subunit protein L10			
rplL	*b3986*	-3.25	-2.30	50S ribosomal subunit protein L7, L12			

rpsF	*b4200*	-2.83	-2.14	30S ribosomal subunit protein S6			
rpsR	*b4202*	-3.03	-2.14	30S ribosomal subunit protein S18			
prfC	*b4375*	2.30	3.73	peptide chain release factor RF-3			
lasT	*b4403*	3.03	4.92	hypothetical protein			
Transcription							
yahB	*b0316*	2.46	6.06	putative transcriptional regulator (LysR family)			
ybaO	*b0447*	5.28	4.92	putative LRP-like transcriptional regulator			
hha	*b0460*	6.96	7.46	haemolysin expression modulating protein	(3)		
ybeF	*b0629*	2.14	2.30	putative transcriptional regulator or putative periplasmic binding protein			
cspD	*b0880*	-3.73	-3.03	DNA replication inhibitor, nucleic acid-binding domain, transcriptional regulator			
ymfK	*b1145*	2.64	5.66	e14 prophage, putative phage repressor	(5)		
cysB	*b1275*	8.00	4.92	positive transcriptional regulator for cysteine regulon			
ydcN	*b1434*	3.03	6.96	putative regulator			
ydeO	*b1499*	2.83	18.38	putative ARAC-type regulatory protein			
cspF	*b1558*	2.64	18.38	transcriptional regulator, Qin prophage, cold shock protein			
sdiA	*b1916*	8.00	10.56	transcriptional activator for cell division (LuxR, UhpA family)	(3)	(2)	(6)
rcsA	*b1951*	2.14	2.46	positive regulator for ctr capsule biosynthesis, positive transcription factor			
yegW	*b2101*	2.14	2.64	putative transcriptional regulator			
molR_1	*b2115*	2.64	2.64	molybdate metabolism regulator, interrupted			
molR_2	*b2116*	2.46	8.00	twice split molybdate metabolism regulator			
yfaH	*b2238*	3.25	11.31	hypothetical protein			
alpA	*b2624*	4.92	9.85	CP4-57 prophage, transcriptional acitvator of a P4-like cryptic prophage			
ygaV	*b2667*	12.13	4.59	hypothetical protein			
gutM	*b2706*	4.92	3.48	glucitol operon transcriptional activator			
hycA	*b2725*	2.64	2.30	regulatory protein for HycE (part of the FHL complex), transcriptional regulator			
rpoS	*b2741*	-3.73	-3.25	RNA polymerase, sigma S factor, synthesis of many growth phase related proteins	(3)	(2)	
ygfI	*b2921*	2.30	13.93	putative transcriptional regulator (LysR familiy)			
ygiT	*b3021*	6.96	4.59	hypothetical protein			
tdcR	*b3119*	3.25	6.06	threonine dehydratase operon transcriptional activator protein			
nlp	*b3188*	2.46	2.83	transcriptional regulatory factor of maltose metabolism			
yhcF	*b3219*	2.46	11.31	putative transcriptional regulator			
rpoA	*b3295*	-4.92	-3.48	RNA polymerase, alpha subunit			
xylR	*b3569*	2.30	3.25	putative transcriptional regulator of xyl operon			
yidL	*b3680*	2.83	4.92	putative ARAC-type regulatory protein			
yidP	*b3684*	2.83	6.96	putative transcriptional regulator			
bglG	*b3723*	2.14	2.30	positive regulation of bgl operon			
asnC	*b3743*	3.03	3.48	AsnC transcriptional dual regulator	(5)		
rpoB	*b3987*	-2.83	-2.14	RNA polymerase, beta subunit			
cadC	*b4133*	2.83	4.29	transcriptional activator of cad operon			
yjfJ	*b4182*	2.14	2.14	conserved hypothetical protein			

ytfA	*b4205*	2.46	8.00	hypothetical protein	
DNA replication, recombination and repair					
insA_2	*b0275*	2.64	3.48	CP4-6 prophage, IS1 protein InsA	(5)
pinR	*b1374*	4.00	4.59	Rac prophage, putative transposon resolvase	
yi22_2	*b1402*	2.30	2.14	IS2 hypothetical protein	
ydcM	*b1432*	2.30	9.19	putative virulence protein	
intQ	*b1579*	2.46	3.73	Qin prophage, putative transposase	
tus	*b1610*	8.00	4.59	DNA-binding protein, inhibition of replication at Ter sites	
nth	*b1633*	6.96	10.56	endonuclease III, specific for apurinic and, or apyrimidinic sites	
insA_5	*b1894*	3.25	4.92	IS1 protein InsA	(5)
yfjY	*b2644*	2.64	2.64	CP4-57 prophage, putative DNA repair protein	
priB	*b4201*	-2.83	-2.30	primosomal replication protein N	
yjhS	*b4309*	2.64	8.57	conserved hypothetical protein	
yigW_2	*b4483*	2.64	6.50	magnesium-dependent cytoplasmic DNase	
Cellular processes					
Cell division and chromosome partitioning					
ftsL	*b0083*	-3.48	-2.14	essential cell division protein, ingrowth of wall at septum	
yefM	*b2017*	6.06	3.48	antitoxin of the YoeB-YefM toxin-antitoxin pair	
yhdJ	*b3262*	2.30	2.83	cell cycle-regulated methyltransferase	
Posttranslational modification, protein turnover, chaperones					
clpX	*b0438*	-2.46	-2.30	ATP-dependent specificity component of clpP serine protease, chaperone	
citC	*b0618*	7.46	6.96	citrate lyase synthetase (citrate (pro-3S)-lyase ligase	
ybiY	*b0824*	2.83	13.93	putative pyruvate formate lyase activating enzyme	
nrfE	*b4074*	2.46	8.00	formate-dependent nitrite reductase, possible assembly function	
nrfG	*b4076*	2.30	4.92	part of formate-dependent nitrite reductase complex	
Cell envelope biogenesis, outer membrane					
murE	*b0085*	-2.46	-2.14	UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate ligase	
phoE	*b0241*	3.03	2.00	Outer membrane pore protein E	(6)
lpxC	*b0096*	-2.46	-3.48	UDP-3-O-acyl N-acetylglucosamine deacetylase	
yaeT	*b0177*	-3.48	-2.14	protein with possible extracytoplasmic function	(3)
hlpA	*b0178*	-2.64	-2.30	periplasmic molecular chaperone for outer membrane proteins	
csgE	*b1039*	3.25	8.57	curli production assembly, transport component, 2nd curli operon	
rspA	*b1581*	2.30	18.38	putative dehydratase, starvation-sensing protein	
cfa	*b1661*	-2.46	-2.14	cyclopropane fatty acyl phospholipid synthase	
ydiY	*b1722*	2.14	6.50	conserved hypothetical protein	
yeeZ	*b2016*	2.14	3.03	putative enzyme of sugar metabolism	
wcaE	*b2055*	3.03	19.70	putative colanic acid biosynthesis glycosyl transferase	
wcaA	*b2059*	4.00	3.48	putative glycosyl transferase, colanic acid synthesis	
ompC	*b2215*	-2.83	-2.14	outer membrane pore protein, OmpC	(6)
ypdI	*b2376*	2.83	9.85	colanic acid synthesis lipoprotein	

yfiB	*b2605*	3.03	6.96	putative outer membrane protein			
pbl	*b2854*	4.00	7.46	conserved protein, lysozyme-like			
agaS	*b3136*	3.25	3.25	putative tagatose-6-phosphate aldose, ketose isomerase			
acrE	*b3265*	18.38	9.19	indole transport, transmembrane protein, cell membrane permeability			(8)
yhfN	*b3371*	3.03	10.56	fructoselysine 6-phosphate deglycase monomer			
yiaT	*b3584*	2.14	2.46	putative outer membrane protein			
yibD	*b3615*	2.64	2.14	putative glycosyltransferase			
gidB	*b3740*	2.46	3.48	glucose-inhibited division protein, protein with a methyltransferase fold and role in chromosome replication			
Cell motility and secretion							
yadC	*b0135*	2.46	2.64	putative fimbrial-like protein			
ybgP	*b0717*	2.14	4.00	putative chaperone			
ybgD	*b0719*	2.14	3.25	putative fimbrial-like protein			
flgI	*b1080*	7.46	4.92	homolog of Salmonella P-ring of flagella basal body	(5)	(4)	
flhA	*b1879*	2.14	8.00	flagellar biosynthesis, possible export of flagellar proteins			
cheZ	*b1881*	2.30	6.50	chemotactic response, CheY protein phophatase	(5)	(2)	
fliL	*b1944*	2.46	3.25	flagellar biosynthesis	(5)		
fliQ	*b1949*	3.25	5.66	flagellar biosynthesis	(5, 7)		
fliR	*b1950*	2.64	2.46	flagellar biosynthesis	(7)		
yehC	*b2110*	2.14	2.83	putative chaperone			
yfcV	*b2339*	3.03	4.92	putative fimbrial-like protein			
ygiL	*b3043*	2.83	2.83	putative fimbrial-like protein			
yhcA	*b3215*	4.29	14.93	putative chaperone			
yhcD	*b3216*	2.14	3.25	putative outer membrane protein			
fimC	*b4316*	2.14	3.03	periplasmic chaperone, required for type 1 fimbriae			
fimD	*b4317*	3.03	7.46	outer membrane protein, export and assembly of type 1 fimbriae, interrupted			
Inorganic ion transport and metabolism							
phoA	*b0383*	2.00	3.73	Alkaline phosphatase protein			(6)
phoR	*b0400*	2.00	2.64	Phosphate regulon sensor protein PhoR			(6)
ybjW	*b0873*	4.00	4.92	hybrid-cluster protein , hydroxylamine reductase			
yncD	*b1451*	2.30	2.64	Probable TonB-dependent receptor			
ydiE	*b1705*	3.73	3.25	conserved hypothetical protein			
ftn	*b1905*	2.30	2.83	cytoplasmic ferritin (an iron storage protein)			
b1995	*b1995*	6.06	8.00	CP4-44 prophage, putative hemine receptor, predicted zinc-regulated protein			
yfeO	*b2389*	2.30	3.48	hypothetical protein			
focB	*b2492*	14.93	2.64	probable formate transporter (formate channel 2)			
ygaP	*b2668*	9.19	5.66	putative phosphatase			
nirD	*b3366*	3.73	8.57	nitrite reductase (NAD(P)H) subunit			
yieL	*b3719*	6.06	6.50	putative xylanase			
phnG	*b4101*	2.46	3.03	phosphonate metabolism			

phnC	*b4106*	2.14	3.48	ATP-binding component of phosphonate transport, ABC transporter	
Signal transduction mechanisms					
fimZ	*b0535*	2.14	13.93	fimbiral protein Z, putative transcriptional regulator of fimbrial expression	
ycdT	*b1025*	4.29	4.00	hypothetical protein	
ydiV	*b1707*	3.03	12.13	conserved hypothetical protein	
yedW	*b1969*	3.48	4.00	putative 2-component transcriptional regulator	
evgS	*b2370*	2.64	3.73	hybrid sensory histidine kinase in two-component regulatory system, regulates multidrug resistance	(3)
pphB	*b2734*	2.64	2.14	protein phosphatase 2 , protein-tyrosine-phosphatase , phosphoprotein phosphatase	
chpA	*b2782*	2.64	2.64	putative growth inhibitor A, exhibits ribonuclease activity	
barA	*b2786*	2.30	2.14	hybrid sensory histidine kinase in two-component regulatory system with UvrY	
b2856	*b2856*	2.30	6.06	hypothetical protein	
yjjQ	*b4365*	2.46	4.59	putative regulator	
creC	*b4399*	3.48	4.00	catabolite repression sensor kinase for PhoB, alternative sensor for pho regulon	
Intracellular trafficking and secretion					
ecfA	*b2970*	3.03	6.50	putative general secretion pathway for protein export (GSP)	
prlA	*b3300*	-4.00	-3.25	preprotein translocase, membrane component, transport across inner membrane	
yheE	*b3324*	3.03	2.83	putative export protein C for general secretion pathway (GSP)	
yheI	*b3331*	2.83	12.13	putative export protein J for general secretion pathway (GSP)	
Defense mechanisms					
emrK	*b2368*	2.64	2.30	multidrug resistance protein K, putative membrane fusion protein	
acrF	*b3266*	4.29	8.57	integral transmembrane protein, acridine resistance, Drug Efflux Transport System	(8)
dinF	*b4044*	2.30	9.85	DNA-damage-inducible protein F, MATE Transporter	
mcrC	*b4345*	2.83	2.14	component of 5-methylcytosine-specific restriction enzyme McrBC	
Metabolism					
Energy production and conversion					
fixA	*b0041*	2.30	14.93	probable flavoprotein subunit required for anaerobic carnitine metabolism	
aceE	*b0114*	-2.14	-2.30	subunit of E1p component of pyruvate dehydrogenase complex	
prpC	*b0333*	5.28	3.03	methylcitrate synthase (citrate synthase 2)	
ylbC	*b0517*	2.64	4.59	ureidoglycolate dehydrogenase	
dcuC	*b0621*	3.03	3.25	dicarboxylate transport protein (DcuC family)	
gltA	*b0720*	-3.03	-3.03	citrate synthase monomer	(5)
sdhC	*b0721*	-4.29	-3.25	succinate dehydrogenase membrane protein	
sdhD	*b0722*	-4.00	-2.83	succinate dehydrogenase membrane protein	
sdhA	*b0723*	-4.29	-3.73	succinate dehydrogenase, catalytic and NAD, flavoprotein subunit	
sucA	*b0726*	-4.00	-3.73	2-oxoglutarate decarboxylase, component of the 2-oxoglutarate dehydrogenase complex, thiamin-binding	
sucB	*b0727*	-5.66	-3.48	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 component)	
sucC	*b0728*	-4.92	-2.64	succinyl-CoA synthetase, beta subunit	(5)
yceJ	*b1057*	2.30	2.83	putative cytochrome	

icdA	*b1136*	-2.14	-2.64	e14 prophage, isocitrate dehydrogenase, specific for NADP+			
aldA	*b1415*	-2.64	-3.73	putative succinate-semialdehyde dehydrogenase , aldehyde dehydrogenase			(6)
rsxA	*b1627*	2.83	10.56	integral membrane protein of SoxR-reducing complex, electron transport			
rsxG	*b1631*	3.48	2.30	member of SoxR-reducing complex, electron transport			
ydhV	*b1673*	2.14	3.48	putative oxidoreductase			
astD	*b1746*	-2.30	-2.46	succinylglutamic semialdehyde dehydrogenase	(3)		(1)
napA	*b2206*	6.50	4.00	molybdoprotein, periplasmic nitrate reductase, large subunit, in complex with NapB			
hyfD	*b2484*	9.19	6.50	hydrogenase 4 membrane subunit			
hyfG	*b2487*	2.30	4.92	hydrogenase 4 subunit			
ygeT	*b2867*	3.03	4.59	putative xanthine dehydrogenase subunit, FAD-binding domain			
ttdA	*b3061*	7.46	5.66	L-tartrate dehydratase, alpha subunit			
ebgA	*b3076*	2.46	4.29	beta-D-galactosidase, ebg operon, alpha subunit, cryptic gene			
tdcD	*b3115*	2.83	19.70	propionate kinase, acetate kinase II, anaerobic			
yiaI	*b3573*	2.14	4.92	hypothetical protein			
yiaK	*b3575*	2.14	5.66	2,3-diketo-L-gulonate dehydrogenase, NADH-dependent			
yibA	*b3594*	2.83	4.00	putative lyase	(3)		
atpB	*b3738*	-2.30	-2.14	membrane-bound ATP synthase, F0 sector, subunit a			
fdoG	*b3894*	-2.30	-2.83	formate dehydrogenase-O, major subunit			
nrfB	*b4071*	3.25	6.50	formate-dependent nitrite reductase, a penta-haeme cytochrome c			
fumB	*b4122*	9.19	6.96	fumarase B, anaerobic isozyme			
Carbohydrate transport and metabolism							
prpB	*b0331*	8.57	3.25	2-methylisocitrate lyase, putative carboxyphosphonoenolpyruvate mutase			
torT	*b0994*	5.28	6.50	part of regulation of tor operon, periplasmic, unknown inducer			
ycjT	*b1316*	3.03	17.15	putative enzyme			
ycjV	*b1318*	2.14	6.06	putative ATP-binding component of a transport system			
lsrA	*b1513*	2.00	6.06	ATPase in AI-2 transport	(9)		
lsrD	*b1515*	2.07	4.00	membrane channel proteins involved in transport of AI-2	(9)		
lsrK	*b1511*	2.52	2.14	AI-2 kinase	(9)		
ydjI	*b1773*	2.14	8.00	putative aldolase			
manZ	*b1819*	3.73	4.92	PTS enzyme IID, mannose-specific			
gatZ	*b2095*	-5.66	-2.64	tagatose-1,6-bisphosphate aldolase 2			
gatY	*b2096*	-2.83	-3.25	tagatose-1,6-bisphosphate aldolase 2, subunit with GatZ			
dsdX	*b2365*	2.00	9.19	permease			(6)
emrY	*b2367*	3.48	2.46	putative multidrug MFS transporter			
tktB	*b2465*	-3.73	-2.46	transketolase 2 isozyme		(4)	
srlE	*b2703*	3.03	14.93	PTS family enzyme IIBC, glucitol, sorbitol-specific			
yqcE	*b2775*	2.14	7.46	putative transport protein, MFS transporter			
fucP	*b2801*	2.46	13.00	fucose permease, MFS transporter			
galP	*b2943*	2.30	7.46	galactose-proton symport of transport system, MFS transporter			
agaW	*b3134*	4.00	6.06	PTS family enzyme IIC component 2, N-acetylgalactosamine-specific			

agaB	*b3138*	2.30	6.50	PTS family enzyme IIB component 1, N-acetylgalactosamine-specific		
agaC	*b3139*	2.64	4.92	PTS family enzyme IIC component 1, N-acetylgalactosamine-specific		
agaD	*b3140*	9.19	5.66	PTS family enzyme IID, N-acetylglucosamine-specific		
yhfC	*b3364*	3.48	2.46	putative transport, MFS transporter		
yhjX	*b3547*	2.30	4.92	putative oxalate:formate antiporter (MFS family)		
yiaM	*b3577*	2.46	10.56	YiaMNO Binding Protein-dependent Secondary (TRAP) Transporter		
sgbU	*b3582*	2.46	4.59	3-epimerase, probable 3-hexulose-6-phosphate isomerase		
sgbE	*b3583*	2.30	3.25	L-ribulose-5-phosphate 4-epimerase		
yidY	*b3710*	4.00	19.70	drug, chloramphenicol transport protein (MFS family)		
yieC	*b3720*	3.48	2.83	carbohydrate-specific outer membrane porin putative receptor protein		
yihN	*b3874*	10.56	11.31	putative resistance protein, MFS transporter		
malK	*b4035*	9.19	5.66	ATP-binding component of transport system for maltose and maltodextrin		
idnK	*b4268*	2.14	2.14	D-gluconate kinase, thermosensitive		
yjiJ	*b4332*	2.30	2.64	putative sugar transport protein		
gpmB	*b4395*	2.64	6.50	phosphoglyceromutase 2	(3)	
Amino acid transport and metabolism						
yahI	*b0323*	2.30	3.48	putative carbamate kinase		
pheP	*b0576*	3.25	2.83	phenylalanene transport protein (APC family)		
potG	*b0855*	2.30	5.66	ATP-binding component of putrescine ABC transport system		
potI	*b0857*	2.14	6.96	putrescine transport protein (ABC superfamily, membrane)		
artJ	*b0860*	4.00	5.28	arginine 3rd transport system periplasmic binding protein (ABC transporter)		
ycaM	*b0899*	2.64	7.46	putative amino-acid transport protein (APC family)		
ansP	*b1453*	2.30	2.30	L-asparagine permease		
ydiN	*b1691*	3.03	2.30	putative amino acid, amine transport protein, MFS transporter		
astB	*b1745*	-2.64	-2.30	succinylarginine dihydrolase		(1)
ynjC	*b1755*	2.30	3.48	putative transport protein (ABC superfamily, membrane)		
ydjJ	*b1774*	2.83	4.00	putative dehydrogenase, oxidoreductase, NAD(P)-binding		
ydjL	*b1776*	2.30	2.14	hypothetical zinc-type alcohol dehydrogenase-like protein		
yeaU	*b1800*	2.30	5.66	putative tartrate dehydrogenase		
yeeF	*b2014*	3.03	6.50	putative amino acid transport protein (APC family)		
hisI	*b2026*	2.14	6.50	phosphoribosyl-AMP cyclohydrolase		
eutA	*b2451*	10.56	3.48	CPPZ-55 prophage, chaperonin in ethanolamine utilization		
gabT	*b2662*	-3.73	-2.30	4-aminobutyrate aminotransferase activity	(3)	(1)
proW	*b2678*	4.59	4.92	glycine, betaine, proline transport protein (ABC superfamily, membrane)		
ygeY	*b2872*	3.03	8.57	putative deacetylase		
mtr	*b3161*	-2.46	-6.06	tryptophan-specific transport protein		(8)
nanT	*b3224*	2.30	6.50	sialic acid transport protein (MFS family)		
argR	*b3237*	2.14	4.29	repressor of arg regulon, cer-mediated site specific recombination		
yhdX	*b3269*	3.03	2.64	putative amino acid transport protein (ABC superfamily, membrane)		
yhfM	*b3370*	8.57	5.28	putative amino acid, amine transport protein, APC transporter		

tnaB	*b3709*	2.46	2.46	low affinity tryptophan permease, TnaB tryptophan ArAAP transporter	(3)		(1)
yjdE	*b4115*	2.64	2.64	putative amino acid, amine transport protein, cryptic			
Nucleotide transport and metabolism							
purF	*b2312*	2.46	3.48	amidophosphoribosyltransferase (PRPP amidotransferase)	(5)		
uraA	*b2497*	6.06	6.06	uracil transport			
ygfU	*b2888*	2.14	2.14	putative permease			
yicE	*b3654*	2.64	3.25	putative purine, xanthine transport protein (NCS2 family)	(5)		
Coenzyme transport and metabolism							
citG	*b0613*	6.06	4.59	triphosphoribosyl-dephospho-CoA synthase			
bioD	*b0778*	2.14	3.48	dethiobiotin synthetase			
moeB	*b0826*	2.30	3.03	ATP-dependent adenylate transferase, molybdopterin biosynthesis			
ygcM	*b2765*	2.14	2.14	putative 6-pyruvoyl tetrahydrobiopterin synthase			
btuB	*b3966*	2.46	2.83	outer membrane porin: vitamin B12, cobalamin transport			(6)
thiH	*b3990*	3.03	6.96	thiamin (thiazole moiety) biosynthesis protein	(3)		
Lipid transport and metabolism							
htrL	*b3618*	9.19	8.00	involved in lipopolysaccharide biosynthesis			
yihG	*b3862*	2.30	2.83	putative endonuclease			
acs	*b4069*	-3.03	-2.64	putative hydroxycinnamate-CoA ligase, acetyl-CoA synthetase			
Secondary metabolites biosynthesis, transport and catabolism							
dhaR	*b1201*	2.46	4.59	probable transcription activator for the dha operon, putative 2-component regulator			
kduD	*b2842*	2.83	5.66	2-deoxy-D-gluconate 3-dehydrogenase	(5)		
ygfF	*b2902*	3.73	6.06	putative oxidoreductase			
yjgI	*b4249*	8.57	3.73	putative oxidoreductase			
Poorly characterized							
Prophage genes and phage related functions							
yi82_1	*b0017*	3.03	2.64	IS186 and IS421 hypothetical protein			
ykfI	*b0245*	2.14	4.59	toxin of the YkfI-YafW toxin-antitoxin pair	(3)		
yafX	*b0248*	11.31	7.46	hypothetical protein, CP4-6 prophage			
b0538	*b0538*	2.46	2.30	DLP12 prophage, putative sensory transduction regulator			
ybcQ	*b0551*	2.64	5.28	DLP12 prophage, putative antitermination protein Q			
ybcW	*b0559*	2.14	6.06	DLP12 prophage, hypothetical protein			
ybcY	*b0562*	3.25	11.31	DLP12 prophage, homolog of phage 21 head protein, putative methylase			
ybfL	*b0705*	2.14	2.64	putative receptor protein			
ymfJ	*b1144*	2.30	2.30	e14 prophage, hypothetical protein			
ydaD	*b1352*	2.14	2.83	Kil protein (killing function) of lambdoid prophage Rac		(4)	
sieB	*b1353*	2.46	4.00	Rac prophage, phage superinfection exclusion protein			
b1354	*b1354*	2.46	2.46	Rac prophage, hypothetical protein			
ydaR	*b1356*	2.30	2.14	Rac prophage repressor, hypothetical protein		(4)	
ydaY	*b1366*	2.30	10.56	Rac prophage, hypothetical protein			
ynaE	*b1375*	4.59	7.46	Rac prophage, hypothetical protein			

ynfN	*b1551*	2.14	2.30	Qin prophage, hypothetical protein	
ydfP	*b1553*	2.14	4.59	Qin prophage, hypothetical protein	(3)
rem	*b1561*	2.83	2.64	Qin prophage, hypothetical protein	
b1567	*b1567*	2.30	9.19	Qin prophage, hypothetical protein	(3)
dicB	*b1575*	2.46	2.30	Qin prophage, inhibitior of cell division	(3)
ydfD	*b1576*	2.46	4.92	Qin prophage, hypothetical protein	
yeeT	*b2003*	2.46	2.83	CP4-44 prophage, hypothetical protein	
yeeU	*b2004*	2.64	12.13	CP4-44 prophage, putative structural protein, antitoxin	
wcaD	*b2056*	2.64	2.46	putative colanic acid polymerase	
yfdI	*b2352*	2.14	6.50	CPS-53 (KpLE1) prophage, putative ligase	
yfdL	*b2355*	2.64	3.25	CPS-53 (KpLE1) prophage, putative RNA polymerase beta	
yfdN	*b2357*	3.48	9.85	CPS-53 (KpLE1) prophage, putative transcriptional regulator	
yfdQ	*b2360*	2.14	2.46	CPS-53 (KpLE1) prophage, hypothetical protein	
yfjH	*b2623*	2.14	2.14	CP4-57 prophage, putative histone	
yfjJ	*b2626*	3.03	3.25	CP4-57 prophage, hypothetical protein	
yfjT	*b2637*	3.03	5.28	CP4-57 prophage, hypothetical protein	
b2640	*b2640*	2.14	12.13	CP4-57 prophage, hypothetical protein	
yfjW	*b2642*	3.03	2.14	CP4-57 prophage, hypothetical protein	
yfjZ	*b2645*	2.83	3.03	CP4-57 prophage, hypothetical protein	
yjgY	*b4276*	2.14	3.73	KpLE2 phage-like element	
yi91b	*b4283*	2.14	3.73	KpLE2 phage-like element, IS911 protein	
yjiP	*b4338*	17.15	13.00	hypothetical protein	
General function prediction only					
yahK	*b0325*	-3.25	-2.64	putative dehydrogenase, oxidoreductase, NAD(P)-binding	
prpD	*b0334*	6.96	3.48	2-methyl citrate dehydratase	
yaiX	*b0359*	3.25	2.30	putative acyl transferase	
ylaD	*b0459*	11.31	22.63	maltose O-acetyltransferase	
ybbM	*b0491*	2.30	2.14	putative metal resistance protein	
ybfP	*b0689*	4.00	13.93	putative pectinase	
ybhM	*b0787*	4.29	6.06	hypothetical protein	
ycaK	*b0901*	2.64	14.93	putative NAD(P)H dehydrogenase	
ycgY	*b1196*	2.30	2.46	putative enzyme	
ycjM	*b1309*	2.14	3.48	putative polysaccharide hydrolase	
pqqL	*b1494*	3.03	18.38	putative zinc protease	(3)
yddA	*b1496*	2.30	2.83	putative ABC transport system ATP-binding protein	
ydeM	*b1497*	2.14	5.66	putative enzyme	
ydeQ	*b1502*	2.46	13.93	putative adhesin, similar to FimH protein	(3)
ydfQ	*b1554*	2.14	2.14	Qin prophage, putative lysozyme	
ydiO	*b1695*	3.03	6.50	putative acyl-CoA dehydrogenase	
ydjH	*b1772*	2.64	12.13	putative kinase	

yodA	*b1973*	2.64	3.25	cadmium-induced metal binding protein	
yeeL_2	*b1979*	2.64	2.83	putative transport protein	
yohM	*b2106*	3.73	10.56	hypothetical protein	
yejE	*b2179*	3.73	6.96	putative oligopeptide transport protein	
yejF	*b2180*	2.83	2.30	putative ATP-binding component of a transport system	
yfaV	*b2246*	3.48	12.13	putative transport protein	
yfbJ	*b2258*	2.14	8.57	putative transport, receptor protein	
yfbL	*b2271*	2.30	3.48	putative aminopeptidase	
perM	*b2493*	2.64	6.96	putative permease	
yfgH	*b2505*	2.14	8.57	putative outer membrane lipoprotein	(3)
ygbD	*b2711*	2.64	7.46	NADH:flavorubredoxin (FIRd) oxidoreductase	
ygcW	*b2774*	2.14	2.46	putative deoxygluconate dehydrogenase, oxidoreductase	
hybF	*b2991*	3.73	5.28	protein involved with the maturation of hydrogenases 1 and 2	
ygiU	*b3022*	5.66	3.25	putative cyanide hydratase	
yqiJ	*b3050*	3.03	2.83	putative oxidoreductase	
ygjI	*b3078*	2.46	11.31	putative oxidoreductase, APC transporter	
yhbM	*b3163*	-2.30	-2.83	lipoprotein believed to be involved in cell division	
yheF	*b3325*	2.83	3.03	putative export protein D for general secretion pathway (GSP)	
pshM	*b3334*	2.30	3.03	putative export protein M for general secretion pathway (GSP)	
yrfF	*b3398*	2.30	2.30	putative dehydrogenase	
yidK	*b3679*	2.30	4.29	putative cotransporter	
yihP	*b3877*	6.06	6.06	putative permease, GPH transporter	
yihR	*b3879*	9.85	6.50	putative aldose-1-epimerase	
arp	*b4017*	3.03	2.30	regulator of acetyl CoA synthetase, ankyrin-like regulatory protein	
dcuB	*b4123*	6.50	3.25	anaerobic C4-dicarboxylate transport protein (Dcu family)	
yjgN	*b4257*	2.83	2.46	putative membrane protein possible involved in transport	
ygfQ	*b4464*	2.30	3.25	putative membrane protein	
Function unknown					
yadS	*b0157*	3.73	2.64	putative membrane protein	
yafQ	*b0225*	2.83	4.00	conserved hypothetical protein	
yagZ	*b0293*	2.83	2.83	conserved hypothetical protein	
b0309	*b0309*	3.48	4.59	hypothetical protein	
yahC	*b0317*	2.64	8.00	putative membrane protein	
yaiS	*b0364*	5.66	6.06	conserved hypothetical protein	
b0370	*b0370*	3.03	19.70	hypothetical protein	
ylaC	*b0458*	2.64	4.00	putative membrane protein	
ybaJ	*b0461*	5.66	4.29	conserved hypothetical protein	(6)
ybbC	*b0498*	2.46	4.29	hypothetical protein	
ylbE	*b0519*	5.66	4.59	conserved hypothetical protein	
crcA	*b0622*	3.48	4.59	hypothetical protein, PagP monomer	

ybfG	*b0690*	5.28	5.66	conserved hypothetical protein	
ybfD	*b0706*	2.14	4.00	conserved hypothetical protein	
b0725	*b0725*	-3.73	-2.64	hypothetical protein	
yliH	*b0836*	-2.14	-4.59	putative receptor, induced in stationary phase	(4)
ycdF	*b1005*	-2.30	-5.28	hypothetical protein	
yceP	*b1060*	-73.52	-78.79	conserved hypothetical protein	
ycfR	*b1112*	11.31	3.73	conserved hypothetical protein	
ycfT	*b1115*	3.25	16.00	putative transport protein	
ymfA	*b1122*	2.83	5.28	conserved hypothetical protein	
ychP	*b1220*	2.83	6.50	conserved protein, invasin-like, putative factor	
ynbE	*b1382*	3.03	2.46	hypothetical protein	
b1437	*b1437*	2.64	9.85	hypothetical protein	
ydcX	*b1445*	2.64	2.46	hypothetical protein	(3)
ydcZ	*b1447*	2.64	3.25	putative transport protein	
yddJ	*b1470*	2.46	3.03	hypothetical protein	
yddK	*b1471*	3.03	4.00	putative glycoportein	
b1500	*b1500*	2.83	2.14	hypothetical protein, gene is in an operon associated with acid resistance	
yneK	*b1527*	2.83	4.00	conserved hypothetical protein	
ydhI	*b1643*	2.30	3.25	hypothetical protein	
arpB_1	*b1720*	2.30	8.57	hypothetical protein	
arpB_2	*b1721*	2.46	2.64	hypothetical protein	
ydjC	*b1733*	2.30	3.48	hypothetical protein, encoded by an operon required for growth on N,N	
ynjI	*b1762*	3.73	3.03	conserved hypothetical protein	
b1788	*b1788*	2.30	9.85	hypothetical protein	
yoaG	*b1796*	3.03	9.85	hypothetical protein	
yobD	*b1820*	2.30	2.14	conserved hypothetical protein	
mgrB	*b1826*	2.30	12.13	hypothetical protein, product of a gene induced by low magnesium	
yebV	*b1836*	-4.59	-2.30	hypothetical protein	
yecT	*b1877*	3.73	13.00	hypothetical protein	
yecR	*b1904*	2.30	2.64	conserved hypothetical protein	
yedN	*b1934*	3.73	6.50	conserved hypothetical protein	
yedM	*b1935*	2.14	3.48	hypothetical protein	
yeeN	*b1983*	2.83	5.28	conserved hypothetical protein	
sanA	*b2144*	2.30	2.14	vancomycin sensitivity	
yejG	*b2181*	9.85	4.00	conserved hypothetical protein	
yfaA	*b2230*	2.64	2.64	conserved hypothetical protein	
ais	*b2252*	2.46	3.25	protein induced by aluminum	
yfbM	*b2272*	2.30	12.13	conserved hypothetical protein	
yfbO	*b2274*	2.30	5.28	hypothetical protein	
yfdF	*b2345*	2.46	3.03	hypothetical protein	

yfeS	*b2420*	2.30	3.03	conserved hypothetical protein			
yfgF	*b2503*	2.14	4.29	putative cytochrome C-type biogenesis protein, oxidative protein			
yfiP	*b2583*	2.14	2.14	conserved hypothetical protein			
b2596	*b2596*	2.83	2.14	hypothetical protein			
b2651	*b2651*	2.46	4.92	hypothetical protein			
ygaU	*b2665*	-2.14	-2.14	conserved hypothetical protein		(4)	
ygcJ	*b2758*	2.14	9.85	conserved hypothetical protein			
ygeF	*b2850*	2.14	4.29	conserved hypothetical protein	(3)		
ygeO	*b2859*	2.14	2.64	conserved hypothetical protein	(3)		
yqgC	*b2940*	2.30	2.30	hypothetical protein			
yqgD	*b2941*	2.83	18.38	hypothetical protein			(6)
yghG	*b2971*	14.93	11.31	hypothetical protein			
yhaI	*b3104*	2.30	3.25	putative cytochrome			
yhaB	*b3120*	3.03	2.46	conserved hypothetical protein			
yhaC	*b3121*	2.46	6.50	conserved hypothetical protein			
yhcR	*b3242*	21.11	12.13	hypothetical protein			
yhfL	*b3369*	2.14	3.73	hypothetical protein			
yrhA	*b3443*	2.46	3.48	conserved hypothetical protein			
yhhH	*b3483*	4.92	5.66	hypothetical protein			
yhhI	*b3484*	5.66	4.29	conserved protein, similar to H-repeat-associated proteins			
yhiS	*b3504*	2.64	2.46	conserved hypothetical protein			
yiaH	*b3561*	2.46	9.19	putative membrane protein			
yiaA	*b3562*	3.25	4.00	hypothetical protein			
yiaB	*b3563*	4.29	29.86	inner membrane protein			
yibJ	*b3595*	2.30	19.70	hypothetical protein			
yibG	*b3596*	2.83	8.00	conserved hypothetical protein			
yicG	*b3646*	2.83	4.29	putative membrane protein			
yieI	*b3716*	2.30	3.48	putative membrane protein			
b3808	*b3808*	2.64	9.19	hypothetical protein			
yigF	*b3817*	2.30	10.56	conserved hypothetical protein			
yigG	*b3818*	3.25	6.06	inner membrane protein			
yiiL	*b3901*	2.30	2.30	conserved hypothetical protein			
yjaA	*b4011*	2.83	3.73	conserved hypothetical protein			
yjbL	*b4047*	5.66	55.72	hypothetical protein			
yjcF	*b4066*	3.25	8.00	conserved hypothetical protein			
yjdK	*b4128*	2.14	4.29	hypothetical protein			
yjeJ	*b4145*	2.64	2.64	conserved hypothetical protein			
yjfM	*b4185*	3.48	9.85	conserved hypothetical protein			
yjfZ	*b4204*	2.46	9.19	hypothetical protein			
yjgG	*b4247*	2.46	8.57	hypothetical protein			

yjgL	*b4253*	2.14	5.28	conserved hypothetical protein
yjhA	*b4311*	2.30	9.19	conserved hypothetical protein
ygaR	*b4462*	2.30	34.30	hypothetical protein
Not classified				
citE	*b0616*	3.25	3.25	citrate lyase beta chain (acyl lyase subunit)
ycfZ	*b1121*	3.03	21.11	homolog of virulence factor
yiaN	*b3578*	2.46	18.38	YiaMNO Binding Protein-dependent Secondary (TRAP) Transporter

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