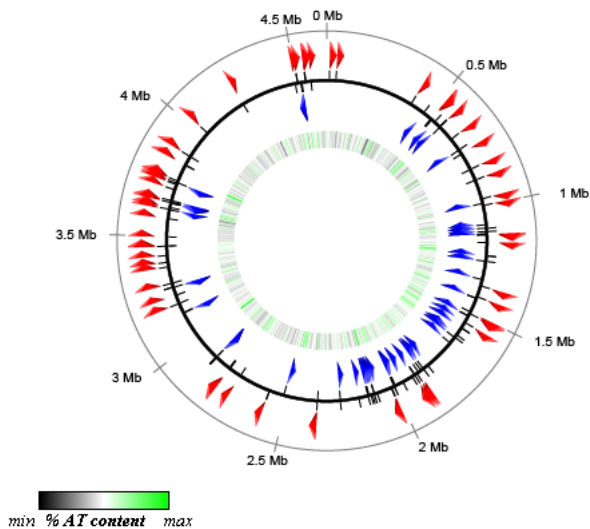


4. Analysis of the composite set of genes [\(back\)](#)

Predicted H-NS binding sites



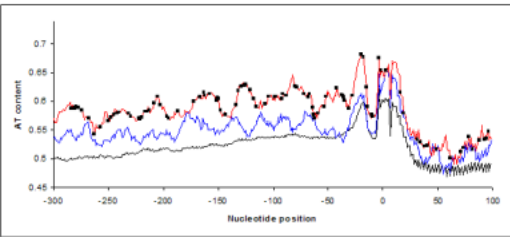
Input motif



Resulting motif



Average AT content



[More details](#)


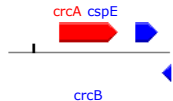

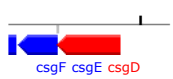

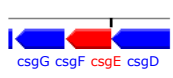



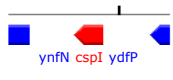

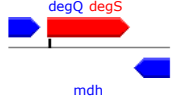


GO term overrepresentation


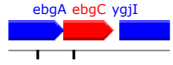

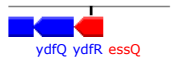





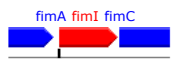

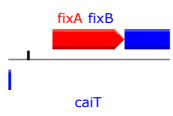


Propensity	Count	Annotation term
3.187	5	motor activity
3.187	5	flagellum (sensu Bacteria)
2.501	3	structural molecule activity
1.806	2	cytolysis
1.806	2	type II protein secretion system
1.806	2	type II protein secretion system complex
1.642	5	ciliary or flagellar motility
1.405	7	flagellum
1.355	2	ATPase activity, coupled to transmembrane movement of substances
1.260	5	cell adhesion
1.204	2	porin activity
1.032	2	transposase activity

Genes with a predicted H-NS binding site [\(back\)](#)










Gene	Binding site logo	Motif alignment	bs (u,d)	rel bs pos.	abs gene pos. + len	fold change	Gene locus	PID	Interactions	Annotation
acrE		TCGTTAAATA	1	(1,0)	-286	3411886 3413043 n/a 1158		1789665	H-NS & acrE	<div>cytoplasmic membrane lipoprotein<ul style="list-style-type: none">cell cycleprotein transporter activityprotein secretionmembranecell division</div>
ade		GCGATTATT GGGATTAAAT	2	(2,0)	-233, -153	3841987 n/a 3843753 1767		1790098	H-NS & ade	<div>cryptic adenine deaminase<ul style="list-style-type: none">adenine deaminase activityadenine catabolismhydrolase activity</div>

agaB		GGGATAAATC CCGATTAATA 2 (2,0) -150, -130	3282192 3282668 n/a 477		1789527 H-NS & agaB	<ul style="list-style-type: none"> manganese ion binding N-acetylgalactosamine-specific enzyme IIB component of PTS sugar porter activit cytoplasm transport protein-N(PI)-phosphohistidine-sugar phosphotransferase activity phosphoenolpyruva dependent sugar phosphotransferase system transferase activity
allC		CCGATTAATA 1 (1,0) -262	543281 544516 n/a 1236		1786726 H-NS & allC	allantoate amidohydrolase <ul style="list-style-type: none"> purine base metabolism proteolysis metabolism metallopeptidase activity hydrolase activity hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines protein dimerization activity
bdm		CCGATTAATA 1 (1,0) -167	1554089 1554304 n/a 216		87081920 H-NS & bdsm	biofilm-dependent modulation protein
chbR		TCAATTAATT 1 (1,0) -33	1816629 1817471 n/a 843		1788030 H-NS & chbR	DNA-binding transcriptional dual regulator <ul style="list-style-type: none"> DNA binding transcription factor activity intracellular transcription regulation of transcription, DNA-dependent sequence-specific DNA binding regulation of transcription
cpsB		TCGATAAAGA 1 (1,0) -43	2121108 2122544 n/a 1437		1788362 H-NS & cpsB	mannose-1-phosphate guanylttransferase

crcA		TCGTTAAAA 1 (1,0) -255	655780 n/a 656340 561		1786840 H-NS & crcA	palmitoyl transferase for Lipid A	
csgD		TCGTTATATT 1 (1,0) -208	1101769 1102419 n/a 651		1787277 H-NS & csgD	DNA-binding transcriptional activator in two-component regulatory system	<ul style="list-style-type: none"> DNA binding transcription factor activity intracellular transcription regulation of transcription, DNA-dependent sequence-specific DNA binding
csgE		GCGATAAAGC 1 (1,0) -2	1101375 1101764 n/a 390		1787276 H-NS & csgE	predicted transport protein	
cspA		CCGATTAATC 1 (1,0) -225	3718072 3718284 n/a 213		1789979 H-NS & cspA	major cold shock protein	<ul style="list-style-type: none"> nucleic acid binding DNA binding transcription regulation of transcription, DNA-dependent
cspI		CAGATAAATT 1 (1,0) -123	1636479 1636691 n/a 213		1787834 H-NS & cspI	Qin prophage; cold shock protein	<ul style="list-style-type: none"> nucleic acid binding DNA binding transcription regulation of transcription, DNA-dependent
degS		TGGATTAATT 1 (0,1) +33	3380222 3381289 n/a 1068		1789630 H-NS & degS	serine endoprotease, periplasmic	<ul style="list-style-type: none"> serine-type endopeptidase activity protein binding proteolysis peptidase activity hydrolase activity periplasmic space
dnaK		GCGATTCATT 1 (1,0) -253	12163 n/a 14079 1917		1786196 H-NS & dnaK	chaperone Hsp70, co-chaperone with DnaJ	<ul style="list-style-type: none"> nucleotide binding protein binding ATP binding DNA replication

ebgC		TCGTTACAGT TCGATATTTT	2 (1,1)	-240, +83	3223744 3224193 n/a 450		1789458 H-NS & ebgC	<p>cryptic beta-D-galactosidase, beta subunit</p> <ul style="list-style-type: none"> protein folding response to unfolded protein unfolded protein binding
essQ		TCGATAAAGT	1 (0,1)	+91	1638394 1638609 n/a 216		87081934 H-NS & essQ	<p>Qin prophage; predicted S lysis protein</p> <ul style="list-style-type: none"> molecular function unknown cell wall catabolism cytolysis
fimA		TCTATAAATA	1 (1,0)	-213	4541138 4541686 n/a 549		1790769 H-NS & fimA	<p>major type 1 subunit fimbriae (pilin)</p> <ul style="list-style-type: none"> cell adhesion fimbrium
fimD		CGGTTAAATT	1 (1,0)	-163	4543119 4545755 n/a 2637		1790772 H-NS & fimD	<p>outer membrane usher protein, type 1 fimbriae synthesis</p> <ul style="list-style-type: none"> transporter activity transport fimbrium membrane integral to membrane outer membrane
fimI		GCGATAAAAA	1 (1,0)	-14	4541751 4542290 n/a 540		87082421 H-NS & fimI	<p>fimbriae protein involved in type 1 pilus biosynthesis</p> <ul style="list-style-type: none"> glycine-tRNA ligase activity ATP binding glycyl-tRNA aminoacylation cell adhesion fimbrium
fixA		TCGTTAATTT	1 (1,0)	-284	42403 43173 n/a 771		87081682 H-NS & fixA	<p>predicted electron transfer flavoprotein subunit, ETFP adenine nucleotide-binding domain</p> <ul style="list-style-type: none"> electron transport transport electron carrier activity carnitine metabolism
flgC		CCGTTAATTT	1 (1,0)	-9	1130661 n/a 1131065 405		1787314 H-NS & flgC	<p>flagellar component of cell-proximal portion of basal-body rod</p> <ul style="list-style-type: none"> ciliary or flagellar motility motor activity

5/18

							<ul style="list-style-type: none">transcription factor activityDNA-directed RNA polymerase activitytranscriptiontranscription initiationregulation of transcription, DNA-dependentsigma factor activityregulation of transcription
							flagellar motor switching and energizing component <ul style="list-style-type: none">ciliary or flagellar motilitymotor activitychemotaxisflagellum (sensu Bacteria)membraneflagellum
fliG		TGGATAAATA 1 (1,0) -15	2012904 2013899 n/a 996		1788249	H-NS & fliG	
							flagellar protein <ul style="list-style-type: none">ciliary or flagellar motilitymotor activitychemotaxisflagellum (sensu Bacteria)membraneflagellum
fliJ		TCGATAAAGC 1 (1,0) -139	2015970 2016413 n/a 444		1788252	H-NS & fliJ	
							predicted regulator of FliA activity <ul style="list-style-type: none">DNA integration
fliZ		CCGTTTAAATA 1 (1,0) -73	1998497 1999048 n/a 552		87082001	H-NS & fliZ	
							glutamate decarboxylase A, PLP-dependent <ul style="list-style-type: none">glutamate decarboxylase activityglutamate metabolismlyase activitycarboxy-lyase activitycarboxylic acid metabolismpyridoxal phosphate binding
gadA		TCCTTAAATT CGGATAAATC 2 (2,0) -8, -42	3664203 3665603 n/a 1401		1789934	H-NS & gadA	
gadE		TCCATATATT 2 (2,0) -175, -157 TGGATAAATC	3656389 n/a 3656916 528		1789928	H-NS & gadE	DNA-binding transcriptional activator



- DNA binding
- transcription factor activity
- pyruvate kinase activity
- intracellular
- glycolysis
- transcription
- regulation of transcription, DNA-dependent
- sequence-specific DNA binding

galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P) binding

- zinc ion binding
- galactitol-1-phosphate 5-dehydrogenase activity
- oxidoreductase activity
- galactitol metabolism
- metal ion binding

UDP-galactopyranose mutase, FAD/NAD(P)-binding

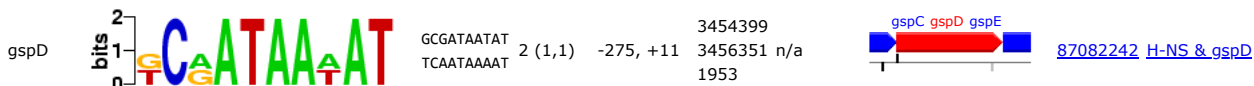
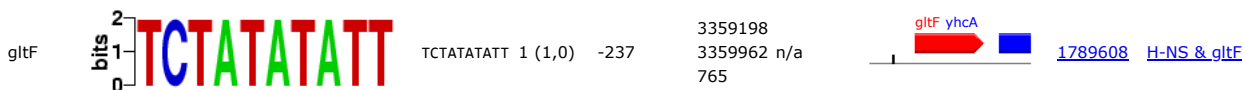
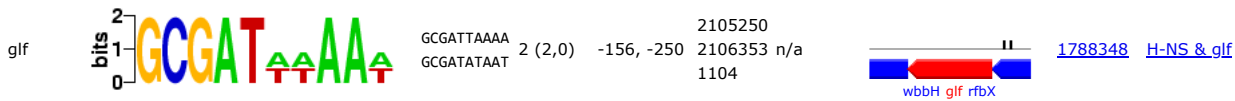
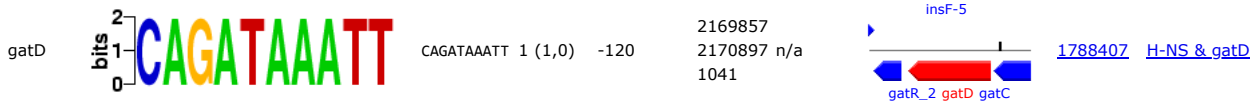
- protein binding
- UDP-galactopyranose mutase activity
- lipopolysaccharide biosynthesis
- isomerase activity

periplasmic protein

- membrane
- integral to membrane

general secretory pathway component, cryptic

- transport
- protein transporter activity
- protein secretion
- type II protein secretion system complex
- type II protein secretion system
- membrane
- outer membrane



gspE CCGATAAATA 1 (1,0) -202 3456361 n/a [gspD gspE gspF](#) [1789723](#) [H-NS & gspE](#) **general secretory**



3457842
1482

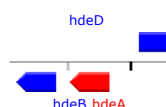


**pathway component,
cryptic**

- nucleotide binding
- ATP binding
- intracellular
- transport
- protein transporter activity
- type II protein secretion system complex
- type II protein secretion system
- nucleoside-triphosphatase activity



3654431
3654763 n/a
333



[1789926](#) [H-NS & hdeA](#)

**stress response protein
acid-resistance protein**

- periplasmic space



3653989
3654315 n/a
327



[87082279](#) [H-NS & hdeB](#)

acid-resistance protein



1228706
1229617 n/a
912



[87081853](#) [H-NS & hlyE](#)

hemolysin E

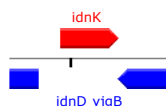
- pathogenesis
- membrane
- integral to membra
- cytolysis
- hemolysis of host n blood cells

**D-gluconate kinase,
thermosensitive**

- nucleotide binding
- shikimate kinase activity
- ATP binding
- carbohydrate metabolism
- amino acid biosynthesis
- kinase activity
- transferase activity
- D-gluconate metabolism
- gluconokinase activ



4492646
4493209 n/a
564



[1790719](#) [H-NS & idnK](#)



478591 n/a
479142
552






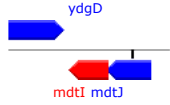

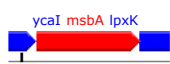

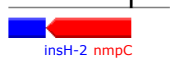


[1786664](#) [H-NS & maa](#)

maltose O-acetyltransferase

- acyltransferase activity
- maltose O-acetyltransferase activity

11/5/2020

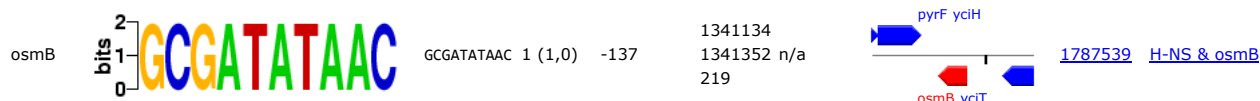
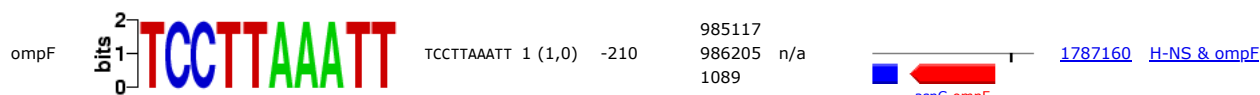
k12.setC.html

mdtF		TCAATAAAAT 1 (0,1) +11	3658437 3661550 n/a 3114		1789930 H-NS & mdtF	<ul style="list-style-type: none">transferase activity multidrug transporter, RpoS-dependent <ul style="list-style-type: none">transporter activitytransportmembraneintegral to membraresponse to antibio
mdtI		CCGTTAAAAA 1 (1,0) -192	1670844 1671173 n/a 330		1787883 H-NS & mdtI	multidrug efflux system transporter <ul style="list-style-type: none">transportmembraneintegral to membra
msbA		GCCATTAATT 1 (1,0) -285	965844 967592 n/a 1749		1787143 H-NS & msbA	fused lipid transporter subunits of ABC superfamily: membrane component/ATP-binding component <ul style="list-style-type: none">nucleotide bindingATP bindingtransportlipid transportcell wall (sensu Proteobacteria)membraneintegral to membraATPase activitynucleoside-triphosphatase activityATPase activity, coupled to transmembrane movement of substances
nmpC		GCGATAAAATA 1 (0,1) +14	574981 576108 n/a 1128		1786765 H-NS & nmpC	DLP12 prophage; truncated outer membrane porin (pseudogene) <ul style="list-style-type: none">transporter activitytransportion transportporin activitymembraneintegral to membraouter membrane
nrdH		CCGATAAAAA 1 (1,0) -284	2798745 n/a 2798990 246		1789028 H-NS & nrdH	glutaredoxin-like prote <ul style="list-style-type: none">electron transporttransport

- electron carrier activity
- protein disulfide oxidoreductase activity
- cell redox homeostasis

outer membrane porin (Ia;b;F)

- transporter activity
- transport
- ion transport
- detection of virus
- porin activity
- membrane
- integral to membra
- outer membrane
- entry of virus into host cell



lipoprotein

- membrane

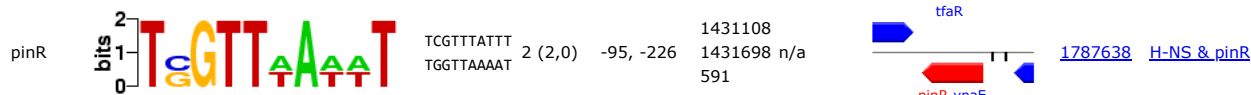
osmotically inducible, stress-inducible membrane protein

- peroxidase activity
- response to stress
- antioxidant activity
- oxidoreductase activity
- peroxiredoxin activ



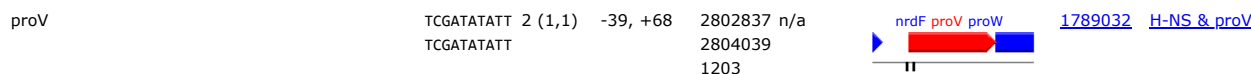
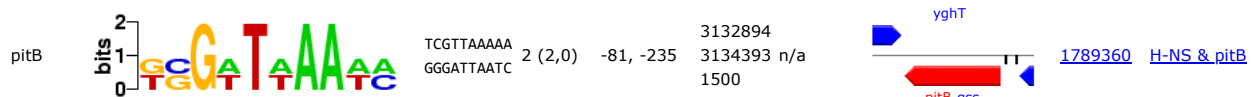
Rac prophage; predicte site-specific recombina

- recombinase activit
- DNA binding
- DNA recombination
- transposition, DNA-mediated
- regulation of transcription





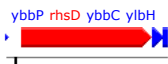

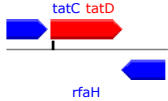

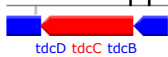





phosphate transporter

- inorganic phosphat transporter activity
- transport
- phosphate transpor
- membrane
- integral to membra



glycine betaine transporter subunit

						<ul style="list-style-type: none">nucleotide bindingATP bindingtransportamino acid transpoamino acid transporter activitymembraneATPase activitynucleoside-triphosphatase activity
rhsA		CCGATAAAAC 1 (1,0) -20	3760206 3764339 n/a 4134		1790020 H-NS & rhsA	rhsA element core protein RshA <ul style="list-style-type: none">membraneintegral to membra
rhsD		TGGATAATAT 1 (1,0) -220	522485 526765 n/a 4281		1786706 H-NS & rhsD	rhsD element protein <ul style="list-style-type: none">membraneintegral to membra
tatD		GCGTTAATTT 1 (0,1) +14	4021577 4022359 n/a 783		48994985 H-NS & tatD	DNase, magnesium-dependent <ul style="list-style-type: none">magnesium ion bindingnuclease activityhydrolase activity
tdcC		TGGACAAT TCGACTAATT 2 (1,1) +27, -245	3261708 3263039 n/a 1332		1789504 H-NS & tdcC	L-threonine/L-serine transporter <ul style="list-style-type: none">transporter activitytransportsymporter activitymembraneintegral to membra
tdcD		TCGATTAAGT 1 (0,1) +66	3260474 3261694 n/a 1221		1789503 H-NS & tdcD	propionate kinase/acetate kinase (anaerobic) <ul style="list-style-type: none">protein bindingintracellularorganic acid metabolismmetabolismacetate kinase activitykinase activityphosphorylationtransferase activityphosphotransferase activity, carboxyl group as acceptor
tnaA		TCGTTTATTT 2 (2,0) -120, -68 CCGATTAATT	3886753 n/a 3888168		87082323 H-NS & tnaA	tryptophanase/L-cysteine desulfhydrase,



1416



PLP-dependent

- protein binding
- amino acid metabolism
- tryptophan metabolism
- tryptophan catabolism
- tryptophanase activ
- aromatic amino aci family metabolism
- lyase activity
- carbon-carbon lyas activity

trimethylamine N-oxide reductase system III, catalytic subunit

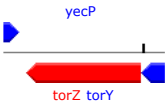
- electron transport
- oxidoreductase activity
- molybdenum ion binding
- periplasmic space
- trimethylamine-N-oxide reductase (cytochrome c) activity

torZ



GCGTTAAAAT 1 (1,0) -69

1952602
1955031 n/a
2430



[87081994](#) [H-NS & torZ](#)

ugd



GCGTTAAAC
TGGTTAAATC 3 (3,0) -67, -236,
TGGATTAATC -247

2096471
2097637 n/a
1167



[1788340](#) [H-NS & ugd](#)

UDP-glucose 6-dehydrogenase

- UDP-glucose 6-dehydrogenase activity
- electron transport
- oxidoreductase activity

uvrC



GCGTTACATT 1 (1,0) -279

1990898 n/a
1992730
1833






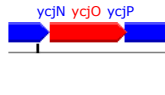





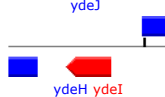





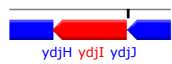



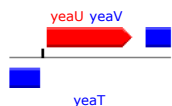

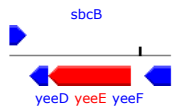





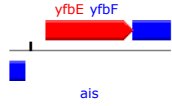

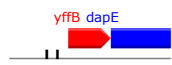

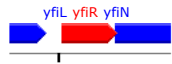
[87081999](#) [H-NS & uvrC](#)

excinuclease UvrABC, endonuclease subunit



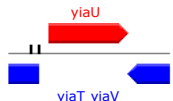





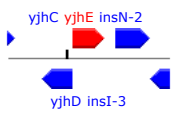

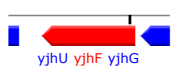

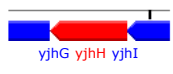


- DNA binding
- nuclease activity
- intracellular
- cytoplasm
- DNA repair
- base-excision repai
- nucleotide-excision repair
- response to DNA damage stimulus
- excinuclease ABC complex
- excinuclease ABC activity
- SOS response

								<ul style="list-style-type: none">sequence-specific DNA binding
wcaE		GCGTTAAATA CCGTTAAATA	2 (2,0)	-22, -279	2126928 2127674 n/a 747		1788368 H-NS & wcaE	<p>predicted glycosyl transferase</p> <ul style="list-style-type: none">lipopolysaccharide biosynthesistransferase activity
wcaM		TGGTTAAAAT TGGTTAAAAT	1 (1,0)	-57	2112526 2113920 n/a 1395		1788356 H-NS & wcaM	<p>predicted colanic acid biosynthesis protein</p> <ul style="list-style-type: none">lipopolysaccharide biosynthesis
xapR		GCGTTTAAAT GCGTTTAAAT	1 (0,1)	+95	2519615 2520499 n/a 885		2367136 H-NS & xapR	<p>DNA-binding transcriptional activator</p> <ul style="list-style-type: none">DNA bindingtranscription factor activitytranscriptionregulation of transcription, DNA-dependent
ybbD		TCGACAAAAT TGGATTAATA	2 (2,0)	-271, -40	527864 528124 n/a 261		1786709 H-NS & ybbD	<p>predicted protein</p> <ul style="list-style-type: none">membraneintegral to membra
ybcW		GCGATAAAAA GCGACAAAAT	2 (2,0)	-237, -7	579103 579309 n/a 207		1786772 H-NS & ybcW	<p>DLP12 prophage; predicted protein</p>
ybfD		TCGTTAAAAT CCGATAATTT	2 (1,1)	-240, +73	737315 738076 n/a 762		1786924 H-NS & ybfD	<p>conserved protein</p> <ul style="list-style-type: none">DNA bindingtransposase activitytransposition, DNA-mediated
ybfH		TGGATAAAGT TCCATACATT	2 (2,0)	-98, -104	715611 715820 n/a 210		87081772 H-NS & ybfH	<p>predicted protein</p>
ybhM		TCAATAAATT GCAATAAATT CCGTTTAAATA	3 (1,2)	-48, +23, +56	820016 820729 n/a 714		1787005 H-NS & ybhM	<p>conserved inner membrane protein</p> <ul style="list-style-type: none">membraneintegral to membra
ycbQ		TCTATAAAAT TCTATAAAAT	1 (1,0)	-131	997091 997630 n/a 540		87081804 H-NS & ycbQ	<p>predicted fimbrial-like adhesin protein</p> <ul style="list-style-type: none">cell adhesionfimbrium
ycdP		CCGTTAAATA CCGTTAAATA	1 (1,0)	-268	1085329 1085742 n/a 414		1787258 H-NS & ycdP	<p>predicted inner membrane protein</p>
yceI		TCGATAAAGA GCCATAAATC	2 (2,0)	-56, -83	1117124 1117699 n/a 576		1787295 H-NS & yceI	<p>predicted protein</p> <ul style="list-style-type: none">molecular function unknownperiplasmic space
ycfR		TCTTTAAATT TCTTTAAATT	1 (1,0)	-134	1168296 n/a 1168553 258		1787355 H-NS & ycfR	<p>predicted protein</p>


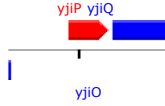

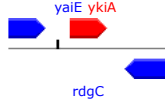

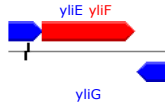

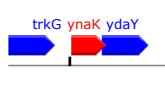

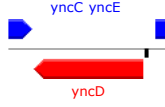

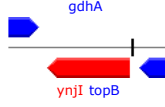

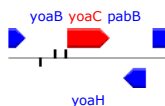

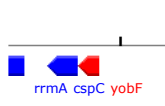

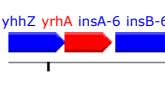
								
ycgV		TCGATATAAA TCGTTACTTA 2 (2,0) -200, -226	1252308 1255175 n/a 2868			1787452 H-NS & ycgV	predicted adhesin	<ul style="list-style-type: none"> cell adhesion
ycjO		GGGATAAAAA 1 (1,0) -168	1371246 1372127 n/a 882			1787570 H-NS & ycjO	predicted sugar transporter subunit: membrane component ABC superfamily	<ul style="list-style-type: none"> transporter activity transport membrane integral to membra
ycdL		TCGATAAAAA 1 (1,0) -227	1500481 1501149 n/a 669			1787701 H-NS & ycdL	predicted lipoprotein	<ul style="list-style-type: none"> membrane
ydcR		TGGTTTAATT 1 (1,0) -85	1508027 1509433 n/a 1407			1787710 H-NS & ydcR	fused predicted DNA-binding transcriptional regulator/predicted amino transferase	<ul style="list-style-type: none"> DNA binding transcription factor activity intracellular transcription regulation of transcription, DNA-dependent transaminase activi biosynthesis transferase activity transferase activity, transferring nitrogenous groups
ydeI		GAGATAAAAAT 1 (1,0) -289	1622129 1622521 n/a 393			1787817 H-NS & ydeI	conserved protein	
ydeP		TGGATATATA 1 (1,0) -83	1582231 1584510 n/a 2280			1787778 H-NS & ydeP	predicted oxidoreducta	<ul style="list-style-type: none"> iron ion binding formate dehydrogenase activity oxidoreductase activity molybdenum ion binding metal ion binding iron-sulfur cluster binding 4 iron, 4 sulfur clus binding
ydjI		GCGATTAATT 1 (1,0) -19	1854957 n/a			1788072 H-NS & ydjI	predicted aldolase	

				1855793 837			<ul style="list-style-type: none">fructose-bisphosphatasealdolase activity
yeaJ		GCGATAAAAT 1 (0,1) +29	1870065 1871555 n/a 1491		87081974 H-NS & yeaJ	<p>predicted diguanylate cyclase</p>	<ul style="list-style-type: none">molecular function unknownmembraneintegral to membrane
yeaU		GGGATTAATT 1 (1,0) -72	1879936 1881021 n/a 1086		1788101 H-NS & yeaU	<p>predicted dehydrogenase</p>	<ul style="list-style-type: none">protein bindingmetabolismtartrate dehydrogenase activityoxidoreductase activityoxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptorlyase activityD-malate dehydrogenase (decarboxylating) activitytartrate decarboxylase activityNAD binding
yeeE		TCGATACAAA 1 (1,0) -109	2082491 2083549 n/a 1059		1788323 H-NS & yeeE	<p>predicted inner membrane protein</p>	<ul style="list-style-type: none">membraneintegral to membrane
yeiC		TCATTAAATT GCGATAAAAT 2 (1,1) +78, -177	2256377 2257318 n/a 942		1788491 H-NS & yeiC	<p>predicted kinase</p>	<ul style="list-style-type: none">kinase activitytransferase activity
yfaO		TCGATAAAGT 1 (1,0) -126	2362576 2363001 n/a 426		1788585 H-NS & yfaO	<p>predicted NUDIX hydrolase</p>	<ul style="list-style-type: none">hydrolase activity
yfbE		GCGATAATTTC 1 (1,0) -226	2363932 2365089 n/a 1158		87082073 H-NS & yfbE	<p>uridine 5'-(beta-1-threopentapyranosyl-4-ulosate diphosphate) aminotransferase, PLP-dependent</p>	
yffB		TGGTTAAAT TCGATAATGT 2 (2,0) -185, -93	2589269 2589625 n/a 357		1788815 H-NS & yffB	<p>conserved protein</p>	<ul style="list-style-type: none">electron transportoxidoreductase activity
yfiR		TCGATATTTT 1 (1,0) -42	2739897 2740415 n/a 519		1788955 H-NS & yfiR	<p>predicted protein</p>	
ygbT		GCGTTTAATA 1 (1,0) -283	2876877 n/a 2877794		1789113 H-NS & ygbT	<p>conserved protein</p>	

				918			
ygcI		GC GTTTAATC 1 (1,0) -155	2878396 2879070 n/a 675		87082154 H-NS & ygcI	predicted protein	
ygcJ		TCAATTAATT TCGTTAATTC 2 (2,0) -178, -200	2879073 2880164 n/a 1092		1789116 H-NS & ygcJ	predicted protein	
ygcK		TCGATATAAA 1 (0,1) +35	2880177 2880659 n/a 483		1789117 H-NS & ygcK	predicted protein	
ygcL		TCGTTTTATT 1 (1,0) -222	2880652 2882160 n/a 1509		1789118 H-NS & ygcL	predicted protein	
ygiL		TCGATTAAGT TCCTTAAATA 2 (2,0) -132, -59	3183436 3183987 n/a 552		1789422 H-NS & ygiL	predicted fimbrial-like adhesin protein	<ul style="list-style-type: none"> cell adhesion fimbrium
yhfl		GGGTAAATT 1 (1,0) -247	3497470 3497637 n/a 168		1789770 H-NS & yhfl	conserved secreted peptide	<ul style="list-style-type: none"> membrane integral to membra
yhhI		CCGATAATT 1 (0,1) +73	3622401 3623537 n/a 1137		1789896 H-NS & yhhI	predicted transposase	<ul style="list-style-type: none"> DNA binding transposase activity transposition, DNA-mediated
yhhJ		GGGATAAAAA 1 (1,0) -67	3623702 3624826 n/a 1125		87082274 H-NS & yhhJ	predicted transporter subunit: membrane component of ABC superfamily	<ul style="list-style-type: none"> ATP binding transport membrane integral to membra ATPase activity, coupled to transmembrane movement of substances
yhiM		CCGATATATA GGGATTAATT 3 (0,3) +8, +29, +56 GCGATACAAA	3632864 3633916 n/a 1053		87082276 H-NS & yhiM	conserved inner membrane protein	<ul style="list-style-type: none"> membrane integral to membra
viaN		GCGATTATTC 1 (1,0) -153	3742827 3744104 n/a 1278		48994950 H-NS & yiaN	predicted transporter	<ul style="list-style-type: none"> transport membrane integral to membra
yiaT		GCGATTAATT 1 (0,1) +14	3749151 n/a 3749891 741		1790010 H-NS & yiaT	predicted protein	<ul style="list-style-type: none"> membrane

								<ul style="list-style-type: none"> outer membrane
yiaU		GCGATTTCATT GCGATTAAATT	2 (2,0)	-228, -137	3750015 3750989 n/a 975		1790011 H-NS & yiaU	<ul style="list-style-type: none"> predicted DNA-binding transcriptional regulator DNA binding transcription factor activity transcription regulation of transcription, DNA-dependent
yiaW		TCGTTATATA	1 (1,0)	-77	3752128 3752451 n/a 324		1790013 H-NS & yiaW	<ul style="list-style-type: none"> conserved inner membrane protein membrane integral to membrane
yjbE		CCGTTAAATT	1 (1,0)	-284	4233929 4234171 n/a 243		1790458 H-NS & yjbE	<ul style="list-style-type: none"> predicted protein
yjhE		TAGATACATT	1 (1,0)	-47	4504884 4505132 n/a 249		87082407 H-NS & yjhE	<ul style="list-style-type: none"> KpLE2 phage-like element; predicted membrane protein (pseudogene) transporter activity transport membrane integral to membrane
yjhF		TCGTTAATTA	1 (0,1)	+87	4518694 4520043 n/a 1350		2367370 H-NS & yjhF	<ul style="list-style-type: none"> KpLE2 phage-like element; predicted transporter transport gluconate transport activity gluconate transport membrane integral to membrane
yjhH		CCGATAAAAA	1 (1,0)	-273	4522128 4523033 n/a 906		87082415 H-NS & yjhH	<ul style="list-style-type: none"> KpLE2 phage-like element; predicted lyase/synthase catalytic activity metabolism dihydrodipicolinate synthase activity lysine biosynthesis lyase activity diaminopimelate biosynthesis
yjhI		TGGATTCATT	1 (1,0)	-121	4523038 n/a 4523826 789		1790752 H-NS & yjhI	<ul style="list-style-type: none"> KpLE2 phage-like element; predicted DNA-binding transcriptional regulator DNA binding transcription

- regulation of transcription, DNA-dependent

yjiP		TCCATAAAAT 1 (0,1) +77	4567021 4567332 n/a 312		1790795 H-NS & yjiP	predicted transposase (pseudogene)
ykiA		CCGATATATT 1 (1,0) -112	407893 408174 n/a 282		1786591 H-NS & ykiA	predicted protein
yliF		TGGATTAATT GCGATATTTT 2 (2,0) -259, -218	874558 875886 n/a 1329		1787056 H-NS & yliF	predicted diguanylate cyclase • molecular function unknown • membrane • integral to membra
ynaK		GCGTTTTTATT 1 (1,0) -25	1423401 1423664 n/a 264		1787628 H-NS & ynaK	Rac prophage; conserved protein • DNA binding
yncD		TCCATAAATT CCGTTTCATT 2 (2,0) -53, -64	1518987 1521089 n/a 2103		1787723 H-NS & yncD	predicted iron outer membrane transporter • receptor activity • transporter activity • transport • membrane • outer membrane
ynjI		GCGATAAATT TGGATAAAAT 2 (2,0) -30, -36	1841855 1842895 n/a 1041		87081969 H-NS & ynjI	predicted inner membrane protein • membrane • integral to membra
yoaC		TAGATAAAAT CCGTTAAATT 3 (3,0) -230, -111, -23	1892097 1892456 n/a 360		1788112 H-NS & yoaC	predicted protein
yobF		CCGATATATC 1 (1,0) -148	1905472 1905615 n/a 144		1788127 H-NS & yobF	predicted protein
yrhA		TCGATTAATA 1 (1,0) -156	3581064 3581477 n/a 414		87082266 H-NS & yrhA	conserved protein

116 of 248 genes (or 46.8%) contained a predicted H-NS binding site. These are:

acrE, ade, agaB, allC, bdm, chbR, cpsB, crcA, csd, csge, cspA, cspI, degS, dnaK, ebqC, essQ, fimA, fimD, fimI, fixA, flgC, flgE, flgG, flgM, flgN, fliA, fliG, fliJ, fliZ, gadA, gadE, gatD, glf, gltF, gspD, gspE, hdeA, hdeB, hlyE, idnK, maa, mdtF, mdtI, msbA, nmpC, nrdH, ompF, osmB, osmC, pinR, pitB, proV, rhsA, rhsD, tatD, tdcC, tdcD, tnaA, torZ, ugd, uvrC, wcaE, wcaM, xapR, ybbD, ybcW, ybfD, ybfH, ybhM, ycbQ, ycdP, yceI, ycfR, ycgV, ycjO, ydcl, ydcR, ydeI, ydeP, ydjI, yeaJ, yeaU, yeeE, yeiC, yfaO, yfbE, yffB, yfiR, ygbT, ygcI, ygcJ, ygcK, ygcL, ygiL, yhlF, yhhI, yhhJ, yhiM, yiaN, yiaT, yiaU, yiaW, yjbE, yjhE, yjhF, yjhH, yjhi, yjiP, ykiA, yliF, ynaK, yncD, ynjI, yoaC, yobF, yrhA

No strong binding sites were predicted for the following genes (132 of 248):

acrA, acrF, artJ, bcsF, borD, cadA, cchB, citA, cspC, cutC, emrE, emrY, entA, fhuB, fhuC, fimB, fimE, flgA, flgB, flgD, flgF, flgH, flgI, flgJ, flhB, flhC, flhD, flhE, flhF, flhH, flhI, flhL, flhM, flhN, fliQ, fliS, folC, frlB, fxaA, gadC, glpG, gltJ, gmd, hdhA, hipA, hns, kbl, kdsB, mdtJ, mntH, motB, nagA, nudD, parE, pflB, puuR, pyrB, rbsD, rcsA, recA, serB, sgbU, slp, stpA, tauA, wcaC, wcaD, wcaF, wzc, wzxE, yadL, yagX, yagZ, yahA, ybaJ, ybjL, yccU, yceJ, ycgH_1, ycgX, yciA, yciF, ydcC, ydeK, ydeS, ydfJ, ydfW, ydiA, ydjJ, yebN, yecR, yedS_2, yedS_3, yedv yeeN, yegJ, yfdP, yfgH, yfjK, ygaX, yhdX, yhjB, yhjD, yhjR, yiaA, yiaV, yibA, yibJ, yiiS, yjeJ, yjfJ, yjgM, yjhA, yjhG, yjiW, ykgA, ykgB, ykgF, ykgI, ymgD, ymgG, ynaE, ynaI, yncI, yneK ynfN, yodA, yqeA, yqeI, yrah, ytfT