

Supplementary Table 2. Relationship between H-NS associated genes and horizontally acquired genes.

Locus tag	Gene	Length(nt)	Position ^a		Product ^b	Nakamura ^c	Lawrence ^d	H-NS ^e	Conservation ^f
b0001	thrL	66	190	255	+ thr operon leader				1
b0002	thrA	2463	337	2799	+ bifunctional: aspartokinase I (N-terminal); homoserine dehydrogenase I (C-terminal)				21
b0003	thrB	933	2801	3733	+ homoserine kinase				21
b0004	thrC	1287	3734	5020	+ threonine synthase				21
b0005	yaaX	297	5234	5530	+ orf, hypothetical protein	1			20
b0006	yaaA	777	5683	6459	- orf, hypothetical protein				21
b0007	yaaJ	1431	6529	7959	- inner membrane transport protein	1			11
b0008	talB	954	8238	9191	+ transaldolase B				21
b0009	mog	588	9306	9893	+ putative molybdochetalase in molybdopterin biosynthesis				21
b0010	yaaH	567	9928	10494	- orf, hypothetical protein				21
b0012	htgA	591	10725	11315	+ positive regulator for sigma 32 heat shock promoters	1			5
b0013	yaal	405	11382	11786	- orf, hypothetical protein				14
b0014	dnaK	1917	12163	14079	+ chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins				21
b0015	dnaJ	1131	14168	15298	+ chaperone with DnaK; heat shock protein				21
b0016	yi81_1	1113	15445	16557	+ IS186 hypothetical	1	1		5
b4412	hokC	153	16751	16903	- small toxic membrane polypeptide	1		1	10
b0019	nhaA	1167	17489	18655	+ Na ⁺ /H antiporter, pH dependent			1	21
b0020	nhaR	906	18715	19620	+ transcriptional activator of nhaA				21
b0021	insB_1	504	19811	20314	- IS1 protein InsB	1	1		15
b0022	insA_1	276	20233	20508	- IS1 protein InsA	1	1		15
b0023	rpsT	264	20815	21078	- 30S ribosomal subunit protein S20	1			21
b0024	yaaY	219	21181	21399	+ orf, hypothetical protein	1			14
b0025	ribF	942	21407	22348	+ flavokinase and FAD synthetase				21
b0026	ileS	2817	22391	25207	+ isoleucine tRNA synthetase				21
b0027	lspA	495	25207	25701	+ prolipoprotein signal peptidase (SPase II)				21
b0028	fkpB	450	25826	26275	+ FKBP-type 16KD peptidyl-prolyl cis-trans isomerase (a rotamase)				21
b0029	ispH	951	26277	27227	+ lspH protein				21
b0030	rihC	915	27293	28207	+ nucleoside hydrolase				14
b0031	dapB	822	28374	29195	+ dihydrodipicolinate reductase				21
b0032	carA	1149	29651	30799	+ carbamoyl-phosphate synthetase, glutamine (small) subunit				21
b0033	carB	3222	30817	34038	+ carbamoyl-phosphate synthase large subunit				21
b0034	caiF	501	34195	34695	+ transcriptional regulator of cai operon	1		1	14
b0035	caiE	612	34781	35392	- possible synthesis of cofactor for carnitine racemase and dehydratase			1	14
b0036	caiD	894	35377	36270	- carnitine racemase			1	15
b0037	caiC	1569	36271	37839	- probable crotonobetaine/carnitine -CoA liqase				14
b0038	caiB	1218	37898	39115	- l-carnitine dehydratase				13

b0039	caiA	1143	39244	40386	- probable carnitine operon oxidoreductase				16
b0040	caiT	1515	40417	41931	- probable carnitine transporter		1		19
b0041	fixA	807	42367	43173	+ probable flavoprotein subunit, carnitine metabolism		1		14
b0042	fixB	942	43188	44129	+ probable flavoprotein subunit, carnitine metabolism				12
b0043	fixC	1287	44180	45466	+ flavoprotein; electron transport				14
b0044	fixX	288	45463	45750	+ putative ferredoxin				14
b0045	yaaU	1332	45807	47138	+ putative transport				14
b0046	yabF	531	47246	47776	+ putative NAD(P)H oxidoreductase				14
b0047	kefC	1863	47769	49631	+ K ⁺ efflux antiporter, glutathione-regulated				15
b0048	folA	480	49823	50302	+ dihydrofolate reductase type I; trimethoprim resistance				21
b0049	apaH	843	50380	51222	- diadenosine tetraphosphatase				21
b0050	apaG	378	51229	51606	- orf, hypothetical protein	1			21
b0051	ksgA	822	51609	52430	- S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase				21
b0052	pdxA	990	52427	53416	- pyridoxine biosynthesis				21
b0053	surA	1287	53416	54702	- survival protein				21
b0054	imp	2355	54755	57109	- organic solvent				21
b0055	djlA	816	57364	58179	+ DnaJ-like membrane chaperone protein				21
b0056	yabP	651	58474	59124	+ orf, hypothetical protein	1	1	1	5
b0057	yabQ	159	59121	59279	+ orf, hypothetical protein	1	1	1	5
b0058	rluA	660	59687	60346	- Ribosomal large subunit pseudouridine				21
b0059	hepA	2907	60358	63264	- probable ATP-dependent RNA				21
b0060	polB	2352	63429	65780	- DNA polymerase II				19
b0061	araD	696	65855	66550	- L-ribose-5-phosphate 4-epimerase				20
b0062	araA	1503	66835	68337	- L-arabinose isomerase				19
b0063	araB	1701	68348	70048	- L-ribulokinase				19
b0064	araC	879	70387	71265	+ transcriptional regulator for ara operon				18
b0065	yabI	765	71351	72115	+ orf, hypothetical protein				20
b0066	yabJ	699	72229	72927	- putative ATP-binding component of a transport system				21
b0067	yabK	1611	72911	74521	- putative transport system permease				21
b0068	tbpA	984	74497	75480	- thiamin-binding periplasmic protein				21
b0069	yabN	1656	75644	77299	- putative transport				21
b0070	setA	1179	77621	78799	+ Sugar efflux protein	1			9
b0071	leuD	606	78848	79453	- isopropylmalate isomerase subunit				21
b0072	leuC	1401	79464	80864	- 3-isopropylmalate isomerase				21
b0073	leuB	1095	80867	81961	- (dehydratase) subunit				21
b0074	leuA	1572	81958	83529	- 3-isopropylmalate dehydrogenase			1	21
b0075	leuL	87	83622	83708	- leu operon leader			1	15
b0076	leuO	1122	84191	85312	+ probable transcriptional activator for leuABCD operon	1		1	18
b0077	ilvI	1815	85540	87354	+ acetolactate synthase III, valine sensitive, large subunit			1	21

b0078	ilvH	492	87357	87848	+ acetolactate synthase III, valine sensitive, small subunit	21
b0079	fruL	87	87860	87946	+ fruR leader peptide	9
b0080	fruR	1005	88028	89032	+ transcriptional repressor of fru operon	21
b0081	yabB	459	89634	90092	+ orf, hypothetical protein	21
b0082	yabC	942	90094	91035	+ putative apolipoprotein	21
b0083	ftsL	366	91032	91397	+ cell division protein; ingrowth of wall at septum formation; penicillin-binding protein 3; peptidoglycan meso-diaminopimelate-adding enzyme	21
b0084	ftsI	1767	91413	93179	+ D-alanine:D-alanine-adding enzyme	21
b0085	murE	1488	93166	94653	+ phospho-N-acetylmuramoyl-pentapeptide	21
b0086	murF	1359	94650	96008	+ UDP-N-acetylmuramoylalanine-D-glutamate ligase	21
b0087	mraY	1083	96002	97084	+ cell division; membrane protein involved in shape determination	21
b0088	murD	1317	97087	98403	+ UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	21
b0089	ftsW	1245	98403	99647	+ L-alanine adding enzyme, UDP-N-acetyl-muramate:alanine	21
b0090	murG	1068	99644	100711	+ D-alanine-D-alanine ligase B, affects cell division protein; ingrowth of wall at	21
b0091	murC	1476	100765	102240	+ ATP-binding cell division protein, septation process, complexes with FtsZ, associated with	21
b0092	ddlB	921	102233	103153	+ junctions of inner and cell division; forms circumferential ring; tubulin-like GTP-binding protein and GTPase	21
b0093	ftsQ	831	103155	103985	+ UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis	21
b0094	ftsA	1263	103982	105244	+ orf, hypothetical protein	21
b0095	ftsZ	1152	105305	106456	+ preprotein translocase; secretion protein	21
b0096	lpxC	918	106557	107474	+ 7,8-dihydro-8-oxoguanine-triphosphatase, prefers dGTP. causes AT-GC	21
b0097	yacA	588	107630	108217	- orf, hypothetical protein	21
b0098	secA	2706	108279	110984	+ orf, hypothetical protein	21
b0099	mutT	390	111044	111433	+ orf, hypothetical protein	21
b0100	-	135	111564	111698	- putative DNA repair protein	8
b0101	yacG	198	111649	111846	- orf, hypothetical protein	21
b0102	yacF	744	111856	112599	- orf, hypothetical protein	21
b0103	yacE	621	112599	113219	- orf, hypothetical protein	21
b0104	guaC	1044	113444	114487	+ GMP reductase	20
b0105	-	108	114407	114514	- orf, hypothetical protein	8

b0106	hofC	1203	114522	115724	- putative integral membrane protein involved in biogenesis of fimbriae, protein	1				20
b0107	hofB	1386	115714	117099	transport DNA uptake putative integral membrane protein involved in biogenesis of fimbriae, protein	1				17
b0108	ppdD	441	117109	117549	transport DNA uptake prelipin peptidase dependent protein					20
b0109	nadC	894	117752	118645	quinolinate phosphoribosyltransferase					21
b0110	ampD	552	118733	119284	+ regulates ampC					20
b0111	ampE	855	119281	120135	+ regulates ampC					21
b0112	aroP	1374	120178	121551	- aromatic amino acid transport protein					21
b0113	pdhR	765	122092	122856	+ transcriptional regulator for pyruvate dehydrogenase					21
b0114	aceE	2664	123017	125680	+ pyruvate dehydrogenase (decarboxylase)					21
b0115	aceF	1893	125695	127587	+ pyruvate dehydrogenase (dihydrolipoyltransacetylase)					20
b0116	lpdA	1425	127912	129336	+ lipoamide dehydrogenase (NADH); component of 2-oxodehydrogenase and pyruvate complexes; lipoamide dehydrogenase					21
b0117	yacH	1854	129407	131260	- putative membrane protein	1				13
b0118	acnB	2598	131615	134212	+ aconitate hydratase B					21
b0119	yacL	411	134340	134750	+ orf, hypothetical protein					21
b0120	speD	795	134788	135582	- S-adenosylmethionine decarboxylase					21
b0121	speE	867	135598	136464	- spermidine synthase = putrescine aminopropyltransferase					21
b0122	yacC	471	136570	137040	- orf, hypothetical protein	1				21
b0123	cueO	1551	137083	138633	+ Probable periplasmic copper oxidase					20
b0124	gcd	2391	138835	141225	- glucose dehydrogenase					14
b0125	hpt	549	141419	141967	+ hypoxanthine phosphoribosyltransferase					21
b0126	yadF	663	142008	142670	- putative carbonic anhydrase					21
b0127	yadG	927	142779	143705	+ putative ATP-binding component of a transport system					21
b0128	yadH	771	143702	144472	+ orf, hypothetical protein					21
b0129	yadI	441	144577	145017	+ putative PTS enzyme II B component					20
b0130	yadE	1230	145081	146310	+ conserved hypothetical protein					17
b0131	panD	381	146314	146694	- aspartate 1-decarboxylase					21
b0132	yadD	903	146968	147870	+ orf, hypothetical protein	1				21
b0133	panC	852	147944	148795	- pantothenate					21
b0134	panB	795	148807	149601	- 3-methyl-2-oxobutanoate					21
b0135	yadC	1239	149715	150953	- putative fimbrial-like protein	1	1	1		9
b0136	yadK	597	151003	151599	- putative fimbrial protein	1	1	1		10
b0137	yadL	606	151626	152231	- putative fimbrial protein	1	1	1		9
b0138	yadM	612	152243	152854	- putative fimbrial-like protein	1	1	1		8

b0139	htrE	2598	152829	155426	- probable outer membrane porin protein involved in fimbrial	1	1	1	9
b0140	ecpD	741	155461	156201	probable pilin	1	1	1	14
b0141	yadN	585	156299	156883	chaperone similar to putative fimbrial-like protein	1	1	1	10
b0142	folK	480	157253	157732	- 7,8-dihydro-6-hydroxymethylpterin-ovrophosphokinase				21
b0143	pcnB	1365	157729	159093	- poly(A) polymerase I				21
b0144	yadB	927	159186	160112	- putative tRNA				21
b0145	dksA	456	160149	160604	- dnaK suppressor				21
b0146	sfsA	705	160782	161486	- probable regulator for maltose metabolism	1			21
b0147	ligT	540	161501	162040	- 2'-5' RNA ligase				20
b0148	hrpB	2475	162060	164534	+ helicase, ATP-				20
b0149	mrcB	2535	164730	167264	+ peptidoglycan synthetase; penicillin-binding protein 1B				21
b0150	fhuA	2244	167484	169727	+ outer membrane protein receptor for ferrichrome, colicin M, and phages T1. T5. and				20
b0151	fhuC	798	169778	170575	+ ATP-binding component of hydroxamate-				20
b0152	fhuD	891	170575	171465	+ hydroxamate-dependent iron uptake, cytoplasmic membrane				20
b0153	fhuB	1983	171462	173444	+ hydroxamate-dependent iron uptake, cytoplasmic membrane				20
b0154	hemL	1281	173602	174882	- glutamate-1-semialdehyde aminotransferase (aminomutase)				21
b0155	yadQ	1422	175107	176528	+ putative channel transporter				19
b0156	yadR	345	176610	176954	+ orf, hypothetical protein				21
b0157	yadS	624	177001	177624	- orf, hypothetical protein				19
b0158	yadT	801	177662	178462	- orf, hypothetical protein				21
b0159	pfs	699	178455	179153	- orf, hypothetical protein				21
b0160	dgt	1518	179237	180754	+ deoxyguanosine triphosphate triphosphohydrolase			1	19
b0161	degP	1425	180884	182308	+ periplasmic serine protease Do; heat shock protein HtrA				20
b0162	cdaR	1176	182445	183620	+ regulator of D-galactarate, D-glucarate and D-glycerate				18
b0163	yaeH	387	183709	184095	- putative structural				21
b0164	yael	744	184257	185000	- orf, hypothetical protein				5
b0165	-	132	184987	185118	- orf, hypothetical protein				1
b0166	dapD	825	185123	185947	- 2,3,4,5-tetrahydropyridine-2-carboxylate N-protein PII; uridylyltransferase acts on regulator of qlnA				21
b0167	glnD	2673	185978	188650	- methionine aminopeptidase				21
b0168	map	795	188712	189506	+ 30S ribosomal subunit protein S2				21
b0169	rpsB	726	189874	190599	+ protein chain elongation factor EF-Ts				21
b0170	tsf	852	190857	191708	+ uridylylate kinase				21
b0171	pyrH	726	191855	192580	+ ribosome releasing				21
b0172	frr	558	192872	193429					21

b0173	ispC	1197	193521	194717	+ 2-C-methyl-D-erythritol 4-phosphate synthase; 1-deoxy-D-xylulose 5-phosphate reductoisomerase		20
b0174	uppS	762	194903	195664	+ undecaprenyl pyrophosphate synthetase (di-trans.poly-cis- CDP-diglyceride synthetase	1	21
b0175	cdsA	750	195785	196534	+ putative protease		21
b0176	yaeL	1353	196546	197898	+ putative outer membrane antigen		21
b0177	yaeT	2433	197928	200360	+ periplasmic molecular chaperone for outer membrane proteins		21
b0178	hlpA	486	200482	200967	+ UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acetyltransferase		21
b0179	lpxD	1026	200971	201996	+ (3R)-hydroxymyristol acyl carrier protein dehydratase		21
b0180	fabZ	456	202101	202556	+ UDP-N-acetylglucosamine acetyltransferase; lipid A biosynthesis		21
b0181	lpxA	789	202560	203348	+ tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step		21
b0182	lpxB	1149	203348	204496	+ RNase HII, degrades RNA of DNA-RNA		21
b0183	rnhB	597	204493	205089	+ DNA polymerase III, alpha subunit		21
b0184	dnaE	3483	205126	208608	+ acetylCoA carboxylase, carboxytransferase component, alpha		21
b0185	accA	960	208621	209580	+ lysine decarboxylase 2, constitutive		13
b0186	ldcC	2142	209679	211820	+ orf, hypothetical protein		20
b0187	yaeR	417	211850	212266	+ tRNA(Ile)-lysine synthetase		21
b0188	tilS	1299	212331	213629	- modulator of Rho-dependent transcription termination		21
b0189	rof	261	213678	213938	- conserved hypothetical protein		16
b4406	yaeP	201	213925	214125	+ orf, hypothetical protein		20
b0190	yaeQ	546	214291	214836	+ orf, hypothetical protein	1	18
b0191	yaeJ	423	214833	215255	+ copper homeostasis protein (lipoprotein)		19
b0192	cutF	711	215269	215979	- orf, hypothetical protein	1	14
b0193	yaeF	879	216179	217057	- proline tRNA		21
b0194	proS	1719	217057	218775	- orf, hypothetical protein		21
b0195	yaeB	708	218887	219594	- regulator in colanic acid synthesis; interacts with RcsB	1	21
b0196	rscF	405	219591	219995	- D-methionine transport protein (ABC superfamily, peri bind)		21
b0197	metQ	816	220113	220928	- D- and L-methionine transport protein (ABC superfamily, D- and L-methionine transport protein (ABC superfamily, atp bind)		21
b0198	metI	654	220968	221621	+ D,D-heptose 1,7-bisphosphate phosphatase		21
b0199	metN	1032	221614	222645	+ rrnH_16S		21
b0200	gmhB	576	222833	223408	+ tRNA-Ile		21
rrnH_16S	rrnH_16S	1542	223771	225312	+ tRNA-Ala		
tRNA-Ile1	tRNA-Ile	77	225381	225457			
tRNA-Ala1	tRNA-Ala	76	225500	225575			

rrnH_23S	rrnH_23S	2904	225759	228662	+ rrnH_23S						
rrnH_5S	rrnH_5S	120	228756	228875	+ rrnH_5S						
tRNA-Asp ¹	tRNA-Asp	77	228928	229004	+ tRNA-Asp						
b0207	dkgB	804	229167	229970	+ 2,5-diketo-D-gluconate reductase B						20
b0208	yafC	915	229967	230881	- putative transcriptional regulator LYSR-type	1					21
b0209	yafD	801	231122	231922	+ orf, hypothetical protein						21
b0210	yafE	624	231926	232549	+ putative biotin synthesis protein	1					20
b0211	mltD	1359	232597	233955	- membrane-bound lytic murein transglycosylase D						21
b0212	gloB	756	234027	234782	- probable hydroxyacylglutathione hydrolase	1		1			21
b0213	yafS	741	234798	235538	+ orf, hypothetical protein	1					21
b0214	rnhA	468	235535	236002	- RNase HI, degrades RNA of DNA-RNA hybrids, participates in DNA replication						21
b0215	dnaQ	732	236067	236798	+ DNA polymerase III, epsilon subunit						21
tRNA-Asp ²	tRNA-Asp	77	236931	237007	+ tRNA-Asp					1	
b0217	yafT	786	237335	238120	+ putative	1		1		1	4
b0218	yafU	339	238746	239084	- orf, hypothetical protein	1		1		1	9
b0219	yafV	771	239419	240189	- putative amidase-type enzyme						17
b0220	ykfE	474	240343	240816	+ orf, hypothetical protein						14
b0221	fadE	2481	240859	243339	- medium-long-chain fatty acyl-CoA						19
b0222	lpcA	579	243543	244121	+ phosphoheptose isomerase						21
b0223	yafJ	768	244327	245094	+ putative						21
b0224	yafK	741	245065	245805	- orf, hypothetical protein					1	21
b0225	yafQ	279	245961	246239	- orf, hypothetical protein	1		1		1	8
b0226	dinJ	261	246242	246502	- damage-inducible protein J			1		1	12
b0227	yafL	750	246712	247461	+ putative lipoprotein	1				1	8
b0228	yafM	498	247637	248134	+ orf, hypothetical protein	1					11
b0229	fhiA	1740	248358	250097	- flagellar biosynthesis			1			9
b0230	mbhA	786	250042	250827	+ putative motility protein						12
b0231	dinB	1056	250898	251953	+ DNA polymerase IV						20
b0232	yafN	294	252005	252298	+ orf, hypothetical protein	1		1		1	11
b0233	yafO	399	252301	252699	+ orf, hypothetical protein	1		1		1	7
b0234	yafP	453	252709	253161	+ orf, hypothetical protein	1		1		1	13
b0235	ykfJ	267	253467	253733	+ orf, hypothetical protein	1				1	13
b0236	prfH	501	253702	254202	+ probable peptide chain release factor						16
b0237	pepD	1458	254259	255716	- aminoacyl-histidine dipeptidase (peptidase						21
b0238	gpt	459	255977	256435	+ guanine-hypoxanthine phosphoribosyltransferase						21
b0239	yafA	1245	256527	257771	+ orf, hypothetical protein						21
b0240	crl	402	257829	258230	+ transcriptional regulator of cryptic csgA gene for curli surface fibers					1	20
b0241	phoE	1056	258269	259324	- outer membrane pore protein E (E.Ic,NmpAB)					1	21
b0242	proB	1104	259612	260715	+ gamma-glutamate						21
b0243	proA	1254	260727	261980	+ gamma-glutamylphosphate reductase						21
tRNA-Thr ¹	tRNA-Thr	76	262095	262170	+ tRNA-Thr						
b0245	ykfl	342	262552	262893	- orf, hypothetical protein						11
b0246	yafW	318	262914	263231	- orf, hypothetical protein	1		1			11
b0247	ykfG	477	263480	263956	- putative DNA repair protein						11
b0248	yafX	459	263972	264430	- orf, hypothetical protein						11
b0249	ykfB	240	264528	264767	- orf, hypothetical protein	1					8
b0250	ykfF	468	264844	265311	- orf, hypothetical protein						3

b0251	yafY	858	265334	266191	-	hypothetical transcriptional regulator orf, hypothetical protein	1			2
b0252	yafZ	837	266408	267244	-	putative GTP-binding protein	1	1		8
b0253	ykfA	867	267321	268187	-	peroxide resistance protein	1	1		9
b0254	perR	894	268513	269406	-	transposase insN for insertion sequence element IS911A	1	1		2
b0255	yi91a	405	269466	269870	+	IS30 transposase	1			13
b0256	tra8_1	1152	269827	270978	+	putative transposase	1			7
b0257	-	426	271054	271479	+	orf, hypothetical protein	1			14
b0258	ykfC	1131	272086	273216	+	IS5 transposase	1	1		12
b0259	trs5_1	1017	273325	274341	-	S-methylmethionine permease	1			2
b0260	mmuP	1428	274525	275952	+	S-methylmethionine:homocysteine				3
b0261	mmuM	933	275939	276871	+	putative ATP-binding component of a transport system		1		3
b0262	afuC	1059	276980	278038	-	putative transport system permease		1		6
b0263	afuB	363	278038	278400	-	IS1 protein InsB	1	1		9
b0264	insB_2	504	278402	278905	-	IS1 protein InsA	1	1		15
b0265	insA_2	276	278824	279099	-	orf, hypothetical protein	1	1		15
b0266	yagB	378	279609	279986	-	orf, hypothetical protein		1		11
b0267	yagA	1155	280053	281207	-	putative lyase/synthase		1		18
b0268	yagE	930	281481	282410	+	putative dehydratase		1		4
b0269	yagF	1968	282425	284392	+	putative permease		1	1	2
b0270	yagG	1383	284619	286001	+	putative beta-putative regulator		1		20
b0271	yagH	1611	286013	287623	+	ornithine carbamoyltransferase		1		8
b0272	yagI	759	287628	288386	-	2. chain F		1		2
b0273	argF	1005	288525	289529	-	IS1 protein InsB	1	1		21
b0274	insB_3	504	289873	290376	-	IS1 protein InsA	1	1		15
b0275	insA_3	276	290295	290570	-	orf, hypothetical protein	1			15
b0276	yagJ	732	290724	291455	+	orf, hypothetical protein	1		1	2
b0277	yagK	627	291546	292172	-	DNA-binding protein	1	1	1	4
b0278	yagL	699	292444	293142	-	orf, hypothetical protein	1		1	2
b0279	yagM	855	293169	294023	-	orf, hypothetical protein	1		1	4
b0280	yagN	441	294363	294803	-	orf, hypothetical protein	1		1	2
b0281	intF	1401	294920	296320	-	putative phage	1		1	3
b0282	yagP	411	296605	297015	-	putative transcriptional regulator LYSR-type	1			4
b0283	yagQ	957	296994	297950	-	orf, hypothetical protein	1			4
b0284	yagR	2199	297960	300158	-	orf, hypothetical protein		1		4
b0285	yagS	957	300155	301111	-	orf, hypothetical protein				4
b0286	yagT	690	301108	301797	-	putative xanthine dehydrogenase				4
b0287	yagU	615	302215	302829	+	orf, hypothetical protein	1		1	11
b0288	ykgJ	330	303077	303406	-	putative ferredoxin	1		1	9
b0289	yagV	756	303719	304474	-	orf, hypothetical protein	1			5
b0290	yagW	1644	304398	306041	-	putative receptor				5
b0291	yagX	2526	306031	308556	-	putative enzyme				15
b0292	yagY	669	308582	309250	-	orf, hypothetical protein				6
b0293	yagZ	588	309308	309895	-	orf, hypothetical protein			1	6
b0294	ykgK	591	309970	310560	-	putative regulator	1		1	6
b0295	ykgL	228	311336	311563	+	orf, hypothetical protein	1		1	4
b0296	ykgM	264	311738	312001	-	putative ribosomal			1	17
b0297	eaeH	888	313581	314468	+	attaching and effacing protein, pathogenesis factor	1	1	1	5
b0298	-	309	314506	314814	+	transposase insE for insertion sequence IS3			1	9
b0299	tra5_5	867	314811	315677	+	transposase insF for insertion sequence IS3	1		1	15
b0300	ykgA	720	315674	316393	-	putative ARAC-type regulatory protein	1	1	1	10
b0301	ykgB	603	316950	317552	-	orf, hypothetical protein		1	1	11
b0303	ykgI	252	317555	317806	-	orf, hypothetical protein	1	1	1	11
b0304	ykgC	1353	317900	319252	-	putative oxidoreductase	1	1	1	11

b0305	ykgD	855	319451	320305	+ putative ARAC-type regulatory protein	1		1	11
b0306	ykgE	720	320832	321551	+ putative dehydrogenase subunit			1	9
b0307	ykgF	1428	321562	322989	+ orf, hypothetical protein			1	9
b0308	ykgG	849	322829	323677	+ putative transporter	1		1	9
b0309	-	213	323632	323844	- orf, hypothetical protein			1	4
b0310	ykgH	669	323920	324588	- orf, hypothetical protein	1	1	1	12
b0311	betA	1671	324801	326471	- choline dehydrogenase, a flavoprotein				9
b0312	betB	1473	326485	327957	- NAD+-dependent betaine aldehyde				13
b0313	betI	588	327971	328558	- probably transcriptional repressor of bet genes				9
b0314	betT	2034	328687	330720	+ high-affinity choline transport				9
b0315	yahA	1089	331595	332683	+ orf, hypothetical protein	1		1	5
b0316	yahB	933	332725	333657	- putative transcriptional regulator LYSR-type			1	5
b0317	yahC	498	333749	334246	- orf, hypothetical protein	1		1	5
b0318	yahD	606	334504	335109	+ putative transcription factor	1	1	1	5
b0319	yahE	864	335149	336012	+ orf, hypothetical protein	1	1	1	6
b0320	yahF	1548	336002	337549	+ putative oxidoreductase subunit		1		6
b0321	yahG	1419	337549	338967	+ orf, hypothetical protein		1		11
b0323	yahI	951	339389	340339	+ putative kinase				6
b0324	yahJ	1383	340349	341731	+ putative deaminase				6
b0325	yahK	1050	342108	343157	+ putative oxidoreductase				7
b0326	yahL	816	343400	344215	+ orf, hypothetical protein	1	1	1	5
b0327	yahM	276	344598	344873	+ orf, hypothetical protein	1	1	1	5
b0328	yahN	672	344890	345561	- putative cytochrome subunit of	1	1	1	17
b0329	yahO	276	345708	345983	+ orf, hypothetical protein		1	1	10
b0330	prpR	1587	346081	347667	- regulator for prp operon			1	11
b0331	prpB	891	347906	348796	+ putative phosphonmutase 2				12
b0333	prpC	1170	349236	350405	+ putative citrate synthase; propionate				11
b0334	prpD	1452	350439	351890	+ orf, hypothetical protein				11
b0335	prpE	1887	351930	353816	+ putative propionyl-CoA synthetase				11
b0336	codB	1260	354146	355405	+ cytosine permease/transport				11
b0337	codA	1284	355395	356678	+ cytosine deaminase				14
b0338	cynR	900	357015	357914	- cyn operon positive regulator	1			5
b0339	cynT	660	358023	358682	+ carbonic anhydrase				5
b0340	cynS	471	358713	359183	+ cyanate aminohydrolase,				5
b0341	cynX	1155	359216	360370	+ cyanate transport				17
b0342	lacA	612	360473	361084	- thiogalactoside acetyltransferase	1	1	1	14
b0343	lacY	1254	361150	362403	- galactoside permease (lactose permease, M protein) (MFS family)		1	1	9
b0344	lacZ	3075	362455	365529	- beta-D-galactosidase		1		12
b0345	lacI	1083	365652	366734	- transcriptional repressor of the lac		1		11
b0346	mhpR	948	366811	367758	- transcriptional regulator for mhp operon				4
b0347	mhpA	1665	367835	369499	+ 3-(3-hydroxyphenyl)propionate hydroxylase				11
b0348	mhpB	945	369501	370445	+ 2,3-dihydroxyphenylpropionate 1,2-dioxygenase				6
b0349	mhpC	930	370400	371329	+ 2-hydroxy-6-ketono-2,4-dienedioic acid				8
b0350	mhpD	816	371333	372148	+ 2-keto-4-pentenoate hydratase				18
b0351	mhpF	951	372145	373095	+ acetaldehyde dehydrogenase				6

b0352	mhpE	1014	373092	374105	+ 4-hydroxy-2-ketovalerate aldolase					7
b0353	mhpT	1257	374638	375894	+ putative transport					11
b0354	yaiL	657	375879	376535	+ nucleoprotein/polynucleotide-associated	1				16
b0355	frmB	834	376759	377592	- putative S-formylglutathione hydrolase					7
b0356	frmA	1110	377686	378795	- alcohol dehydrogenase class III; formaldehyde dehydrogenase, glutathione-dependent					14
b0357	frmR	297	378830	379126	- repressor of frmRAB	1				8
b0358	yaiO	774	379293	380066	- orf, hypothetical protein				1	4
b0359	-	444	380068	380511	- putative transferase	1	1		1	4
b0360	yi21_1	411	380530	380940	+ IS2 hypothetical protein	1	1		1	8
b0361	yi22_1	906	380898	381803	+ IS2 hypothetical protein	1	1		1	18
b0362	-	387	381728	382114	- orf, hypothetical protein	1	1		1	3
b0363	yaiP	1197	381963	383159	- polysaccharide metabolism	1			1	3
b0364	yaiS	411	383283	383693	- orf, hypothetical protein	1	1		1	4
b0365	tauA	1020	384399	385418	+ taurine transport system periplasmic				1	15
b0366	tauB	768	385431	386198	+ taurine ATP-binding component of a transport system					14
b0367	tauC	828	386195	387022	+ taurine transport system permease					15
b0368	tauD	852	387019	387870	+ taurine dioxygenase, 2-oxoglutarate-dependent					15
b0369	hemB	1008	387977	388984	- 5-aminolevulinatase = porphobilinogen				1	21
b0370	-	270	389121	389390	- orf, hypothetical protein	1	1		1	4
b0371	yaiT	1461	389475	390935	+ orf, hypothetical protein	1	1		1	12
b0372	tra5_1	867	390963	391829	- transposase insF for insertion sequence IS3	1	1			15
b0373	-	309	391826	392134	- transposase insE for insertion sequence IS3		1			9
b0374	yaiU	1404	392239	393642	+ putative flagellin structural protein					19
b0375	yaiV	669	393685	394353	+ orf, hypothetical protein	1	1		1	14
b0376	ampH	1158	394354	395511	- beta-lactamase/D-alanine carboxypeptidase, penicillin binding					20
b0377	sbmA	1221	395863	397083	+ sensitivity to microcin B17, possibly envelop protein					15
b0378	yaiW	1095	397096	398190	+ orf, hypothetical protein					16
b0379	yaiY	309	398249	398557	- orf, hypothetical protein					15
b0380	yaiZ	345	398685	399029	+ orf, hypothetical protein	1				15
b0381	ddlA	1095	399053	400147	- D-alanine-D-alanine ligase A					14
b0382	yaiB	261	400610	400870	+ orf, hypothetical protein				1	16
b0383	phoA	1416	400971	402386	+ alkaline phosphatase				1	15
b0384	psiF	339	402487	402825	+ induced by phosphate starvation	1				19
b0385	yaiC	1116	402927	404042	+ orf, hypothetical protein	1				16
b0386	proC	810	404059	404868	- pyrroline-5-carboxylate reductase					21
b0387	yaiI	579	404868	405446	+ orf, hypothetical protein	1				20
b0388	aroL	525	405629	406153	+ shikimate kinase II					21
b0389	yaiA	192	406203	406394	+ orf, hypothetical protein	1	1			15
b0390	aroM	678	406652	407329	+ protein of aro operon, regulated by aroR				1	14
b0391	yaiE	285	407401	407685	+ orf, hypothetical protein				1	20
b0392	ykiA	282	407893	408174	+ orf, hypothetical protein		1		1	9
b0393	yaiD	912	408332	409243	- orf, hypothetical protein					21
b0394	yajF	1047	409230	410276	+ possible NAGC-like transcriptional regulator					19
b0396	araJ	1185	410521	411705	- involved in either transport or processing of arabinose polymers					12

b0397	sbcC	3147	411831	414977	- ATP-dependent dsDNA exonuclease	20
b0398	sbcD	1203	414974	416176	- ATP-dependent dsDNA exonuclease	20
b0399	phoB	690	416366	417055	+ positive response regulator for pho regulon, sensor is PhoR	21
b0400	phoR	1296	417113	418408	+ positive and negative sensor protein for pho regulon	20
b0401	brnQ	1320	418815	420134	+ branched chain amino acid transport system II carrier protein	21
b0402	proY	1374	420210	421583	+ proline permease transport protein	20
b0403	malZ	1818	421739	423556	+ maltodextrin	17
b0404	yajB	582	423561	424142	- putative glycoprotein	20
b0405	queA	1071	424235	425305	+ synthesis of queuine in tRNA; probably S-adenosylmethionine:tRNA ribosyltransferase-isomerase	21
b0406	tgt	1128	425361	426488	+ tRNA-guanine transglycosylase	21
b0407	yajC	333	426511	426843	+ orf, hypothetical protein	21
b0408	secD	1848	426871	428718	+ protein secretion; membrane protein, part of the channel	21
b0409	secF	972	428729	429700	+ protein secretion, membrane protein	21
b0410	yajD	348	429829	430176	+ orf, hypothetical protein	20
b0411	tsx	885	430353	431237	- nucleoside channel; receptor of phage T6 and colicin K	17
b0412	yajI	600	431536	432135	- orf, hypothetical lipoprotein	16
b0413	ybaD	450	432226	432675	+ orf, hypothetical protein	20
b0414	ribD	1104	432679	433782	+ diaminohydroxyphosphoribosylaminopyrimidine deaminase; 5-amino-6-(5-phosphoribosylamino)uracil	21
b0415	ribE	471	433871	434341	+ riboflavin synthase, beta chain	21
b0416	nusB	420	434361	434780	+ transcription termination; L factor	21
b0417	thiL	978	434858	435835	+ thiamin-monophosphate kinase	21
b0418	pgpA	519	435813	436331	+ phosphatidylglycerophosphatase	21
b0419	yajO	1047	436385	437431	- putative NAD(P)H-dependent xylose reductase	19
b0420	dxs	1863	437539	439401	- 1-deoxyxylulose-5-phosphate synthase; flavoprotein	21
b0421	ispA	900	439426	440325	- geranyltransferase (farnesyl-diphosphate synthase)	21
b0422	xseB	243	440325	440567	- exonuclease VII, small subunit	21
b0423	thiI	1449	440773	442221	+ sulfur transfer protein	21
b0424	thiJ	597	442275	442871	- 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthase	20
b0425	apbA	912	442828	443739	- 2-dehydropanoate 2-reductase	21
b0426	yajQ	510	443889	444398	+ orf, hypothetical protein	21
b0427	yajR	1371	444526	445896	- putative transport	19
b0428	cyoE	891	446039	446929	- protoheme IX farnesyltransferase (haeme O biosynthesis)	20

b0429	cyoD	330	446941	447270	- cytochrome o ubiquinol oxidase subunit IV				19
b0430	cyoC	615	447270	447884	- cytochrome o ubiquinol oxidase subunit III				20
b0431	cyoB	1992	447874	449865	- cytochrome o ubiquinol oxidase subunit I				18
b0432	cyoA	948	449887	450834	- cytochrome o ubiquinol oxidase subunit II		1		18
b0433	ampG	1476	451294	452769	- regulates beta-lactamase synthesis				21
b0434	yajG	681	452813	453493	- putative polymerase/proteinase	1			21
b0435	bolA	351	453663	454013	+ possible regulator of murein genes	1			21
b0436	tig	1299	454357	455655	+ trigger factor; a molecular chaperone involved in cell division				21
b0437	clpP	624	455901	456524	+ ATP-dependent proteolytic subunit of clpA-clpP serine protease. heat shock				21
b0438	clpX	1275	456650	457924	+ ATP-dependent specificity component of clpP serine protease, DNA-binding, ATP-dependent protease La; heat shock K-protein				21
b0439	lon	2355	458112	460466	+ DNA-binding, ATP-dependent protease La; heat shock K-protein				21
b0440	hupB	273	460675	460947	+ DNA-binding protein HU-beta, NS1 (HU-1)				21
b0441	ppiD	1872	461139	463010	+ peptidyl-prolyl cis-trans isomerase D				21
b0442	ybaV	372	463161	463532	+ orf, hypothetical protein				21
b0443	ybaW	399	463626	464024	+ orf, hypothetical protein				21
b0444	ybaX	696	464076	464771	- orf, hypothetical protein				21
b0445	ybaE	1701	464836	466536	- orf, hypothetical protein				18
b0446	cof	831	466624	467454	+ orf, hypothetical protein				19
b0447	ybaO	546	467520	468065	+ putative LRP-like transcriptional regulator				21
b0448	mdlA	1773	468095	469867	+ ATP-binding component of a putative ATP-binding component of a transport system				21
b0449	mdlB	1782	469860	471641	+ nitrogen regulatory protein P-II 2				21
b0450	glnK	339	471822	472160	+ probable ammonium transporter				21
b0451	amtB	1287	472190	473476	- acyl-CoA thioesterase II				21
b0452	tesB	861	473525	474385	+ glycoprotein/polysaccharide metabolism				20
b0453	ybaY	573	474603	475175	- orf, hypothetical protein				20
b0454	ybaZ	390	475206	475595	+ orf, hypothetical protein	1			10
b0456	ybaA	354	475896	476249	- orf, hypothetical protein				16
b0457	ylaB	1557	476291	477847	- orf, hypothetical protein				20
b0458	ylaC	510	478005	478514	- orf, hypothetical protein				14
b0459	maa	552	478591	479142	- maltose O-acetyltransferase			1	21
b0460	hha	219	479314	479532	- haemolysin expression modulating protein		1	1	20
b0461	ybaJ	375	479558	479932	- orf, hypothetical protein	1	1	1	21
b0462	acrB	3150	480478	483627	- acridine efflux pump				21
b0463	acrA	1194	483650	484843	- acridine efflux pump				20
b0464	acrR	648	484985	485632	+ acrAB operon repressor	1			19
b0465	kefA	3363	485760	489122	+ component of the MscS mechanosensitive channel				21
b0466	ybaM	162	489334	489495	- orf, hypothetical protein				19
b0467	priC	528	489509	490036	- primosomal replication protein N"				19
b0468	ybaN	378	490106	490483	+ putative gene 58				21
b0469	apt	552	490636	491187	+ adenine phosphoribosyltransferase				21

b0470	dnaX	1932	491316	493247	+ DNA polymerase III, tau and gamma subunits; DNA elongation factor					21
b0471	ybaB	330	493300	493629	+ orf, hypothetical protein					21
b0472	recR	606	493629	494234	+ recombination and					21
b0473	htpG	1875	494344	496218	+ chaperone Hsp90, heat shock protein C 62.5					21
b0474	adk	645	496399	497043	+ adenylate kinase activity; pleiotropic effects on glycerol-3-phosphate					21
b0475	hemH	963	497279	498241	+ ferroxidase: final enzyme of heme biosynthesis					21
b0476	aes	960	498238	499197	- acetyl esterase	1				20
b0477	gsk	1305	499349	500653	+ inosine-guanosine					20
b0478	ybaL	1677	500786	502462	- putative transport					21
b0479	fsr	1221	502700	503920	- fosmidomycin resistance protein					19
b0480	ushA	1653	504138	505790	+ UDP-sugar hydrolase (5'-nucleotidase)					15
b0481	ybaK	480	505827	506306	- orf, hypothetical protein					21
b0482	ybaP	795	506510	507304	- putative ligase					21
b0483	ybaQ	396	507388	507783	+ orf, hypothetical protein					11
b0484	copA	2505	508099	510603	- Cu(I)-translocating P-type ATPase					21
b0485	ybaS	933	510865	511797	+ putative glutaminase					13
b0486	ybaT	1293	511800	513092	+ putative amino acid/amine transport					11
b0487	cueR	408	513217	513624	+ copper responsive transcription regulator		1			21
b0488	ybbJ	456	513625	514080	- orf, hypothetical protein					21
b0489	ybbK	918	514080	514997	- putative protease					20
b0490	ybbL	678	515143	515820	+ putative ATP-binding component of a transport system			1		15
b0491	ybbM	807	515780	516586	+ putative metal resistance protein			1		14
b0492	ybbN	891	516649	517539	- putative thioredoxin-like protein					20
b0493	ybbO	810	517564	518373	- putative oxidoreductase					21
b0494	tesA	627	518363	518989	- acyl-CoA thioesterase I; also functions as protease I					19
b0495	ybbA	687	518957	519643	+ putative ATP-binding component of a transport system					21
b0496	ybbP	2415	519640	522054	+ putative oxidoreductase					18
b0497	rhsD	4281	522485	526765	+ rhsD protein in rhs element	1	1	1		18
b0498	ybbC	369	526805	527173	+ orf, hypothetical protein	1	1	1		2
b0499	-	711	527173	527883	+ orf, hypothetical protein	1	1	1		
b0500	ybbD	261	527864	528124	+ orf, hypothetical protein	1	1	1		5
b0501	-	192	528163	528354	+ orf, hypothetical protein	1	1	1		4
b0502	-	408	528869	529276	- orf, hypothetical protein					6
b0503	ybbB	1095	529356	530450	- putative capsule anchoring protein					15
b0504	ybbS	927	530519	531445	- putative transcriptional regulator LYSR-type					13
b0505	allA	483	531675	532157	+ ureidoglycolate					12
b0506	allR	816	532235	533050	+ repressor of allantoin and glyoxylate utilization operons					14
b0507	gcl	1782	533140	534921	+ glyoxylate carboligase					13
b0508	hyi	777	534934	535710	+ hydroxypyruvate			1		19
b0509	glxR	879	535810	536688	+ tartronic semialdehyde reductase			1		21
b0510	ybbV	279	536720	536998	+ orf, hypothetical protein	1	1	1		5
b0511	allP	1314	536998	538311	+ putative allantoin permease			1		11
b0512	allB	1362	538371	539732	+ allantoinase			1		10
b0513	ybbY	1308	539783	541090	+ possible uracil	1		1		10
b0514	glxK	1146	541112	542257	+ glycerate kinase			1		21

b0515	yIbA	786	542485	543270	- orf, hypothetical protein			1	12
b0516	allC	1236	543281	544516	- allantate			1	17
b0517	allD	1050	544538	545587	- ureidoglycolate dehydrogenase			1	16
b0518	fdrA	1668	545904	547571	+ involved in protein transport; multicopy suppressor of dominant negative ftsH mutants			1	10
b0519	yIbE	1002	547838	548839	+ orf, hypothetical protein				13
b0520	yIbF	816	548850	549665	+ putative carboxylase				14
b0521	arcC	894	549662	550555	+ putative carbamate				13
b0522	purK	1068	550750	551817	- phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO(2)-fixing subunit				21
b0523	purE	510	551814	552323	- phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit				21
b0524	ybbF	723	552441	553163	- orf, hypothetical protein				21
b0525	ppiB	495	553166	553660	- peptidyl-prolyl cis-trans isomerase B (rotamase B)				21
b0526	cysS	1386	553834	555219	+ cysteine tRNA				21
b0527	ybcI	522	555255	555776	- orf, hypothetical protein	1			19
b0528	ybcJ	234	555884	556117	- orf, hypothetical protein				21
b0529	folD	867	556098	556964	- 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase				21
b0530	sfmA	576	557402	557977	+ putative fimbrial-like protein	1	1	1	11
b0531	sfmC	693	558197	558889	+ putative chaperone	1	1	1	16
b0532	sfmD	2604	558920	561523	+ putative outer membrane protein, involved in fimbrial assembly	1	1	1	14
b0533	sfmH	978	561565	562542	+ putative fimbrial-like protein	1	1	1	15
b0534	sfmF	516	562553	563068	+ fimbrial Z protein; probable signal	1	1	1	10
b0535	fimZ	633	563071	563703	- tRNA-Arg				19
tRNA-Arg1	tRNA-Arg	77	563946	564022	- prophage DLP12 integrase			1	
b0537	intD	1164	564038	565201	+ putative sensory transduction regulator	1	1	1	13
b0538	-	561	565195	565755	transposase insE for insertion sequence IS3			1	2
b0540	-	309	566056	566364	transposase insF for insertion sequence IS3		1	1	9
b0541	tra5_2	867	566361	567227	+ orf, hypothetical protein	1	1	1	15
b0542	-	138	567333	567470	+ methylviologen	1	1	1	5
b0543	emrE	333	567538	567870	+ orf, hypothetical protein	1	1	1	19
b0544	ybcK	1527	568125	569651	+ orf, hypothetical protein	1	1	1	8
b0545	ybcL	552	570116	570667	+ orf, hypothetical protein	1	1	1	16
b0546	ybcM	798	570677	571474	+ putative ARAC-type regulatory protein	1	1	1	15
b0547	ybcN	456	571689	572144	+ orf, hypothetical protein	1	1	1	6
b0548	ninE	171	572144	572314	+ similar to phage 82 and lambda proteins	1	1	1	4
b0549	ybcO	291	572307	572597	+ orf, hypothetical protein	1	1	1	9
b0550	rus	363	572594	572956	+ endodeoxyribonuclease RUS (Holliday junction resolvase)		1	1	7
b0551	ybcQ	384	573179	573562	+ orf, hypothetical protein	1	1	1	15
b0552	trs5_2	1017	573960	574976	- IS5 transposase	1	1	1	2
b0553	nmpC	1128	574981	576108	- outer membrane porin protein; locus of qsr prophage		1	1	21
b0554	ybcR	216	576621	576836	+ orf, hypothetical protein		1	1	10
b0555	ybcS	498	576836	577333	+ bacteriophage lambda lysozyme homolog	1	1	1	19

b0556	ybcT	462	577330	577791	+	bacteriophage lambda endopeptidase homolog		1	1	15
b0557	ybcU	294	577823	578116	-	bacteriophage lambda Bor protein homolog	1	1	1	6
b0558	ybcV	453	578407	578859	-	putative an envelop protein	1	1	1	11
b0559	ybcW	207	579103	579309	+	orf, hypothetical protein	1	1	1	4
b0560	nohB	546	580057	580602	+	bacteriophage DNA packaging protein		1	1	8
b0561	ybcX	744	580577	581320	+	orf, hypothetical protein	1	1	1	11
b0562	ybcY	585	581375	581959	-	orf, hypothetical protein	1	1	1	17
b0563	ylcE	186	582098	582283	+	orf, hypothetical protein			1	16
b0564	appY	750	582904	583653	+	regulatory protein affecting appA and outer membrane protein 3b (a), protease VII	1	1	1	2
b0565	ompT	954	583903	584856	-		1	1	1	18
b0566	envY	762	585370	586131	-	envelope protein; thermoregulation of porin biosynthesis	1	1		7
b0567	ybcH	891	586314	587204	-	orf, hypothetical protein				9
b0568	nfrA	2973	587205	590177	-	bacteriophage N4 receptor, outer membrane protein				6
b0569	nfrB	2238	590164	592401	-	bacteriophage N4 receptor, subunit, inner membrane protein				7
b0570	cusS	1443	592551	593993	-	sensor kinase of copper sensing two-component system				19
b0571	cusR	684	593983	594666	-	response regulator of copper sensing system				20
b0572	cusC	1374	594823	596196	+	putative outer membrane protein involved in copper				16
b0573	ylcC	333	596354	596686	+	orf, hypothetical protein				9
b0574	cusB	1224	596702	597925	+	possible component of copper transport				8
b0575	cusA	3144	597937	601080	+	putative copper transport protein				11
b0576	pheP	1377	601182	602558	+	phenylalanine-specific transport system				15
b0577	ybdG	1248	602639	603886	-	putative transport				20
b0578	nfnB	654	603994	604647	-	oxygen-insensitive NAD(P)H				14
b0579	ybdF	369	604741	605109	-	orf, hypothetical protein	1			16
b0580	ybdJ	249	605174	605422	-	orf, hypothetical protein				14
b0581	ybdK	1119	605488	606606	-	orf, hypothetical protein				15
b4415	hokE	153	607059	607211	+	small toxic membrane polypeptide				5
b0582	yi81_2	1113	607288	608400	+	IS186 hypothetical	1	1		5
b0583	entD	630	608682	609311	-	enterochelin synthetase, component	1			21
b0584	fepA	2241	609477	611717	-	outer membrane receptor for ferric enterobactin				16
b0585	fes	1125	612038	613162	+	(enterochelin) and enterochelin esterase				16
b0586	entF	3882	613380	617261	+	ATP-dependent serine activating enzyme (may be part of enterobactin synthase as component F)				21
b0587	fepE	1134	617477	618610	+	ferric enterobactin (enterochelin) transport	1		1	16
b0588	fepC	816	618607	619422	-	ATP-binding component of ferric enterobactin transport				21
b0589	fepG	993	619419	620411	-	ferric enterobactin transport protein				21
b0590	fepD	1005	620408	621412	-	ferric enterobactin (enterochelin) transport				20
b0591	ybdA	1251	621523	622773	+	putative transport				16

b0592	fepB	957	622777	623733	- ferric enterobactin (enterochelin) binding protein; periplasmic component				19
b0593	entC	1176	624108	625283	+ isochorismate hydroxymutase 2, enterochelin				14
b0594	entE	1611	625293	626903	+ 2,3-dihydroxybenzoate-AMP ligase				21
b0595	entB	858	626917	627774	+ 2,3-dihydro-2,3-dihydroxybenzoate synthetase,				17
b0596	entA	747	627774	628520	+ isochorismatase 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin				17
b0597	ybdB	414	628523	628936	+ orf, hypothetical protein				15
b0598	cstA	2106	629117	631222	+ carbon starvation				20
b0599	ybdH	1089	631612	632700	- putative oxidoreductase				20
b0600	ybdL	1161	632809	633969	+ putative				16
b0601	ybdM	630	633970	634599	- orf, hypothetical protein				15
b0602	ybdN	1221	634572	635792	- orf, hypothetical protein	1		1	12
b0603	ybdO	903	635939	636841	- putative transcriptional regulator LYSR-type	1	1	1	11
b0604	dsbG	807	637050	637856	- thiol:disulfide interchange protein				14
b0605	ahpC	564	638168	638731	+ alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides				16
b0606	ahpF	1596	638946	640541	+ alkyl hydroperoxide reductase, F52a subunit; detoxification of hydroperoxides				16
b0607	ybdQ	429	640662	641090	- orf, hypothetical protein				17
b0608	ybdR	1239	641311	642549	+ putative oxidoreductase	1			11
b0610	rnk	411	642780	643190	- regulator of nucleoside diphosphate kinase				20
b0611	rna	807	643420	644226	- RNase I, cleaves phosphodiester bond between any two nucleotides	1			13
b0612	citT	1464	644340	645803	- citrate carrier				12
b0613	citG	879	645854	646732	- orf, hypothetical protein				14
b0614	ybdU	552	646707	647258	- orf, hypothetical protein				14
b0615	citF	1533	647262	648794	- citrate lyase alpha				14
b0616	citE	924	648805	649728	- citrate lyase beta chain (acyl lyase subunit)				19
b0617	citD	297	649710	650006	- citrate lyase acyl carrier protein (gamma chain)				13
b0618	citC	1146	650021	651166	- citrate lyase synthetase (citrate (pro-3S)-lyase liqase			1	14
b0619	citA	1659	651458	653116	+ putative sensor-type protein			1	12
b0620	citB	681	653085	653765	+ sequence similarity to Shigella regulator				13
b0621	dcuC	1386	653806	655191	- transport of			1	15
b0622	crcA	561	655780	656340	+ orf, hypothetical protein	1		1	20
b0623	cspE	210	656515	656724	+ cold shock protein			1	21
b0624	crcB	384	656778	657161	- orf, hypothetical protein	1			21
b0625	ybeH	228	657254	657481	+ orf, hypothetical protein				14
b0626	ybeM	564	657478	658041	+ putative amidase				19
b0627	tatE	204	658170	658373	+ component of Sec-independent				20
b0628	lipA	966	658474	659439	- lipoate synthesis, sulfur insertion?				21
b0629	ybeF	801	659648	660448	- putative transcriptional regulator LYSR-type	1		1	14
b0630	lipB	576	660860	661435	- protein of lipoate biosynthesis	1			21
b0631	ybeD	264	661602	661865	- orf, hypothetical protein				21

b0632	dacA	1212	661975	663186	- D-alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5	21
b0633	rlpA	1089	663325	664413	- a minor lipoprotein	21
b0634	mrdB	1113	664424	665536	- rod shape-determining membrane protein; sensitivity to radiation and drugs	21
b0635	mrDA	1902	665539	667440	- cell elongation, e phase; peptidoglycan synthetase; penicillin- orf, hypothetical protein	21
b0636	ybeA	468	667471	667938	- orf, hypothetical protein	21
b0637	ybeB	210	667942	668151	- orf, hypothetical protein	21
b0638	phpB	612	668519	669130	- homolog of Salmonella cobC, a phosphohistidine NAMN	14
b0639	nadD	642	669154	669795	- DNA polymerase III, delta subunit	21
b0640	holA	1032	669797	670828	- a minor lipoprotein	21
b0641	rlpB	582	670828	671409	- leucine tRNA	21
b0642	leuS	2583	671424	674006	- putative alpha helical protein	21
b0643	ybeL	483	674241	674723	- orf, hypothetical protein	20
b0644	ybeQ	984	674793	675776	- orf, hypothetical protein	21
b0645	ybeR	708	675934	676641	- putative enzyme of polynucleotide modification	10
b0646	ybeS	1428	676638	678065	- orf, hypothetical protein	10
b0647	ybeT	555	678075	678629	- putative tRNA ligase	21
b0648	ybeU	708	678731	679438	- orf, hypothetical protein	9
b0649	ybeV	1452	679435	680886	- chaperone protein	10
b0650	hscC	1671	680946	682616	- pyrimidine specific nucleoside hydrolase	9
b0651	rihA	936	682700	683635	- ATP-binding protein of glutamate/aspartate transport system	16
b0652	gltL	726	683753	684478	- glutamate/aspartate transport system	20
b0653	gltK	675	684478	685152	- permease	21
b0654	gltJ	741	685152	685892	- glutamate/aspartate transport system	20
b0655	gltI	909	686062	686970	- permease	21
b0656	trs5_3	1017	687220	688236	- glutamate/aspartate periplasmic binding protein	2
b0657	Int	1539	688566	690104	- IS5 transposase	21
b0658	ybeX	879	690129	691007	- apolipoprotein N-acyltransferase, copper homeostasis protein, inner membrane	21
b0659	ybeY	468	691097	691564	- putative transport	21
b0660	ybeZ	1080	691561	692640	- orf, hypothetical protein	21
b0661	yleA	1425	692754	694178	- putative ATP-binding protein in pho regulon	21
b0662	ubiF	1176	694324	695499	- orf, hypothetical protein	21
tRNA-Gln1	tRNA-Gln	75	695653	695727	- 2-octoprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase	
tRNA-Gln2	tRNA-Gln	75	695765	695839	- tRNA-Gln	
tRNA-Met1	tRNA-Met	77	695887	695963	- tRNA-Gln	
tRNA-Gln3	tRNA-Gln	75	695979	696053	- tRNA-Met	
tRNA-Gln3	tRNA-Gln	75	696088	696162	- tRNA-Gln	
tRNA-Leu	tRNA-Leu	85	696186	696270	- tRNA-Leu	
tRNA-Met	tRNA-Met	77	696280	696356	- tRNA-Met	
b0674	asnB	1665	696736	698400	- asparagine synthetase	20
b0675	nagD	753	698797	699549	- N-acetylglucosamine metabolism	16

b0676	nagC	1221	699597	700817	- transcriptional repressor of nag (N-acetylglucosamine) operon					21
b0677	nagA	1149	700826	701974	- N-acetylglucosamine-6-phosphate deacetylase					21
b0678	nagB	801	702034	702834	- glucosamine-6-phosphate deaminase					21
b0679	nagE	1947	703167	705113	+ PTS system, N-acetylglucosamine-specific enzyme IIABC					21
b0680	glnS	1665	705316	706980	+ glutamine tRNA synthetase					21
b0681	ybfM	1407	707557	708963	+ orf, hypothetical protein				1	18
b0682	ybfN	327	709013	709339	+ orf, hypothetical protein					14
b0683	fur	447	709423	709869	- negative regulator	1				21
b0684	fldA	531	710158	710688	- flavodoxin 1					21
b0685	ybfE	363	710828	711190	- orf, hypothetical protein					21
b0686	ybfF	765	711261	712025	- orf, hypothetical protein					21
b0687	seqA	546	712210	712755	+ negative modulator of initiation of replication	1				21
b0688	pgm	1641	712781	714421	+ phosphoglucomutase					21
b0689	ybfP	495	714635	715129	+ putative pectinase	1	1	1		3
b0690	ybfG	363	715170	715532	- orf, hypothetical protein	1	1	1		3
b0691	ybfH	318	715611	715928	- orf, hypothetical protein	1	1	1		2
b0692	potE	1320	716169	717488	- putrescine transport protein					13
b0693	speF	2199	717485	719683	- ornithine decarboxylase isozyme, inducible				1	10
b0694	kdpE	678	720279	720956	- regulator of kdp operon (transcriptional effector)					19
b0695	kdpD	2685	720953	723637	- sensor for high-affinity potassium transport system					18
b0696	kdpC	573	723630	724202	- high-affinity potassium transport system					19
b0697	kdpB	2049	724211	726259	- ATPase of high-affinity potassium transport system. B chain					18
b0698	kdpA	1674	726282	727955	- ATPase of high-affinity potassium transport system. A chain					20
b0699	ybfA	207	728357	728563	+ orf, hypothetical protein				1	20
b0700	rhsC	4194	728806	732999	+ rhsC protein in rhs element	1	1			18
b0702	ybfB	327	732999	733325	+ orf, hypothetical protein	1	1	1		3
b0703	ybfO	1434	733443	734876	+ orf, hypothetical protein	1	1	1		
b0704	ybfC	570	734873	735442	+ orf, hypothetical protein	1	1	1		4
b0705	ybfL	858	736327	737184	+ putative receptor				1	7
b0706	ybfD	762	737315	738076	+ putative DNA ligase	1	1	1		7
b0707	ybgA	510	738224	738733	+ orf, hypothetical protein				1	20
b0708	phrB	1419	738730	740148	+ deoxyribodipyrimidine photolyase (photoreactivation)					20
b0709	ybgH	1482	740298	741779	- putative transport					14
b0710	ybgI	744	742050	742793	+ orf, hypothetical protein					21
b0711	ybgJ	657	742816	743472	+ putative carboxylase					19
b0712	ybgK	933	743466	744398	+ putative carboxylase					19
b0713	ybgL	735	744388	745122	+ putative lactam utilization protein					21
b0714	nei	792	745158	745949	+ endonuclease VIII and DNA N-glycosylase with an AP lyase activity					16
b0715	abrB	1092	745946	747037	- putative transport					16
b0716	ybgO	1089	747144	748232	- orf, hypothetical protein	1				17
b0717	ybgP	729	748202	748930	- putative chaperone					12
b0718	ybgQ	2457	748945	751401	- putative outer membrane protein				1	15
b0719	ybgD	567	751452	752018	- putative fimbrial-like protein	1	1	1		19
b0720	gltA	1284	752408	753691	- citrate synthase				1	21
b0721	sdhC	390	754400	754789	+ succinate dehydrogenase,	1				21

b0722	sdhD	348	754783	755130	+ succinate dehydrogenase,		20
b0723	sdhA	1767	755130	756896	+ succinate dehydrogenase,		21
b0724	sdhB	717	756912	757628	+ succinate dehydrogenase, iron		21
b0725	-	261	757687	757947	+ orf, hypothetical protein	1	8
b0726	sucA	2802	757929	760730	+ 2-oxoglutarate dehydrogenase (decarboxylase component)		21
b0727	sucB	1218	760745	761962	+ 2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinyl-CoA synthetase, beta synthetase, alpha synthetase, transcriptional regulator of succinylCoA synthetase operon		21
b0728	sucC	1167	762237	763403	+ protein modification enzyme, induction of ompC		21
b0729	sucD	870	763403	764272	+ putative sugar		21
b0730	farR	723	764376	765098	+ cytochrome d terminal oxidase, polypeptide subunit I	1	16
b0731	hrsA	1977	765207	767183	+ cytochrome d terminal oxidase polypeptide subunit II		6
b0732	ybgG	2634	767201	769834	+ orf, hypothetical protein		6
b0733	cydA	1572	770678	772249	+ orf, hypothetical protein		21
b0734	cydB	1140	772265	773404	+ inner membrane protein, membrane-spanning, maintains integrity of cell envelope: tolerance to		21
b0735	ybgE	294	773532	773825	+ putative inner membrane protein, involved in the tonB-independent uptake of		20
b0736	ybgC	405	773975	774379	+ membrane spanning protein, required for		21
b0737	tolQ	693	774376	775068	+ periplasmic protein involved in the tonB-independent uptake of		21
b0738	tolR	429	775072	775500	+ group A colicins		21
b0739	tolA	1266	775565	776830	+ peptidoglycan-associated lipoprotein		21
b0740	tolB	1293	776963	778255	+ orf, hypothetical protein		21
b0741	pal	522	778290	778811	+ tRNA-Lys		21
b0742	ybgF	792	778821	779612	+ tRNA-Val		21
tRNA-Lys1	tRNA-Lys	76	779777	779852	+ tRNA-Lys		
tRNA-Val1	tRNA-Val	76	779988	780063	+ tRNA-Lys		
tRNA-Lys	tRNA-Lys	76	780066	780141	+ tRNA-Val		
tRNA-Val2	tRNA-Val	76	780291	780366	+ tRNA-Lys		
tRNA-Lys	tRNA-Lys	76	780370	780445	+ tRNA-Val		
tRNA-Lys2	tRNA-Lys	76	780592	780667	+ tRNA-Lys		
tRNA-Lys3	tRNA-Lys	76	780800	780875	+ tRNA-Lys		
b0750	nadA	1044	781308	782351	+ quinolinate synthetase, A protein		20
b0751	pnuC	720	782389	783108	+ required for NMN		21
b0752	ybgR	942	783105	784046	- putative transport system permease		20
b0753	ybgS	381	784160	784540	- putative homeobox		15
b0754	aroG	1053	784856	785908	+ 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, phenylalanine phosphoglyceromutase		20
b0755	gpmA	753	786066	786818	-		21

b0756	galM	1041	787020	788060	- galactose-1-epimerase (mutarotase)					18
b0757	galK	1149	788054	789202	- galactokinase					21
b0758	galT	1047	789206	790252	- galactose-1-phosphate uridylyltransferase					21
b0759	galE	1017	790262	791278	- UDP-galactose-4-epimerase					21
b0760	modF	1473	791539	793011	- ATP-binding component of molybdate transport					21
b0761	modE	789	793079	793867	- molybdate uptake regulatory protein					21
b0762	ybhT	150	793996	794145	+ orf, hypothetical protein		1			20
b0763	modA	774	794312	795085	+ molybdate-binding periplasmic protein; permease					21
b0764	modB	690	795085	795774	+ molybdate transport permease protein					21
b0765	modC	1059	795777	796835	+ ATP-binding component of putative phosphatase					21
b0766	ybhA	819	796836	797654	- putative phosphatase					19
b0767	ybhE	996	797809	798804	+ putative isomerase					21
b0768	ybhD	1017	798845	799861	- putative transcriptional regulator LYSR-type	1			1	8
b0769	ybhH	1053	799982	801034	+ orf, hypothetical protein		1		1	7
b0770	ybhI	1434	801110	802543	+ putative membrane pump protein				1	17
b0771	ybhJ	2286	802702	804987	+ putative enzyme					9
b0772	ybhC	1284	805221	806504	- putative pectinesterase					19
b0773	ybhB	477	806656	807132	- orf, hypothetical protein					16
b0774	bioA	1290	807191	808480	- 7,8-diaminopelargonic acid synthetase					21
b0775	bioB	1041	808567	809607	+ biotin synthesis, sulfur insertion?					21
b0776	bioF	1155	809604	810758	+ 8-amino-7-oxononanoate synthase					21
b0777	bioC	756	810745	811500	+ biotin biosynthesis; reaction prior to pimeloyl CoA					21
b0778	bioD	678	811493	812170	+ dethiobiotin synthetase					21
b0779	uvrB	2022	812749	814770	+ DNA repair; excision nuclease subunit B					21
b0780	ybhK	909	814962	815870	- putative structural					21
b0781	moaA	990	816267	817256	+ molybdopterin biosynthesis, protein A					21
b0782	moaB	513	817278	817790	+ molybdopterin biosynthesis, protein B					16
b0783	moaC	486	817793	818278	+ molybdopterin biosynthesis, protein C					21
b0784	moaD	246	818271	818516	+ molybdopterin biosynthesis					21
b0785	moaE	453	818518	818970	+ molybdopterin converting factor,					21
b0786	ybhL	705	819107	819811	+ orf, hypothetical protein			1		19
b0787	ybhM	714	820016	820729	+ orf, hypothetical protein	1		1	1	13
b0788	ybhN	957	820765	821721	- orf, hypothetical protein					14
b0789	ybhO	1242	821721	822962	- cardiolipin synthase activity					14
b0790	ybhP	762	822959	823720	- orf, hypothetical protein					14
b0791	ybhQ	411	823853	824263	+ orf, hypothetical protein					15
b0792	ybhR	1107	824225	825331	- orf, hypothetical protein			1		19
b0793	ybhS	1134	825342	826475	- orf, hypothetical protein			1		19
b0794	ybhF	1752	826468	828219	- putative ATP-binding component of a transport system			1		18
b0795	ybhG	999	828197	829195	- putative membrane protein					19
b0796	ybiH	684	829195	829878	- putative transcriptional regulator	1				19
b0797	rhIE	1365	830095	831459	+ putative ATP-dependent RNA					19
b0798	ybiA	483	831691	832173	- orf, hypothetical protein					7

b0799	dinG	2151	832293	834443	+ probably ATP-dependent helicase				19
b0800	ybiB	963	834471	835433	+ putative enzyme				18
b0801	ybiC	1086	835574	836659	+ putative dehydrogenase				16
b0802	ybiJ	261	836888	837148	- orf, hypothetical protein				21
b0803	ybiI	267	837413	837679	- orf, hypothetical protein				20
b0804	ybiX	714	837753	838466	- putative enzyme				10
b0805	ybiL	2283	838472	840754	- putative outer membrane receptor for				6
b0806	ybiM	405	841019	841423	- orf, hypothetical protein	1			21
b0807	ybiN	1008	841474	842481	+ orf, hypothetical protein				17
b0808	ybiO	2361	842478	844838	- putative transport				13
b0809	glnQ	723	844964	845686	- ATP-binding component of glutamine high-affinity transport				20
b0810	glnP	660	845683	846342	- glutamine high-affinity transport system;				20
b0811	glnH	747	846481	847227	- membrane component periplasmic glutamine-binding protein;				20
b0812	dps	504	847631	848134	- global regulator, starvation conditions		1		20
b0813	ybiF	888	848433	849320	- putative transmembrane subunit		1		19
b0814	ompX	516	849673	850188	+ outer membrane protein				20
b0815	ybiP	1584	850237	851820	- putative enzyme				16
b0816	-	270	851894	852163	+ orf, hypothetical protein	1			2
b0817	mntR	468	852406	852873	+ transcriptional regulator MntR				15
b0818	ybiR	1119	852870	853988	+ orf, hypothetical protein				15
b0819	ybiS	921	854047	854967	- orf, hypothetical protein				16
b0820	ybiT	1593	855186	856778	+ putative ATP-binding component of a transport system				21
b0821	ybiU	1266	857019	858284	- orf, hypothetical protein				18
b0822	ybiV	816	858436	859251	- orf, hypothetical protein				16
b0823	ybiW	2433	859397	861829	- putative formate acetyltransferase 3				16
b0824	ybiY	927	861835	862761	- putative pyruvate formate-lyase 3				16
b0825	fsa	735	862793	863527	+ fructose-6-phosphate aldolase				20
b0826	moeB	750	863603	864352	- molybdopterin biosynthesis				21
b0827	moeA	1236	864352	865587	- molybdopterin biosynthesis				21
b0828	ybiK	966	865791	866756	+ putative asparaginase				16
b0829	yliA	1839	866776	868614	+ putative ATP-binding component of a transport system				16
b0830	yliB	1539	868634	870172	+ putative transport				16
b0831	yliC	921	870190	871110	+ putative transport system permease				16
b0832	yliD	912	871113	872024	+ putative transport system permease				16
b0833	yliE	2349	872202	874550	+ orf, hypothetical protein	1	1	1	6
b0834	yliF	1329	874558	875886	+ orf, hypothetical protein	1	1	1	9
b0835	yliG	1326	875933	877258	- orf, hypothetical protein				15
b0836	yliH	384	877471	877854	+ putative receptor	1			13
b0837	yliI	1116	877965	879080	+ putative dehydrogenase				15
b0838	yliJ	633	879077	879709	- putative transferase				21
b0839	dacC	1203	879950	881152	+ D-alanyl-D-alanine carboxypeptidase;				18
b0840	deoR	759	881199	881957	- penicillin-binding transcriptional repressor for deo				20
b0841	ybjG	597	882015	882611	- orf, hypothetical protein				20
b0842	cmr	1233	882896	884128	+ proton motive force efflux pump				17
b0843	ybjH	285	884169	884453	- orf, hypothetical protein				9
b0844	ybjI	789	884539	885327	- orf, hypothetical protein				16
b0845	ybjJ	1209	885354	886562	- putative DEOR-type transcriptional regulator				21

b0846	ybjK	537	886646	887182	+ putative DEOR-type transcriptional regulator				16
b0847	ybjL	1686	887357	889042	- putative transport			1	20
b0848	ybjM	378	889312	889689	+ orf, hypothetical protein	1			16
b0849	grxA	258	889719	889976	- glutaredoxin1 redox coenzyme for glutathione-dependent ribonucleotide		1		21
b0850	ybjC	288	890136	890423	+ orf, hypothetical protein				20
b0851	nfsA	723	890407	891129	+ oxygen insensitive NADPH nitroreductase (nitrofurane reductase I activitv B)				15
b0852	rimK	903	891190	892092	+ ribosomal protein S6 modification protein				16
b0853	ybjN	477	892180	892656	+ putative sensory transduction regulator	1			21
b0854	potF	1113	893007	894119	+ periplasmic putrescine-binding protein; permease protein				20
b0855	potG	1215	894133	895347	+ ATP-binding component of putrescine transport				20
b0856	potH	954	895357	896310	+ putrescine transport protein; permease				20
b0857	potI	846	896307	897152	+ putrescine transport protein; permease				19
b0858	ybjO	489	897212	897700	+ orf, hypothetical protein				20
b0859	ybjF	1128	897741	898868	+ putative enzyme				21
b0860	artJ	732	899067	899798	- arginine 3rd transport system periplasmic binding protein				18
b0861	artM	669	900089	900757	- arginine 3rd transport system permease				21
b0862	artQ	717	900757	901473	- arginine 3rd transport system permease				21
b0863	artI	732	901480	902211	- arginine 3rd transport system periplasmic binding protein				21
b0864	artP	729	902229	902957	- ATP-binding component of 3rd arginine transport				21
b0865	ybjP	516	903175	903690	- putative lipoprotein				18
b0866	ybjQ	324	903816	904139	+ orf, hypothetical protein				16
b0867	ybjR	831	904136	904966	+ probable N-acetylmutamoyl-L-alanine amidase				21
b0868	ybjS	1050	904963	906012	- orf, hypothetical protein				19
b0869	ybjT	1461	906075	907535	- orf, hypothetical protein				20
b0870	ltaE	1002	907516	908517	- low-specificity L-threonine aldolase				19
b0871	poxB	1719	908554	910272	- pyruvate oxidase				19
b0872	hcr	969	910405	911373	- NADH oxidoreductase for HCP				20
b0873	hcp	1659	911385	913043	- Hybrid cluster protein (HCP)				20
b0874	ybjE	948	913181	914128	- putative surface protein				21
b0875	aqpZ	696	914575	915270	- transmembrane water channel; aquaporin Z			1	11
b0876	ybjD	1659	915696	917354	+ orf, hypothetical protein			1	20
b0877	ybjX	993	917351	918343	- putative enzyme				20
b0878	macA	1143	918431	919573	+ macrolide-specific efflux protein				20
b0879	macB	1947	919570	921516	+ macrolide-specific ABC-type efflux carrier				21
b0880	cspD	225	921589	921813	- stress induced DNA replication inhibitor				20
b0881	yljA	321	922136	922456	+ orf, hypothetical protein	1			21
b0882	clpA	2277	922487	924763	+ ATP-binding component of serine				21
tRNA-Ser1	tRNA-Ser	88	925107	925194	- tRNA-Ser				
b0884	infA	219	925448	925666	- protein chain initiation factor IF-1				21

b0885	aat	705	925951	926655	- leucyl, phenylalanyl-tRNA-protein				21
b0886	cydC	1722	926697	928418	- ATP-binding component of cytochrome-related				21
b0887	cydD	1767	928419	930185	- ATP-binding component of cytochrome-related				21
b0888	trxB	966	930308	931273	- thioredoxin reductase				21
b0889	lrp	495	931818	932312	+ regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system		1		21
b0890	ftsK	3990	932447	936436	+ cell division protein				21
b0891	lolA	615	936592	937206	+ periplasmic protein effects translocation of lipoproteins from inner membrane to outer				21
b0892	ycaJ	1344	937217	938560	+ putative polynucleotide enzyme				21
b0893	serS	1293	938651	939943	+ serine tRNA synthetase; also charges selenocystein				21
b0894	dmsA	2358	940269	942626	+ tRNA with serine anaerobic dimethyl sulfoxide reductase subunit A				21
b0895	dmsB	618	942637	943254	+ anaerobic dimethyl sulfoxide reductase subunit B				18
b0896	dmsC	864	943256	944119	+ anaerobic dimethyl sulfoxide reductase subunit C				18
b0897	ycaC	627	944154	944780	- orf, hypothetical protein				16
b0898	ycaD	1149	945094	946242	+ putative transport protein (MFS family)				21
b0899	ycaM	1623	946260	947882	+ putative transporter	1		1	14
b0900	ycaN	909	947883	948791	- putative transcriptional regulator LYSR-type	1	1	1	18
b0901	ycaK	591	948891	949481	+ orf, hypothetical protein	1	1	1	4
b0902	pflA	741	949563	950303	- pyruvate formate lyase activating enzyme 1				20
b0903	pflB	2283	950495	952777	- formate acetyltransferase 1				20
b0904	focA	858	952832	953689	- probable formate transporter (formate channel 1)			1	21
b0905	ycaO	1770	954095	955864	- orf, hypothetical protein				21
b0906	ycaP	693	955985	956677	+ orf, hypothetical protein				15
b0907	serC	1089	956876	957964	+ 3-phosphoserine aminotransferase				21
b0908	aroA	1284	958035	959318	+ 5-enolpyruvylshikimate-3-phosphate synthetase				21
b0909	ycaL	789	959463	960251	+ putative heat shock protein				14
b0910	cmk	684	960424	961107	+ cytidylate kinase				21
b0911	rpsA	1674	961218	962891	+ 30S ribosomal subunit protein S1				21
b0912	himD	285	963051	963335	+ integration host factor (IHF), beta subunit; site-specific				21
b0913	ycal	2343	963465	965807	+ orf, hypothetical protein	1			17
b0914	msbA	1749	965844	967592	+ ATP-binding transport protein; multicopy suppressor of htrB				21
b0915	lpxK	987	967589	968575	+ lipid A 4' kinase				20
b0916	ycaQ	1233	968612	969844	+ orf, hypothetical protein				13
b0917	ycaR	183	969896	970078	+ orf, hypothetical protein				20
b0918	kdsB	747	970075	970821	+ CTP:CMP-3-deoxy-D-manno-octulosonate transferase				21
b0919	ycbJ	894	970975	971868	+ orf, hypothetical protein				20

b0920	ycbC	780	971845	972624	- orf, hypothetical protein					17
b0921	smtA	786	972760	973545	+ S-adenosylmethionine-dependent methyltransferase					21
b0922	mukF	1323	973542	974864	+ mukF protein (killing factor KICB)					21
b0923	mukE	678	974872	975549	+ orf, hypothetical protein					21
b0924	mukB	4461	975549	980009	+ kinesin-like cell division protein involved in chromosome					20
b0925	ycbB	1848	980270	982117	+ putative amidase					20
b0926	ycbK	549	982298	982846	+ orf, hypothetical protein					21
b0927	ycbL	648	982873	983520	+ orf, hypothetical protein					21
b0928	aspC	1191	983742	984932	- aspartate aminotransferase					21
b0929	ompF	1089	985117	986205	- outer membrane protein 1a (Ia;b;F)			1		21
b0930	asnS	1401	986808	988208	- asparagine tRNA synthetase					21
b0931	pncB	1203	988377	989579	- nicotinate phosphoribosyltransferase					21
b0932	pepN	2613	989845	992457	+ aminopeptidase N					21
b0933	ssuB	768	992500	993267	- probable ATP-binding component of ABC transporter					14
b0934	ssuC	837	993264	994100	- probable permease component of ABC transporter					13
b0935	ssuD	1146	994066	995211	- alkanesulfonate monooxygenase					13
b0936	ssuA	1002	995208	996209	- putative aliphatic sulfonates binding					14
b0937	ssuE	576	996160	996735	- NAD(P)H-dependent FMN reductase			1		14
b0938	ycbQ	549	997082	997630	+ putative fimbrial-like protein	1		1	1	10
b0939	ycbR	702	997713	998414	+ putative fimbrial chaperone	1		1	1	16
b0940	ycbS	2601	998439	1001039	+ putative outer membrane usher	1		1	1	14
b0941	ycbT	1071	1001030	1002100	+ putative fimbrial-like protein	1		1		15
b0942	ycbU	543	1002112	1002654	+ putative fimbrial-like protein	1		1		14
b0943	ycbV	564	1002614	1003177	+ putative fimbrial-like protein	1				12
b0944	ycbF	738	1003143	1003880	+ putative fimbrial chaperone	1				15
b0945	pyrD	1011	1003991	1005001	+ dihydro-orotate dehydrogenase					21
b0946	ycbW	579	1005139	1005717	+ orf, hypothetical protein	1			1	21
b0947	ycbX	1110	1005714	1006823	- orf, hypothetical protein					21
b0948	ycbY	2109	1007067	1009175	+ putative oxidoreductase					21
b0949	uup	1908	1009187	1011094	+ putative ATP-binding component of a transport system					20
b0950	pqiA	1254	1011224	1012477	+ paraquat-inducible protein A	1				21
b0951	pqiB	1641	1012482	1014122	+ paraquat-inducible protein B					21
b0952	ymbA	549	1014134	1014682	+ orf, hypothetical protein					21
b0953	rmf	168	1014938	1015105	+ ribosome modulation factor	1		1		17
b0954	fabA	519	1015175	1015693	- beta-hydroxydecanoyl thioester dehydrase, trans-2-decenoyl-ACP isomerase					21
b0955	ycbZ	1761	1015762	1017522	- putative ATP-dependent protease					20
b0956	ycbG	453	1017708	1018160	+ putative dehydrogenase	1				21
b0957	ompA	1041	1018236	1019276	- outer membrane protein 3a (II*;G;d)					21

b0958	sulA	510	1019633	1020142	- suppressor of lon; inhibits cell division and ftsZ ring formation	1			20
b0959	yccR	630	1020361	1020990	+ orf, hypothetical protein	1			20
b0960	yccS	2163	1020953	1023115	- orf, hypothetical protein				21
b0961	yccF	447	1023125	1023571	- orf, hypothetical protein				20
b0962	helD	2055	1023694	1025748	+ DNA helicase IV				21
b0963	mgsA	468	1025780	1026247	- methylglyoxal synthase				21
b0964	yccT	663	1026334	1026996	- orf, hypothetical protein				20
b0965	yccU	495	1027088	1027582	+ protein (unknown)				21
b0966	yccV	369	1027627	1027995	- orf, hypothetical protein				21
b0967	yccW	1104	1028002	1029105	- putative oxidoreductase				18
b0968	yccX	279	1029287	1029565	+ orf, hypothetical protein				21
b0969	yccK	387	1029562	1029948	- putative sulfite				21
b0970	yccA	660	1029982	1030641	- putative carrier/transport protein				16
tRNA-Ser2	tRNA-Ser	88	1030848	1030935	- tRNA-Ser				
b0972	hyaA	1119	1031362	1032480	+ hydrogenase-1 small subunit				15
b0973	hyaB	1794	1032477	1034270	+ hydrogenase-1 large subunit				14
b0974	hyaC	708	1034289	1034996	+ probable Ni/Fe- hydrogenase 1 b-type cytochrome subunit				14
b0975	hyaD	588	1034993	1035580	+ processing of HyaA and HyaB proteins				15
b0976	hyaE	399	1035577	1035975	+ processing of HyaA and HyaB proteins				15
b0977	hyaF	858	1035972	1036829	+ nickel incorporation into hydrogenase-1 proteins				14
b0978	appC	1545	1036963	1038507	+ probable third cytochrome oxidase,				13
b0979	appB	1137	1038519	1039655	+ probable third cytochrome oxidase,				14
b0980	appA	1299	1039840	1041138	+ phosphoanhydride phosphorylase; pH 2.5 acid phosphatase;	1			20
b0981	yccC	2181	1041253	1043433	- orf, hypothetical protein				17
b0982	yccY	459	1043453	1043911	- putative phosphatase				17
b0983	yccZ	1140	1043887	1045026	- putative function in exopolysaccharide production				17
b0984	ymcA	2097	1045072	1047168	- orf, hypothetical protein				16
b0985	ymcB	747	1047168	1047914	- orf, hypothetical protein	1		1	16
b0986	ymcC	645	1047911	1048555	- putative regulator			1	16
b0987	ymcD	324	1048662	1048985	- orf, hypothetical protein	1		1	9
b0988	insB_4	504	1049250	1049753	+ IS1 protein InsB			1	15
b0989	cspH	213	1050186	1050398	- cold shock-like protein	1		1	15
b0990	cspG	213	1050684	1050896	+ homolog of Salmonella cold shock protein	1		1	21
b0991	sfa	231	1051070	1051300	+ suppresses fabA and ts growth mutation	1	1	1	9
b0992	yccM	1074	1051512	1052585	- orf, hypothetical protein	1			10
b0993	torS	2715	1052657	1055371	- sensor protein torS (regulator TorR)				13
b0994	torT	1029	1055484	1056512	+ part of regulation of tor operon, periplasmic				14
b0995	torR	693	1056485	1057177	- response transcriptional regulator for torA (sensor TorS)				13
b0996	torC	1173	1057307	1058479	+ trimethylamine N-oxide reductase, cytochrome c-type subunit				13
b0997	torA	2547	1058479	1061025	+ trimethylamine N-oxide reductase subunit				21
b0998	torD	600	1061022	1061621	+ part of trimethylamine- N-oxide oxidoreductase				12
b0999	yccD	306	1061773	1062078	- orf, hypothetical protein				15
b1000	cbpA	921	1062078	1062998	- curved DNA-binding protein; functions closely related to DnaJ			1	15
b1001	yccE	1257	1063259	1064515	+ orf, hypothetical protein	1	1	1	8

b1002	agp	1242	1064808	1066049	+ periplasmic glucose-1-phosphatase			1	20
b1003	yccJ	228	1066087	1066314	- orf, hypothetical protein				14
b1004	wrbA	597	1066335	1066931	- flavoprotein WrbA (Trp repressor binding				19
b1005	ycdF	231	1067141	1067371	+ orf, hypothetical protein				3
b1006	ycdG	1395	1067734	1069128	- putative transport				9
b1007	ycdH	459	1069083	1069541	- putative flavin:NADH reductase	1			21
b1008	ycdI	591	1069588	1070178	- putative NADH dehydrogenase/NAD(P) H nitroreductase				9
b1009	ycdJ	801	1070188	1070988	- hypothetical protein				10
b1010	ycdK	387	1070996	1071382	- hypothetical protein				8
b1011	ycdL	735	1071394	1072128	- hypothetical isochorismatase family protein				
b1012	ycdM	1149	1072086	1073234	- putative				10
b1013	ycdC	639	1073465	1074103	+ hypothetical transcriptional regulator				16
b1014	putA	3963	1074143	1078105	- proline dehydrogenase, P5C dehydrogenase				18
b1015	putP	1509	1078528	1080036	+ major sodium/proline symporter			1	19
b4490	b4490	120	1080570	1080689	+ orf, hypothetical protein			1	
b1018	ycdO	1128	1081466	1082593	+ orf, hypothetical protein			1	13
b1019	ycdB	1272	1082599	1083870	+ orf, hypothetical protein			1	13
b1020	phoH	1065	1084215	1085279	+ PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation	1		1	19
b1021	ycdP	414	1085329	1085742	- orf, hypothetical protein	1	1	1	10
b1022	ycdQ	1326	1085744	1087069	- orf, hypothetical protein	1	1	1	10
b1023	ycdR	2019	1087062	1089080	- orf, hypothetical protein	1	1	1	10
b1024	ycdS	2424	1089089	1091512	- putative outer membrane protein	1	1	1	10
b1025	ycdT	1359	1092099	1093457	+ orf, hypothetical protein	1	1	1	5
b1026	tra5_3	867	1093498	1094364	- transposase insF for insertion sequence IS3	1	1	1	15
b1027	-	309	1094361	1094669	- transposase insE for insertion sequence IS3	1	1	1	9
b1028	-	324	1094746	1095069	+ orf, hypothetical protein	1	1	1	4
b1029	ycdU	987	1095066	1096052	+ orf, hypothetical protein	1	1	1	6
tRNA-Ser3tRNA-Ser		88	1096788	1096875	- tRNA-Ser			1	
b1033	ycdW	978	1097070	1098047	+ putative dehydrogenase	1	1	1	15
b1034	ycdX	738	1098102	1098839	+ orf, hypothetical protein			1	20
b1035	ycdY	555	1098863	1099417	+ putative oxidoreductase component			1	21
b1036	ycdZ	540	1099471	1100010	+ orf, hypothetical protein			1	15
b1037	csgG	834	1100074	1100907	- curli production assembly/transport component, 2nd curli operon		1	1	18
b1038	csgF	417	1100934	1101350	- curli production assembly/transport component, 2nd curli operon		1	1	12
b1039	csgE	390	1101375	1101764	- curli production assembly/transport component, 2nd curli operon	1	1	1	14
b1040	csgD	651	1101769	1102419	- putative 2-component transcriptional regulator for 2nd curli operon	1	1	1	13
b1041	csgB	456	1103174	1103629	+ minor curlin subunit precursor, similar ro	1	1	1	13
b1042	csgA	456	1103670	1104125	+ curlin major subunit, coiled surface structures: crvptc		1	1	12
b1043	csgC	333	1104184	1104516	+ putative curli production protein	1	1	1	13
b1044	ymdA	312	1104637	1104948	+ orf, hypothetical protein	1	1	1	21

b1045	ymdB	534	1105043	1105576	+ putative polyprotein	1	1	1	14
b1046	ymdC	1482	1105518	1106999	+ putative synthase	1		1	15
b1047	mdoC	1158	1107007	1108164	- essential for succinylation of osmoregulated periplasmic glucans biosynthesis protein	1		1	15
b1048	mdoG	1536	1108558	1110093	+ membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO)			1	17
b1049	mdoH	2544	1110086	1112629	+ orf, hypothetical protein				16
b1050	yceK	228	1112802	1113029	- acidic protein				14
b1051	msyB	378	1113030	1113407	- suppresses mutants lacking function of orf, hypothetical protein				13
b1052	-	99	1113434	1113532	- putative transport				6
b1053	yceE	1227	1113487	1114713	- heat shock protein				12
b1054	htrB	921	1114885	1115805	+ orf, hypothetical protein				18
b1055	yceA	1053	1116030	1117082	- orf, hypothetical protein				21
b1056	yceI	576	1117124	1117699	- cytochrome b561			1	20
b1057	yceJ	567	1117703	1118269	- homolog 2	1		1	19
b1058	yceO	141	1118530	1118670	- orf, hypothetical protein		1	1	14
b1059	solA	1119	1118691	1119809	- sarcosine oxidase-like protein			1	20
b1060	yceP	255	1119924	1120178	- orf, hypothetical protein	1		1	16
b1061	dinI	246	1120465	1120710	- damage-inducible			1	20
b1062	pyrC	1047	1120784	1121830	- dihydro-orotase				21
b1063	yceB	561	1121936	1122496	- orf, hypothetical protein				20
b1064	grxB	648	1122630	1123277	- glutaredoxin 2				16
b1065	yceL	1239	1123341	1124579	- orf, hypothetical protein				21
b1066	rimJ	585	1124785	1125369	+ acetylation of N-terminal alanine of 30S ribosomal subunit				21
b1067	yceH	648	1125380	1126027	+ orf, hypothetical protein				20
b1068	mviM	924	1126029	1126952	+ putative virulence factor				18
b1069	mviN	1536	1127062	1128597	+ putative virulence factor				21
b1070	flgN	417	1128637	1129053	- protein of flagellar biosynthesis				20
b1071	flgM	294	1129058	1129351	- anti-FlhA (anti-sigma) factor; also known as RflB protein	1			21
b1072	flgA	660	1129427	1130086	- flagellar biosynthesis; assembly of basal-body	1			21
b1073	flgB	417	1130241	1130657	+ flagellar biosynthesis, cell-proximal portion of basal-body rod				21
b1074	flgC	405	1130661	1131065	+ flagellar biosynthesis, cell-proximal portion of basal-body rod				19
b1075	flgD	696	1131077	1131772	+ flagellar biosynthesis, initiation of hook				21
b1076	flgE	1209	1131797	1133005	+ flagellar biosynthesis, hook protein				21
b1077	flgF	756	1133025	1133780	+ flagellar biosynthesis, cell-proximal portion of basal-body rod				18
b1078	flgG	783	1133952	1134734	+ flagellar biosynthesis, cell-distal portion of basal-body rod				19
b1079	flgH	699	1134787	1135485	+ flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein				21
b1080	flgI	1098	1135497	1136594	+ homolog of Salmonella P-ring of flagella basal				21
b1081	flgJ	942	1136594	1137535	+ flagellar biosynthesis				20
b1082	flgK	1644	1137601	1139244	+ flagellar biosynthesis, hook-filament junction protein 1				18

b1083	flgL	954	1139256	1140209	+ flagellar biosynthesis; hook-filament junction protein					19
b1084	rne	3186	1140405	1143590	- RNase E, membrane attachment, mRNA turnover, maturation 5S RNA					21
b1085	-	375	1143671	1144045	+ orf, hypothetical protein	1				14
b1086	rluC	960	1144163	1145122	+ Ribosomal large subunit pseudouridine					21
b1087	yceF	624	1145234	1145857	- orf, hypothetical protein					20
b1088	yceD	522	1146017	1146538	+ orf, hypothetical protein	1				21
b1089	rpmF	174	1146590	1146763	+ 50S ribosomal subunit protein L32					20
b1090	plsX	1041	1146874	1147914	+ glycerolphosphate auxotrophy in plsB background	1				21
b1091	fabH	954	1147982	1148935	+ 3-oxoacyl-[acyl-carrier-protein] synthase III; acetylCoA ACP transacylase					21
b1092	fabD	930	1148951	1149880	+ malonyl-CoA-[acyl-carrier-protein]					21
b1093	fabG	735	1149893	1150627	+ 3-oxoacyl-[acyl-carrier-protein] reductase					20
b1094	acpP	237	1150838	1151074	+ acyl carrier protein					21
b1095	fabF	1242	1151162	1152403	+ 3-oxoacyl-[acyl-carrier-protein] synthase II					21
b1096	pabC	810	1152523	1153332	+ 4-amino-4-deoxychorismate lyase					21
b1097	yceG	1023	1153335	1154357	+ putative thymidylate kinase					21
b1098	tmk	642	1154347	1154988	+ thymidylate kinase					21
b1099	holB	1005	1154985	1155989	+ DNA polymerase III, delta prime subunit					21
b1100	ycfH	798	1156000	1156797	+ orf, hypothetical protein					21
b1101	ptsG	1434	1157092	1158525	+ PTS system, glucose-specific IIBC					20
b1102	fhuE	2190	1158585	1160774	- outer membrane receptor for ferric iron					16
b1103	ycfF	360	1161108	1161467	+ orf, hypothetical protein					21
b1104	ycfL	378	1161470	1161847	+ orf, hypothetical protein	1				20
b1105	ycfM	642	1161861	1162502	+ orf, hypothetical protein					21
b1106	ycfN	825	1162483	1163307	+ putative beta-	1				21
b1107	nagZ	1026	1163318	1164343	+ beta-N-acetylglucosaminidase					21
b1108	ycfP	600	1164309	1164908	+ orf, hypothetical protein					20
b1109	ndh	1305	1165308	1166612	+ respiratory NADH dehydrogenase					21
b1110	ycfJ	540	1166822	1167361	+ orf, hypothetical protein					20
b1111	ycfQ	711	1167423	1168133	- orf, hypothetical protein	1				17
b1112	ycfR	258	1168296	1168553	+ orf, hypothetical protein					21
b1113	ycfS	963	1168635	1169597	- orf, hypothetical protein					19
b1114	mfd	3447	1169741	1173187	- transcription-repair coupling factor; mutation frequency					21
b1115	ycfT	1074	1173315	1174388	- orf, hypothetical protein					10
b1116	ycfU	1200	1174650	1175849	+ orf, hypothetical protein					21
b1117	ycfV	687	1175857	1176543	+ putative ATP-binding component of a transport system					21
b1118	ycfW	1245	1176543	1177787	+ putative kinase					21
b1119	ycfX	912	1177816	1178727	+ putative NAGC-like transcriptional regulator					20
b1120	cobB	840	1178743	1179582	+ putative nicotinic acid mononucleotide:5,6-dimethylbenzimidazole (DMB) phosphoribosyltransferase					21
b1121	ycfZ	789	1179702	1180490	- -	1	1	1		3
b1122	ymfA	471	1180487	1180957	- orf, hypothetical protein	1		1		3

b1123	potD	1047	1181006	1182052	- spermidine/putrescine periplasmic transport protein					16
b1124	potC	795	1182049	1182843	- spermidine/putrescine transport system permease					16
b1125	potB	828	1182840	1183667	- spermidine/putrescine transport system permease					16
b1126	potA	1137	1183681	1184817	- ATP-binding component of spermidine/putrescine putative peptidase T					16
b1127	pepT	1227	1185067	1186293	+ orf, hypothetical protein					21
b1128	ycfD	1131	1186342	1187472	- sensor protein PhoQ					21
b1129	phoQ	1461	1187539	1188999	- transcriptional regulatory protein					21
b1130	phoP	672	1188999	1189670	- adenylosuccinate lyase					21
b1131	purB	1371	1189839	1191209	- orf, hypothetical protein					21
b1132	ycfC	642	1191213	1191854	- tRNA (5-methylaminomethyl-2-thiouridylate)-methvltransferase					21
b1133	trmU	1152	1191890	1193041	- putative Nudix orf, hypothetical protein					21
b1134	ymfB	462	1193050	1193511	- isocitrate dehydrogenase, orf, hypothetical protein					21
b1135	ymfC	624	1193521	1194144	- orf, hypothetical protein					21
b1136	icdA	1251	1194346	1195596	+ isocitrate dehydrogenase, orf, hypothetical protein					21
b1137	ymfD	666	1196090	1196755	- orf, hypothetical protein	1	1			2
b1138	ymfE	705	1196756	1197460	- orf, hypothetical protein	1	1			2
b1139	lit	894	1197918	1198811	+ phage T4 late gene expression; at locus of e14 element	1	1	1		2
b1140	intE	1128	1198902	1200029	- prophage e14 integrase	1	1			15
b1141	-	246	1200010	1200255	- excisionase-like protein from lambdoid prophage e14	1	1			8
b1142	ymfH	312	1200292	1200603	- hypothetical protein in lambdoid prophage e14 region	1	1			3
b1143	ymfI	387	1200675	1201061	+ hypothetical protein in lambdoid prophage e14 region	1	1			2
b1144	ymfJ	285	1200999	1201283	- hypothetical protein in lambdoid prophage e14 region	1	1			4
b1145	ymfK	675	1201482	1202156	- putative lambdoid prophage e14 repressor protein	1	1			11
b1146	-	504	1201944	1202447	+ e14 prophage; putative regulator	1	1			3
b1147	ymfL	570	1202479	1203048	+ hypothetical protein in lambdoid prophage e14 region	1	1			5
b1148	ymfM	339	1203045	1203383	+ hypothetical protein in lambdoid prophage e14 region	1	1			2
b1149	ymfN	1368	1203393	1204760	+ hypothetical protein in lambdoid prophage e14 region		1			7
b1150	ymfR	183	1204772	1204954	+ hypothetical protein in lambdoid prophage e14 region		1			3
b1151	ymfO	474	1204954	1205427	+ hypothetical protein in lambdoid prophage e14 region	1	1			7
b1152	ymfP	792	1205354	1206145	+ hypothetical protein in lambdoid prophage e14 region		1			17
b1153	ymfQ	585	1206136	1206720	+ hypothetical protein in lambdoid prophage e14 region		1			9

b1154	ycfK	630	1206724	1207353	+	hypothetical protein in lambdoid prophage e14 region	1	1		10
b1155	ymfS	414	1207355	1207768	+	hypothetical protein in lambdoid prophage e14 region	1	1		10
b1156	tfaE	603	1207740	1208342	-	tail fiber assembly protein homolog from lambdoid prophage e14	1	1		6
b1157	stfE	540	1208342	1208881	-	side tail fiber protein homolog from lambdoid prophage e14	1	1		10
b1158	pin	555	1208908	1209462	+	inversion of adjacent DNA; at locus of e14	1	1		20
b1159	mcrA	834	1209569	1210402	+	restriction of DNA at 5- methylcytosine residues; at locus of	1	1		5
b1160	ycgW	324	1210903	1211226	-	orf, hypothetical protein	1	1	1	9
b1161	ycgX	405	1211926	1212330	-	orf, hypothetical protein	1	1	1	11
b1162	ycgE	732	1212551	1213282	-	putative transcriptional regulator	1	1	1	4
b1163	ycgF	1212	1213487	1214698	-	orf, hypothetical protein	1	1	1	6
b1164	ycgZ	237	1215012	1215248	+	orf, hypothetical protein	1	1	1	3
b1165	ymgA	273	1215291	1215563	+	orf, hypothetical protein	1	1	1	2
b1166	ymgB	267	1215592	1215858	+	orf, hypothetical protein	1	1	1	11
b1167	ymgC	249	1215971	1216219	+	orf, hypothetical protein	1	1	1	2
b1168	ycgG	1566	1216509	1218074	+	putative proteases	1	1	1	5
b4491	ycgH	1521	1218824	1220344	+	-			1	
b1171	ymgD	336	1221528	1221863	-	orf, hypothetical protein			1	7
b1172	-	285	1221867	1222151	-	orf, hypothetical protein		1	1	7
b1173	-	213	1222918	1223130	+	orf, hypothetical protein	1		1	5
b1174	minE	267	1223502	1223768	-	cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation		1	1	21
b1175	minD	813	1223772	1224584	-	cell division inhibitor, a membrane ATPase, activates minC		1	1	21
b1176	minC	696	1224608	1225303	-	cell division inhibitor, inhibits ftsZ ring	1	1	1	21
b1177	ycgJ	369	1225823	1226191	+	orf, hypothetical protein	1	1	1	10
b1178	ycgK	402	1226294	1226695	-	orf, hypothetical protein	1	1	1	9
b1179	ycgL	327	1226904	1227230	+	orf, hypothetical protein	1	1	1	21
b1180	ycgM	660	1227302	1227961	+	putative isomerase			1	21
b1181	ycgN	477	1228023	1228499	+	orf, hypothetical protein			1	21
b1182	hlyE	918	1228706	1229623	-	hemolysin E	1	1	1	8
b1183	umuD	420	1229990	1230409	+	SOS mutagenesis; error-prone repair; processed to UmuD'; forms complex with			1	15
b1184	umuC	1269	1230409	1231677	+	SOS mutagenesis and repair	1			15
b1185	dsbB	531	1231723	1232253	-	reoxidizes DsbA protein following formation of disulfide bond in P-ring of flagella				21
b1186	nhaB	1542	1232399	1233940	-	Na ⁺ /H ⁺ antiporter, pH independent				20
b1187	fadR	720	1234161	1234880	+	negative regulator for fad regulon, and positive activator of				21
b1188	ycgB	1533	1234932	1236464	-	putative sporulation protein				20
b1189	dadA	1299	1236794	1238092	+	D-amino acid dehydrogenase subunit				21
b1190	dadX	1071	1238102	1239172	+	alanine racemase 2, catabolic				14
b1191	ycgO	1611	1239558	1241168	-	putative Na ⁽⁺⁾ /H ⁽⁺⁾ exchanger				16
b1192	ldcA	915	1241389	1242303	-	L,D-carboxypeptidase				15
b1193	mltE	726	1242289	1243014	+	murein transglycosylase E	1			20
b1194	ycgR	735	1243016	1243750	-	orf, hypothetical protein	1			19

b1195	ymgE	255	1243951	1244205	+ transglycosylase associated protein		1	15
b1196	ycgY	441	1244383	1244823	+ orf, hypothetical protein	1	1	3
b1197	treA	1698	1244902	1246599	- trehalase, periplasmic			7
b1198	dhaM	1422	1246919	1248340	- PTS hybrid protein			8
b1199	dhaL	633	1248348	1248980	- dihydroxyacetone kinase, C-terminal			14
b1200	dhaK	1101	1248991	1250091	- dihydroxyacetone kinase, N-terminal			13
b1201	dhaR	1929	1250280	1252208	+ probable transcription activator for the dha operon; Sigma54-dependent activator			7
b1202	ycgV	2868	1252308	1255175	- putative adhesion and penetration protein	1	1	6
b1203	ychF	1092	1255944	1257035	- putative GTP-binding protein			21
b1204	pth	585	1257152	1257736	- peptidyl-tRNA			21
b1205	ychH	279	1258014	1258292	+ orf, hypothetical protein			21
b1206	ychM	1653	1258347	1259999	- putative sulfate transporter			20
b1207	prsA	948	1260151	1261098	- phosphoribosylpyrophosphate synthetase			21
b1208	ispE	852	1261249	1262100	- 4-diphosphocytidyl-2-C-methyl-D-erythritol	1		21
b1209	hemM	624	1262100	1262723	- outer-membrane lipoprotein			21
b1210	hemA	1257	1262937	1264193	+ glutamyl-tRNA			21
b1211	prfA	1083	1264235	1265317	+ peptide chain release factor RF-1			21
b1212	hemK	834	1265317	1266150	+ possible protoporphyrinogen oxidase			21
b1213	ychQ	393	1266147	1266539	+ orf, hypothetical protein			20
b1214	ychA	810	1266543	1267352	+ orf, hypothetical protein			20
b1215	kdsA	855	1267388	1268242	+ 2-dehydro-3-deoxyphosphooctulonate aldolase			21
b4419	ldrA	108	1268391	1268498	- small toxic polypeptide			2
b4421	ldrB	108	1268926	1269033	- small toxic polypeptide			5
b4423	ldrC	108	1269461	1269568	- small toxic polypeptide			2
b1216	chaA	1101	1269972	1271072	- sodium-calcium/proton antiporter			20
b1217	chaB	231	1271342	1271572	+ cation transport			14
b1218	chaC	717	1271709	1272425	+ cation transport			11
b1219	ychN	354	1272469	1272822	- orf, hypothetical protein			19
b1220	ychP	1254	1273148	1274401	+ putative factor			18
b1221	narL	651	1274402	1275052	- pleiotrophic regulation of anaerobic respiration: response regulator for nar, frd, dms and for genes			16
b1222	narX	1797	1275045	1276841	- nitrate/nitrate sensor, histidine protein kinase acts on NarL regulator			21
b1223	narK	1392	1277180	1278571	+ nitrite extrusion protein			16
b1224	narG	3744	1279087	1282830	+ nitrate reductase 1, alpha subunit		1	16
b1225	narH	1539	1282827	1284365	+ nitrate reductase 1, beta subunit			16
b1226	narJ	711	1284362	1285072	+ nitrate reductase 1, delta subunit, assembly function			16
b1227	narI	678	1285072	1285749	+ nitrate reductase 1, cytochrome b(NR), gamma subunit			16
b1228	-	276	1285932	1286207	+ orf, hypothetical protein	1	1	4
b1229	tpr	102	1286310	1286411	- a protaminelike protein	1	1	1
	tRNA-Tyr1	85	1286467	1286551	- tRNA-Tyr			
	tRNA-Tyr2	85	1286761	1286845	- tRNA-Tyr			

b1232	purU	843	1287005	1287847	- formyltetrahydrofolate deformylase; for purT- dependent FGAR synthesis				20
b1233	ychJ	459	1287897	1288355	- orf, hypothetical protein	1	1		19
b1234	ychK	945	1288429	1289373	+ orf, hypothetical protein	1			16
b1235	hnr	1014	1289465	1290478	+ Hnr protein				21
b1236	galU	909	1290680	1291588	+ glucose-1-phosphate uridylyltransferase				21
b1237	hns	414	1291732	1292145	- DNA-binding protein HLP-II (HU, BH2, HD, NS): pleiotropic			1	21
b1238	tdk	618	1292750	1293367	+ thymidine kinase	1	1	1	21
b1239	ychG	591	1293649	1294239	- orf, hypothetical protein	1			11
b1240	-	231	1294191	1294421	- orf, hypothetical protein	1	1		3
b1241	adhE	2676	1294669	1297344	- CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase:				21
b1242	ychE	648	1297821	1298468	+ putative channel protein				19
b1243	oppA	1632	1299206	1300837	+ oligopeptide transport; periplasmic binding protein			1	21
b1244	oppB	921	1300923	1301843	+ oligopeptide transport permease protein				21
b1245	oppC	909	1301858	1302766	+ homolog of Salmonella oligopeptide transport permease protein				19
b1246	oppD	1014	1302778	1303791	+ homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system				21
b1247	oppF	1005	1303788	1304792	+ homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system				21
b1248	yciU	408	1304845	1305252	- orf, hypothetical protein	1			21
b1249	cls	1461	1305209	1306669	- cardiolipin synthase, a major membrane phospholipid; novobiocin sensitivity				21
b1250	kch	1254	1307040	1308293	- putative potassium channel protein	1	1	1	19
b1251	yciI	393	1308593	1308985	- orf, hypothetical protein	1	1	1	20
b1252	tonB	720	1309113	1309832	+ energy transducer; uptake of iron, cyanocobalamin; sensitivity to phages.	1		1	21
b1253	yciA	399	1309872	1310270	- orf, hypothetical protein		1	1	21
b1254	ispZ	540	1310375	1310914	- probable intracellular septation protein			1	21
b1255	yciC	744	1310944	1311687	- orf, hypothetical protein			1	21
b1256	yciD	639	1312044	1312682	+ putative outer membrane protein			1	21
b1257	yciE	507	1312742	1313248	- orf, hypothetical protein		1	1	13
b1258	yciF	501	1313294	1313794	- putative structural		1	1	12
b1259	yciG	237	1313880	1314116	- orf, hypothetical protein	1	1	1	11
b1260	trpA	807	1314440	1315246	- tryptophan synthase, alpha protein				21
b1261	trpB	1194	1315246	1316439	- tryptophan synthase, beta protein				21
b1262	trpC	1362	1316451	1317812	- N-(5- phosphoribosyl)anthrani- late isomerase and indole-3- glycerol phosphate anthranilate synthase				20
b1263	trpD	1596	1317813	1319408	- component II, glutamine amidotransferase and phosphoribosylanthranil- ate transferase				20

b1264	trpE	1563	1319408	1320970	- anthranilate synthase component I				21
b1265	trpL	45	1321062	1321106	- trp operon leader				1
b1266	yciV	882	1321244	1322125	+ putative enzymes	1			21
b1267	yciO	657	1322086	1322742	+ orf, hypothetical protein				21
b1268	yciQ	1896	1322770	1324665	+ orf, hypothetical protein	1			10
b1269	yciL	876	1324876	1325751	+ orf, hypothetical protein				20
b1270	btuR	591	1325791	1326381	- cob(I)alamin adenosyltransferase				21
b1271	yciK	759	1326378	1327136	- putative oxidoreductase				21
b1272	sohB	1050	1327356	1328405	+ putative protease				21
b1273	yciN	252	1328441	1328692	- orf, hypothetical protein				20
b1274	topA	2598	1329072	1331669	+ DNA topoisomerase type I, omega protein				21
b1275	cysB	975	1331879	1332853	+ positive transcriptional regulator for cysteine regulon			1	21
b1276	acnA	2676	1333855	1336530	+ aconitate hydratase 1			1	19
b1277	ribA	591	1336594	1337184	- GTP cyclohydrolase II				21
b1278	pgpB	765	1337354	1338118	+ non-essential phosphatidylglycerophosphate phosphatase, membrane bound	1			20
b1279	yciS	309	1338267	1338575	+ orf, hypothetical protein				21
b1280	yciM	1170	1338582	1339751	+ putative heat shock protein				21
b1281	pyrF	738	1339945	1340682	+ orotidine-5'-phosphate decarboxylase				21
b1282	yciH	330	1340679	1341008	+ orf, hypothetical protein		1		21
b1283	osmB	219	1341134	1341352	- osmotically inducible lipoprotein		1	1	19
b1284	yciT	750	1341621	1342370	- putative DEOR-type transcriptional regulator			1	16
b1285	yciR	1986	1342781	1344766	- orf, hypothetical protein	1			16
b1286	rnb	1935	1345002	1346936	- RNase II, mRNA degradation				21
b1287	yciW	1206	1347004	1348209	- putative oxidoreductase	1			19
b1288	fabI	789	1348275	1349063	- enoyl-[acyl-carrier-protein] reductase				21
b1289	ycjD	354	1349431	1349784	- orf, hypothetical protein	1			6
b1290	sapF	807	1349852	1350658	- putative ATP-binding protein of peptide transport system				21
b1291	sapD	993	1350660	1351652	- putative ATP-binding protein of peptide transport system				21
b1292	sapC	891	1351652	1352542	- homolog of Salmonella peptide transport permease protein				21
b1293	sapB	966	1352529	1353494	- homolog of Salmonella peptide transport permease protein				21
b1294	sapA	1644	1353491	1355134	- homolog of Salmonella peptide transport periplasmic protein				21
b1295	ymjA	246	1355447	1355692	- orf, hypothetical protein				10
b1296	ycjJ	1440	1355826	1357265	- putative amino acid/amine transport				8
b1297	ycjK	1497	1357514	1359010	- putative glutamine synthetase				9
b1298	ycjL	777	1359132	1359908	+ probable amidotransferase	1			7
b1299	ycjC	558	1359935	1360492	+ orf, hypothetical protein				9
b1300	aldH	1488	1360767	1362254	+ aldehyde dehydrogenase, prefers				13
b1301	ordL	1281	1362256	1363536	+ probable				16
b1302	goaG	1266	1363574	1364839	+ 4-aminobutyrate aminotransferase				20
b1303	pspF	993	1364959	1365951	- psp operon transcriptional activator				21
b1304	pspA	669	1366103	1366771	+ phage shock protein, inner membrane protein				21
b1305	pspB	225	1366825	1367049	+ phage shock protein				21

b1306	pspC	360 1367049 1367408	+ phage shock protein: activates phage shock- protein expression					21
b1307	pspD	222 1367417 1367638	+ phage shock protein					18
b1308	pspE	315 1367713 1368027	+ phage shock protein				1	19
b1309	ycjM	1707 1368213 1369919	+ putative polysaccharide hydrolase	1			1	5
b1310	ycjN	1293 1369933 1371225	+ putative ABC transporter periplasmic binding protein				1	11
b1311	ycjO	882 1371246 1372127	+ putative binding-protein dependent transport protein		1			8
b1312	ycjP	843 1372114 1372956	+ putative transport system permease		1			8
b1313	ycjQ	1053 1372987 1374039	+ putative oxidoreductase					8
b1314	ycjR	798 1374049 1374846	+ orf, hypothetical protein					7
b1315	ycjS	1056 1374856 1375911	+ putative dehydrogenase					14
b1316	ycjT	2268 1375908 1378175	+ orf, hypothetical protein					8
b1317	ycjU	660 1378172 1378831	+ putative beta- phosphoglucomutase					8
b1318	ycjV	969 1378845 1379813	+ putative ATP-binding component of a transport system					7
b1319	ompG	906 1379971 1380876	+ outer membrane protein				1	5
b1320	ycjW	999 1380987 1381985	- putative LACI-type transcriptional regulator		1		1	8
b1321	ycjX	1398 1382141 1383538	+ putative enzymes					21
b1322	ycjF	1062 1383535 1384596	+ orf, hypothetical protein					21
b1323	tyrR	1542 1384744 1386285	+ transcriptional regulation of aroF, aroG, tyrA and aromatic amino acid transport					21
b1324	tpx	507 1386329 1386835	- thiol peroxidase					21
b1325	ycjG	1008 1386912 1387919	+ putative muconate cycloisomerase I					20
b1326	ycjI	789 1387894 1388682	- putative					19
b1327	ycjY	933 1388957 1389889	- orf, hypothetical protein					13
b1328	ycjZ	900 1390015 1390914	+ putative transcriptional regulator LYSR-type	1	1		1	18
b1329	mppA	1635 1391230 1392864	+ periplasmic murein tripeptide (L-Ala- gamma-D-Glut-m-DAP)		1		1	21
b1330	ynal	1032 1392915 1393946	- orf, hypothetical protein	1	1		1	14
b1331	trs5_4	1017 1394100 1395116	+ IS5 transposase	1	1			2
b1332	ynaJ	258 1395389 1395646	+ orf, hypothetical protein					12
b1333	ydaA	951 1395696 1396646	- orf, hypothetical protein					21
b1334	fnr	753 1396798 1397550	- transcriptional regulation of aerobic, anaerobic respiration, osmotic balance					21
b1335	ogt	516 1397745 1398260	- O-6-alkylguanine- DNA/cysteine-protein methyltransferase	1				21
b1336	abgT	1533 1398271 1399803	- aminobenzoyl- glutamate transport					10
b1337	abgB	1446 1399834 1401279	- aminobenzoyl- glutamate utilization					8
b1338	abgA	1326 1401279 1402604	- aminobenzoyl- glutamate utilization					9
b1339	abgR	909 1402765 1403673	+ putative transcriptional regulator LYSR-type				1	21
b1340	ydaL	564 1404003 1404566	+ orf, hypothetical protein				1	13
b1341	ydaM	1293 1404587 1405879	- orf, hypothetical protein					8
b1342	ydaN	984 1406074 1407057	+ orf, hypothetical protein					21
b1343	dbpA	1374 1407535 1408908	+ ATP-dependent RNA helicase					17
b1344	ydaO	936 1409037 1409972	- orf, hypothetical protein					21
b1345	intR	1236 1410024 1411259	- lambdoid prophage Rac integrase	1	1		1	15
b1346	xisR	240 1411261 1411500	- putative lambdoid prophage Rac excisionase	1	1		1	5

b1347	ydaC	210	1411555	1411764	-	orf, hypothetical protein	1	1	1	6
b1348	lar	195	1411757	1411951	-	restriction alleviation	1	1	1	5
b1349	recT	810	1412008	1412817	-	and modification recombinase, DNA		1		10
b1350	recE	2601	1412810	1415410	-	renaturation exonuclease VIII, ds	1	1	1	13
b1351	racC	276	1415512	1415787	-	DNA exonuclease, 5' --				
b1352	kil	234	1416032	1416265	-	> 3' specific RacC protein	1	1	1	7
					-	Kil protein (killing	1	1	1	8
b1353	sieB	612	1416572	1417183	+	function) of lambdoid phage superinfection	1	1	1	4
b1354	-	177	1417192	1417368	+	exclusion protein				
b1355	ydaG	180	1417346	1417525	-	orf, hypothetical protein	1	1	1	3
b1356	racR	477	1417789	1418265	-	orf, hypothetical protein	1	1	1	4
b1357	ydaS	297	1418389	1418685	+	Rac prophage	1	1	1	4
b1358	ydaT	423	1418708	1419130	+	orf, hypothetical protein		1		11
b1359	ydaU	858	1419143	1420000	+	orf, hypothetical protein	1	1		10
b1360	ydaV	747	1420007	1420753	+	putative DNA	1	1		9
						replication factor				
b1361	ydaW	612	1420725	1421336	+	orf, hypothetical protein	1	1		6
b1362	rzpR	306	1421363	1421668	+	putative Rac prophage		1		15
						endopeptidase				
b1363	trkG	1458	1421806	1423263	+	trk system potassium	1	1	1	2
b1364	-	282	1423202	1423483	+	uptake protein	1	1	1	1
b1365	ynaK	264	1423401	1423664	+	orf, hypothetical protein		1	1	7
b1366	ydaY	360	1423645	1424004	+	orf, hypothetical protein		1	1	2
b1367	-	234	1424079	1424312	+	orf, hypothetical protein	1	1	1	1
b1368	ynaA	1029	1424478	1425506	+	putative alpha helix	1	1	1	4
b1369	-	156	1425482	1425637	+	orf, hypothetical protein		1		1
b1370	trs5_5	981	1425770	1426750	-	IS5Y transposase		1		2
b1371	-	462	1426547	1427008	+	orf, hypothetical protein	1	1		16
b1372	stfR	3369	1427067	1430435	+	side tail fiber protein	1	1		12
						homolog from lambdoid				
b1373	tfaR	576	1430435	1431010	+	prophage Rac		1	1	11
						tail fiber assembly				
b1374	pinR	591	1431108	1431698	-	protein homolog from				
						lambdoid prophage Rac	1	1	1	20
b1375	ynaE	267	1432015	1432281	-	putative DNA-invertase				
b1376	ynaF	507	1433209	1433715	-	from lambdoid				
b1377	ompN	1134	1433784	1434917	-	prophage Rac	1	1	1	3
b1378	ydbK	3525	1435284	1438808	-	orf, hypothetical protein	1			15
						putative filament protein			1	21
						outer membrane porin			1	20
						putative				
b1379	hslJ	423	1439345	1439767	-	oxidoreductase, Fe-S				17
b1380	ldhA	990	1439878	1440867	-	heat shock protein hslJ				21
						fermentative D-lactate				
						dehydrogenase, NAD-				
						dependent				
b1381	ydbH	2640	1441075	1443714	+	orf, hypothetical protein				20
b1382	ynbE	186	1443711	1443896	+	orf, hypothetical protein		1		20
b1383	ydbL	333	1443898	1444230	+	orf, hypothetical protein		1		19
b1384	feaR	906	1444402	1445307	-	regulatory protein for 2-				3
						phenylethylamine				
						catabolism				
b1385	feaB	1503	1445540	1447042	+	phenylacetaldehyde				8
b1386	tynA	2274	1447100	1449373	-	dehydrogenase				2
b1387	paaZ	2046	1449621	1451666	-	copper amine oxidase				2
						(tyramine oxidase)				
						phenylacetic acid				
						degradation protein;				
						putative aldehyde				
b1388	paaA	930	1451951	1452880	+	dehydrogenase				2
b1389	paaB	288	1452892	1453179	+	phenylacetic acid				2
b1390	paaC	747	1453188	1453934	+	degradation protein				2
						phenylacetic acid				
						degradation protein				

b1391	paaD	504	1453943	1454446	+ phenylacetic acid degradation protein	1			2
b1392	paaE	1071	1454454	1455524	+ probable phenylacetic acid degradation NADH oxidoreductase				2
b1393	paaF	768	1455521	1456288	+ probable enoyl-CoA hydratase				15
b1394	paaG	789	1456288	1457076	+ probable enoyl-CoA hydratase				15
b1395	paaH	1428	1457078	1458505	+ probable 3-hydroxybutyryl-CoA				3
b1396	paal	423	1458495	1458917	+ phenylacetic acid degradation protein				2
b1397	paaJ	1206	1458917	1460122	+ probable beta-ketoadipyl CoA thiolase				3
b1398	paaK	1314	1460149	1461462	+ phenylacetate-CoA				3
b1399	paaX	951	1461563	1462513	+ transcriptional repressor for phenylacetic acid degradation protein; putative transferase				2
b1400	paaY	591	1462495	1463085	+ phenylacetic acid degradation protein; putative transferase				2
b4492	ydbA	8622	1463416	1472037	+ -			1	
b1406	ydbC	861	1472245	1473105	+ putative dehydrogenase			1	5
b1407	ydbD	2313	1473162	1475474	+ orf, hypothetical protein	1	1	1	7
b1408	ynbA	612	1475639	1476250	+ orf, hypothetical protein	1	1	1	14
b1409	ynbB	897	1476250	1477146	+ putative phosphatidate cytidyltransferase	1	1	1	12
b1410	ynbC	1758	1477162	1478919	+ orf, hypothetical protein	1		1	14
b1411	ynbD	1293	1478933	1480225	+ putative enzymes	1			14
b1412	acpD	606	1480279	1480884	- acyl carrier protein phosphodiesterase				21
b1413	hrpA	3846	1481142	1484987	+ helicase, ATP-				21
b1414	ydcF	801	1485259	1486059	+ orf, hypothetical protein	1			12
b1415	aldA	1440	1486256	1487695	+ aldehyde dehydrogenase, NAD-				9
b4493	gapC	653	1487737	1488389	- -				
b1418	cybB	567	1488890	1489456	+ cytochrome b561				18
b1419	ydcA	174	1489701	1489874	+ orf, hypothetical protein	1	1		9
b4428	hokB	150	1489946	1490095	- small toxic membrane polypeptide				4
b1420	mokB	168	1489986	1490153	- regulatory peptide whose translation enables hokB	1	1		5
b1421	trg	1641	1490494	1492134	+ methyl-accepting chemotaxis protein III, ribose sensor receptor	1			12
b1422	ydcI	1065	1492172	1493236	- putative transcriptional regulator LYSR-type	1			21
b1423	ydcJ	1344	1493312	1494655	+ orf, hypothetical protein				16
b1424	ydcG	1656	1494880	1496535	+ putative glycoprotein				15
b1425	-	204	1496456	1496659	- orf, hypothetical protein				8
b1426	ydcH	168	1496732	1496899	+ orf, hypothetical protein	1			10
b1427	rimL	540	1496962	1497501	+ ribosomal-protein-serine acetyltransferase	1			16
b1428	ydcK	981	1497493	1498473	- orf, hypothetical protein	1			14
b1429	tehA	993	1498597	1499589	+ tellurite resistance				15
b1430	tehB	594	1499586	1500179	+ tellurite resistance				21
b1431	ydcL	669	1500481	1501149	+ orf, hypothetical protein	1		1	15
b1432	ydcM	1209	1501681	1502889	+ orf, hypothetical protein	1			16
b1433	ydcO	1437	1502929	1504365	- putative membrane transport protein	1			11
b1434	ydcN	537	1504196	1504732	+ orf, hypothetical protein	1			12
b1435	ydcP	2004	1504763	1506766	+ putative protease				12
b1436	yncJ	231	1506858	1507088	- orf, hypothetical protein	1			11
b1437	-	198	1507274	1507471	- orf, hypothetical protein				4
b1438	ydcQ	438	1507511	1507948	+ orf, hypothetical protein	1			12
b1439	ydcR	1407	1508027	1509433	+ multi modular; putative transcriptional regulator; also putative ATP-binding component of a				18

b1440	ydcS	1146	1509678	1510823	+ putative ABC transporter periplasmic binding protein					7
b1441	ydcT	1014	1510841	1511854	+ putative ABC transporter ATP-binding					12
b1442	ydcU	942	1511855	1512796	+ putative ABC transporter permease					5
b1443	ydcV	795	1512786	1513580	+ putative ABC transporter permease					8
b1444	ydcW	1425	1513602	1515026	+ putative aldehyde dehydrogenase					16
b1445	ydcX	249	1515338	1515586	+ orf, hypothetical protein	1				14
b1446	ydcY	234	1515672	1515905	+ orf, hypothetical protein					14
b1447	ydcZ	450	1515906	1516355	- orf, hypothetical protein					15
b1448	yncA	519	1516352	1516870	- hypothetical acetyltransferase					16
b1449	yncB	1131	1516958	1518088	+ putative oxidoreductase					14
b1450	yncC	723	1518229	1518951	+ hypothetical transcriptional regulator	1			1	12
b1451	yncD	2103	1518987	1521089	- probable tonB-dependent receptor					19
b1452	yncE	1062	1521331	1522392	+ putative receptor					13
b1453	ansP	1551	1522505	1524055	- L-asparagine permease					17
b1454	yncG	618	1524271	1524888	+ hypothetical GST-like protein				1	8
b1455	yncH	213	1524964	1525176	+ orf, hypothetical protein	1	1		1	6
b1456	rhsE	2049	1525914	1527962	+ rhsE protein	1	1		1	6
b1457	ydcD	483	1527946	1528428	+ orf, hypothetical protein	1	1		1	3
b1458	-	747	1528610	1529356	+ orf, hypothetical protein	1	1		1	7
b1459	-	201	1529400	1529600	+ orf, hypothetical protein	1	1		1	2
b1460	ydcC	1137	1529840	1530976	+ H repeat-associated protein (ORF-H)	1	1		1	7
b1461	ydcE	234	1531076	1531309	+ orf, hypothetical protein	1	1		1	7
b1462	yddH	618	1531306	1531923	- orf, hypothetical protein					6
b1463	nhoA	846	1532048	1532893	+ N-hydroxyarylamine O-acetyltransferase					11
b1464	yddE	894	1532989	1533882	- orf, hypothetical protein					14
b1465	narV	681	1533961	1534641	- cryptic nitrate reductase 2 gamma subunit					11
b1466	narW	696	1534638	1535333	- cryptic nitrate reductase 2 delta subunit					10
b1467	narY	1545	1535333	1536877	- cryptic nitrate reductase 2 beta subunit					12
b1468	narZ	3741	1536874	1540614	- cryptic nitrate reductase 2 alpha subunit					10
b1469	narU	1389	1540696	1542084	- nitrite extrusion protein	1			1	16
b1470	yddJ	336	1542408	1542743	- orf, hypothetical protein	1	1		1	5
b1471	yddK	957	1542782	1543738	- putative glycoprotein	1	1		1	6
b1472	-	291	1543762	1544052	- putative outer membrane porin protein		1		1	3
b1473	yddG	882	1544312	1545193	- orf, hypothetical protein				1	18
b1474	fdnG	3048	1545425	1548472	+ formate dehydrogenase-N, nitrate-inducible, alpha					16
b1475	fdnH	885	1548485	1549369	+ formate dehydrogenase-N, nitrate-inducible, iron-					14
b1476	fdnI	654	1549362	1550015	+ formate dehydrogenase-N, nitrate-inducible, cvtochrome B556(Fdn)					14
b1477	yddM	363	1550422	1550784	- orf, hypothetical protein	1				11
b1478	adhP	1041	1550852	1551892	- alcohol dehydrogenase					13
b1479	sfcA	1725	1551996	1553720	- NAD-linked malate dehydrogenase (malic enzyme)				1	20
b1480	rpsV	138	1553850	1553987	- 30S ribosomal subunit protein S22; stationary phase-induced	1			1	12
b1481	bdm	279	1554089	1554367	- ribosome-associated biofilm-dependent modulation protein	1			1	11

b1482	osmC	432	1554649	1555080	+ osmotically inducible protein			1	16
b1483	yddO	927	1555136	1556062	- putative ABC transport system ATP-binding protein				8
b1484	yddP	987	1556055	1557041	- putative ABC transport system ATP-binding protein				8
b1485	yddQ	897	1557038	1557934	- putative ABC transport system permease				7
b1486	yddR	1023	1557931	1558953	- putative ABC transport system permease				6
b1487	yddS	1551	1558955	1560505	- putative ABC transport system periplasmic binding protein				6
b1488	ddpX	582	1560519	1561100	- D-alanyl-D-alanine dipeptidase				11
b1489	dos	2424	1561358	1563781	- putative phosphodiesterase, oxvden-sensing protein				7
b1490	yddV	1383	1563782	1565164	- orf, hypothetical protein			1	8
b1491	yddW	1320	1565528	1566847	- orf, hypothetical protein	1		1	15
b1492	xasA	1536	1566978	1568513	- acid sensitivity protein, putative transporter			1	15
b1493	gadB	1401	1568669	1570069	- glutamate decarboxylase isozyme			1	9
b1494	pqqL	2796	1570431	1573226	- putative zinc protease			1	9
b1495	yddB	2373	1573271	1575643	- orf, hypothetical protein			1	10
b1496	yddA	1686	1575681	1577366	- putative ABC transport system ATP-binding protein	1		1	7
b1497	ydeM	1173	1577657	1578829	- putative enzyme	1	1	1	12
b1498	ydeN	1716	1578866	1580581	- putative sulfatase	1	1	1	13
b1499	ydeO	762	1580950	1581711	- putative ARAC-type regulatory protein	1	1	1	10
b1500	-	198	1581786	1581983	- orf, hypothetical protein	1	1	1	8
b1501	ydeP	2280	1582231	1584510	- putative oxidoreductase, major	1	1	1	11
b1502	ydeQ	915	1584844	1585758	- putative adhesin; similar to FimH protein	1	1	1	8
b1503	ydeR	504	1585817	1586320	- putative fimbrial-like protein	1	1	1	13
b1504	ydeS	531	1586333	1586863	- putative fimbrial-like protein	1	1	1	5
b1505	ydeT	1149	1586877	1588025	- putative outer membrane protein	1	1	1	5
b1506	yneL	180	1588381	1588560	- orf, hypothetical protein	1	1	1	4
b1507	hipA	1323	1588878	1590200	- persistence to inhibition of murein or DNA biosynthesis, DNA-binding reulator	1		1	7
b1508	hipB	267	1590200	1590466	- persistence to inhibition of murein or DNA biosynthesis; regulatory protein	1		1	5
b1509	ydeU	1401	1590689	1592089	- putative ATP-binding component of a transport system and adhesin protein			1	17
b1510	ydeK	3978	1592133	1596110	- orf, hypothetical protein	1		1	16
b1511	ydeV	1593	1596641	1598233	- putative kinase				14
b1512	ydeW	954	1598312	1599265	- putative transcriptional regulator, sorC family				15
b1513	ego	1536	1599514	1601049	- putative ATP-binding component of a transport system; essential for aerobic				15
b1514	ydeY	1029	1601043	1602071	- putative ABC transport system permease				16
b1515	ydeZ	993	1602071	1603063	- putative ABC transport system permease				16
b1516	yneA	1023	1603075	1604097	- putative LACI-type transcriptional regulator				14

b1517	yneB	876	1604124	1604999	+ putative aldolase					17
b1518	yneC	291	1605023	1605313	+ orf, hypothetical protein					17
b1519	tam	759	1605370	1606128	+ trans-aconitate 2-methyltransferase					12
b1520	yneE	966	1606132	1607097	- orf, hypothetical protein	1				13
b1521	uxaB	1452	1607253	1608704	- altronate					12
b1522	yneF	948	1608931	1609878	- orf, hypothetical protein					11
b1523	yneG	360	1609990	1610349	- orf, hypothetical protein					14
b1524	yneH	927	1610349	1611275	- putative glutaminase					18
b1525	ynel	1413	1611339	1612751	- putative aldehyde dehydrogenase					13
b1526	yneJ	882	1612828	1613709	+ putative transcriptional regulator LYSR-type					17
b1527	yneK	1116	1613787	1614902	+ orf, hypothetical protein	1	1		1	8
b1528	sotB	1191	1615052	1616242	+ sugar efflux transporter; L-arabinose and isopropyl-b-D-thiooalactosyranoside				1	16
b1529	marC	666	1616267	1616932	- multiple antibiotic resistance protein				1	20
b1530	marR	378	1617201	1617578	+ multiple antibiotic resistance protein; repressor of mar	1			1	16
b1531	marA	390	1617592	1617981	+ multiple antibiotic resistance; transcriptional activator of defense systems				1	16
b1532	marB	219	1618013	1618231	+ multiple antibiotic resistance protein	1			1	14
b1533	eamA	801	1618262	1619062	- amino acid metabolite efflux pump				1	13
b1534	ydeE	1188	1619356	1620543	+ putative transport	1			1	18
b1535	ydeH	891	1620984	1621874	- orf, hypothetical protein	1			1	18
b1536	ydeI	393	1622129	1622521	- orf, hypothetical protein	1			1	12
b1537	ydeJ	519	1622797	1623315	+ orf, hypothetical protein	1			1	14
b1538	dcp	2046	1623359	1625404	- dipeptidyl carboxypeptidase II				1	15
b1539	ydfG	747	1625541	1626287	+ putative oxidoreductase				1	18
b1540	ydfH	687	1626376	1627062	+ orf, hypothetical protein				1	20
b1541	ydfZ	204	1627239	1627442	+ orf, hypothetical protein				1	19
b1542	ydfI	1461	1627477	1628937	- putative oxidoreductase				1	14
b1543	ydfJ	1284	1629026	1630309	- putative transport				1	13
b1544	ydfK	267	1631063	1631329	+ orf, hypothetical protein	1	1		1	3
b1545	pinQ	591	1631646	1632236	+ putative DNA-invertase from lambdoid prophage Qin	1	1		1	20
b1546	tfaQ	576	1632334	1632909	- tail fiber assembly protein homolog from lambdoid prophage Qin			1	1	11
b1547	stfQ	963	1632909	1633871	- side tail fiber protein homolog from lambdoid prophage Qin	1	1		1	9
b1548	nohA	570	1633822	1634391	- DNA packaging protein NU1 homolog from lambdoid prophage Qin	1	1		1	8
b1549	ydfO	426	1635056	1635481	+ orf, hypothetical protein	1	1		1	11
b1550	gnsB	177	1635633	1635809	- GnsB protein	1	1		1	10
b1551	ynfN	192	1635978	1636169	- orf, hypothetical protein	1	1		1	2
b1552	cspl	213	1636479	1636691	- cold shock-like protein			1	1	21
b1553	ydfP	498	1637054	1637551	- orf, hypothetical protein	1	1		1	7
b1554	ydfQ	534	1637548	1638081	- probable lysozyme from lambdoid prophage Qin	1	1		1	19
b1555	ydfR	312	1638078	1638389	- orf, hypothetical protein	1	1		1	9
b1556	essQ	291	1638394	1638684	- lysis protein S homolog from lambdoid prophage Qin	1	1		1	10
b1557	cspB	216	1639363	1639578	- cold shock-like protein	1	1		1	21
b1558	cspF	213	1639879	1640091	+ cold shock-like protein			1	1	3
b1559	ydfT	783	1640513	1641295	- antitermination protein Q homolog from lambdoid prophage Qin	1	1		1	13
b1560	ydfU	1089	1641279	1642367	- orf, hypothetical protein	1	1		1	12
b1561	rem	252	1642675	1642926	- orf, hypothetical protein	1	1		1	8

b1562	hokD	156	1643143	1643298	- polypeptide destructive to membrane potential	1	1	1	10
b1563	relE	288	1643370	1643657	- orf, hypothetical protein	1	1	1	12
b1564	relB	240	1643657	1643896	- negative regulator of translation		1	1	11
b1565	ydfV	306	1643921	1644226	+ orf, hypothetical protein	1	1	1	2
b1566	fixA	333	1644429	1644761	+ orf, hypothetical protein	1	1	1	14
b1567	ydfW	150	1645198	1645347	- orf, hypothetical protein	1	1	1	2
b1568	ydfX	291	1645370	1645660	- orf, hypothetical protein		1	1	4
b1569	dicC	231	1645644	1645874	- regulator of dicB	1	1	1	7
b1570	dicA	408	1645958	1646365	+ regulator of dicB	1	1	1	18
b1571	ydfA	156	1646532	1646687	+ orf, hypothetical protein		1	1	8
b1572	ydfB	171	1646647	1646817	+ orf, hypothetical protein		1	1	5
b1573	ydfC	219	1646847	1647065	+ orf, hypothetical protein		1	1	5
b1575	dicB	189	1647633	1647821	+ inhibition of cell division	1	1	1	5
b1576	ydfD	192	1647818	1648009	+ orf, hypothetical protein	1	1	1	5
b1577	ydfE	921	1648102	1649022	+ orf, hypothetical protein	1	1	1	6
b1578	-	657	1648905	1649561	+ orf, hypothetical protein	1	1	1	18
b1579	intQ	1197	1649536	1650732	+ putative lambdoid prophage Qin defective integrase	1	1	1	15
b1580	rspB	1020	1650920	1651939	- starvation sensing		1	1	9
b1581	rspA	1215	1651951	1653165	- starvation sensing			1	19
b1582	ynfA	327	1653371	1653697	- orf, hypothetical protein	1		1	13
b1583	ynfB	342	1653832	1654173	+ orf, hypothetical protein			1	16
b1584	speG	561	1654208	1654768	+ spermidine N1-acetyltransferase			1	16
b1585	ynfC	747	1654771	1655517	- orf, hypothetical protein	1	1	1	14
b1586	ynfD	348	1655547	1655894	+ orf, hypothetical protein	1		1	15
b1587	ynfE	2427	1656093	1658519	+ putative dimethyl sulfoxide reductase,			1	21
b1588	ynfF	2427	1658577	1661003	+ putative dimethyl sulfoxide reductase,				21
b1589	ynfG	618	1661014	1661631	+ putative dimethyl sulfoxide reductase, Fe-	1			18
b1590	ynfH	855	1661633	1662487	+ putative dimethyl sulfoxide reductase,				15
b1591	ynfI	624	1662521	1663144	+ putative dimethyl sulfoxide reductase				18
b1592	ynfJ	1317	1663279	1664595	+ putative chloride channel protein (eriC-				17
b1593	ynfK	708	1664548	1665255	- putative dethiobiotin synthetase				21
b1594	mlc	1221	1665368	1666588	- putative NAGC-like transcriptional regulator				21
b1595	ynfL	894	1666723	1667616	- putative transcriptional regulator LYSR-type				19
b1596	ynfM	1254	1667723	1668976	+ putative transport				17
b1597	asr	336	1669373	1669708	+ acid shock protein		1	1	1
b1598	ydgD	822	1669984	1670805	+ putative protease			1	20
b1599	ydgE	330	1670844	1671173	- possible chaperone			1	19
b1600	ydgF	366	1671160	1671525	- possible chaperone			1	20
b1601	ydgG	1035	1671937	1672971	+ putative transport			1	18
b1602	pntB	1389	1672996	1674384	- pyridine nucleotide transhydrogenase, beta subunit				21
b1603	pntA	1533	1674395	1675927	- pyridine nucleotide transhydrogenase, alpha subunit				21
b1604	ydgH	945	1676451	1677395	+ orf, hypothetical protein				21
b1605	ydgl	1383	1677581	1678963	+ putative arginine/ornithine				20
b1606	ydgB	723	1679000	1679722	+ putative oxidoreductase				11
b1607	ydgC	336	1679719	1680054	- orf, hypothetical protein				20
b1608	rstA	729	1680174	1680902	+ response transcriptional regulatory protein (RstB sensor)				20
b1609	rstB	1302	1680906	1682207	+ sensor histidine protein kinase (RstA regulator)				19
b1610	tus	930	1682283	1683212	+ DNA-binding protein; inhibition of replication at Ter sites				21

b1611	fumC	1404 1683209 1684612	- fumarase C= fumarate hydratase Class II; isozyme			21
b1612	fumA	1647 1684755 1686401	- fumarase A = fumarate hydratase Class I; aerobic isozyme			20
b1613	manA	1176 1686600 1687775	+ mannose-6-phosphate isomerase			21
b1614	ydgA	1509 1687876 1689384	+ orf, hypothetical protein			21
b1615	uidC	1254 1689610 1690863	- membrane-associated protein	1	1	9
b1616	uidB	1374 1690914 1692287	- glucuronide permease			20
b1617	uidA	1812 1692284 1694095	- beta-D-glucuronidase			8
b1618	uidR	591 1694486 1695076	- repressor for uid operon	1		10
b1619	hdhA	768 1695297 1696064	- NAD-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids		1	13
b1620	mall	1029 1696176 1697204	- maltose regulon regulatory protein			11
b1621	malX	1593 1697379 1698971	+ PTS system, maltose and glucose-specific IIBC component			14
b1622	malY	1173 1698981 1700153	+ cystathionine beta-lyase; maltose regulon modulator			20
b1623	add	1002 1700257 1701258	+ adenosine deaminase			17
b1624	ydgJ	1080 1701292 1702371	- hypothetical oxidoreductase			20
b4409	blr	126 1702575 1702700	+ beta-lactam resistance protein		1	3
b1625	ydgT	216 1702973 1703188	+ orf, hypothetical protein		1	15
b1626	ydgK	465 1703250 1703714	+ orf, hypothetical protein		1	20
b1627	rfmA	582 1703791 1704372	+ electron transport complex protein			21
b1628	rfmB	579 1704372 1704950	+ electron transport complex protein			21
b1629	rfmC	2223 1704943 1707165	+ electron transport complex protein			21
b1630	rfmD	1059 1707166 1708224	+ electron transport complex protein			21
b1631	rfmG	621 1708228 1708848	+ electron transport complex protein			21
b1632	rfmE	696 1708852 1709547	+ electron transport complex protein			21
b1633	nth	636 1709547 1710182	+ endonuclease III; specific for apurinic and/or apyrimidinic			21
b1634	ydgR	1503 1710793 1712295	+ putative transport		1	20
b1635	gst	606 1712401 1713006	+ glutathionine S-transferase			20
b1636	pdxY	864 1713050 1713913	- pyridoxal kinase 2 / pyridoxine kinase			21
b1637	tyrS	1275 1713972 1715246	- tyrosine tRNA			21
b1638	pdxH	657 1715375 1716031	- pyridoxinephosphate oxidase			21
b1639	ydhA	249 1716090 1716338	- orf, hypothetical protein			20
b1640	ydhH	1110 1716517 1717626	- orf, hypothetical protein		1	21
b1641	slyB	468 1717900 1718367	+ putative outer membrane protein		1	21
b1642	slyA	441 1718414 1718854	- transcriptional regulator for cryptic hemolysin		1	21
b1643	ydhl	237 1719049 1719285	+ orf, hypothetical protein	1	1	13
b1644	ydhJ	900 1719246 1720145	+ putative membrane protein	1		15
b1645	ydhK	2013 1720145 1722157	+ orf, hypothetical protein			13
b1646	sodC	522 1722158 1722679	- superoxide dismutase precursor (Cu-Zn)			20
b1647	ydhF	897 1722760 1723656	- orf, hypothetical protein			19
b1648	ydHL	378 1723705 1724082	- orf, hypothetical protein	1		20
b1649	ydHM	600 1724047 1724646	+ hypothetical transcriptional regulator			21

b1650	nemA	1098	1724683	1725780	+ N-ethylmaleimide reductase				20
b1651	gloA	408	1725861	1726268	+ lactoylglutathione lyase				21
b1652	rnt	648	1726371	1727018	+ RNase T, degrades				21
b1653	lhr	4617	1727111	1731727	+ member of ATP-dependent helicase superfamily II				9
b1654	ydhD	348	1731778	1732125	- orf, hypothetical protein				21
b1655	ydhO	816	1732459	1733274	+ putative lipoprotein	1			20
b1656	sodB	582	1733402	1733983	+ superoxide dismutase, iron				19
b1657	ydhP	1170	1734145	1735314	- putative transport				20
b1658	purR	1026	1735868	1736893	+ transcriptional repressor for pur regulon, glyA, glnB, putative transcriptional regulator LYSR-type				21
b1659	ydhB	933	1736890	1737822	- putative transport				20
b1660	ydhC	1212	1737935	1739146	+ putative transport				20
b1661	cfa	1149	1739437	1740585	+ cyclopropane fatty acyl phospholipid synthase				21
b1662	ribC	642	1740625	1741266	- riboflavin synthase, alpha chain				21
b1663	norM	1374	1741481	1742854	+ multidrug resistance protein norM (Na ⁺)/drug antiporter				20
b1664	ydhQ	1257	1742895	1744151	- possible enzyme				10
tRNA-Val3	tRNA-Val	77	1744459	1744535	+ tRNA-Val				
tRNA-Val3	tRNA-Val	77	1744540	1744616	+ tRNA-Val				
b1667	ydhR	306	1744724	1745029	+ protein of unknown function		1		18
b1668	ydhS	1605	1745155	1746759	+ orf, hypothetical protein	1	1		8
b1669	ydhT	813	1746771	1747583	- orf, hypothetical protein	1			11
b1670	ydhU	786	1747587	1748372	- orf, hypothetical protein	1			15
b1671	ydhX	720	1748369	1749088	- putative oxidoreductase, Fe-S	1			10
b1672	ydhW	648	1749101	1749748	- orf, hypothetical protein				10
b1673	ydhV	2103	1749752	1751854	- orf, hypothetical protein			1	8
b1674	ydhY	627	1751875	1752501	- putative oxidoreductase, Fe-S	1		1	9
b1675	ydhZ	210	1752956	1753165	- orf, hypothetical protein			1	15
b1676	pykF	1413	1753722	1755134	+ pyruvate kinase I (formerly F), fructose murein lipoprotein			1	21
b1677	lpp	237	1755445	1755681	+ murein lipoprotein				20
b1678	ynhG	1005	1755745	1756749	- orf, hypothetical protein				13
b1679	sufE	417	1756898	1757314	- orf, hypothetical protein				21
b1680	sufS	1221	1757327	1758547	- selenocysteine lyase; involved in formation of FhuF [2Fe-2S] cluster required for stability of the [2Fe-2S] FhuF				19
b1681	sufD	1272	1758544	1759815	- putative ATP-binding component of a transport system				20
b1682	sufC	747	1759790	1760536	- orf, hypothetical protein				21
b1683	sufB	1527	1760546	1762072	- orf, hypothetical protein				21
b1684	sufA	369	1762042	1762410	- orf, hypothetical protein				20
b1685	ydiH	270	1762958	1763227	- orf, hypothetical protein		1		16
b1686	ydiI	411	1763246	1763656	- orf, hypothetical protein				21
b1687	ydiJ	3057	1763653	1766709	- putative oxidase				21
b1688	ydiK	1113	1767098	1768210	+ orf, hypothetical protein				21
b1689	ydiL	384	1768612	1768995	+ orf, hypothetical protein	1		1	12
b1690	ydiM	1215	1769095	1770309	+ putative transport system permease	1		1	21
b1691	ydiN	1272	1770530	1771801	+ putative amino acid/amine transport			1	21
b1692	ydiB	867	1771813	1772679	+ putative oxidoreductase			1	11
b1693	aroD	759	1772710	1773468	+ 3-dehydroquinate dehydratase			1	15
b1694	ydiF	1596	1773611	1775206	+ putative enzyme			1	11
b1695	ydiO	1206	1775166	1776371	+ putative oxidoreductase			1	16
b1696	ydiP	912	1776414	1777325	- putative ARAC-type regulatory protein	1	1	1	10
b1697	ydiQ	765	1777641	1778405	+ putative transport				9

b1698	ydiR	939	1778425	1779363	+ putative flavoprotein				10
b1699	ydiS	1290	1779419	1780708	+ flavoprotein; probably electron transport				11
b1700	ydiT	294	1780705	1780998	+ orf, hypothetical protein				11
b1701	ydiD	1701	1781001	1782701	+ putative				10
b1702	ppsA	2379	1782758	1785136	- phosphoenolpyruvate synthase			1	21
b1703	ydiA	834	1785469	1786302	+ orf, hypothetical protein			1	21
b1704	aroH	1047	1786459	1787505	+ 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, trvntnnhan renressible)			1	21
b1705	ydiE	192	1787637	1787828	+ orf, hypothetical protein	1		1	14
b1706	ydiU	1437	1787832	1789268	- orf, hypothetical protein			1	17
b1707	ydiV	714	1789331	1790044	- orf, hypothetical protein	1		1	16
b1708	nlpC	465	1790291	1790755	- lipoprotein	1			21
b1709	btuD	750	1790833	1791582	- ATP-binding component of vitamin B12 transport system				21
b1710	btuE	552	1791582	1792133	- vitamin B12 transport				20
b1711	btuC	981	1792196	1793176	- vitamin B12 transport permease protein				21
b1712	himA	300	1793277	1793576	- integration host factor (IHF), alpha subunit; site specific				21
b1713	pheT	2388	1793581	1795968	- phenylalanine tRNA synthetase, beta-				20
b1714	pheS	984	1795983	1796966	- phenylalanine tRNA synthetase, alpha-				21
b1715	pheM	45	1797250	1797294	- phenylalanyl-tRNA synthetase (pheST)				1
b1716	rplT	357	1797417	1797773	- operon leader peptide				21
b1717	rpml	198	1797826	1798023	- 50S ribosomal subunit protein L20, and				19
b1718	infC	543	1798120	1798662	- 50S ribosomal subunit protein A	1			21
b1719	thrS	1929	1798666	1800594	- protein chain initiation factor IF-3				21
b4494	arpB	1900	1801118	1803017	- threonine tRNA synthetase			1	21
b1722	ydiY	759	1803349	1804107	-			1	18
b1723	pfkB	930	1804394	1805323	- orf, hypothetical protein			1	15
b1724	ydiZ	291	1805424	1805714	+ 6-phosphofructokinase II; suppressor of pfkA	1			15
b1725	yniA	861	1805820	1806680	+ orf, hypothetical protein				21
b1726	yniB	537	1806721	1807257	+ orf, hypothetical protein	1			21
b1727	yniC	669	1807404	1808072	- orf, hypothetical protein				21
b1728	ydjM	603	1808223	1808825	+ putative phosphatase	1			21
b1729	ydjN	1392	1808958	1810349	+ orf, hypothetical protein				20
b1730	ydjO	816	1810353	1811168	+ hypothetical symporter	1	1	1	5
b1731	cedA	264	1811445	1811708	- orf, hypothetical protein			1	13
b1732	katE	2262	1811891	1814152	- cell division modulator, affects inhibition after overreplication of chromosome in dnaAcos mutants				19
b1733	ydjC	750	1814410	1815159	+ catalase; hydroperoxidase				17
b1734	celF	1353	1815172	1816524	- orf, hypothetical protein			1	17
b1735	celD	843	1816629	1817471	- phospho-beta-glucosidase; cryptic negative transcriptional regulator of cel operon			1	16
b1736	celC	351	1817479	1817829	- PEP-dependent phosphotransferase enzyme III for cellobiose. arbutin. and			1	18
b1737	celB	1359	1817880	1819238	- PEP-dependent phosphotransferase enzyme II for cellobiose. arbutin. and			1	17

b1738	celA	321 1819323 1819643	- PEP-dependent phosphotransferase enzyme IV for cellobiose, arbutin, and		1	20
b1739	osmE	339 1819942 1820280	- activator of ntrL gene		1	16
b1740	nadE	828 1820482 1821309	+ NAD synthetase, prefers NH3 over			16
b1741	ydjQ	888 1821539 1822426	+ putative excinuclease subunit			15
b1742	ydjR	639 1822386 1823024	- orf, hypothetical protein	1		14
b1743	spy	486 1823164 1823649	- periplasmic protein related to spheroblast		1	16
b1744	astE	969 1823979 1824947	- succinylglutamate desuccinylase			20
b1745	astB	1344 1824940 1826283	- succinylarginine dihydrolase			17
b1746	astD	1479 1826280 1827758	- succinylglutamic semialdehyde dehydrogenase			18
b1747	astA	1035 1827755 1828789	- arginine succinyltransferase			19
b1748	astC	1221 1828786 1830006	- acetylornithine delta-aminotransferase		1	17
b1749	xthA	807 1830452 1831258	+ exonuclease III		1	21
b1750	ydjX	759 1831377 1832135	+ orf, hypothetical protein	1		10
b1751	ydjY	840 1831978 1832817	+ orf, hypothetical protein	1		10
b1752	ydjZ	708 1832832 1833539	+ orf, hypothetical protein			10
b1753	ynjA	549 1833539 1834087	+ orf, hypothetical protein			16
b1754	ynjB	1170 1834094 1835263	+ orf, hypothetical protein			13
b1755	ynjC	1491 1835281 1836771	+ putative transport system permease			6
b1756	ynjD	654 1836771 1837424	+ putative ATP-binding component of a transport system	1		10
b1757	ynjE	1323 1837476 1838798	+ putative thiosulfate sulfur transferase			7
b1758	ynjF	627 1838807 1839433	- putative cytochrome oxidase			9
b1759	nudG	408 1839514 1839921	+ CTP pyrophosphohydrolase			19
b1760	ynjH	273 1839887 1840159	- orf, hypothetical protein	1		20
b1761	gdhA	1344 1840395 1841738	+ NADP-specific glutamate			20
b1762	ynjI	1164 1841855 1843018	- orf, hypothetical protein	1	1	8
b1763	topB	1962 1843023 1844984	- DNA topoisomerase III			21
b1764	selD	1044 1844989 1846032	- selenophosphate synthase, H(2)Se added to acrylyl-tRNA			20
b1765	ydjA	552 1846149 1846700	- orf, hypothetical protein			21
b1766	sppA	1857 1846861 1848717	+ protease IV, a signal peptide peptidase			21
b1767	ansA	1017 1848884 1849900	+ cytoplasmic L-asparaginase I			21
b1768	pncA	660 1849893 1850552	+ nicotinamidase and pyrazinamidase			21
b1769	ydjE	1359 1850645 1852003	- putative transport	1	1	8
b1770	ydjF	759 1852120 1852878	- putative DEOR-type transcriptional regulator	1	1	9
b1771	ydjG	981 1853015 1853995	- hypothetical oxidoreductase		1	9
b1772	ydjH	969 1854005 1854973	- putative kinase	1	1	13
b1773	ydjI	837 1854957 1855793	- putative aldolase		1	8
b1774	ydjJ	1044 1855814 1856857	- putative oxidoreductase		1	12
b1775	ydjK	1380 1856874 1858253	- putative transport			9
b1776	ydjL	1077 1858280 1859356	- hypothetical zinc-type alcohol dehydrogenase-like protein			9
b1777	yeaC	318 1859726 1860043	- orf, hypothetical protein			21
b1778	yeaA	414 1860040 1860453	- orf, hypothetical protein	1		21
b1779	gapA	996 1860795 1861790	+ glyceraldehyde-3-phosphate dehydrogenase A			21
b1780	yeaD	906 1861853 1862758	+ orf, hypothetical protein			18

b1781	yeaE	855 1862806 1863660	- putative an aldehyde reductase				16
b1782	mipA	747 1863750 1864496	- scaffolding protein for murein-synthesising holoenzyme				21
b1783	yeaG	1935 1864932 1866866	+ orf, hypothetical protein				17
b1784	yeaH	1284 1866979 1868262	+ orf, hypothetical protein				17
b1785	yeaI	1476 1868409 1869884	+ orf, hypothetical protein	1	1	1	7
b1786	yeaJ	1671 1869885 1871555	+ orf, hypothetical protein	1	1	1	10
b1787	yeaK	504 1871598 1872101	+ orf, hypothetical protein			1	16
b1788	-	153 1872102 1872254	- orf, hypothetical protein	1		1	9
b1789	yeaL	447 1872376 1872822	+ orf, hypothetical protein			1	21
b1790	yeaM	822 1872779 1873600	- putative ARAC-type regulatory protein	1		1	20
b1791	yeaN	1182 1873697 1874878	+ putative amino acid/amine transport	1		1	17
b1792	yeaO	369 1874912 1875280	+ orf, hypothetical protein			1	16
b1793	yoaF	255 1875302 1875556	- orf, hypothetical protein	1		1	15
b1794	yeaP	1155 1875610 1876764	+ orf, hypothetical protein	1		1	10
b1795	yeaQ	249 1877031 1877279	- orf, hypothetical protein	1		1	17
b1796	yeaG	183 1877427 1877609	- orf, hypothetical protein			1	14
b1797	yeaR	360 1877613 1877972	- orf, hypothetical protein	1		1	19
b1798	yeaS	639 1878145 1878783	- orf, hypothetical protein			1	14
b1799	yeaT	945 1878910 1879854	- putative transcriptional regulator LYSR-type			1	17
b1800	yeaU	1086 1879936 1881021	+ putative tartrate dehydrogenase			1	11
b1801	yeaV	1446 1881212 1882657	+ putative transport			1	19
b1802	yeaW	1125 1882689 1883813	+ orf, hypothetical protein				10
b1803	yeaX	966 1883869 1884834	+ putative diogenase beta subunit				13
b1804	rnd	1128 1884888 1886015	- RNase D, processes tRNA precursor				21
b1805	fadD	1686 1886085 1887770	- acyl-CoA synthetase, long-chain-fatty-acid--CoA liqase				21
b1806	yeaY	582 1887975 1888556	- putative outer membrane protein				21
b1807	yeaZ	696 1888596 1889291	- orf, hypothetical protein				21
b1808	yoaA	1911 1889349 1891259	- putative enzyme				21
b1809	yoaB	393 1891343 1891735	+ orf, hypothetical protein			1	21
b1810	yoaC	360 1892097 1892456	+ orf, hypothetical protein	1	1	1	12
b1811	yoaH	180 1892576 1892755	- orf, hypothetical protein			1	21
b1812	pabB	1362 1892829 1894190	+ p-aminobenzoate synthetase, component				21
b1813	yeaB	579 1894194 1894772	+ orf, hypothetical protein				21
b1814	sdaA	1365 1894956 1896320	+ L-serine deaminase				21
b1815	yoaD	1629 1896421 1898049	+ orf, hypothetical protein				15
b1816	yoaE	1557 1898053 1899609	- putative transport				20
b1817	manX	972 1900072 1901043	+ PTS enzyme IIAB, mannose-specific			1	21
b1818	manY	801 1901106 1901906	+ PTS enzyme IIC, mannose-specific			1	20
b1819	manZ	861 1901910 1902770	+ PTS enzyme IID, mannose-specific			1	21
b1820	yobD	459 1902825 1903283	+ orf, hypothetical protein	1		1	21
b1821	yebN	621 1903658 1904278	+ orf, hypothetical protein			1	20
b1822	rrmA	810 1904275 1905084	- 23S rRNA m1G745 methyltransferase			1	21
b1823	cspC	210 1905250 1905459	- cold shock protein	1		1	20
b1824	yobF	144 1905472 1905615	- orf, hypothetical protein	1	1	1	16
b1825	yebO	288 1906285 1906572	- orf, hypothetical protein	1	1	1	20
b1826	yobG	144 1906647 1906790	- orf, hypothetical protein			1	15
b1827	kdgR	792 1907332 1908123	- regulator of kdgK, kdgT, and eda			1	20
b1828	yebQ	1485 1908189 1909673	+ putative transport	1		1	16
b1829	htpX	882 1909719 1910600	- heat shock protein, integral membrane				21
b1830	prc	2049 1910792 1912840	- carboxy-terminal protease for penicillin-binding protein 3				21
b1831	proQ	699 1912860 1913558	- regulator of ProP				20
b1832	yebR	552 1913655 1914206	- orf, hypothetical protein	1			21

b1833	yebS	1284	1914282	1915565	+ orf, hypothetical protein	1				20
b1834	yebT	2640	1915528	1918167	+ orf, hypothetical protein					18
b1835	yebU	1446	1918241	1919686	+ orf, hypothetical protein					15
b1836	yebV	252	1919789	1920040	+ orf, hypothetical protein			1		19
b1837	yebW	276	1920061	1920336	+ orf, hypothetical protein	1		1		16
b1838	pphA	660	1920337	1920996	- protein phosphatase 1	1		1		11
b1839	yebY	342	1921389	1921730	- orf, hypothetical protein			1		21
b1840	yebZ	873	1921743	1922615	- putative resistance					17
b1841	yobA	375	1922619	1922993	- orf, hypothetical protein					20
b1842	holE	231	1923132	1923362	+ DNA polymerase III, theta subunit					21
b1843	yobB	657	1923464	1924120	+ orf, hypothetical protein	1				14
b1844	exoX	663	1924144	1924806	+ exodeoxyribonuclease					15
b1845	ptrB	2061	1924803	1926863	- protease II					20
b1846	yebE	660	1927072	1927731	- orf, hypothetical protein					16
b1847	yebF	369	1928058	1928426	- orf, hypothetical protein	1				20
b1848	yobG	291	1928481	1928771	- orf, hypothetical protein					16
b1849	purT	1179	1928905	1930083	+ phosphoribosylglycinamide formyltransferase 2					19
b1850	eda	642	1930139	1930780	- 2-keto-3-deoxygluconate 6-phosphate aldolase and					20
b1851	edd	1812	1930817	1932628	- 2-keto-4-6-phosphogluconate dehydratase					20
b1852	zwf	1476	1932863	1934338	- glucose-6-phosphate dehydrogenase					20
b1853	yebK	870	1934676	1935545	+ orf, hypothetical protein	1				21
b1854	pykA	1443	1935673	1937115	+ pyruvate kinase II, glucose stimulated					21
b1855	msbB	972	1937246	1938217	- suppressor of htrB, heat shock protein					21
b1856	yebA	1260	1938337	1939596	- orf, hypothetical protein					21
b1857	znuA	987	1939675	1940661	- High-affinity zinc uptake system periplasmic protein	1		1		21
b1858	znuC	756	1940686	1941441	+ High-affinity zinc uptake system ATP-binding protein			1		21
b1859	znuB	786	1941438	1942223	+ High-affinity zinc uptake system membrane			1		21
b1860	ruvB	1011	1942370	1943380	- Holliday junction helicase subunit A;					21
b1861	ruvA	612	1943389	1944000	- branch migration; repair Holliday junction helicase subunit B;				1	21
b1862	yebB	702	1944176	1944877	+ orf, hypothetical protein	1		1	1	12
b1863	ruvC	522	1944879	1945400	- Holliday junction nuclease; resolution of structures; repair					21
b1864	yebC	741	1945435	1946175	- orf, hypothetical protein					20
b1865	ntpA	453	1946204	1946656	- dATP pyrophosphohydrolase					21
b1866	aspS	1773	1946774	1948546	- aspartate tRNA synthetase					21
b1867	yecD	600	1948823	1949422	+ orf, hypothetical protein					13
b1868	yecE	819	1949419	1950237	+ orf, hypothetical protein					16
b1869	yecN	426	1950260	1950685	+ orf, hypothetical protein					21
b1870	yecO	744	1950726	1951469	+ orf, hypothetical protein					21
b1871	yecP	972	1951466	1952437	+ putative enzyme					21
b1872	torZ	2448	1952602	1955049	- TMAO-reductase				1	21
b1873	torY	1101	1955056	1956156	- pentahaem c-type cytochrome	1			1	8
b1874	cutC	441	1956544	1956984	- copper homeostasis protein	1		1		20
b1875	yecM	573	1957304	1957876	- orf, hypothetical protein					21
b1876	argS	1734	1958086	1959819	+ arginine tRNA					21
b1877	yecT	510	1959975	1960484	+ orf, hypothetical protein	1		1	1	12
b1878	flhE	393	1960604	1960996	- flagellar protein	1				19
b1879	flhA	2079	1960996	1963074	- flagellar biosynthesis; possible export of flagellar proteins					17

b1880	flhB	1149	1963067	1964215	- putative part of export apparatus for flagellar proteins					20
b1881	cheZ	645	1964417	1965061	- chemotactic response; CheY protein phosphatase; antagonist of CheY as switch					20
b1882	cheY	390	1965072	1965461	- chemotaxis regulator transmits chemoreceptor signals to flagellar motor					20
b1883	cheB	1050	1965476	1966525	- response regulator for chemotaxis (cheA sensor); protein methylesterase					20
b1884	cheR	861	1966528	1967388	- response regulator for chemotaxis; protein glutamate methyltransferase					20
b1885	tap	1602	1967407	1969008	- methyl-accepting chemotaxis protein IV, peptide sensor receptor					11
b1886	tar	1662	1969054	1970715	- methyl-accepting chemotaxis protein II, aspartate sensor					12
b1887	cheW	504	1970860	1971363	- positive regulator of CheA protein activity					19
b1888	cheA	1965	1971384	1973348	- sensory transducer kinase between chemo-signal receptors and CheB and CheY					19
b1889	motB	927	1973353	1974279	- enables flagellar motor rotation, linking torque machinery to cell wall					20
b1890	motA	888	1974276	1975163	- proton conductor component of motor; no effect on switching					20
b1891	flhC	579	1975290	1975868	- regulator of flagellar biosynthesis acting on class 2 operons; transcription initiation factor?	1				20
b1892	flhD	360	1975871	1976230	- regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor?					16
b1893	insB_5	504	1976542	1977045	- IS1 protein InsB	1	1			15
b1894	insA_5	276	1976964	1977239	- IS1 protein InsA	1	1			15
b1895	yecG	429	1977777	1978205	+ putative regulator	1	1	1		13
b1896	otsA	1425	1978212	1979636	- trehalose-6-phosphate synthase					12
b1897	otsB	801	1979611	1980411	- trehalose-6-phosphate phosphatase,					13
b4460	araH	990	1980578	1981567	- high-affinity L-arabinose transport protein (ABC superfamily.					15
b1900	araG	1515	1981579	1983093	- ATP-binding component of high-affinity L-arabinose					15
b1901	araF	990	1983163	1984152	- L-arabinose-binding periplasmic protein				1	12
b1902	yecI	504	1984949	1985452	+ ferritin-like protein	1			1	15
b1903	-	339	1985468	1985806	+ orf, hypothetical protein				1	6
b1904	yecR	324	1986246	1986569	+ orf, hypothetical protein	1			1	15
b1905	ftn	498	1986740	1987237	+ cytoplasmic ferritin (an iron storage protein)				1	21
b1906	yecH	240	1987275	1987514	- orf, hypothetical protein		1		1	16
b1907	tyrP	1212	1987705	1988916	+ tyrosine-specific transport system					21
b1908	yecA	666	1988978	1989643	- orf, hypothetical protein					15
tRNA-Leu	tRNA-Leu	87	1989839	1989925	- tRNA-Leu					
tRNA-Cys	tRNA-Cys	74	1989938	1990011	- tRNA-Cys					

tRNA-Gly1 b1912	tRNA-Gly pgsA	76 1990066 1990141 549 1990293 1990841	- tRNA-Gly phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl-sn-glycero-3-phosphate						21
b1913	uvrC	1767 1990898 1992664	- excinuclease ABC, subunit C; repair of UV damage to DNA						21
b1914	uvrY	657 1992727 1993383	- putative 2-component transcriptional regulator				1		21
b1915	yecF	225 1993842 1994066	+ orf, hypothetical protein				1		20
b1916	sdhA	723 1994134 1994856	- transcriptional regulator of ftsQAZ gene cluster	1			1		20
b1917	yecC	753 1995086 1995838	- putative ATP-binding component of a transport system						20
b1918	yecS	669 1995835 1996503	- putative transport system permease protein (former vecC)						21
b1919	yedO	1083 1996518 1997600	- putative 1-aminocyclopropane-1-carboxylate deaminase						20
b1920	fliY	801 1997609 1998409	- putative periplasmic binding transport						20
b1921	fliZ	588 1998497 1999084	- orf, hypothetical protein	1					20
b1922	fliA	720 1999094 1999813	- flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons						19
b1923	fliC	1497 2000134 2001630	- flagellar biosynthesis; flagellin, filament structural protein	1					20
b1924	fliD	1407 2001896 2003302	+ flagellar biosynthesis; filament capping protein; enables filament assembly						21
b1925	fliS	411 2003327 2003737	+ flagellar biosynthesis; repressor of class 3a and 3b operons (RfIA)						21
b1926	fliT	366 2003737 2004102	+ flagellar biosynthesis; repressor of class 3a and 3b operons (RfIA)						19
b1927	amyA	1488 2004180 2005667	+ cytoplasmic alpha-amylase						15
b1928	yedD	414 2005701 2006114	- orf, hypothetical protein						15
b1929	yedE	1206 2006301 2007506	+ putative transport system permease						19
b1930	yedF	234 2007503 2007736	+ orf, hypothetical protein				1		19
b1931	yedK	669 2007845 2008513	+ orf, hypothetical protein				1		10
b1932	yedL	480 2008624 2009103	+ orf, hypothetical protein	1			1	1	4
b4495	yedL	192 2009372 2009563	-					1	
b1935	yedM	351 2010025 2010375	- orf, hypothetical protein	1			1	1	4
b1936	-	279 2010526 2010804	+ orf, hypothetical protein	1				1	4
b1937	fliE	315 2010724 2011038	- flagellar biosynthesis; basal-body component, possibly at (MS-ring)-rod junction						20
b1938	fliF	1659 2011253 2012911	+ flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein						18
b1939	fliG	996 2012904 2013899	+ flagellar biosynthesis; component of motor switching and energizing, enabling rotation and flagellar biosynthesis; export of flagellar proteins?						19
b1940	fliH	708 2013871 2014578	+ flagellar biosynthesis; export of flagellar proteins?						19
b1941	fliI	1374 2014578 2015951	+ flagellum-specific ATP synthase						19

b1942	fliJ	444	2015970	2016413	+ flagellar fliJ protein				19
b1943	fliK	1128	2016410	2017537	+ flagellar hook-length control protein				19
b1944	fliL	465	2017642	2018106	+ flagellar biosynthesis				20
b1945	fliM	1005	2018111	2019115	+ flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction				20
b1946	fliN	414	2019112	2019525	+ flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction				20
b1947	fliO	306	2019588	2019893	+ flagellar biosynthesis				20
b1948	fliP	738	2019893	2020630	+ flagellar biosynthesis				18
b1949	fliQ	270	2020640	2020909	+ flagellar biosynthesis				20
b1950	fliR	786	2020917	2021702	+ flagellar biosynthesis	1		1	20
b1951	rcsA	624	2021992	2022615	+ positive regulator for ctr capsule biosynthesis, positive transcription factor	1	1	1	19
b1952	dsrB	189	2022659	2022847	- orf, hypothetical protein			1	19
b1953	yodD	243	2022995	2023237	+ orf, hypothetical protein			1	14
b1955	yedP	816	2023535	2024350	+ orf, hypothetical protein				14
b1956	yedQ	1710	2024347	2026056	- orf, hypothetical protein				14
b1957	yodC	183	2026212	2026394	- orf, hypothetical protein				15
b1958	yedI	918	2026473	2027390	- orf, hypothetical protein				12
b1959	yedA	921	2027563	2028483	+ putative transmembrane subunit				18
b1960	vsr	471	2028472	2028942	- DNA mismatch endonuclease, patch repair protein				16
b1961	dcm	1419	2028923	2030341	- DNA cytosine				16
b1962	yedJ	696	2030408	2031103	- orf, hypothetical protein				14
b1963	yedR	384	2031143	2031526	- orf, hypothetical protein	1		1	12
b4496	yedS	516	2032045	2032560	+ -			1	
b1967	yedU	852	2033859	2034710	+ orf, hypothetical protein			1	9
b1968	yedV	1359	2034818	2036176	- putative 2-component sensor protein	1	1	1	19
b1969	yedW	720	2036176	2036895	- putative 2-component transcriptional regulator	1	1	1	20
b1970	yedX	414	2036980	2037393	+ orf, hypothetical protein	1	1	1	14
b1971	yedY	1005	2037502	2038506	+ putative reductase			1	17
b1972	yedZ	636	2038507	2039142	+ orf, hypothetical protein	1		1	20
b1973	yodA	651	2039399	2040049	+ orf, hypothetical protein	1	1	1	15
b1974	yodB	561	2040362	2040922	+ cytochrome b561 homolog 1	1	1	1	14
tRNA-Ser4	tRNA-Ser	90	2041492	2041581	- tRNA-Ser			1	
b1976	yeeI	837	2041636	2042472	+ orf, hypothetical protein	1	1		20
tRNA-Asn1	tRNA-Asn	76	2042573	2042648	+ tRNA-Asn				
b1978	yeeJ	7152	2042887	2050038	+ putative factor	1			9
b4497	yeeL	1053	2050300	2051352	- -			1	
b1981	shiA	1317	2051667	2052983	+ shikimate transporter			1	20
b1982	amn	1455	2053085	2054539	+ AMP nucleosidase		1	1	19
b1983	yeeN	717	2054882	2055598	+ orf, hypothetical protein	1	1	1	14
tRNA-Asn2	tRNA-Asn	76	2056051	2056126	- tRNA-Asn			1	
b1985	yeeO	1644	2056227	2057870	- orf, hypothetical protein	1			18
tRNA-Asn	tRNA-Asn	76	2057875	2057950	+ tRNA-Asn				
b1987	cbl	951	2057988	2058938	- transcriptional regulator cys regulon; accessory regulatory circuit	1			10
b1988	nac	918	2059040	2059957	- affecting cvsM nitrogen assimilation control protein	1			15
tRNA-Asn3	tRNA-Asn	76	2060284	2060359	+ tRNA-Asn				
b1990	erfK	933	2060415	2061347	- orf, hypothetical protein	1			14
b1991	cobT	1080	2061412	2062491	- nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl				16
b1992	cobS	744	2062503	2063246	- cobalamin 5'-phosphate synthase				16

b1993	cobU	546 2063243 2063788	- cobinamide kinase/cobinamide phosphate quanylvitransferase	1			14
b1994	trs5_6	1017 2064329 2065345	- IS5 transposase	1	1		2
b1995	-	420 2066632 2067051	+ orf, hypothetical protein	1	1	1	5
b1996	yi22_3	906 2066976 2067881	- IS2 hypothetical protein	1	1		18
b1997	yi21_3	411 2067839 2068249	- IS2 hypothetical protein	1	1		8
b1998	-	261 2068268 2068528	+ orf, hypothetical protein	1	1		5
b1999	yeeP	711 2068525 2069235	+ putative histone	1			9
b2000	flu	3120 2069563 2072682	+ antigen 43, phase-variable bipartite outer membrane fluffing	1			17
b2001	yeeR	1539 2072797 2074335	+ orf, hypothetical protein	1			5
b2002	yeeS	447 2074332 2074778	+ putative DNA repair protein, RADC family	1			11
b2003	yeeT	222 2074841 2075062	+ orf, hypothetical protein				8
b2004	yeeU	369 2075136 2075504	+ putative structural	1			11
b2005	yeeV	375 2075593 2075967	+ orf, hypothetical protein				11
b2006	yeeW	195 2075964 2076158	+ orf, hypothetical protein				5
b2007	yeeX	396 2077056 2077451	- putative alpha helix				21
b2008	yeeA	1059 2077557 2078615	- orf, hypothetical protein				13
b2009	sbmC	474 2078813 2079286	- SbmC protein				11
b2010	dacD	1173 2079405 2080577	- penicillin binding protein 6b				9
b2011	sbcB	1428 2080780 2082207	+ exonuclease I, 3' --> 5' specific; deoxyribophosphodiesterase				21
b2012	yeeD	228 2082250 2082477	- orf, hypothetical protein				9
b2013	yeeE	1059 2082491 2083549	- putative transport system permease			1	7
b2014	yeeF	1365 2083728 2085092	- putative amino acid/amine transport				21
b2015	yeeY	951 2085353 2086303	- putative transcriptional regulator LYSR-type				15
b2016	yeeZ	825 2086328 2087152	- putative enzyme of sugar metabolism				21
b2017	yefM	279 2087486 2087764	- orf, hypothetical protein	1			12
b2018	hisL	51 2088020 2088070	+ his operon leader				1
b2019	hisG	900 2088216 2089115	+ ATP phosphoribosyltransferase				21
b2020	hisD	1305 2089121 2090425	+ L-histidinol:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase				21
b2021	hisC	1071 2090422 2091492	+ histidinol-phosphate aminotransferase				21
b2022	hisB	1071 2091489 2092559	+ imidazoleglycerolphosphate dehydratase and histidinol-phosphate phosphatase				21
b2023	hisH	591 2092559 2093149	+ glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme				21
b2024	hisA	741 2093146 2093886	+ N-(5'-phospho-L-ribosyl-formimino)-5-amino-1- (5'-phosphoribosyl)-4-imidazolecarboxamide				21
b2025	hisF	777 2093868 2094644	+ imidazole glycerol phosphate synthase subunit in heterodimer with HisH = imidazole glycerol phosphate synthase holoenzyme				21

b2026	hisI	612	2094638	2095249	+ phosphoribosyl-amp cyclohydrolase;					21
b2027	wzzB	1017	2095345	2096361	- pyrophosphatase regulator of length of O- antigen component of			1		15
b2028	ugd	1167	2096471	2097637	- UDP-glucose 6- dehydrogenase	1		1		19
b2029	gnd	1407	2097886	2099292	- gluconate-6-phosphate dehydrogenase, decarboxylating			1		21
b2030	trs5_7	1017	2099919	2100935	- IS5 transposase	1	1	1		2
b2031	wbbL	474	2100940	2101413	- putative lipopolysaccharide biosynthesis glycosyl transferase	1	1	1		2
b2032	wbbK	1119	2101415	2102533	- putative glucose transferase	1	1	1		2
b2033	wbbJ	591	2102518	2103108	- putative O-acetyl transferase	1	1	1		5
b2034	wbbI	993	2103089	2104081	- putative Galf	1	1	1		2
b2035	wbbH	1167	2104084	2105250	- O-antigen polymerase	1	1	1		2
b2036	glf	1104	2105250	2106353	- UDP-galactopyranose mutase	1	1	1		6
b2037	rfbX	1248	2106361	2107608	- putative O-antigen transporter	1	1	1		6
b2038	rfbC	558	2107605	2108162	- dTDP-6-deoxy-D- glucose-3,5 epimerase	1	1	1		11
b2039	rfbA	882	2108162	2109043	- glucose-1-phosphate thymidyltransferase	1	1	1		10
b2040	rfbD	900	2109101	2110000	- dTDP-6-deoxy-L- mannose-	1	1	1		11
b2041	rfbB	1086	2110000	2111085	- dTDP-glucose 4,6 dehydratase	1	1	1		10
b2042	galF	894	2111458	2112351	- homolog of Salmonella UTP--glucose-1-P uridyltransferase, probably a UDP-gal orf, hypothetical protein			1		18
b2043	wcaM	1395	2112526	2113920	- putative colanic acid biosynthesis glycosyl transferase					13
b2044	wcaL	1221	2113931	2115151	- putative galactokinase probable export protein					14
b2045	wcaK	1281	2115148	2116428	- putative colanic acid biosynthesis UDP- glucose lipid carrier					10
b2046	wxC	1479	2116704	2118182	- phosphomannomutase			1		13
b2047	wcaJ	1395	2118184	2119578	- mannose-1-phosphate quanyltransferase			1		16
b2048	cpsG	1371	2119633	2121003	- putative colanic biosynthesis glycosyl transferase					19
b2049	cpsB	1437	2121108	2122544	- GDP-mannose mannosyl hydrolase					18
b2050	wcaI	1224	2122547	2123770	- putative nucleotide di- P-sugar epimerase or dehydratase					14
b2051	wcaH	483	2123767	2124249	- GDP-D-mannose dehydratase			1		14
b2052	wcaG	966	2124249	2125214	- putative transferase					17
b2053	gmd	1122	2125217	2126338	- putative colanic acid biosynthesis glycosyl transferase					15
b2054	wcaF	549	2126364	2126912	- putative colanic acid biosynthesis glycosyl transferase	1		1		14
b2055	wcaE	747	2126928	2127674	- putative colanic acid polymerase	1		1		16
b2056	wcaD	1218	2127685	2128902	- putative glycosyl transferase	1		1		10
b2057	wcaC	1218	2128877	2130094	- putative transferase			1		13
b2058	wcaB	489	2130091	2130579	- putative regulator			1		15
b2059	wcaA	840	2130582	2131421	- tyrosine-protein kinase			1		12
b2060	wzc	2199	2131514	2133712				1		17

b2061	wzb	444 2133679 2134122	- low molecular weight protein-tyrosine-phosphatase			1	17
b2062	wza	1140 2134128 2135267	- putative polysaccharide export protein			1	17
b2063	yegH	1650 2135860 2137509	+ putative transport			1	21
b2064	asmA	1854 2137783 2139636	- suppressor of ompF assembly mutants				21
b2065	dcd	582 2139658 2140239	- 2'-deoxycytidine 5'-triphosphate deaminase				21
b2066	udk	696 2140331 2141026	- uridine/cytidine kinase				21
b2067	yegE	3318 2141290 2144607	+ putative sensor-type protein				12
b2068	alkA	849 2144716 2145564	- 3-methyl-adenine DNA glycosylase II, inducible				21
b2069	yegD	1416 2145635 2147050	+ putative heat shock protein				18
b2070	yegI	1947 2147063 2149009	- putative chaperonin	1		1	9
b2071	yegJ	462 2149209 2149670	+ orf, hypothetical protein	1	1	1	2
b2072	yegK	762 2149735 2150496	- orf, hypothetical protein				10
b2073	yegL	660 2150493 2151152	- orf, hypothetical protein				14
b2074	yegM	1395 2151893 2153287	+ putative membrane protein				18
b2075	yegN	3123 2153287 2156409	+ orf, hypothetical protein				18
b2076	yegO	3078 2156410 2159487	+ orf, hypothetical protein				20
b2077	yegB	1416 2159488 2160903	+ putative transport				19
b2078	baeS	1404 2160900 2162303	+ sensor protein (for				19
b2079	baeR	723 2162300 2163022	+ transcriptional response regulatory protein (sensor BaeS)				21
b2080	yegP	372 2163174 2163545	+ orf, hypothetical protein				14
b2081	yegQ	1362 2163692 2165053	+ orf, hypothetical protein				21
b2082	ogrK	219 2165326 2165544	- prophage P2 ogr	1	1	1	15
b2083	-	147 2165626 2165772	- orf, hypothetical protein	1	1	1	12
b2084	-	267 2165759 2166025	- orf, hypothetical protein	1	1	1	2
b2085	yegR	378 2166013 2166390	- orf, hypothetical protein	1	1	1	10
b2086	yegS	900 2166736 2167635	+ orf, hypothetical protein		1	1	17
b4498	gatR	2041 2167717 2169757	- -			1	
b2091	gatD	1041 2169857 2170897	- galactitol-1-phosphate dehydrogenase	1		1	15
b2092	gatC	1356 2170945 2172300	- PTS system galactitol-specific enzyme IIC			1	15
b2093	gatB	285 2172304 2172588	- galactitol-specific enzyme IIB of phosphotransferase		1	1	15
b2094	gatA	453 2172619 2173071	- galactitol-specific enzyme IIA of phosphotransferase	1	1	1	13
b2095	gatZ	1263 2173081 2174343	- putative tagatose 6-phosphate kinase 1			1	10
b2096	gatY	861 2174372 2175232	- tagatose-bisphosphate aldolase 1			1	21
b2097	fbaB	1125 2175534 2176658	- fructose-bisphosphate aldolase class I				16
b2098	yegT	1278 2176843 2178120	+ putative nucleoside permease protein				14
b2099	yegU	1005 2178117 2179121	+ orf, hypothetical protein				13
b2100	yegV	966 2179118 2180083	+ putative kinase				16
b2101	yegW	747 2180057 2180803	- putative transcriptional regulator				19
b2102	yegX	828 2180855 2181682	- orf, hypothetical protein	1			10
b2103	thiD	801 2181738 2182538	- phosphomethylpyrimidine kinase				21
b2104	thiM	789 2182535 2183323	- hydroxyethylthiazole	1			16
b2105	yohL	273 2183546 2183818	- orf, hypothetical protein				14
b2106	yohM	825 2183939 2184763	+ orf, hypothetical protein	1			15
b2107	yohN	519 2184802 2185320	+ orf, hypothetical protein	1		1	13
b2108	yehA	1035 2185402 2186436	- putative type-1 fimbrial protein	1	1	1	13
b2109	yehB	2481 2186452 2188932	- putative outer membrane protein	1	1	1	13
b2110	yehC	720 2188948 2189667	- putative chaperone	1	1	1	12

b2111	yehD	543 2189702 2190244	- putative fimbrial-like protein	1	1	1	13
b2112	yehE	282 2190537 2190818	- orf, hypothetical protein	1	1	1	13
b2113	mrp	1140 2191081 2192220	- putative ATPase				21
b2114	metG	2034 2192322 2194355	+ methionine tRNA synthetase				21
b4499	molR	3796 2194496 2198291	+ -			1	
b2118	yehI	3633 2198301 2201933	+ putative regulator	1			8
b2119	yehL	1155 2202552 2203706	+ orf, hypothetical protein			1	8
b2120	yehM	2280 2203717 2205996	+ orf, hypothetical protein				8
b2121	yehP	1137 2205989 2207125	+ orf, hypothetical protein				9
b2122	yehQ	1869 2207098 2208966	+ orf, hypothetical protein				10
b2123	yehR	474 2209235 2209708	+ orf, hypothetical protein				15
b2124	yehS	471 2209748 2210218	- orf, hypothetical protein				19
b2125	yehT	735 2210265 2210999	- orf, hypothetical protein				21
b2126	yehU	1686 2210981 2212666	- putative 2-component sensor protein				20
b2127	yehV	732 2212888 2213619	+ putative transcriptional regulator				13
b2128	yehW	732 2213767 2214498	- putative transport system permease				19
b2129	yehX	927 2214503 2215429	- putative ATP-binding component of a transport system				18
b2130	yehY	1158 2215422 2216579	- putative transport system permease				18
b2131	yehZ	918 2216586 2217503	- putative transport system permease				17
b2132	bglX	2298 2217714 2220011	- beta-D-glucoside glucohydrolase, periplasmic				20
b2133	dld	1716 2220207 2221922	+ D-lactate dehydrogenase, FAD protein, NADH				21
b2134	pbpG	942 2221960 2222901	- penicillin-binding				18
b2135	yohC	612 2223066 2223677	- orf, hypothetical protein				19
b2136	yohD	615 2223787 2224401	+ orf, hypothetical protein				15
b2137	yohF	762 2224531 2225292	- putative oxidoreductase				13
b2138	yohG	1197 2225345 2226541	- putative channel/filament				13
b2139	yohH	291 2226571 2226861	- orf, hypothetical protein	1		1	11
b2140	yohI	948 2227460 2228407	- putative regulator				20
b2141	yohJ	399 2228646 2229044	+ orf, hypothetical protein				21
b2142	yohK	696 2229041 2229736	+ putative serotonin transporter				21
b2143	cdd	885 2229866 2230750	+ cytidine/deoxycytidine deaminase				21
b2144	sanA	720 2230900 2231619	+ vancomycin sensitivity		1	1	21
b2145	yeiS	240 2231622 2231861	+ orf, hypothetical protein	1	1	1	15
b2146	yeiT	1239 2232055 2233293	+ putative oxidoreductase			1	14
b2147	yeiA	1242 2233281 2234522	+ putative oxidoreductase				10
b2148	mglC	1011 2234765 2235775	- methyl-galactoside transport and galactose taxis			1	19
b2149	mglA	1521 2235791 2237311	- ATP-binding component of methyl-galactoside transport and galactose taxis			1	14
b2150	mglB	999 2237372 2238370	- galactose-binding transport protein; receptor for galactose				19
b2151	galS	1041 2238650 2239690	- mgl repressor, galactose operon				15
b2152	yeiB	1158 2239832 2240989	- orf, hypothetical protein				21
b2153	folE	669 2241006 2241674	- GTP cyclohydrolase I				21
b2154	yeiG	837 2241932 2242768	+ putative esterase				17
b2155	cirA	1992 2242800 2244791	- outer membrane receptor for iron-regulated colicin I				16
b2156	lysP	1470 2245085 2246554	- lysine-specific				21
b2157	yeiE	882 2246759 2247640	- putative transcriptional regulator LYSR-type				21

b2158	yeiH	1050 2247739 2248788	+ orf, hypothetical protein				21
b2159	nfo	858 2248862 2249719	+ endonuclease IV				21
b2160	yeiI	1089 2249722 2250810	+ putative kinase				10
b2161	yeiJ	1251 2250917 2252167	- putative pyrimidine nucleoside transporter				16
b2162	rihB	942 2252267 2253208	- pyrimidine specific nucleoside hydrolase			1	10
b2163	yeiL	660 2253377 2254036	+ stationary phase nitrogen starvation	1		1	10
b2164	yeiM	1251 2254107 2255357	- putative transport system permease			1	16
b2165	yeiN	939 2255451 2256389	- orf, hypothetical protein			1	9
b2166	yeiC	942 2256377 2257318	- putative kinase	1		1	9
b2167	fruA	1692 2257741 2259432	- PTS system, fructose-specific transport				21
b2168	fruK	939 2259449 2260387	- fructose-1-phosphate kinase				21
b2169	fruB	1131 2260387 2261517	- PTS system, fructose-specific IIA/fpr				21
b2170	setB	1182 2261885 2263066	+ sugar efflux protein				16
b2171	yeiP	828 2263217 2264044	+ putative elongation	1			20
b2172	yeiQ	1467 2264267 2265733	+ putative oxidoreductase				15
b2173	yeiR	987 2265851 2266837	+ orf, hypothetical protein				20
b2174	yeiU	750 2266840 2267589	+ orf, hypothetical protein	1			21
b2175	spr	567 2268001 2268567	+ putative lipoprotein	1			21
b2176	rtn	1557 2268748 2270304	+ orf, hypothetical protein				19
b2177	yejA	1821 2270380 2272200	+ orf, hypothetical protein				20
b2178	yejB	1095 2272201 2273295	+ putative transport system permease				20
b2179	yejE	1026 2273295 2274320	+ putative transport system permease				20
b2180	yejF	1590 2274322 2275911	+ putative ATP-binding component of a transport system				20
b2181	yejG	345 2275915 2276259	- orf, hypothetical protein				21
b2182	bcr	1191 2276592 2277782	- bicyclomycin resistance protein; transmembrane protein				19
b2183	rsuA	696 2277810 2278505	- 16S pseudouridylate 516 synthase				21
b2184	yejH	1761 2278654 2280414	+ putative ATP-dependent helicase				21
b2185	rpLY	285 2280539 2280823	+ 50S ribosomal subunit protein L25				21
b2186	yejK	1008 2280962 2281969	- protein present in spermidine nucleoids				21
b2187	yejL	228 2282151 2282378	+ orf, hypothetical protein				21
b2188	yejM	1761 2282398 2284158	+ putative sulfatase				21
tRNA-Pro1		77 2284233 2284309	+ tRNA-Pro				
b2190	yejO	2511 2284412 2286922	- putative ATP-binding component of a transport system	1			19
b2191	-	123 2286927 2287049	+ orf, hypothetical protein	1		1	1
b2192	trs5_8	1017 2287087 2288103	- IS5 transposase	1		1	2
b2193	narP	648 2288522 2289169	+ nitrate/nitrite response regulator (sensor NarQ)				21
b2194	ccmH	1053 2289380 2290432	- possible subunit of heme lyase				20
b2195	ccmG	558 2290429 2290986	- heme lyase/disulfide oxidoreductase (thiol:disulfide interchange protein)				20
b2196	ccmF	1944 2290983 2292926	- cytochrome c-type biogenesis protein				20
b2197	ccmE	480 2292923 2293402	- cytochrome c biogenesis, possible subunit of a heme lyase				20
b2198	ccmD	210 2293399 2293608	- heme exporter protein				20
b2199	ccmC	738 2293605 2294342	- heme exporter protein				20
b2200	ccmB	663 2294384 2295046	- heme exporter protein B, cytochrome c-type biogenesis protein				20

b2201	ccmA	618 2295043 2295660	- ATP binding protein of heme exporter A			20
b2202	napC	603 2295679 2296281	- cytochrome c-type			20
b2203	napB	471 2296291 2296761	- cytochrome c-type			20
b2204	napH	864 2296737 2297600	- ferredoxin-type protein: electron transfer			16
b2205	napG	696 2297587 2298282	- ferredoxin-type protein: electron transfer			16
b2206	napA	2487 2298289 2300775	- probable nitrate reductase 3			19
b2207	napD	264 2300772 2301035	- orf, hypothetical protein			20
b2208	napF	495 2301025 2301519	- ferredoxin-type protein: electron transfer	1		19
b2209	eco	489 2301927 2302415	+ ecotin, a serine protease inhibitor			18
b2210	mgo	1647 2303130 2304776	- malate:quinone oxidoreductase			9
b2211	yoiJ	1644 2304994 2306637	- putative ATP-binding component of a transport system			17
b2212	alkB	651 2306713 2307363	- DNA repair system specific for alkylated			16
b2213	ada	1065 2307363 2308427	- O6-methylguanine-DNA methyltransferase; transcription activator/repressor	1		21
b2214	yoiL	1056 2308501 2309556	- orf, hypothetical protein			21
b2215	ompC	1104 2309668 2310771	- outer membrane protein 1b (lb;c)		1	21
b2216	yoiN	2673 2311510 2314182	+ putative 2-component sensor protein			19
b2217	rscB	651 2314199 2314849	+ positive response regulator for colanic capsule biosynthesis, (sensor. RcsC)			21
b2218	rscC	2802 2315049 2317850	- sensor for ctr capsule biosynthesis, probable histidine kinase acting on RcsB			21
b2219	atoS	1827 2318065 2319891	+ sensor protein AtoS for response regulator			4
b2220	atoC	1386 2319888 2321273	+ response regulator of ato, ornithine decarboxylase antizyme			4
b2221	atoD	663 2321469 2322131	+ acetyl-CoA:acetoacetyl-CoA transferase alpha subunit			11
b2222	atoA	651 2322131 2322781	+ acetyl-CoA:acetoacetyl-CoA transferase beta subunit			
b2223	atoE	1323 2322778 2324100	+ short chain fatty acid transporter			4
b2224	atoB	1185 2324131 2325315	+ acetyl-CoA acetyltransferase			5
b2225	yfaP	777 2325389 2326165	- orf, hypothetical protein			10
b2226	yfaQ	1650 2326170 2327819	- orf, hypothetical protein			10
b4500	yfaS	4515 2327820 2332334	-			
b2229	yfaT	651 2332358 2333008	- orf, hypothetical protein	1		8
b2230	yfaA	1737 2332978 2334714	- orf, hypothetical protein			6
b2231	gyrA	2628 2334815 2337442	- DNA gyrase, subunit A, type II topoisomerase			21
b2232	ubiG	723 2337589 2338311	+ 3-demethylubiquinone-9 3-methyltransferase and 2-octaprenyl-6-hydroxy phenol			21
b2233	yfaL	3753 2338439 2342191	- putative ATP-binding component of a transport system	1	1	17
b2234	nrdA	2286 2342887 2345172	+ ribonucleoside diphosphate reductase 1, alpha subunit. B1			21

b2235	nrdB	1131	2345406	2346536	+ ribonucleoside-diphosphate reductase 1, beta subunit, B2				21
b2236	yfaE	255	2346536	2346790	+ orf, hypothetical protein				21
b2237	inaA	651	2346844	2347494	- pH-inducible protein involved in stress response				9
b2238	yfaH	207	2347709	2347915	+ orf, hypothetical protein	1	1		14
b2239	glpQ	1077	2347957	2349033	- glycerophosphodiester phosphodiesterase, periplasmic				21
b2240	glpT	1359	2349038	2350396	- sn-glycerol-3-phosphate permease				17
b2241	glpA	1629	2350669	2352297	+ sn-glycerol-3-phosphate dehydrogenase				20
b2242	glpB	1260	2352287	2353546	+ sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane				20
b2243	glpC	1191	2353543	2354733	+ sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small				21
b2244	yfaD	900	2354926	2355825	+ orf, hypothetical protein				13
b2245	-	804	2356064	2356867	- orf, hypothetical protein				16
b2246	yfaV	1329	2356885	2358213	- putative transport				19
b2247	yfaW	1218	2358231	2359448	- putative racemase				12
b2248	yfaX	783	2359451	2360233	- putative regulator				18
b2249	-	1203	2360453	2361655	- orf, hypothetical protein				18
b2250	yfaZ	564	2361755	2362318	- orf, hypothetical protein			1	13
b2251	yfaO	426	2362576	2363001	+ orf, hypothetical protein			1	14
b2252	ais	603	2363040	2363642	- protein induced by aluminum	1	1	1	21
b2253	yfbE	1173	2363917	2365089	+ putative enzyme			1	21
b2254	yfbF	969	2365093	2366061	+ putative sugar				20
b2255	yfbG	1983	2366061	2368043	+ putative transformylase				21
b2256	-	891	2368040	2368930	+ orf, hypothetical protein				21
b2257	arnT	1653	2368930	2370582	+ 4-amino-4-deoxy-L-arabinose transferase (lipid A modification)				21
b2258	yfbJ	669	2370632	2371300	+ putative transport/receptor	1			13
b2259	pmrD	297	2371294	2371590	- polymyxin resistance protein B	1			21
b2260	menE	1356	2371670	2373025	- o-succinylbenzoate-CoA liqase				21
b2261	menC	963	2373022	2373984	- o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA				21
b2262	menB	858	2373984	2374841	- dihydroxynaphtic acid synthetase				21
b2263	yfbD	759	2374856	2375614	- putative enzyme				21
b2264	menD	1671	2375611	2377281	- 2-oxoglutarate decarboxylase; SHCHC synthase				21
b2265	menF	1071	2377370	2378440	- isochorismate hydroxymutase 2, menaquinone biosynthesis				21
b2266	elaB	306	2378744	2379049	- orf, hypothetical protein			1	20
b2267	elaA	462	2379104	2379565	- orf, hypothetical protein			1	16
b2268	elaC	936	2379612	2380547	+ orf, hypothetical protein			1	15
b2269	elaD	1212	2380735	2381946	+ putative sulfatase / phosphatase	1	1	1	9
b2270	yfbK	1728	2382017	2383744	- orf, hypothetical protein	1	1	1	9
b2271	yfbL	978	2383876	2384853	+ putative	1	1	1	6
b2272	yfbM	504	2384956	2385459	+ orf, hypothetical protein		1	1	9
b2273	yfbN	717	2385732	2386448	- orf, hypothetical protein	1	1	1	2
b2274	-	477	2386603	2387079	+ orf, hypothetical protein	1	1	1	2
b2275	-	852	2387135	2387986	+ orf, hypothetical protein	1	1	1	2

b2276	nuoN	1278 2388070 2389347	- NADH dehydrogenase I chain N	21
b2277	nuoM	1530 2389534 2391063	- NADH dehydrogenase I chain M	21
b2278	nuoL	1842 2391227 2393068	- NADH dehydrogenase I chain L	21
b2279	nuoK	303 2393065 2393367	- NADH dehydrogenase I chain K	21
b2280	nuoJ	555 2393364 2393918	- NADH dehydrogenase I chain J	21
b2281	nuoI	543 2393930 2394472	- NADH dehydrogenase I chain I	21
b2282	nuoH	978 2394487 2395464	- NADH dehydrogenase I chain H	21
b2283	nuoG	2733 2395461 2398193	- NADH dehydrogenase I chain G	21
b2284	nuoF	1338 2398240 2399577	- NADH dehydrogenase I chain F	21
b2285	nuoE	501 2399574 2400074	- NADH dehydrogenase I chain E	21
b2286	nuoC	1803 2400077 2401879	- NADH dehydrogenase I chain C, D	21
b2287	nuoB	663 2401973 2402635	- NADH dehydrogenase I chain B	21
b2288	nuoA	444 2402651 2403094	- NADH dehydrogenase I chain A	21
b2289	lrhA	939 2403725 2404663	- NADH dehydrogenase transcriptional regulator, LysR family; modulates SsrE(RssB)	21
b2290	yfbQ	1218 2405583 2406800	+ putative	21
b2291	-	600 2406884 2407483	+ putative alpha helix	20
b2292	yfbS	1833 2407542 2409374	- putative transport	21
b2293	yfbT	669 2409461 2410129	- putative phosphatase	19
b2294	yfbU	513 2410122 2410634	- orf, hypothetical protein	20
b2295	-	456 2410699 2411154	- orf, hypothetical protein	21
b2296	ackA	1203 2411492 2412694	+ acetate kinase	21
b2297	pta	2145 2412769 2414913	+ phosphotransacetylase	21
b2298	yfcC	1542 2415082 2416623	+ putative S-transferase	15
b2299	-	543 2416656 2417198	- putative regulator	21
b2300	yfcE	555 2417256 2417810	- orf, hypothetical protein	20
b2301	yfcF	645 2417863 2418507	- orf, hypothetical protein	16
b2302	yfcG	648 2418643 2419290	+ putative S-transferase	17
b2303	folX	363 2419347 2419709	+ D-erythro-7,8-dihydroneopterin tri P epimerase	11
b2304	yfcH	894 2419730 2420623	+ putative sugar nucleotide epimerase	21
b2305	yfcI	891 2420671 2421561	- orf, hypothetical protein	21
b2306	hisP	774 2421758 2422531	- ATP-binding component of histidine	20
b2307	hisM	717 2422539 2423255	- histidine transport, membrane protein M	20
b2308	hisQ	687 2423252 2423938	- histidine transport system permease	20
b2309	hisJ	783 2424028 2424810	- histidine-binding periplasmic protein of high-affinity histidine transport system	20
b2310	argT	783 2425031 2425813	- lysine-, arginine-, ornithine-binding periplasmic protein	14
b2311	ubiX	570 2426079 2426648	- 3-octaprenyl-4-hydroxybenzoate carboxylase	21
b2312	purF	1518 2426743 2428260	- amidophosphoribosyltransferase = PRPP amidotransferase	21
b2313	cvpA	489 2428297 2428785	- membrane protein required for colicin V production	21
b2314	dedD	636 2429044 2429679	- putative lipoprotein	21

b2315	folC	1269 2429696 2430964	- dihydrofolate:folylpolyglutaminate synthetase;					21
b2316	accD	915 2431034 2431948	- dihydrofolate acetylCoA carboxylase, carboxytransferase component, beta					21
b2317	dedA	660 2432104 2432763	- orf, hypothetical protein					21
b2318	truA	813 2432846 2433658	- pseudouridylate synthase I					21
b2319	usg	1014 2433658 2434671	- putative PTS system enzyme II A component					21
b2320	pdxB	1137 2434737 2435873	- erythronate-4-phosphate					21
b2321	flk	996 2435972 2436967	+ flagellar assembly					20
b2322	-	1179 2436964 2438142	- putative transport					13
b2323	fabB	1221 2438407 2439627	- 3-oxoacyl-[acyl-carrier-protein] synthase I					21
b2324	-	2067 2439726 2441792	+ putative peptidase					21
b2325	yfcL	279 2441913 2442191	- orf, hypothetical protein					21
b2326	yfcM	549 2442225 2442773	- putative transporting ATPase					19
b2327	yfcA	810 2442773 2443582	- putative structural					20
b2328	mepA	825 2443582 2444406	- murein DD-endopeptidase,					20
b2329	aroC	1086 2444410 2445495	- penicillin-insensitive chorismate synthase					21
b2330	yfcB	1266 2445530 2446795	- putative adenine-specific methylase	1				21
b2331	yfcN	552 2446628 2447179	+ orf, hypothetical protein					21
b2332	yfcO	837 2447250 2448086	- orf, hypothetical protein	1				12
b2333	yfcP	540 2448073 2448612	- putative fimbrial-like protein					16
b2334	yfcQ	489 2448609 2449097	- orf, hypothetical protein					15
b2335	yfcR	513 2449094 2449606	- putative fimbrial protein	1				13
b2336	yfcS	753 2449606 2450358	- putative chaperone					19
b2337	yfcT	897 2450378 2451274	- putative outer membrane protein					19
b2338	yfcU	1737 2451287 2453023	- putative outer membrane protein				1	19
b2339	yfcV	564 2453105 2453668	- putative fimbrial-like protein				1	12
b2340	sixA	486 2454349 2454834	- phosphohistidine phosphatase				1	21
b2341	yfcX	2145 2455037 2457181	- putative enzyme				1	21
b2342	yfcY	1311 2457181 2458491	- putative acyltransferase				1	21
b2343	yfcZ	309 2458672 2458980	- orf, hypothetical protein				1	19
b2344	fadL	1347 2459322 2460668	+ long-chain fatty acid transport protein (outer membrane flp protein)				1	21
b2345	-	1059 2461034 2462092	+ orf, hypothetical protein	1	1		1	6
b2346	vacJ	756 2462274 2463029	- lipoprotein precursor				1	21
b2347	yfcC	933 2463323 2464255	- putative transport				1	16
tRNA-Arg2	tRNA-Arg	75 2464331 2464405	+ tRNA-Arg				1	
b2349	intS	1158 2464567 2465724	+ putative prophage CPS-53 integrase	1	1		1	16
b2350	yfdG	363 2465877 2466239	+ bactoprenol-linked glucose translocase homolog from prophage CPS-53	1	1		1	9
b2351	yfdH	921 2466236 2467156	+ bactoprenol glucosyl transferase homolog from prophage CPS-53	1	1		1	9
b2352	yfdI	1332 2467153 2468484	+ putative ligase	1	1		1	2
b2353	tfaS	345 2468783 2469127	+ tail fiber assembly protein homolog from prophage CPS-53		1		1	2
b2354	yfdK	441 2469099 2469539	- orf, hypothetical protein		1		1	10
b2355	yfdL	519 2469566 2470084	- putative RNA polymerase beta	1			1	10
b2356	yfdM	309 2470134 2470442	- orf, hypothetical protein				1	9
b2357	yfdN	495 2470409 2470903	- orf, hypothetical protein	1			1	4
b2358	yfdO	369 2470900 2471268	- orf, hypothetical protein				1	5
b2359	yfdP	447 2471542 2471988	+ orf, hypothetical protein				1	4

b2360	yfdQ	825	2472054	2472878	+	orf, hypothetical protein		1	1	4
b2361	yfdR	564	2472979	2473542	+	orf, hypothetical protein	1	1	1	3
b2362	yfdS	363	2473533	2473895	+	orf, hypothetical protein	1	1	1	3
b2363	yfdT	306	2473895	2474200	+	orf, hypothetical protein		1	1	5
b2364	dsdC	936	2474716	2475651	-	D-serine dehydratase (deaminase)	1		1	9
						transcriptional activator				
b2365	dsdX	1338	2475869	2477206	+	transport system			1	9
						permease (serine?)				
b2366	dsdA	1329	2477224	2478552	+	D-serine dehydratase (deaminase)			1	16
b2367	emrY	1539	2478660	2480198	-	multidrug resistance protein Y	1	1	1	10
b2368	emrK	1164	2480198	2481361	-	multidrug resistance protein K	1	1	1	10
b2369	evgA	615	2481777	2482391	+	putative positive transcription regulator (sensor EvgS)	1	1	1	19
b2370	evgS	3594	2482396	2485989	+	putative sensor for regulator EvgA	1	1	1	14
b2371	yfdE	1185	2486045	2487229	-	putative enzyme	1	1	1	10
b2372	yfdV	945	2487264	2488208	-	putative receptor	1	1	1	15
b2373	yfdU	1695	2488278	2489972	-	probable oxalyl-CoA decarboxylase	1	1	1	10
b2374	yfdW	1251	2490026	2491276	-	putative enzyme		1	1	10
b2375	yfdX	636	2491789	2492424	-	orf, hypothetical protein	1	1	1	15
b2376	ypdI	276	2492720	2492995	+	orf, hypothetical protein	1		1	9
b2377	yfdY	243	2493072	2493314	-	orf, hypothetical protein			1	15
b2378	ddg	987	2493601	2494587	+	putative heat shock protein			1	20
b2379	yfdZ	1239	2495079	2496317	-	putative			1	20
b2380	ypdA	1698	2496693	2498390	+	putative sensor protein			1	8
b2381	ypdB	735	2498405	2499139	+	putative 2-component transcriptional regulator				10
b2382	ypdC	858	2499152	2500009	+	putative ARAC-type regulatory protein				8
b2383	ypdD	2496	2500012	2502507	-	putative PTS system enzyme IIA component, enzyme I				8
b2384	ypdE	1038	2502532	2503569	-	orf, hypothetical protein				15
b2385	ypdF	1086	2503569	2504654	-	putative peptidase				7
b2386	ypdG	1248	2504669	2505916	-	putative PTS system enzyme IIC component				10
b2387	ypdH	327	2505938	2506264	-	putative PTS system enzyme IIB component				10
b2388	glk	966	2506483	2507448	-	glucokinase				21
b2389	yfeO	1257	2507652	2508908	+	orf, hypothetical protein				14
b2390	ypeC	327	2509023	2509349	+	orf, hypothetical protein				20
b2392	mntH	1239	2509490	2510728	-	high-affinity manganese transporter				20
b2393	nupC	1203	2511064	2512266	+	permease of transport system for 3				20
b2394	yi81_3	1119	2512347	2513465	+	putative transposase insL for insertion sequence IS186	1	1		5
b2395	yfeA	2307	2513665	2515971	-	orf, hypothetical protein	1			11
tRNA-Ala2	tRNA-Ala	76	2516063	2516138	-	tRNA-Ala				
tRNA-Ala3	tRNA-Ala	76	2516178	2516253	-	tRNA-Ala				
b2398	yfeC	360	2516474	2516833	+	orf, hypothetical protein		1		15
b2399	yfeD	393	2516835	2517227	+	orf, hypothetical protein	1	1		15
b2400	gltX	1416	2517279	2518694	-	glutamate tRNA synthetase, catalytic subunit				21
tRNA-Val4	tRNA-Val	76	2518953	2519028	+	tRNA-Val				
tRNA-Val5	tRNA-Val	76	2519073	2519148	+	tRNA-Val				
tRNA-Val6	tRNA-Val	76	2519195	2519270	+	tRNA-Val				
tRNA-Lys	tRNA-Lys	76	2519275	2519350	+	tRNA-Lys				
b2405	xapR	885	2519615	2520499	-	regulator for xapA	1		1	10
b2406	xapB	1257	2520751	2522007	-	xanthosine permease			1	8
b2407	xapA	834	2522067	2522900	-	xanthosine			1	10
b2408	yfeN	765	2523149	2523913	+	putative sugar			1	12
b2409	yfeR	927	2523952	2524878	-	putative transcriptional regulator LYSR-type				14

b2410	yfeH	999 2524968 2525966	+ putative cytochrome oxidase			21
b2411	ligA	2016 2526183 2528198	- DNA ligase			21
b2412	zipA	987 2528269 2529255	- cell division protein involved in FtsZ ring	1		21
b2413	cysZ	762 2529485 2530246	+ required for sulfate transport			21
b2414	cysK	972 2530431 2531402	+ cysteine synthase A, O-acetylserine sulphydrolase A			21
b2415	ptsH	258 2531786 2532043	+ PTS system protein			21
b2416	ptsI	1728 2532088 2533815	+ PEP-protein phosphotransferase system enzyme I			20
b2417	crr	510 2533856 2534365	+ PTS system, glucose-specific IIA component			21
b2418	pdxK	852 2534408 2535259	- pyridoxal/pyridoxine/pyridoxamine kinase			14
b2419	yfeK	375 2535364 2535738	+ orf, hypothetical protein			15
b2420	yfeS	735 2535771 2536505	+ orf, hypothetical protein	1	1	2
b2421	cysM	912 2536694 2537605	- cysteine synthase B, O-acetylserine sulphydrolase B			21
b2422	cysA	1098 2537739 2538836	- ATP-binding component of sulfate permease A protein; chromate resistance			20
b2423	cysW	450 2538826 2539275	- sulfate transport system permease W protein			20
b2424	cysU	834 2539701 2540534	- sulfate, thiosulfate transport system permease T protein			21
b2425	cysP	1017 2540534 2541550	- thiosulfate binding			21
b2426	ucpA	858 2541854 2542711	- putative oxidoreductase			19
b2427	yfeT	858 2542774 2543631	- orf, hypothetical protein			9
b2428	yfeU	897 2543795 2544691	+ putative regulator			21
b2429	yfeV	1425 2544695 2546119	+ putative PTS enzyme IIBC component			15
b2430	yfeW	1392 2546037 2547428	+ putative beta-lactamase			12
b2431	yfeX	927 2547668 2548594	- orf, hypothetical protein			20
b2432	yfeY	576 2548663 2549238	- orf, hypothetical protein			21
b2433	yfeZ	456 2549299 2549754	- orf, hypothetical protein			15
b2434	ypeA	537 2549735 2550271	- orf, hypothetical protein	1		21
b2435	amiA	870 2550374 2551243	+ N-acetylmuramoyl-L-alanine amidase I			15
b2436	hemF	900 2551247 2552146	+ coproporphyrinogen III oxidase			20
b2437	yfeG	1053 2552152 2553204	- putative ARAC-type regulatory protein			14
b2438	yffI	507 2553250 2553756	- orf, hypothetical protein	1		14
b2439	eutL	660 2553763 2554422	- orf, hypothetical protein			15
b2440	eutC	888 2554432 2555319	- ethanolamine ammonia-lyase, light			13
b2441	eutB	1404 2555340 2556743	- ethanolamine ammonia-lyase, heavy			12
b2442	intZ	1296 2556793 2558088	+ putative prophage integrase	1	1	16
b2443	-	642 2558279 2558920	+ orf, hypothetical protein	1	1	1
b2444	-	246 2559390 2559635	+ orf, hypothetical protein	1	1	1
b2445	-	384 2559632 2560015	+ orf, hypothetical protein	1	1	1
b2446	yffO	417 2560133 2560549	+ orf, hypothetical protein	1	1	1
b2447	-	594 2560546 2561139	+ orf, hypothetical protein	1	1	1
b2448	-	393 2561599 2561991	+ orf, hypothetical protein	1	1	1
b2449	-	393 2562002 2562394	+ orf, hypothetical protein	1	1	1
b2450	-	840 2562515 2563354	+ orf, hypothetical protein	1	1	1
b2451	eutA	1404 2563503 2564906	- orf, hypothetical protein			12
b2452	eutH	1227 2564903 2566129	- ethanolamine utilization; homolog of Salmonella putative			11

b2453	eutG	1215 2566346 2567560	- ethanolamine utilization; homolog of Salmonella enzyme, similar to iron-containing alcohol		11
b2454	eutJ	837 2567523 2568359	- ethanolamine utilization; homolog of Salmonella gene		12
b2455	eutE	1404 2568370 2569773	- ethanolamine utilization; similar to acetaldehyde		12
b2456	cchB	288 2569785 2570072	- detox protein		12
b2457	cchA	336 2570179 2570514	- detox protein		12
b2458	eutI	1017 2570511 2571527	- ethanolamine utilization; homolog of Salmonella		12
b2459	eutT	804 2571524 2572327	- acetvl/butvrvl P orf, hypothetical protein		12
b2460	eutQ	702 2572324 2573025	- orf, hypothetical protein	1	12
b2461	eutP	480 2573000 2573479	- orf, hypothetical protein	1	14
b2462	ypfE	408 2573492 2573899	- orf, hypothetical protein	1	15
b2463	maeB	2280 2574120 2576399	- putative multimodular enzyme	1	21
b2464	talA	951 2576688 2577638	+ transaldolase A		14
b2465	tktB	2004 2577658 2579661	+ transketolase 2		13
b2466	ypfG	1044 2579756 2580799	- orf, hypothetical protein		16
b2467	yffH	576 2580925 2581500	- orf, hypothetical protein		20
b2468	aegA	1980 2581568 2583547	- putative oxidoreductase, Fe-S subunit (anaerobically expressed gene)		20
b2469	narQ	1701 2583753 2585453	+ sensor for nitrate reductase system, protein histidine kinase (acts on NarP and narL)		12
b2470	acrD	3114 2585617 2588730	+ aminoglycoside efflux pump		19
b2471	yffB	357 2589269 2589625	+ orf, hypothetical protein	1	21
b2472	dapE	1128 2589629 2590756	+ N-succinyl-diaminopimelate deacylase		21
b2473	ypfH	723 2591094 2591816	- orf, hypothetical protein		11
b2474	ypfI	2016 2591866 2593881	- orf, hypothetical protein		21
b2475	-	864 2593896 2594759	- orf, hypothetical protein		19
b2476	purC	714 2594927 2595640	- phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase		21
b2477	nlpB	1038 2595853 2596890	- lipoprotein-34		21
b2478	dapA	879 2596904 2597782	- dihydrodipicolinate synthase		21
b2479	gcvR	639 2597862 2598500	+ transcriptional regulation of gcv	1	19
b2480	bcp	471 2598500 2598970	+ bacterioferritin	1	21
b2481	hyfA	657 2599184 2599840	+ comigratory protein	1	8
b2482	hyfB	2019 2599840 2601858	+ hydrogenase 4 subunit		7
b2483	hyfC	969 2601848 2602816	+ hydrogenase 4 membrane subunit		10
b2484	hyfD	1440 2602833 2604272	+ hydrogenase 4 membrane subunit		8
b2485	hyfE	651 2604284 2604934	+ hydrogenase 4 membrane subunit		10
b2486	hyfF	1581 2604939 2606519	+ hydrogenase 4 membrane subunit		10
b2487	hyfG	1668 2606509 2608176	+ hydrogenase 4 subunit		8
b2488	hyfH	546 2608186 2608731	+ hydrogenase 4 Fe-S subunit		9
b2489	hyfI	759 2608728 2609486	+ hydrogenase 4 Fe-S subunit		10

b2490	hyfJ	477 2609416 2609892	+ putative protein processing element; hydrogenase 4 component J					10
b2491	hyfR	1992 2609943 2611934	+ putative 2-component regulator, interaction with sigma 54					16
b2492	focB	849 2611956 2612804	+ probable formate transporter (formate channel 2)					5
b2493	perM	1062 2612842 2613903	- putative permease					19
b2494	-	1464 2614116 2615579	+ orf, hypothetical protein					21
b2495	yfgD	360 2615600 2615959	+ putative oxidoreductase					21
b2496	hda	747 2616097 2616843	- putative DNA replication factor					21
b2497	uraA	1290 2616893 2618182	- uracil transport					17
b2498	upp	654 2618268 2618921	- uracil phosphoribosyltransferase					21
b2499	purM	1038 2619219 2620256	+ phosphoribosylaminoimidazole synthetase = AIR synthetase					21
b2500	purN	639 2620256 2620894	+ phosphoribosylglycinamide formyltransferase 1					21
b2501	ppk	2067 2621066 2623132	+ polyphosphate kinase					21
b2502	ppx	1542 2623137 2624678	+ exopolyphosphatase					21
b2503	yfgF	2244 2624717 2626960	- putative cytochrome C-type biogenesis protein	1			1	11
b2504	yfgG	192 2627312 2627503	+ orf, hypothetical protein	1			1	14
b2505	yfgH	519 2627814 2628332	+ putative outer membrane lipoprotein	1	1		1	10
b2506	yfgI	540 2628348 2628887	+ putative membrane protein				1	13
b2507	guaA	1578 2628980 2630557	- GMP synthetase (glutamine-hydrolyzing)					21
b2508	guaB	1467 2630626 2632092	- IMP dehydrogenase					21
b2509	xseA	1371 2632254 2633624	+ exonuclease VII, large subunit					21
b2510	yfgJ	252 2633621 2633872	- orf, hypothetical protein	1	1			18
b2511	yfgK	1512 2633906 2635417	- putative GTP-binding factor					21
b2512	yfgL	1179 2635496 2636674	- putative dehydrogenase					21
b2513	yfgM	621 2636685 2637305	- orf, hypothetical protein					21
b2514	hisS	1275 2637323 2638597	- histidine tRNA					21
b2515	ispG	1119 2638708 2639826	- 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase					21
b2516	yfgA	1014 2639853 2640866	- putative membrane protein					21
b2517	yfgB	1155 2641151 2642305	- orf, hypothetical protein					21
b2518	ndk	432 2642455 2642886	- nucleoside diphosphate kinase					21
b2519	pbpC	2313 2643035 2645347	- penicillin binding protein 1C (PBP 1C)					16
b2520	yfhM	4962 2645348 2650309	- orf, hypothetical protein					16
b2521	sseA	1005 2650357 2651361	+ putative thiosulfate sulfurtransferase				1	19
b2522	sseB	786 2652179 2652964	- enhanced serine sensitivity				1	21
b2523	pepB	1371 2653097 2654467	- putative peptidase					21
b2524	yfhJ	201 2654558 2654758	- orf, hypothetical protein					21
b2525	fdx	336 2654770 2655105	- [2FE-2S] ferredoxin, electron carrier protein					21
b2526	hscA	1851 2655107 2656957	- DnaK-homologue chaperone Hsc66					20
b2527	hscB	516 2656974 2657489	- DnaJ-homologue co-chaperone protein					21
b2528	iscA	324 2657585 2657908	- involved in Fe-S biosynthesis					21
b2529	iscU	387 2657925 2658311	- involved in Fe-S biosynthesis					21
b2530	iscS	1215 2658339 2659553	- cysteine desulfurase					21

b2531	iscR	489 2659665 2660153	- Fe-S cluster-containing transcription factor				21
b2532	yfhQ	741 2660605 2661345	- hypothetical tRNA/rRNA				21
b2533	suhB	804 2661464 2662267	+ inositol-1-monophosphatase				20
b2534	yfhR	882 2662385 2663266	+ putative enzyme				20
b2535	csiE	1302 2663436 2664737	+ stationary phase inducible protein	1			19
b2536	hcaT	1140 2664729 2665868	- MFS (major facilitator superfamily) transporter				21
b2537	hcaR	891 2666028 2666918	- transcriptional activator of hca cluster				8
b2538	hcaE	1362 2667054 2668415	+ 3-phenylpropionate dioxygenase, alpha subunit				9
b2539	hcaF	519 2668412 2668930	+ small terminal subunit of phenylpropionate dioxygenase				9
b2540	hcaC	321 2668930 2669250	+ ferredoxin subunit of phenylpropionate dioxygenase				13
b2541	hcaB	813 2669247 2670059	+ 2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase				9
b2542	hcaD	1203 2670069 2671271	+ ferredoxin reductase subunit of phenylpropionate dioxygenase				6
b2543	yphA	495 2671296 2671790	+ orf, hypothetical protein	1			8
b2544	yphB	873 2671838 2672710	- orf, hypothetical protein				9
b2545	yphC	1095 2672722 2673816	- putative oxidoreductase				9
b2546	yphD	999 2673849 2674847	- putative transport system permease				13
b2547	yphE	1512 2674872 2676383	- putative ATP-binding component of a transport system				9
b2548	yphF	984 2676406 2677389	- putative LACI-type transcriptional regulator		1	1	7
b2549	yphG	3375 2677486 2680860	- orf, hypothetical protein				8
b2550	yphH	1200 2680879 2682078	+ putative NAGC-like transcriptional regulator				9
b2551	glyA	1254 2682276 2683529	- serine hydroxymethyltransferase				21
b2552	hmpA	1191 2683857 2685047	+ dihydropteridine reductase, ferrisiderophore reductase activity				21
b2553	glnB	339 2685092 2685430	- regulatory protein P-II for glutamine				21
b2554	yfhA	1335 2685491 2686825	- putative 2-component transcriptional regulator				21
b2555	yfhG	714 2686815 2687528	- putative alpha helix				21
b2556	yfhK	1491 2687693 2689183	- putative 2-component sensor protein				21
b2557	purL	3888 2689678 2693565	- phosphoribosylformylglycineamide synthetase = FGAM				21
b2558	yfhD	1419 2693961 2695379	+ putative periplasmic binding transport				21
b2559	tadA	537 2695376 2695912	- tRNA-specific adenosine deaminase				21
b2560	yfhB	573 2695937 2696509	- orf, hypothetical protein				19
b2561	yfhH	921 2696709 2697629	+ orf, hypothetical protein				18
b2562	yfhL	261 2697685 2697945	+ orf, hypothetical protein	1		1	21
b2563	acpS	381 2698640 2699020	- CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase				21
b2564	pdxJ	732 2699020 2699751	- pyridoxine biosynthesis				21
b2565	recO	729 2699763 2700491	- protein interacts with RecR and possibly RecF proteins				21

b2566	era	906	2700503	2701408	- GTP-binding protein				21
b2567	rnc	681	2701405	2702085	- RNase III, ds RNA				21
b2568	lepB	975	2702357	2703331	- leader peptidase (signal peptidase I)				21
b2569	lepA	1800	2703347	2705146	- GTP-binding elongation factor, may be inner membrane protein				21
b2570	rseC	480	2705344	2705823	- sigma-E factor, negative regulatory	1			21
b2571	rseB	957	2705820	2706776	- regulates activity of sigma-E factor				21
b2572	rseA	651	2706776	2707426	- sigma-E factor, negative regulatory				21
b2573	rpoE	576	2707459	2708034	- RNA polymerase, sigma-E factor; heat shock and oxidative	1			21
b2574	nadB	1623	2708442	2710064	+ quinolinate synthetase, B protein				17
b2575	yfiC	858	2710049	2710906	- putative enzyme	1			21
b2576	srmB	1335	2710918	2712252	+ ATP-dependent RNA helicase				21
b2577	yfiE	927	2712461	2713387	- putative transcriptional regulator LYSR-type	1			13
b2578	yfiK	588	2713445	2714032	+ orf, hypothetical protein				21
b2579	yfiD	384	2714088	2714471	- putative formate acetyltransferase				20
b2580	ung	690	2714776	2715465	+ uracil-DNA-glycosylase				21
b2581	yfiF	1038	2715513	2716550	- orf, hypothetical protein				21
b2582	trxC	420	2716757	2717176	+ putative thioredoxin-like protein				20
b2583	yfiP	723	2717221	2717943	+ orf, hypothetical protein	1			20
b2584	yfiQ	2661	2717975	2720635	+ orf, hypothetical protein				21
b2585	pssA	1359	2720746	2722104	+ phosphatidylserine synthase; phospholipid synthesis				21
b2586	yfiM	273	2722201	2722473	+ orf, hypothetical protein				20
b2587	kgfP	1299	2722470	2723768	- alpha-ketoglutarate permease	1			20
rrnG_5S	rrnG_5S	120	2724091	2724210	- rrnG_5S				
rrnG_23S	rrnG_23S	2904	2724303	2727206	- rrnG_23S				
tRNA-Glu1	tRNA-Glu	76	2727391	2727466	- tRNA-Glu				
rrnG_16S	rrnG_16S	1542	2727638	2729179	- rrnG_16S				
b2592	clpB	2574	2729622	2732195	- heat shock protein				21
b2593	yfiH	732	2732325	2733056	- orf, hypothetical protein				21
b2594	rluD	981	2733053	2734033	- 23S rRNA pseudouridine synthase				21
b2595	yfiO	738	2734168	2734905	+ orf, hypothetical protein				21
b2596	-	207	2734935	2735141	+ orf, hypothetical protein	1	1		5
b2597	yfiA	342	2735176	2735517	+ putative yhbH sigma 54 modulator				21
b2598	pheL	48	2735621	2735668	+ leader peptide of chorismate mutase-P-prephenate				1
b2599	pheA	1161	2735767	2736927	+ chorismate mutase-P and prephenate				19
b2600	tyrA	1122	2736970	2738091	- chorismate mutase-T and prephenate				21
b2601	aroF	1071	2738102	2739172	- dehydrogenase 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible)				21
b2602	yfiL	405	2739343	2739747	+ orf, hypothetical protein	1	1	1	11
b2603	yfiR	519	2739897	2740415	+ orf, hypothetical protein	1	1	1	18
b2604	yfiN	1227	2740405	2741631	+ orf, hypothetical protein			1	17
b2605	yfiB	483	2741647	2742129	+ putative outer membrane protein	1			14
b2606	rplS	348	2742205	2742552	- 50S ribosomal subunit protein L19				21
b2607	trmD	768	2742594	2743361	- tRNA methyltransferase; tRNA (guanine-7-)-				21

b2608	rimM	558 2743392 2743949	- 16S rRNA processing protein						21
b2609	rpsP	249 2743959 2744207	- 30S ribosomal subunit protein S16						21
b2610	ffh	1362 2744456 2745817	- GTP-binding export factor binds to signal sequence, GTP and						21
b2611	-	867 2745909 2746775	+ orf, hypothetical protein						21
b4461	yfjD	1263 2746820 2748082	+ putative membrane protein						20
b2614	grpE	594 2748137 2748730	- phage lambda replication; host DNA synthesis; heat shock protein: protein repair						21
b2615	yfjB	879 2748853 2749731	+ orf, hypothetical protein						21
b2616	recN	1662 2749817 2751478	+ protein used in recombination and DNA repair						21
b2617	smpA	153 2751816 2751968	+ small membrane						21
b2618	yfjF	309 2752030 2752338	- orf, hypothetical protein						21
b2619	yfjG	477 2752310 2752786	- orf, hypothetical protein	1					21
b2620	smpB	483 2752918 2753400	+ small protein B						21
b2622	intA	1242 2754181 2755422	+ prophage CP4-57 integrase	1	1				11
b2623	yfjH	957 2755666 2756622	- putative histone	1	1		1		2
b2624	alpA	213 2756666 2756878	+ prophage CP4-57 regulatory protein alpA	1	1		1		13
b2625	yfjI	1410 2757007 2758416	+ orf, hypothetical protein	1	1		1		5
b2626	yfjJ	627 2758569 2759195	+ orf, hypothetical protein	1	1		1		4
b2627	yfjK	2190 2759373 2761562	- orf, hypothetical protein	1					2
b2628	yfjL	1617 2761559 2763175	- orf, hypothetical protein	1					2
b2629	yfjM	264 2763535 2763798	- orf, hypothetical protein	1					2
b2630	yfjN	1074 2763940 2765013	+ putative cell division protein	1	1				3
b2631	yfjO	321 2765057 2765377	+ orf, hypothetical protein	1					2
b2632	yfjP	864 2765732 2766595	+ putative GTP-binding protein						9
b2633	yfjQ	822 2766687 2767508	+ orf, hypothetical protein						8
b2634	yfjR	702 2767725 2768426	+ orf, hypothetical protein	1					3
b2635	ypjK	393 2768311 2768703	+ orf, hypothetical protein	1					1
b2636	yfjS	693 2768454 2769146	+ orf, hypothetical protein	1					2
b2637	yfjT	468 2769170 2769637	+ orf, hypothetical protein	1					3
b2638	yfjU	315 2769862 2770176	- orf, hypothetical protein	1					2
b2639	-	519 2770189 2770707	- putative pump protein						1
b2640	-	201 2770858 2771058	- orf, hypothetical protein				1		2
b2641	-	117 2770998 2771114	- orf, hypothetical protein	1			1		2
b2642	yfjW	1704 2771340 2773043	+ orf, hypothetical protein	1	1		1		2
b2643	yfjX	459 2773941 2774399	+ orf, hypothetical protein	1					11
b2644	yfjY	483 2774408 2774890	+ putative DNA repair protein	1					11
b2645	yfjZ	318 2775137 2775454	+ orf, hypothetical protein	1					11
b2646	ypjF	330 2775475 2775804	+ orf, hypothetical protein	1					11
b2647	ypjA	4710 2776168 2780877	- putative ATP-binding component of a transport system	1			1		19
b2648	-	144 2781087 2781230	- orf, hypothetical protein	1	1		1		5
b2649	-	792 2781660 2782451	- orf, hypothetical protein	1	1		1		5
b2650	-	483 2782551 2783033	- orf, hypothetical protein	1	1		1		5
b2651	-	132 2783243 2783374	+ orf, hypothetical protein	1	1		1		1
tRNA-Ile2	tRNA-Ile	76 2783784 2783859	- tRNA-Ile					1	
b2653	-	174 2783822 2783995	- orf, hypothetical protein	1	1		1		2
b2654	-	333 2784419 2784751	+ orf, hypothetical protein	1	1		1		4
b4462	ygaR	687 2784770 2785456	+ orf, hypothetical protein					1	4
b2657	-	633 2785628 2786260	+ putative enzyme	1	1		1		5
b2658	-	273 2786399 2786671	+ orf, hypothetical protein	1	1		1		7
b2659	-	1083 2786902 2787984	+ orf, hypothetical protein				1		14
b2660	ygaF	1335 2787938 2789272	+ orf, hypothetical protein						14
b2661	gabD	1449 2789295 2790743	+ succinate-semialdehyde dehydrogenase, NADP-4-aminobutyrate aminotransferase						17
b2662	gabT	1281 2790757 2792037	+ 4-aminobutyrate aminotransferase						20

b2663	gabP	1401 2792275 2793675	+ transport permease protein of gamma-aminobutyrate					14
b2664	ygaE	681 2793678 2794358	+ putative transcriptional regulator					15
b2665	ygaU	450 2794359 2794808	- orf, hypothetical protein					13
b2666	yqaE	159 2794892 2795050	- orf, hypothetical protein				1	15
b2667	-	300 2795233 2795532	+ orf, hypothetical protein				1	16
b2668	ygaP	525 2795542 2796066	+ orf, hypothetical protein		1		1	16
b2669	stpA	405 2796113 2796517	- DNA-binding protein; H-NS-like protein; chaperone activity:				1	15
b2670	-	450 2797186 2797635	+ orf, hypothetical protein	1			1	20
b2671	ygaC	345 2797672 2798016	- orf, hypothetical protein		1			19
b2672	ygaM	342 2798156 2798497	+ orf, hypothetical protein					13
b2673	nrdH	246 2798745 2798990	+ glutaredoxin-like protein; hydrogen donor					21
b2674	nrdI	411 2798987 2799397	+ orf, hypothetical protein					19
b2675	nrdE	2145 2799370 2801514	+ ribonucleoside-diphosphate reductase 2, alpha subunit					21
b2676	nrdF	960 2801524 2802483	+ ribonucleoside-diphosphate reductase 2, beta chain, frag					20
b2677	proV	1203 2802837 2804039	+ ATP-binding component of transport system for glycine, betaine and proline				1	19
b2678	proW	1065 2804032 2805096	+ high-affinity transport system for glycine betaine and proline					21
b2679	proX	993 2805154 2806146	+ high-affinity transport system for glycine betaine and proline					20
b2680	-	267 2806338 2806604	+ orf, hypothetical protein					21
b2681	-	918 2806598 2807515	+ putative transport					21
b2682	ygaZ	738 2807639 2808376	+ orf, hypothetical protein					21
b2683	ygaH	336 2808366 2808701	+ orf, hypothetical protein					16
b2684	emrR	531 2808792 2809322	+ regulator of plasmid mcrB operon (microcin B17 synthesis)					21
b2685	emrA	1173 2809449 2810621	+ multidrug resistance secretion protein					19
b2686	emrB	1539 2810638 2812176	+ multidrug resistance; probably membrane translocase					20
b2687	ygaG	516 2812240 2812755	- orf, hypothetical protein					21
b2688	gshA	1557 2812905 2814461	- gamma-glutamyl-cysteine ligase					21
b2689	yqaA	429 2814534 2814962	- orf, hypothetical protein	1				20
b2690	yqaB	567 2814959 2815525	- putative phosphatase					20
tRNA-Arg3 tRNA-Arg		77 2815806 2815882	- tRNA-Arg					
tRNA-Arg4 tRNA-Arg		77 2816081 2816157	- tRNA-Arg					
tRNA-Arg5 tRNA-Arg		77 2816220 2816296	- tRNA-Arg					
tRNA-Arg6 tRNA-Arg		77 2816495 2816571	- tRNA-Arg					
tRNA-Ser tRNA-Ser		93 2816575 2816667	- tRNA-Ser					
b2696	csrA	186 2816983 2817168	- carbon storage regulator; controls glycogen synthesis, gluconeogenesis, cell size and surface					21
b2697	alaS	2631 2817403 2820033	- alanyl-tRNA synthetase					20
b2698	oraA	501 2820161 2820661	- regulator, OraA protein					21
b2699	recA	1062 2820730 2821791	- DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent					21
b2700	ygaD	498 2821871 2822368	- orf, hypothetical protein					21
b2701	mltB	1086 2822513 2823598	- membrane-bound lytic murein transglycosylase B					20

b2702	srlA	564 2823854 2824417	+ PTS system, glucitol/sorbitol-specific IIC component, one of	13
b2703	srlE	960 2824414 2825373	+ PTS system, glucitol/sorbitol-specific IIB component and	13
b2704	srlB	372 2825384 2825755	+ second of two IIC PTS system, glucitol/sorbitol-specific	15
b2705	srlD	780 2825759 2826538	+ enzyme IIA component glucitol (sorbitol)-6- phosphate	16
b2706	gutM	360 2826643 2827002	+ dehydrogenase glucitol operon activator	14
b2707	srlR	774 2827069 2827842	+ regulator for gut (srl), glucitol operon	15
b2708	gutQ	927 2827874 2828800	+ orf, hypothetical protein	15
b2709	ygaA	1590 2828797 2830386	- putative 2-component transcriptional regulator	16
b2710	norV	1440 2830498 2831937	+ putative flavodoxin	15
b2711	ygbD	1134 2831934 2833067	+ putative oxidoreductase	16
b2712	hypF	2253 2833195 2835447	- transcriptional regulatory protein	16
b2713	hydN	528 2835600 2836127	- involved in electron transport from formate to hydrogen, Fe-S	20
b2714	ascG	1014 2836276 2837289	- ascBF operon	19
b2715	ascF	1458 2837546 2839003	+ PTS system enzyme II ABC (asc), cryptic, transports specific beta- glucosides	7
b2716	ascB	1425 2839012 2840436	+ 6-phospho-beta- glucosidase; cryptic	11
b2717	hycl	471 2840595 2841065	- protease involved in processing C-terminal end of the large subunit of hvdooenase 3	14
b2718	hycH	411 2841058 2841468	- processing of large subunit (HycE) of hydrogenase 3 (part of the FHL complex)	13
b2719	hycG	768 2841465 2842232	- hydrogenase activity	12
b2720	hycF	543 2842232 2842774	- probable iron-sulfur protein of hydrogenase 3 (part of FHL complex)	13
b2721	hycE	1710 2842784 2844493	- large subunit of hydrogenase 3 (part of FHL complex)	15
b2722	hycD	924 2844511 2845434	- membrane-spanning protein of hydrogenase 3 (part of FHL complex)	15
b2723	hycC	1827 2845437 2847263	- membrane-spanning protein of hydrogenase 3 (part of FHL complex)	14
b2724	hycB	612 2847260 2847871	- probable small subunit of hydrogenase-3, iron- sulfur protein (part of formate hydrogenlyase (FHL) complex)	15
b2725	hycA	462 2847996 2848457	- transcriptional repression of hyc and	14
b2726	hypA	351 2848669 2849019	+ pleiotrophic effects on 3 hydrogenase isozymes	16
b2727	hypB	873 2849023 2849895	+ guanine-nucleotide binding protein, functions as nickel donor for large subunit	21
b2728	hypC	273 2849886 2850158	+ pleiotrophic effects on 3 hydrogenase isozymes	16
b2729	hypD	1122 2850158 2851279	+ pleiotrophic effects on 3 hydrogenase isozymes	16

b2730	hypE	969 2851318 2852286	+	plays structural role in maturation of all 3 hydrogenases				16
b2731	fhIA	2079 2852360 2854438	+	formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons				16
b2732	ygbA	354 2854475 2854828	-	orf, hypothetical protein				16
b2733	mutS	2562 2855115 2857676	+	methyl-directed mismatch repair				21
b2734	pphB	657 2857782 2858438	+	protein phosphatase 2	1	1	1	10
b2735	ygbI	798 2858489 2859286	-	putative DEOR-type transcriptional regulator				17
b2736	ygbJ	909 2859452 2860360	+	putative dehydrogenase				21
b2737	ygbK	1167 2860357 2861523	+	orf, hypothetical protein				14
b2738	ygbL	639 2861615 2862253	+	putative epimerase/aldolase				15
b2739	ygbM	777 2862258 2863034	+	orf, hypothetical protein				19
b2740	ygbN	1365 2863123 2864487	+	putative transport				6
b2741	rpoS	993 2864581 2865573	-	RNA polymerase, sigma S (sigma38) factor; synthesis of manv growth phase lipoprotein				20
b2742	nlpD	1140 2865636 2866775	-	L-isoaspartate protein	1			21
b2743	pcm	627 2866915 2867541	-	carboxymethyltransferase type II				21
b2744	surE	762 2867535 2868296	-	survival protein				20
b2745	ygbO	1050 2868277 2869326	-	putative hydrogenase subunit				21
b2746	ispF	480 2869323 2869802	-	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase				21
b2747	ispD	711 2869802 2870512	-	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase				21
b2748	ygbQ	312 2870531 2870842	-	orf, hypothetical protein				21
b2749	ygbE	324 2871036 2871359	-	putative cytochrome oxidase subunit				20
b2750	cysC	606 2871409 2872014	-	adenosine 5'-phosphosulfate kinase				21
b2751	cysN	1428 2872014 2873441	-	ATP-sulfurylase (ATP:sulfate adenylyltransferase), subunit 1, probably a GTPase				21
b2752	cysD	909 2873443 2874351	-	ATP:sulfurylase (ATP:sulfate adenylyltransferase), subunit 2				21
b2753	iap	1038 2874603 2875640	+	alkaline phosphatase isozyme conversion protein: aminopeptidase	1			15
b2754	ygbF	351 2876591 2876941	-	orf, hypothetical protein	1	1		12
b2755	ygbT	918 2876877 2877794	-	orf, hypothetical protein	1	1		16
b2756	ygcH	600 2877810 2878409	-	orf, hypothetical protein	1	1		13
b2757	ygcI	681 2878396 2879076	-	orf, hypothetical protein	1	1		12
b2758	ygcJ	1092 2879073 2880164	-	orf, hypothetical protein	1	1		12
b2759	ygcK	483 2880177 2880659	-	orf, hypothetical protein	1	1	1	2
b2760	ygcL	1509 2880652 2882160	-	orf, hypothetical protein	1	1	1	10
b2761	ygcB	2667 2882575 2885241	-	orf, hypothetical protein	1	1	1	16
b2762	cysH	735 2885600 2886334	-	3'-phosphoadenosine 5'-phosphosulfate sulfite reductase, alpha subunit				18
b2763	cysI	1713 2886409 2888121	-	sulfite reductase, alpha subunit				21
b2764	cysJ	1800 2888121 2889920	-	sulfite reductase (NADPH), flavoprotein beta subunit				21
b2765	ygcM	366 2890236 2890601	+	putative 6-pyruvoyl tetrahydrobiopterin synthase				21
b2766	ygcN	1302 2890649 2891950	+	orf, hypothetical protein	1			10
b2767	ygcO	297 2891905 2892201	+	orf, hypothetical protein				10

b2768	ygcP	576 2892218 2892793	+ putative anti-terminator regulatory protein	1			7
b2769	ygcQ	894 2892941 2893834	- putative flavoprotein				9
b2770	ygcR	786 2893798 2894583	- putative transport				9
b2771	ygcS	1410 2894555 2895964	- putative transport				13
b4463	-	1455 2895986 2897440	- orf, hypothetical protein			1	9
b2774	ygcW	861 2897510 2898370	- putative oxidoreductase			1	6
b2775	yqcE	1278 2898614 2899891	+ putative transport			1	6
b2776	ygcE	1479 2899918 2901396	+ putative kinase			1	6
b2777	ygcF	672 2902769 2903440	- orf, hypothetical protein			1	21
b2778	ygcG	942 2903664 2904605	+ orf, hypothetical protein	1	1	1	8
b2779	eno	1299 2904665 2905963	- enolase				21
b2780	pyrG	1638 2906051 2907688	- CTP synthetase				21
b2781	mazG	792 2907916 2908707	- orf, hypothetical protein				21
b2782	chpA	336 2908778 2909113	- probable growth inhibitor, PemK-like, suppressor of inhibitory function of ChpA, Pemi-like, autoregulated (p)ppGpp synthetase I (GTP pyrophosphokinase); regulation of RNA synthesis: stringent 23S rRNA (uracil-5-)-methyltransferase	1			8
b2783	chpR	249 2909113 2909361	-				8
b2784	relA	2235 2909439 2911673	-				21
b2785	rumA	1302 2911721 2913022	-				17
b2786	barA	2757 2913079 2915835	+ sensor-regulator, activates OmpR by phosphorylation (D)-glucarate dehydratase 1				21
b2787	gudD	1341 2916067 2917407	- putative (D)-glucarate dehydratase 2				15
b2788	gudX	1341 2917428 2918768	- putative D-glucarate dehydratase 2				13
b2789	gudP	1353 2918770 2920122	- putative D-glucarate permease (MFS family)				15
b2790	yqcA	450 2920557 2921006	- orf, hypothetical protein				21
b2791	yqcB	783 2921024 2921806	- orf, hypothetical protein				21
b2792	yqcC	330 2921806 2922135	- orf, hypothetical protein				21
b2793	syd	546 2922757 2923302	- interacts with secY	1			21
b2794	yqcD	849 2923370 2924218	+ orf, hypothetical protein				21
b2795	ygdH	1365 2924330 2925694	+ orf, hypothetical protein				21
b2796	sdaC	1290 2926251 2927540	+ probable serine transporter				21
b2797	sdaB	1368 2927598 2928965	+ L-serine dehydratase (deaminase), L-SD2				15
b2798	exo	846 2928987 2929832	+ 5'-3' exonuclease				21
b2799	fucO	1152 2929887 2931038	- L-1,2-propanediol oxidoreductase				15
b2800	fucA	648 2931063 2931710	- L-fucose-1-phosphate aldolase	1		1	15
b2801	fucP	1317 2932257 2933573	+ fucose permease	1		1	12
b2802	fucI	1776 2933606 2935381	+ L-fucose isomerase				14
b2803	fucK	1449 2935460 2936908	+ L-fuculokinase				11
b2804	fucU	423 2936910 2937332	+ protein of fucose	1			15
b2805	fucR	732 2937390 2938121	+ positive regulator of the fuc operon	1			20
b2806	ygdE	1101 2938165 2939265	- orf, hypothetical protein				21
b2807	ygdD	396 2939258 2939653	- orf, hypothetical protein				21
b2808	gcvA	918 2939672 2940589	- positive regulator of gcv operon	1			21
b2809	ygdI	231 2940940 2941170	- orf, hypothetical protein				16
b2810	csdA	1206 2941359 2942564	+ cysteine sulfinate desulfinate				21
b2811	ygdK	444 2942564 2943007	+ orf, hypothetical protein				21
b2812	ygdL	807 2943058 2943864	- putative enzyme				21
b2813	mltA	1098 2944103 2945200	- membrane-bound lytic murein transglycosylase				21
tRNA-Met ²	tRNA-Met	77 2945409 2945485	+ tRNA-Met				
tRNA-Met ³	tRNA-Met	77 2945519 2945595	+ tRNA-Met				
tRNA-Met ⁴	tRNA-Met	77 2945629 2945705	+ tRNA-Met				
b2817	amiC	1344 2945779 2947122	- N-acetylmuramoyl-L-alanine amidase				21

b2818	argA	1332 2947264 2948595	+ N-acetylglutamate synthase; amino acid acetyltransferase						21
b2819	recD	1827 2948657 2950483	- DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit.						21
b2820	recB	3543 2950483 2954025	- DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit.						21
b2821	ptr	2889 2954018 2956906	- protease III						21
b2822	recC	3369 2957082 2960450	- DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit.						21
b2823	ppdC	324 2960463 2960786	- prepilin peptidase dependent protein C	1					21
b2824	ygdB	366 2960771 2961136	- orf, hypothetical protein						21
b2825	ppdB	564 2961175 2961738	- prepilin peptidase dependent protein B						19
b2826	ppdA	471 2961729 2962199	- prepilin peptidase dependent protein A	1					19
b2827	thyA	795 2962383 2963177	- thymidylate synthetase						21
b2828	lgt	876 2963184 2964059	- phosphatidylglycerol-prolipoprotein diacylglycerol transferase; a major membrane phospholipid						21
b2829	ptsP	2247 2964210 2966456	- PTS system, enzyme I, transcriptional regulator (with NPR and NTR proteins)						21
b2830	ygdP	531 2966469 2966999	- putative invasion	1					21
b2831	mutH	690 2967684 2968373	+ methyl-directed mismatch repair						21
b2832	ygdQ	714 2968442 2969155	+ putative transport						17
b2833	ygdR	219 2969293 2969511	+ orf, hypothetical protein		1				16
b2834	tas	1041 2969619 2970659	+ putative reductase, NAD(P)-linked						20
b2835	ygeD	1194 2970691 2971884	- putative resistance proteins						21
b2836	aas	2160 2971877 2974036	- 2-acyl-glycerophospho-ethanolamine acyltransferase; acyl-acyl-carrier protein						21
b2837	galR	1032 2974621 2975652	+ repressor of galETK operon						20
b2838	lysA	1263 2975659 2976921	- diaminopimelate decarboxylase						21
b2839	lysR	936 2977043 2977978	+ positive regulator for lys						21
b2840	ygeA	693 2977965 2978657	- putative resistance proteins						19
b2841	araE	1419 2978786 2980204	- low-affinity L-arabinose transport system proton symport protein				1		14
b2842	kduD	762 2980519 2981280	- 2-deoxy-D-gluconate 3-dehydrogenase				1		19
b2843	kduI	837 2981310 2982146	- homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase				1		19
b2844	yqeF	1185 2982433 2983617	- putative acyltransferase				1		14
b2845	yqeG	1230 2983869 2985098	+ putative transporter protein	1	1		1		13
b2846	yqeH	693 2985498 2986190	+ orf, hypothetical protein	1	1		1		10
b2847	yqeI	810 2986524 2987333	+ putative sensory transducer	1	1		1		10
b2848	yqeJ	495 2987314 2987808	+ orf, hypothetical protein	1			1		11
b2849	yqeK	438 2987957 2988394	- orf, hypothetical protein	1			1		4
b2850	ygeF	447 2988576 2989022	+ orf, hypothetical protein	1			1		5
b2851	ygeG	492 2989290 2989781	+ orf, hypothetical protein	1	1		1		12
b2852	ygeH	1377 2990116 2991492	+ putative invasion	1	1		1		9

b2853	ygeI	219 2991660 2991878	+ orf, hypothetical protein	1	1	1	4
b2854	-	417 2992021 2992437	+ orf, hypothetical protein	1	1	1	7
b2855	ygeK	447 2992482 2992928	- putative 2-component transcriptional regulator	1	1	1	4
b2856	-	156 2992959 2993114	- orf, hypothetical protein	1	1	1	3
b2857	-	432 2993336 2993767	- orf, hypothetical protein	1	1	1	12
b2858	-	222 2993770 2993991	- orf, hypothetical protein	1	1	1	4
b2859	-	426 2993984 2994409	- orf, hypothetical protein	1	1	1	11
b2860	yi22_4	906 2994394 2995299	- IS2 hypothetical protein	1	1	1	18
b2861	yi21_4	366 2995257 2995622	- IS2 hypothetical protein		1	1	8
b2862	ygeP	300 2995711 2996010	- orf, hypothetical protein	1	1	1	5
b2863	ygeQ	837 2996056 2996892	- orf, hypothetical protein	1	1	1	6
tRNA-Gly2 tRNA-Gly		74 2997006 2997079	- tRNA-Gly			1	
b2865	ygeR	780 2997158 2997937	- putative lipoprotein	1		1	14
b2866	xdhA	2259 2998367 3000625	+ xanthine dehydrogenase, molybdenum binding				9
b2867	xdhB	879 3000636 3001514	+ xanthine dehydrogenase, FAD				9
b2868	xdhC	480 3001511 3001990	+ xanthine dehydrogenase iron-				
b2869	ygeV	1779 3002030 3003808	- putative transcriptional regulator	1	1	1	6
b2870	ygeW	1191 3004284 3005474	+ putative carbamoyl transferase			1	6
b2871	ygeX	1197 3005532 3006728	+ putative diaminopropionate ammonia-lyase				10
b2872	ygeY	1212 3006786 3007997	+ putative deacetylase				7
b2873	ygeZ	1398 3008038 3009435	+ orf, hypothetical protein				6
b2874	yqeA	933 3009483 3010415	+ putative kinase				7
b2875	yqeB	1626 3010636 3012261	- putative synthases				7
b2876	yqeC	708 3012309 3013016	- orf, hypothetical protein	1		1	7
b2877	ygfJ	579 3013182 3013760	+ orf, hypothetical protein	1	1	1	7
b2878	ygfK	3099 3014082 3017180	+ putative oxidoreductase, Fe-S			1	5
b2879	ssnA	1395 3017117 3018511	+ soluble protein involved in cell viability at the beginning of stationary phase				10
b2880	ygfM	780 3018562 3019341	+ orf, hypothetical protein				6
b2881	xdhD	2871 3019338 3022208	+ possible hypoxanthine oxidase				6
b2882	ygfO	1458 3022316 3023773	+ probable guanine/xanthin	1			5
b2883	guaD	1320 3023788 3025107	+ guanine deaminase				6
b4464	ygfQ	1368 3025143 3026510	+ orf, hypothetical protein				20
b2886	ygfS	492 3026546 3027037	- putative oxidoreductase, Fe-S				6
b2887	ygfT	1935 3027034 3028968	- putative oxidoreductase, Fe-S	1		1	6
b2888	ygfU	1518 3029320 3030837	+ putative permease	1		1	12
b2889	idi	549 3031087 3031635	+ isopentenyl diphosphate isomerase			1	17
b2890	lysS	1518 3031679 3033196	- lysine tRNA synthetase, constitutive; suppressor of ColE1 mutation in primer RNA				21
b2891	prfB	1023 3033206 3034228	- peptide chain release factor RF-2				18
b2892	recJ	1734 3034395 3036128	- ssDNA exonuclease, 5' --> 3' specific				21
b2893	dsbC	711 3036134 3036844	- protein disulfide isomerase II				21
b2894	xerD	897 3036869 3037765	- site-specific				21
b2895	fldB	522 3037877 3038398	+ flavodoxin 2				21
b2896	ygfX	408 3038438 3038845	- orf, hypothetical protein				21
b2897	ygfY	267 3038826 3039092	- orf, hypothetical protein				21
b2898	ygfZ	981 3039335 3040315	+ orf, hypothetical protein				21
b2899	yqfA	660 3040511 3041170	- putative oxidoreductase				20
b2900	yqfB	312 3041334 3041645	- orf, hypothetical protein				17
b2901	bglA	1440 3041684 3043123	+ 6-phospho-beta-glucosidase A; cryptic				20

b2902	ygfF	744 3043180 3043923	- putative oxidoreductase				7
b2903	gcvP	2874 3044190 3047063	- glycine decarboxylase, P protein of glycine cleavage system				21
b2904	gcvH	390 3047182 3047571	- in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor				21
b2905	gcvT	1095 3047595 3048689	- aminomethyltransferase (T protein; tetrahydrofolate-dependent) of glycine cleavage system		1		21
b2906	visC	1203 3049137 3050339	- orf, hypothetical protein				21
b2907	ubiH	1179 3050362 3051540	- 2-octaprenyl-6-methoxyphenol--> 2-octaprenyl-6-methoxy-1, 4-benzoquinone				21
b2908	pepP	1326 3051537 3052862	- proline aminopeptidase P II				21
b2909	ygfB	585 3052888 3053472	- orf, hypothetical protein				21
b2910	ygfE	330 3053634 3053963	+ orf, hypothetical protein				21
b2912	ygfA	549 3054263 3054811	+ putative ligase	1			21
b2913	serA	1233 3055200 3056432	- D-3-phosphoglycerate dehydrogenase				21
b2914	rpiA	660 3056688 3057347	- ribosephosphate isomerase, constitutive				21
b2915	yqfE	231 3057403 3057633	- orf, hypothetical protein	1	1		3
b2916	iciA	894 3057775 3058668	+ replication initiation inhibitor, binds to 13-mers at oriC				21
b2917	sbm	2145 3058872 3061016	+ methylmalonyl-CoA mutase (MCM)				8
b2918	argK	996 3061009 3062004	+ arginine transport				9
b2919	ygfG	828 3061973 3062800	+ putative enzyme				8
b2920	ygfH	1479 3062824 3064302	+ putative coenzyme A transferase				12
b2921	ygfI	912 3064299 3065210	- putative transcriptional regulator LYSR-type	1			15
b2922	yggE	741 3065362 3066102	- putative actin				21
b2923	yggA	636 3066195 3066830	- orf, hypothetical protein				20
b2924	yggB	861 3066969 3067829	- component of the MscS mechanosensitive channel				21
b2925	fbaA	1080 3068187 3069266	- fructose-bisphosphate aldolase, class II				21
b2926	pgk	1164 3069481 3070644	- phosphoglycerate				21
b2927	epd	1020 3070694 3071713	- D-erythrose 4-phosphate				21
b2928	yggC	714 3071998 3072711	- putative kinase	1			9
b2929	yggD	510 3072708 3073217	- putative transcriptional regulator				9
b2930	yggF	966 3073239 3074204	- orf, hypothetical protein				8
b4465	yggP	1278 3074201 3075478	- orf, hypothetical protein			1	9
b2933	cmtA	1389 3075493 3076881	- PTS system, mannitol-specific enzyme II component, cryptic			1	7
b2934	cmtB	444 3076909 3077352	- PTS system, mannitol-specific enzyme II component, cryptic	1	1	1	8
b2935	tktA	1992 3077666 3079657	- transketolase 1				21
b2936	yggG	885 3079809 3080693	+ orf, hypothetical protein	1			20
b2937	speB	921 3080899 3081819	- agmatinase				16
b2938	speA	1977 3081957 3083933	- biosynthetic arginine decarboxylase				21
b2939	yqgB	147 3083942 3084088	- orf, hypothetical protein	1	1		15
b2940	yqgC	216 3084209 3084424	+ orf, hypothetical protein	1	1		10
b2941	yqgD	252 3084421 3084672	- orf, hypothetical protein	1	1		10

b2942	metK	1155 3084728 3085882	+ methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of <i>met genes</i>				21
b2943	galP	1395 3086306 3087700	+ galactose-proton symport of transport			1	15
b2944	sprT	498 3087777 3088274	+ orf, hypothetical protein	1			21
b2945	endA	708 3088369 3089076	+ DNA-specific endonuclease I				21
b2946	yggJ	759 3089129 3089887	+ orf, hypothetical protein				21
b2947	gshB	951 3089900 3090850	+ glutathione synthetase				21
b2948	yqgE	636 3090887 3091522	+ orf, hypothetical protein				21
b2949	yqgF	417 3091522 3091938	+ orf, hypothetical protein				21
b2950	yggR	1026 3092122 3093147	- putative protein				21
b2951	yggS	705 3093120 3093824	+ orf, hypothetical protein				21
b2952	yggT	567 3093842 3094408	+ conserved hypothetical integral membrane				21
b2953	yggU	303 3094393 3094695	+ orf, hypothetical protein				20
b2954	yggV	594 3094703 3095296	+ putative ribosomal				21
b2955	yggW	1137 3095289 3096425	+ putative oxidase				21
b2956	yggM	1008 3096580 3097587	- putative alpha helix				14
b2957	ansB	1047 3097704 3098750	- periplasmic L-asparaginase II				20
b2958	yggN	720 3098926 3099645	- orf, hypothetical protein				19
b2959	yggL	357 3099829 3100185	- orf, hypothetical protein				21
b2960	yggH	720 3100155 3100874	- orf, hypothetical protein				21
b2961	mutY	1053 3101035 3102087	+ adenine glycosylase; G.C --> T.A				21
b2962	yggX	276 3102115 3102390	+ orf, hypothetical protein				21
b2963	mltC	1083 3102452 3103534	+ membrane-bound lytic murein transglycosylase C				21
b2964	nupG	1305 3103688 3104992	+ transport of nucleosides, permease				15
b2965	speC	2196 3105042 3107237	- ornithine decarboxylase isozyme				17
b2966	yqgA	708 3107575 3108282	+ putative transport				15
b2968	tRNA-Phe	76 3108388 3108463	+ tRNA-Phe				
b2968	yghD	537 3108612 3109148	- putative secretion pathway protein	1			7
b2969	yghE	861 3109150 3110010	- putative general secretion pathway for protein export (GSP)				11
b2970	yghF	867 3110076 3110942	- putative general secretion pathway for protein export (GSP)			1	5
b2971	yghG	411 3111089 3111499	- orf, hypothetical protein	1	1	1	2
b2972	pppA	933 3111565 3112497	- bifunctional prepilin peptidase	1			17
b4466	yghJ	4563 3112572 3117134	- putative lipoprotein			1	2
b2975	yghK	1683 3117619 3119301	- putative permease			1	16
b2976	glcB	2172 3119656 3121827	- malate synthase G				5
b2977	glcG	405 3121849 3122253	- orf, hypothetical protein				12
b4467	glcF	1224 3122258 3123481	- glycolate oxidase iron-sulfur subunit				2
b4468	glcE	1053 3123492 3124544	- glycolate oxidase iron-sulfur subunit				2
b2979	glcD	1500 3124544 3126043	- glycolate oxidase subunit D				3
b2980	glcC	765 3126294 3127058	+ transcriptional activator for glc operon				5
b2981	yghO	1173 3127065 3128237	- orf, hypothetical protein				4
b2982	trs5_9	1017 3128200 3129216	+ IS5 transposase	1	1		2
b2983	yghQ	1068 3129363 3130430	- orf, hypothetical protein				6
b2984	yghR	759 3130476 3131234	- orf, hypothetical protein				6
b2985	yghS	714 3131266 3131979	- orf, hypothetical protein			1	6
b2986	yghT	693 3132153 3132845	+ orf, hypothetical protein	1	1	1	7
b2987	pitB	1500 3132894 3134393	- low-affinity phosphate transport			1	21
b2988	gss	1860 3134685 3136544	- glutathionylspermidine synthetase/amidase				15

b2989	yghU	915 3136701 3137615	+ orf, hypothetical protein		20
b2990	hybG	249 3137738 3137986	- hydrogenase-2 operon protein: may effect maturation of large subunit of		15
b2991	hybF	342 3137999 3138340	- may modulate levels of hydrogenase-2		15
b2992	hybE	489 3138333 3138821	- member of hyb operon		16
b2993	hybD	495 3138814 3139308	- probable processing element for hydrogenase-2		16
b2994	hybC	1704 3139308 3141011	- probable large subunit, hydrogenase-2		16
b2995	hybB	1179 3141008 3142186	- probable cytochrome Ni/Fe component of hydrogenase-2		16
b2996	hybA	987 3142176 3143162	- hydrogenase-2 small subunit		16
b2997	hybO	1119 3143165 3144283	- hydrogenase-2, small chain		16
b2998	yghW	288 3144472 3144759	- orf, hypothetical protein	1	16
b2999	-	411 3144878 3145288	- orf, hypothetical protein		8
b3000	-	426 3145288 3145713	- orf, hypothetical protein		6
b3001	yghZ	1041 3145919 3146959	+ putative reductase		19
b3002	yqhA	495 3146999 3147493	- orf, hypothetical protein		16
b3003	yghA	885 3147684 3148568	+ putative oxidoreductase		15
b3004	-	246 3148744 3148989	+ orf, hypothetical protein	1	5
b3005	exbD	426 3148840 3149265	- uptake of enterochelin; tonB-dependent uptake of B colicins		21
b3006	exbB	735 3149272 3150006	- uptake of enterochelin; tonB-dependent uptake of B colicins		21
b3007	-	156 3149999 3150154	- orf, hypothetical protein	1	13
b3008	metC	1188 3150258 3151445	+ cystathionine beta-lyase (beta-cystathionase)	1	21
b3009	yghB	660 3151585 3152244	+ orf, hypothetical protein		21
b3010	yqhC	1128 3152284 3153411	- putative ARAC-type regulatory protein	1	20
b3011	yqhD	1164 3153377 3154540	+ putative oxidoreductase		20
b3012	dkgA	711 3154762 3155472	+ 2,5-diketo-D-gluconate reductase A (beta-keto ester reductase)		19
b3013	yqhG	927 3155672 3156598	+ orf, hypothetical protein	1	8
b3014	yqhH	258 3156649 3156906	+ orf, hypothetical protein	1	10
b4469	ygiQ	2220 3156949 3159168	- conserved protein		16
b3017	sufI	1413 3159279 3160691	- suppressor of ftsI		21
b3018	plsC	738 3160766 3161503	- 1-acyl-sn-glycerol-3-phosphate acyltransferase		21
b3019	parC	2259 3161737 3163995	- DNA topoisomerase IV subunit A		21
b3020	ygiS	1608 3164133 3165740	- putative transport periplasmic protein		6
b3021	ygiT	396 3165873 3166268	- orf, hypothetical protein	1	6
b3022	ygiU	297 3166270 3166566	- orf, hypothetical protein	1	5
b3023	-	483 3166771 3167253	- orf, hypothetical protein	1	15
b3024	ygiW	393 3167306 3167698	- orf, hypothetical protein		21
b3025	ygiX	660 3167850 3168509	+ putative 2-component transcriptional regulator		16
b3026	ygiY	1350 3168506 3169855	+ putative 2-component sensor protein		16
b3027	ygiZ	333 3169901 3170233	- orf, hypothetical protein	1	4
b3028	mdaB	582 3170552 3171133	+ modulator of drug activity B	1	18
b3029	ygiN	315 3171164 3171478	+ orf, hypothetical protein		15
b3030	parE	1893 3171526 3173418	- DNA topoisomerase IV subunit B		21
b3031	yqiA	582 3173447 3174028	- orf, hypothetical protein		21
b3032	cpdA	828 3174028 3174855	- cyclic 3',5'-adenosine monophosphate phosphodiesterase		21
b3033	yqiB	423 3174880 3175302	- putative enzyme	1	20

b3034	yqiE	630 3175303 3175932	- orf, hypothetical protein	1				21
b3035	tolC	1488 3176131 3177618	+ outer membrane channel; specific tolerance to colicin E1; sequestration of daughter					21
b3036	ygiA	261 3177618 3177878	+ orf, hypothetical protein	1				8
b3037	ygiB	705 3177733 3178437	+ orf, hypothetical protein	1				21
b3038	ygiC	1161 3178443 3179603	+ putative synthetase/amidase					21
b3039	ygiD	816 3179641 3180456	- orf, hypothetical protein					20
b3040	ygiE	774 3180572 3181345	+ orf, hypothetical protein					15
b3041	ribB	654 3181835 3182488	- 3,4 dihydroxy-2-butanone-4-phosphate				1	21
b3042	yqiC	351 3182802 3183152	+ orf, hypothetical protein	1			1	21
b3043	ygiL	552 3183436 3183987	+ putative fimbrial-like protein			1	1	19
b3044	yi21_5	366 3184209 3184574	+ IS2 hypothetical protein			1	1	8
b3045	yi22_5	906 3184532 3185437	+ IS2 hypothetical protein	1		1	1	18
b3046	yqiG	2466 3185422 3187887	+ putative membrane protein	1		1	1	15
b3047	yqiH	759 3187894 3188652	+ putative membrane protein	1		1	1	4
b3048	yqiI	1065 3188654 3189718	+ orf, hypothetical protein	1		1	1	17
b3049	glgS	201 3189761 3189961	- glycogen biosynthesis, rpoS dependent			1	1	14
b3050	yqiJ	630 3190230 3190859	+ putative oxidoreductase	1		1	1	11
b3051	yqiK	1662 3190886 3192547	+ putative membrane protein				1	13
b3052	rfaE	1434 3193342 3194775	- bifunctional protein catalysing steps in LPS core precursor					21
b3053	glnE	2841 3194823 3197663	- adenylylating enzyme for glutamine					21
b3054	ygiF	1302 3197686 3198987	- orf, hypothetical protein					21
b3055	ygiM	621 3199229 3199849	+ orf, hypothetical protein					21
b3056	cca	1239 3199913 3201151	+ tRNA nucleotidyl transferase					21
b3057	bacA	822 3201332 3202153	- bacitracin resistance; possibly phosphorylates undecaprenol					20
b3058	ygiG	372 3202243 3202614	- putative kinase					21
b3059	ygiH	618 3202716 3203333	+ orf, hypothetical protein					21
b3060	ygiP	933 3203346 3204278	- putative transcriptional regulator LYSR-type				1	17
b3061	ttdA	912 3204485 3205396	+ L-tartrate dehydratase, subunit A				1	14
b3062	ttdB	606 3205393 3205998	+ L-tartrate dehydratase, subunit B					14
b3063	ygjE	1464 3206046 3207509	+ orf, hypothetical protein					10
b3064	ygjD	1014 3207552 3208565	- putative O-sialoglycoprotein endopeptidase					21
b3065	rpsU	216 3208803 3209018	+ 30S ribosomal subunit protein S21					21
b3066	dnaG	1746 3209129 3210874	+ DNA biosynthesis; DNA primase					21
b3067	rpoD	1842 3211069 3212910	+ RNA polymerase, sigma(70) factor; regulation of proteins induced at high temperatures					21
b3068	ygjF	507 3212989 3213495	- orf, hypothetical protein	1				14
b3070	tRNA-Ile3	76 3213620 3213695	+ tRNA-Ile					15
b3070	ygjH	765 3213749 3214513	- orf, hypothetical protein					19
b3071	ygjI	624 3214801 3215424	+ orf, hypothetical protein					18
b3072	aer	1521 3215578 3217098	- aerotaxis sensor receptor, flavoprotein					15
b3073	ygjG	1491 3217405 3218895	+ probable ornithine aminotransferase					9
b3074	ygjH	333 3218937 3219269	- putative tRNA					11
b3075	ebgR	984 3219488 3220471	+ regulator of ebg operon					

b3076	ebgA	3093 3220655 3223747	+ evolved beta-D-galactosidase, alpha subunit: cryptic gene					9
b3077	ebgC	450 3223744 3224193	+ evolved beta-D-galactosidase, beta subunit: cryptic gene					9
b3078	ygjI	1434 3224256 3225689	+ putative oxidoreductase			1		14
b3079	ygjJ	1071 3225823 3226893	+ orf, hypothetical protein			1		7
b3080	ygjK	2352 3226910 3229261	+ putative isomerase					9
b3081	fadH	2019 3229687 3231705	+ 2,4-dieonyl-CoA reductase, FMN-linked					19
b3082	ygjM	417 3231750 3232166	- orf, hypothetical protein					16
b3083	ygjN	315 3232163 3232477	- orf, hypothetical protein	1		1		14
b3084	ygjO	1167 3232761 3233927	- putative enzyme					20
b3085	ygjP	540 3233946 3234485	+ orf, hypothetical protein					20
b3086	ygjQ	693 3234562 3235254	+ orf, hypothetical protein					14
b3087	ygjR	1005 3235315 3236319	+ orf, hypothetical protein					20
b3088	ygjT	966 3236602 3237567	+ putative transport					21
b3089	ygjU	1245 3237966 3239210	+ putative transport					21
b3090	ygjV	552 3239215 3239766	- orf, hypothetical protein	1				15
b3091	uxaA	1488 3239849 3241336	- altronate hydrolase					14
b3092	uxaC	1413 3241351 3242763	- uronate isomerase					20
b3093	exuT	1419 3243126 3244544	+ transport of					19
b3094	exuR	792 3244659 3245450	+ negative regulator of exu regulon, exuT, uxaAC, and uxaB					15
b3095	yqjA	663 3245795 3246457	+ orf, hypothetical protein					21
b3096	yqjB	384 3246461 3246844	+ orf, hypothetical protein	1				20
b3097	yqjC	384 3246976 3247359	+ orf, hypothetical protein					18
b3098	yqjD	306 3247397 3247702	+ orf, hypothetical protein					21
b3099	yqjE	405 3247705 3248109	+ orf, hypothetical protein					21
b3100	yqjK	300 3248099 3248398	+ orf, hypothetical protein					21
b3101	yqjF	483 3248494 3248976	+ orf, hypothetical protein					20
b3102	yqjG	987 3249046 3250032	+ putative transferase					16
b3103	yhaH	366 3250326 3250691	+ putative cytochrome				1	16
b3104	yhaI	357 3250933 3251289	+ putative cytochrome	1			1	16
b3105	yhaJ	897 3251340 3252236	- putative transcriptional regulator LYSR-type					20
b3106	yhaK	702 3252341 3253042	+ orf, hypothetical protein					21
b3107	yhaL	171 3253059 3253229	+ orf, hypothetical protein					14
b4470	yhaM	1311 3253363 3254673	- conserved hypothetical protein					15
b3110	yhaO	1332 3254701 3256032	- putative transport system permease					10
b4471	tdcG	1365 3256307 3257671	- L-serine dehydratase					13
b3113	tdcF	453 3257743 3258195	- conserved protein					9
b3114	tdcE	2295 3258146 3260440	- probable formate acetyltransferase 3	1			1	15
b3115	tdcD	1221 3260474 3261694	- putative kinase				1	15
b3116	tdcC	1332 3261708 3263039	- anaerobically inducible L-threonine, L-serine permease			1	1	13
b3117	tdcB	990 3263061 3264050	- threonine dehydratase, catabolic			1	1	17
b3118	tdcA	939 3264149 3265087	- transcriptional activator of tdc operon	1		1	1	21
b3119	tdcR	345 3265276 3265620	+ threonine dehydratase operon activator protein	1		1	1	10
b3120	yhaB	561 3265855 3266415	+ orf, hypothetical protein	1		1	1	5
b3121	yhaC	1188 3266437 3267624	+ orf, hypothetical protein	1		1	1	5
b3124	garK	1227 3268647 3269873	- glycerate kinase I					21
b3125	garR	900 3269889 3270788	- tartronate semialdehyde					21
b3126	garL	771 3270809 3271579	- alpha-dehydro-beta-deoxy-D-glucarate aldolase					14
b3127	garP	1335 3271595 3272929	- putative transport				1	15
b3128	garD	1572 3273304 3274875	+ (D)-galactarate dehydrogenase				1	12
b3129	sohA	336 3275024 3275359	+ putative protease; htrA suppressor protein	1		1		6
b3130	yhaV	465 3275359 3275823	+ orf, hypothetical protein	1		1		7

b3131	agaR	810 3275878 3276687	- putative DEOR-type transcriptional regulator of aqa operon					12
b3132	agaZ	1281 3276936 3278216	+ putative tagatose 6-phosphate kinase 2					12
b3133	agaV	510 3278203 3278712	+ PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component					12
b3134	agaW	402 3278723 3279124	+ PTS system N-acetylgalactosamine-specific IIC component					12
b3135	agaA	504 3279144 3279647	+ putative N-acetylglucosamine-6-phosphate deacetylase					11
b3136	agaS	1155 3279998 3281152	+ putative tagatose-6-phosphate aldose/ketose					10
b3137	agaY	861 3281165 3282025	+ tagatose-bisphosphate aldolase 2					21
b3138	agaB	477 3282192 3282668	+ PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component			1		5
b3139	agaC	804 3282707 3283510	+ PTS system N-acetylglucosamine-specific IIC component			1		6
b3140	agaD	792 3283500 3284291	+ PTS system, N-acetylglucosamine enzyme IID component			1		12
b3141	agal	756 3284292 3285047	+ putative galactosamine-6-phosphate isomerase			1		6
b3142	yraH	585 3285448 3286032	+ putative fimbrial-like protein	1		1	1	9
b3143	yraI	696 3286112 3286807	+ putative chaperone	1		1	1	16
b3144	yraJ	2517 3286836 3289352	+ putative outer membrane protein	1			1	10
b3145	yraK	1092 3289363 3290454	+ putative fimbrial protein	1				8
b3146	yraL	861 3290497 3291357	- orf, hypothetical protein					21
b3147	yraM	2037 3291422 3293458	+ putative glycosylase					21
b3148	yraN	396 3293416 3293811	+ orf, hypothetical protein	1				21
b3149	yraO	591 3293831 3294421	+ orf, hypothetical protein	1				21
b3150	yraP	576 3294431 3295006	+ putative periplasmic protein					21
b3151	yraQ	1041 3295120 3296160	- orf, hypothetical protein					9
b3152	yraR	681 3296233 3296913	- orf, hypothetical protein					20
b3153	yhbO	561 3296954 3297514	+ orf, hypothetical protein					15
b3154	yhbP	444 3297494 3297937	- orf, hypothetical protein	1				21
b3155	yhbQ	303 3297988 3298290	+ orf, hypothetical protein					21
b3156	yhbS	504 3298277 3298780	- orf, hypothetical protein					21
b3157	yhbT	525 3298774 3299298	- orf, hypothetical protein					21
b3158	yhbU	996 3299507 3300502	+ putative collagenase					20
b3159	yhbV	897 3300493 3301389	+ orf, hypothetical protein					20
b3160	yhbW	1008 3301470 3302477	+ putative enzyme					20
b3161	mtr	1245 3302595 3303839	- tryptophan-specific transport protein					21
b3162	deaD	1941 3303993 3305933	- inducible ATP-independent RNA					21
b3163	nlpl	885 3306062 3306946	- lipoprotein					21
b3164	pnp	2205 3307055 3309259	- polynucleotide phosphorylase; cytidylate kinase activity					21
b3165	rpsO	270 3309437 3309706	- 30S ribosomal subunit protein S15					21
b3166	truB	945 3309855 3310799	- tRNA pseudouridine 5S synthase					21
b3167	rbfA	402 3310799 3311200	- ribosome-binding factor					21
b3168	infB	2673 3311364 3314036	- protein chain initiation factor IF-2					21
b3169	nusA	1488 3314061 3315548	- transcription pausing; L factor					21
b3170	yhbC	459 3315576 3316034	- orf, hypothetical protein					21
tRNA-Met	tRNA-Met	77 3316235 3316311	- tRNA-Met					

b3172	argG	1344 3316659 3318002	+ argininosuccinate synthetase		21
b3173	yhbX	1644 3318010 3319653	- putative alkaline phosphatase I	1 1 1	10
tRNA-Leu2	tRNA-Leu	87 3320094 3320180	- tRNA-Leu		
b3175	secG	333 3320195 3320527	- protein export - membrane protein		21
b3176	glmM	1338 3320755 3322092	- phosphoglucosamine mutase		21
b3177	folP	894 3322085 3322978	- 7,8-dihydropteroate synthase		20
b3178	hflB	1935 3323023 3324957	- degrades sigma32, integral membrane peptidase, cell division protein		20
b3179	rrmJ	630 3325057 3325686	- 23 S rRNA methyltransferase		21
b3180	yhbY	294 3325812 3326105	+ orf, hypothetical protein		21
b3181	greA	462 3326261 3326722	- transcription elongation factor: cleaves 3' nucleotide of paused mRNA		21
b3182	dacB	1434 3326985 3328418	+ D-alanyl-D-alanine carboxypeptidase, fraction B; penicillin-binding protein 4		21
b3183	yhbZ	1173 3328604 3329776	- putative GTP-binding factor		21
b3184	yhbE	966 3329792 3330757	- orf, hypothetical protein	1	19
b3185	rpmA	258 3330884 3331141	- 50S ribosomal subunit protein L27		21
b3186	rplU	312 3331162 3331473	- 50S ribosomal subunit protein L21	1	19
b3187	ispB	972 3331732 3332703	+ octaprenyl-diphosphate synthase		21
b3188	nlp	279 3332931 3333209	+ regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu		21
b3189	murA	1260 3333257 3334516	- first step in murein biosynthesis;UDP-N-glucosamine 1-carboxyvinyltransferase		21
b3190	yrbA	270 3334571 3334840	- orf, hypothetical protein	1	21
b3191	yrbB	390 3334985 3335374	- orf, hypothetical protein	1	21
b3192	yrbC	636 3335278 3335913	- orf, hypothetical protein		21
b3193	yrbD	552 3335932 3336483	- orf, hypothetical protein		21
b3194	yrbE	783 3336488 3337270	- orf, hypothetical protein		21
b3195	yrbF	810 3337278 3338087	- putative ATP-binding component of a transport system		21
b3196	yrbG	978 3338297 3339274	+ orf, hypothetical protein		21
b3197	yrbH	987 3339288 3340274	+ putative isomerase		21
b3198	yrbI	567 3340295 3340861	+ orf, hypothetical protein		21
b3199	yrbK	576 3340858 3341433	+ orf, hypothetical protein		21
b3200	yhbN	558 3341402 3341959	+ orf, hypothetical protein		21
b3201	yhbG	726 3341966 3342691	+ putative ATP-binding component of a transport system		21
b3202	rpoN	1434 3342739 3344172	+ RNA polymerase, sigma(54 or 60) factor; nitrogen and fermentation regulation		21
b3203	yhbH	288 3344195 3344482	+ probable sigma-54 modulation protein		18
b3204	ptsN	492 3344600 3345091	+ phosphotransferase system enzyme IIA, regulates N metabolism		21
b3205	yhbJ	855 3345137 3345991	+ orf, hypothetical protein		21

b3206	ptsO	273 3345988 3346260	+ phosphocarrier protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I Hnr					21
b3207	yrbL	633 3346474 3347106	+ orf, hypothetical protein					15
b3208	mtgA	729 3347103 3347831	- putative peptidoglycan enzyme					19
b3209	yhbL	663 3347828 3348490	- sigma cross-reacting protein 27A (SCRIP-					21
b3210	arcB	2337 3348711 3351047	- aerobic respiration sensor-response protein; histidine protein kinase/phosphatase, sensor for arcA					21
b3211	yhcC	930 3351143 3352072	- orf, hypothetical protein					20
b3212	gltB	4554 3352654 3357207	+ glutamate synthase, large subunit					21
b3213	gltD	1419 3357220 3358638	+ glutamate synthase, small subunit					21
b3214	gltF	765 3359198 3359962	+ regulator of gltBDF operon, induction of Ntr enzymes	1	1	1		7
b3215	yhcA	675 3360134 3360808	+ putative chaperone	1	1	1		7
b3216	yhcD	2382 3360829 3363210	+ putative outer membrane protein	1	1	1		8
b3217	yhcE	480 3363207 3363686	+ orf, hypothetical protein	1	1			2
b3218	trs5_10	1017 3363724 3364740	- IS5 transposase	1	1			2
b3219	yhcF	717 3364948 3365664	+ putative transcriptional regulator	1	1			7
b3220	yhcG	1128 3365849 3366976	+ orf, hypothetical protein	1				11
b3221	yhcH	465 3367036 3367500	- orf, hypothetical protein					19
b3222	nanK	909 3367497 3368405	- ManNAc kinase					19
b3223	nanE	690 3368369 3369058	- ManNAc epimerase					19
b3224	nanT	1521 3369106 3370626	- sialic acid transporter					19
b3225	nanA	894 3370705 3371598	- N-acetylneuraminatase (aldolase); catabolism of sialic acid: not K-12?					19
b3226	nanR	792 3371720 3372511	- Nan regulator				1	15
b3227	dcuD	1368 3372891 3374258	+ Cryptic C4-dicarboxylate carrier				1	7
b3228	sspB	498 3374301 3374798	- stringent starvation protein B					21
b3229	sspA	639 3374804 3375442	- regulator of transcription; stringent starvation protein A					21
b3230	rpsI	393 3375837 3376229	- 30S ribosomal subunit protein S9					21
b3231	rplM	429 3376245 3376673	- 50S ribosomal subunit protein L13					21
b3232	yhcM	1128 3376892 3378019	- orf, hypothetical protein	1				21
b3233	yhcB	405 3378207 3378611	+ orf, hypothetical protein					21
b3234	degQ	1368 3378765 3380132	+ serine endoprotease					20
b3235	degS	1068 3380222 3381289	+ protease					21
b3236	mdh	939 3381352 3382290	- malate dehydrogenase					21
b3237	argR	471 3382725 3383195	+ repressor of arg regulon; cer-mediated site specific				1	21
b3238	yhcN	315 3383509 3383823	+ orf, hypothetical protein		1		1	19
b3239	yhcO	273 3383879 3384151	- orf, hypothetical protein		1			20
b3240	yhcP	1968 3384243 3386210	- orf, hypothetical protein					20
b3241	yhcQ	933 3386216 3387148	- putative membrane protein					19
b3242	yhcR	273 3387156 3387428	- orf, hypothetical protein	1				19
b3243	yhcS	930 3387542 3388471	+ putative transcriptional regulator LYSR-type					19
b3244	tldD	1446 3388605 3390050	- suppresses inhibitory activity of CsrA					21
b4472	yhdP	3801 3390480 3394280	- orf, hypothetical protein					21
b3247	rng	1488 3394348 3395835	- RNase G					21
b3248	yhdE	594 3395807 3396400	- orf, hypothetical protein					21

b3249	mreD	489 3396409 3396897	- rod shape-determining protein	1				21
b3250	mreC	1104 3396897 3398000	- rod shape-determining protein					21
b3251	mreB	1104 3398066 3399169	- regulator of ftsI, penicillin binding protein 3, septation function					21
b3252	yhdA	1941 3399414 3401354	- orf, hypothetical protein					20
b3253	yhdH	975 3401506 3402480	+ putative dehydrogenase					21
b3254	-	102 3402538 3402639	- orf, hypothetical protein	1				7
b3255	accB	471 3403458 3403928	+ acetylCoA carboxylase, BCCP subunit; carrier of biotin					21
b3256	accC	1350 3403939 3405288	+ acetyl CoA carboxylase, biotin carboxylase					21
b3257	yhdT	243 3405397 3405639	+ orf, hypothetical protein					20
b3258	panF	1458 3405623 3407080	+ sodium/pantothenate symporter					21
b3259	prmA	882 3407092 3407973	+ methylase for 50S ribosomal subunit protein L11					21
b3260	yhdG	966 3408302 3409267	+ putative dehydrogenase	1				21
b3261	fis	297 3409293 3409589	+ site-specific DNA inversion stimulation factor; DNA-binding protein; a trans activator for					21
b3262	yhdJ	891 3409669 3410559	+ putative					18
b3263	yhdU	180 3410643 3410822	+ orf, hypothetical protein	1	1		1	11
b3264	envR	663 3410825 3411487	- putative transcriptional regulator	1			1	10
b3265	acrE	1158 3411886 3413043	+ transmembrane protein affects septum formation and cell membrane permeability				1	9
b3266	acrF	3105 3413055 3416159	+ integral transmembrane protein; acridine resistance					7
b3267	yhdV	222 3416412 3416633	+ orf, hypothetical protein				1	11
b3268	yhdW	918 3417171 3418088	+ putative periplasmic binding transport					11
b3269	yhdX	1182 3418156 3419337	+ putative transport system permease					7
b3270	yhdY	1107 3419344 3420450	+ putative transport system permease					11
b3271	yhdZ	759 3420458 3421216	+ putative ATP-binding component of a transport system	1				10
rrnD_5S	rrnD_5S	120 3421445 3421564	- rrnD_5S					
tRNA-Thr2	tRNA-Thr	76 3421602 3421677	- tRNA-Thr					
rrnD_5S	rrnD_5S	120 3421690 3421809	- rrnD_5S					
rrnD_23S	rrnD_23S	2904 3421902 3424805	- rrnD_23S					
tRNA-Ala4	tRNA-Ala	76 3424980 3425055	- tRNA-Ala					
tRNA-Ile4	tRNA-Ile	77 3425098 3425174	- tRNA-Ile					
rrnD_16S	rrnD_16S	1542 3425243 3426784	- rrnD_16S					
b3279	yrdA	771 3427042 3427812	+ putative transferase	1				20
b3280	yrdB	258 3427788 3428045	- orf, hypothetical protein	1				17
b3281	aroE	819 3428042 3428860	- dehydroshikimate reductase	1				21
b3282	yrdC	573 3428865 3429437	- orf, hypothetical protein					21
b3283	yrdD	543 3429442 3429984	- putative DNA topoisomerase	1				20
b3284	smg	474 3430013 3430486	- orf, hypothetical protein					20
b4473	smf	1125 3430458 3431582	- orf, hypothetical protein	1		1		21
b3287	def	510 3431712 3432221	+ peptide deformylase			1		21
b3288	fnt	948 3432236 3433183	+ 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase					21
b3289	rrmB	1290 3433229 3434518	+ 16S rRNA m5C967 methyltransferase					21
b3290	trkA	1377 3434540 3435916	+ transport of potassium					21

b3291	mscL	411 3436046 3436456	+ mechanosensitive channel				17
b3292	zntR	426 3436727 3437152	- Zn(II)-responsive transcriptional regulator	1			18
b3293	yhdN	369 3437163 3437531	- orf, hypothetical protein				13
b3294	rplQ	384 3437638 3438021	- 50S ribosomal subunit protein L17				21
b3295	rpoA	990 3438062 3439051	- RNA polymerase, alpha subunit				21
b3296	rpsD	621 3439077 3439697	- 30S ribosomal subunit protein S4				21
b3297	rpsK	390 3439731 3440120	- 30S ribosomal subunit protein S11				21
b3298	rpsM	357 3440137 3440493	- 30S ribosomal subunit protein S13				20
b3299	rpmJ	117 3440640 3440756	- 50S ribosomal subunit protein L36	1			18
b3300	prlA	1332 3440788 3442119	- putative ATPase subunit of translocase				21
b3301	rplO	435 3442127 3442561	- 50S ribosomal subunit protein L15				21
b3302	rpmD	180 3442565 3442744	- 50S ribosomal subunit protein L30				21
b3303	rpsE	504 3442748 3443251	- 30S ribosomal subunit protein S5				21
b3304	rplR	354 3443266 3443619	- 50S ribosomal subunit protein L18				21
b3305	rplF	534 3443629 3444162	- 50S ribosomal subunit protein L6				21
b3306	rpsH	393 3444175 3444567	- 30S ribosomal subunit protein S8, and				21
b3307	rpsN	306 3444601 3444906	- 30S ribosomal subunit protein S14				21
b3308	rplE	540 3444921 3445460	- 50S ribosomal subunit protein L5				21
b3309	rplX	315 3445475 3445789	- 50S ribosomal subunit protein L24				21
b3310	rplN	372 3445800 3446171	- 50S ribosomal subunit protein L14				21
b3311	rpsQ	255 3446336 3446590	- 30S ribosomal subunit protein S17				20
b3312	rpmC	192 3446590 3446781	- 50S ribosomal subunit protein L29				21
b3313	rplP	411 3446781 3447191	- 50S ribosomal subunit protein L16				21
b3314	rpsC	702 3447204 3447905	- 30S ribosomal subunit protein S3				21
b3315	rplV	333 3447923 3448255	- 50S ribosomal subunit protein L22				20
b3316	rpsS	279 3448270 3448548	- 30S ribosomal subunit protein S19	1			20
b3317	rplB	822 3448565 3449386	- 50S ribosomal subunit protein L2				21
b3318	rplW	303 3449404 3449706	- 50S ribosomal subunit protein L23				21
b3319	rplD	606 3449703 3450308	- 50S ribosomal subunit protein L4, regulates expression of S10				21
b3320	rplC	630 3450319 3450948	- 50S ribosomal subunit protein L3				21
b3321	rpsJ	312 3450981 3451292	- 30S ribosomal subunit protein S10	1			21
b3322	pioO	420 3451530 3451949	- calcium-binding protein required for initiation of chromosome replication	1	1		4
b3323	gspA	1470 3451951 3453420	- putative export protein A for general secretion pathway (GSP)	1		1	3
b3324	gspC	816 3453600 3454415	+ putative export protein C for general secretion pathway (GSP)	1	1	1	3

b3325	gspD	1965 3454387 3456351	+ putative export protein D for general secretion pathway (GSP)		10
b3326	gspE	1482 3456361 3457842	+ putative export protein E for general secretion pathway (GSP); Type II		11
b3327	gspF	1197 3457839 3459035	+ putative export protein F for general secretion pathway (GSP)		10
b3328	gspG	438 3459045 3459482	+ putative export protein G for general secretion pathway (GSP); pilin-		11
b3329	gspH	510 3459490 3459999	+ putative export protein H for general secretion pathway (GSP)		5
b3330	gspI	417 3459957 3460373	+ putative export protein I for general secretion pathway (GSP)	1	10
b3331	gspJ	588 3460366 3460953	+ putative export protein J for general secretion pathway (GSP)	1	11
b3332	gspK	984 3460946 3461929	+ putative export protein K for general secretion pathway (GSP)	1	11
b3333	gspL	1167 3461941 3463107	+ putative export protein L for general secretion pathway (GSP)	1	11
b3334	gspM	486 3463080 3463565	+ putative export protein M for general secretion pathway (GSP)	1	3
b3335	gspO	678 3463565 3464242	+ bifunctional prepilin peptidase: leader peptidase; N-methyltransferase; part of general secretion pathway (GSP)	1	17
b3336	bfr	477 3464271 3464747	- bacterioferritin, an iron storage homoprotein	1	20
b3337	bfd	195 3464819 3465013	- regulatory or redox component complexing with Bfr, in iron storage and mobility	1	17
b3338	chiA	2694 3465182 3467875	- periplasmic		7
b3339	tufA	1185 3468167 3469351	- protein chain elongation factor EF-Tu	1	20
b3340	fusA	2115 3469422 3471536	- GTP-binding protein chain elongation factor		21
b3341	rpsG	540 3471564 3472103	- 30S ribosomal subunit protein S7, initiates assembly		21
b3342	rpsL	375 3472200 3472574	- 30S ribosomal subunit protein S12		21
b3343	yheL	288 3472700 3472987	- orf, hypothetical protein	1	20
b3344	yheM	360 3472995 3473354	- orf, hypothetical protein		21
b3345	yheN	387 3473354 3473740	- orf, hypothetical protein		21
b3346	yheO	735 3473740 3474474	- orf, hypothetical protein		21
b3347	fkpA	813 3474629 3475441	- FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)		21
b3348	slyX	219 3475662 3475880	+ host factor for lysis of phiX174 infection		21
b3349	slyD	591 3475929 3476519	- FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)		21
b3350	kefB	1806 3476824 3478629	- K ⁺ efflux; NEM-activable K ⁺ /H ⁺		20
b3351	yheR	555 3478629 3479183	- putative NAD(P)H oxidoreductase		20
b3352	yheS	1914 3479311 3481224	+ putative ATP-binding component of a transport system		20
b3353	yheT	1023 3481224 3482246	+ orf, hypothetical protein		19

b3354	yheU	219	3482240	3482458	+ orf, hypothetical protein			21
b3355	prkB	870	3482512	3483381	+ probable phosphoribulokinase			20
b3356	yhfA	405	3483436	3483840	- orf, hypothetical protein			21
b3357	crp	633	3484142	3484774	+ cyclic AMP receptor protein			21
b3358	yhfK	2091	3484825	3486915	+ orf, hypothetical protein			17
b3359	argD	1221	3486982	3488202	- acetylornithine delta-aminotransferase			20
b3360	pabA	564	3488288	3488851	- p-aminobenzoate synthetase, component			21
b3361	fic	603	3488883	3489485	- induced in stationary phase, recognized by rpoS, affects cell			18
b3362	yhfG	168	3489475	3489642	- orf, hypothetical protein			14
b3363	ppiA	573	3489747	3490319	- peptidyl-prolyl cis-trans isomerase A (rotamase			21
b3364	yhfC	1182	3490590	3491771	+ putative transport			21
b3365	nirB	2544	3492033	3494576	+ nitrite reductase (NAD(P)H) subunit			20
b3366	nirD	327	3494573	3494899	+ nitrite reductase (NAD(P)H) subunit			20
b3367	nirC	555	3495277	3495831	+ nitrite reductase activity			19
b3368	cysG	1374	3495850	3497223	+ uroporphyrinogen III methylase; sirohaeme biosynthesis			20
b3369	yhfL	168	3497470	3497637	+ orf, hypothetical protein		1	13
b3370	yhfM	1389	3497881	3499269	+ putative amino acid/amine transport		1	6
b3371	yhfN	1044	3499269	3500312	+ putative transport	1		13
b4474	frlC	831	3500362	3501192	+ putative fructoselysine or fructoselysine 6-P isomerase			8
b3374	yhfQ	786	3501189	3501974	+ putative kinase			10
b3375	yhfR	798	3502008	3502805	+ putative transcriptional regulator			13
b3376	yhfS	1086	3502957	3504042	- orf, hypothetical protein			8
b3377	yhfT	1305	3504054	3505358	- putative transport system permease			7
b3378	yhfU	393	3505370	3505762	- orf, hypothetical protein			8
b3379	yhfV	879	3505734	3506612	- putative hydrolase			13
b3380	yhfW	1227	3506609	3507835	- putative mutase			7
b3381	yhfX	1164	3507835	3508998	- orf, hypothetical protein			7
b3382	yhfY	405	3509082	3509486	- orf, hypothetical protein	1		8
b3383	yhfZ	906	3509461	3510366	- orf, hypothetical protein			10
b3384	trpS	1005	3510656	3511660	- tryptophan tRNA synthetase			21
b3385	gph	759	3511653	3512411	- phosphoglycolate phosphatase			21
b3386	rpe	678	3512404	3513081	- D-ribulose-5-phosphate 3-epimerase			21
b3387	dam	837	3513099	3513935	- DNA adenine			21
b3388	damX	1287	3514042	3515328	- putative membrane protein; interferes with cell division			21
b3389	aroB	1089	3515420	3516508	- 3-dehydroquinate synthase			21
b3390	aroK	723	3516565	3517287	- shikimate kinase I	1		21
b3391	hofQ	1239	3517487	3518725	- putative transport	1		20
b3392	yrfA	444	3518637	3519080	- orf, hypothetical protein	1		14
b3393	yrfB	441	3519031	3519471	- orf, hypothetical protein	1		15
b3394	yrfC	540	3519455	3519994	- orf, hypothetical protein			20
b3395	yrfD	807	3519994	3520800	- orf, hypothetical protein			20
b3396	mrcA	2577	3520869	3523445	+ peptidoglycan synthetase; penicillin-binding protein 1A			21
b3397	yrfE	561	3523611	3524171	- orf, hypothetical protein			21
b3398	yrfF	2136	3524491	3526626	+ putative dehydrogenase			21
b3399	yrfG	714	3526646	3527359	+ putative phosphatase			20
b3400	hslR	402	3527370	3527771	+ Hsp15; DNA/RNA binding heat shock			21
b3401	hslO	885	3527790	3528674	+ Hsp33; redox regulated chaperone			21

b3402	yhgE	1725 3528737 3530461	- putative transport				15
b3403	pckA	1623 3530840 3532462	+ phosphoenolpyruvate carboxykinase				21
b3404	envZ	1353 3532538 3533890	- protein histidine kinase/phosphatase sensor for OmpR, modulates expression of ompF and ompC				21
b3405	ompR	720 3533887 3534606	- response regulator (sensor, EnvZ) affecting transcription of ompC and ompF: outer membrane protein				21
b3406	greB	513 3534798 3535310	+ transcription elongation factor and transcript cleavage				21
b3407	yhgF	2223 3535506 3537728	+ orf, hypothetical protein				21
b3408	feoA	228 3538185 3538412	+ ferrous iron transport protein A			1	20
b3409	feoB	2322 3538429 3540750	+ ferrous iron transport protein B			1	20
b3410	yhgG	237 3540750 3540986	+ orf, hypothetical protein				20
b3411	yhgA	879 3541189 3542067	+ orf, hypothetical protein	1			21
b3412	bioH	771 3542096 3542866	- biotin biosynthesis; reaction prior to pimeloyl CoA				21
b3413	yhgH	732 3542856 3543587	+ orf, hypothetical protein	1			20
b3414	yhgI	576 3543646 3544221	+ orf, hypothetical protein				21
b3415	gntT	1317 3544581 3545897	+ high-affinity transport of gluconate / gluconate permease				20
b3416	malQ	2085 3546008 3548092	- 4-alpha-glucanotransferase (amylomaltase)				21
b3417	malP	2394 3548102 3550495	- maltodextrin phosphorylase				18
b3418	malT	2706 3551107 3553812	+ positive regulator of mal regulon			1	18
b4475	rtcA	1017 3553855 3554871	- RNA 3'-terminal phosphate cyclase		1		12
b3421	rtcB	1227 3554875 3556101	- orf, hypothetical protein				12
b3422	rtcR	1599 3556290 3557888	+ sigma54-dependent regulator of rtcBA expression				10
b3423	glpR	759 3557870 3558628	- repressor of the glp operon				21
b3424	glpG	831 3558645 3559475	- protein of glp regulon				21
b3425	glpE	327 3559520 3559846	- rhodanese (thiosulfate:cyanide sulfurtransferase)				21
b3426	glpD	1506 3560036 3561541	+ sn-glycerol-3-phosphate				21
b3427	yzgL	294 3561747 3562040	- orf, hypothetical protein	1		1	10
b3428	glgP	2448 3562157 3564604	- glycogen				20
b3429	glgA	1434 3564623 3566056	- glycogen synthase				20
b3430	glgC	1296 3566056 3567351	- glucose-1-phosphate adenylyltransferase				20
b3431	glgX	1974 3567369 3569342	- part of glycogen operon, a glycosyl hydrolase, debranching				21
b3432	glgB	2187 3569339 3571525	- 1,4-alpha-glucan branching enzyme				21
b3433	asd	1104 3571798 3572901	- aspartate-semialdehyde dehydrogenase				21
b3434	yhgN	594 3573094 3573687	+ orf, hypothetical protein				15
b4476	gntU	1341 3573744 3575084	- split gene, low-affinity gluconate transport permease protein in GNT I system				16
b3437	gntK	489 3575088 3575576	- gluconokinase 2, thermoresistant				16
b3438	gntR	996 3575754 3576749	- regulator of gluconate (gnt) operon				21

b3439	yhhW	696 3576973 3577668	- orf, hypothetical protein				21
b3440	yhhX	1038 3577791 3578828	- putative regulator				14
b3441	yhhY	489 3579161 3579649	+ orf, hypothetical protein	1			14
b3442	yhhZ	1179 3579886 3581064	+ orf, hypothetical protein	1	1	1	8
b3443	yrhA	417 3581061 3581477	+ orf, hypothetical protein	1	1	1	7
b3444	insA_6	276 3581506 3581781	+ IS1 protein InsA	1	1	1	15
b3445	insB_6	504 3581700 3582203	+ IS1 protein InsB	1	1	1	15
b3446	yrhB	285 3582782 3583066	+ orf, hypothetical protein	1	1	1	3
b3447	ggt	1743 3583104 3584846	- gamma-glutamyltranspeptidase				19
b3448	yhhA	441 3584966 3585406	+ orf, hypothetical protein				15
b3449	ugpQ	744 3585393 3586136	- glycerophosphodiester phosphodiesterase, cytosolic				19
b3450	ugpC	1110 3586133 3587242	- ATP-binding component of sn-glycerol 3-phosphate transport system				17
b3451	ugpE	846 3587205 3588050	- sn-glycerol 3-phosphate transport system, integral membrane		1		19
b3452	ugpA	888 3588047 3588934	- sn-glycerol 3-phosphate transport system, integral membrane		1		19
b3453	ugpB	1317 3589032 3590348	- sn-glycerol 3-phosphate transport system; periplasmic binding protein				18
b3454	livF	726 3590747 3591472	- ATP-binding component of leucine				21
b3455	livG	768 3591462 3592229	- ATP-binding component of high-affinity branched-chain amino acid transport				21
b3456	livM	1278 3592226 3593503	- high-affinity branched-chain amino acid transport				21
b3457	livH	927 3593500 3594426	- high-affinity branched-chain amino acid transport system; membrane component				21
b3458	livK	1110 3594474 3595583	- high-affinity leucine-specific transport system; periplasmic binding protein				20
b3459	yhhK	384 3596007 3596390	+ orf, hypothetical protein			1	21
b3460	livJ	1104 3596578 3597681	- high-affinity branched-chain amino acid transport protein (ABC superfamily, peribind)				13
b3461	rpoH	855 3597952 3598806	- RNA polymerase, sigma(32) factor; regulation of proteins induced at high temperatures				21
b3462	ftsX	1059 3599051 3600109	- cell division membrane protein				21
b3463	ftsE	669 3600102 3600770	- ATP-binding component of a membrane-associated complex involved in cell				21
b3464	ftsY	1494 3600773 3602266	- cell division membrane protein				21
b3465	yhhF	597 3602416 3603012	+ orf, hypothetical protein				21
b3466	yhhL	270 3603002 3603271	+ orf, hypothetical protein				21
b3467	yhhM	360 3603274 3603633	- putative receptor	1			20
b3468	yhhN	627 3603774 3604400	+ putative enzyme				20
b3469	zntA	2199 3604474 3606672	+ zinc-transporting				21
b3470	sirA	246 3606774 3607019	- small protein required for cell growth; affects RpoS stability				21
b3471	yhhQ	666 3607240 3607905	+ orf, hypothetical protein				21

b3472	dcrB	612 3607924 3608535	+ periplasmic protein; required for phage C1 adsorption					20
b3473	yhhS	1260 3608539 3609798	- putative transport					16
b3474	yhhT	1131 3609807 3610937	+ orf, hypothetical protein					14
b3475	acpT	588 3610992 3611579	+ protein involved in phosphopantetheinyl transfer and holoACP synthesis					15
b3476	nikA	1575 3611690 3613264	+ periplasmic binding protein for nickel		1			10
b3477	nikB	945 3613264 3614208	+ transport of nickel, membrane protein		1			10
b3478	nikC	834 3614205 3615038	+ transport of nickel, membrane protein		1			10
b3479	nikD	765 3615038 3615802	+ ATP-binding protein of nickel transport system		1			11
b3480	nikE	807 3615799 3616605	+ ATP-binding protein of nickel transport system		1			10
b3481	nikR	402 3616611 3617012	+ nickel-responsive transcriptional regulator		1			15
b3482	rhsB	4236 3617215 3621450	+ rhsB protein in rhs element	1	1			18
b3483	yhhH	369 3621437 3621805	+ orf, hypothetical protein	1	1		1	2
b3484	yhhI	1137 3622401 3623537	+ putative receptor	1	1		1	7
b3485	yhhJ	1128 3623702 3624829	- putative transporter					19
b3486	yhiH	2736 3624826 3627561	- ribosome-associated ATPase, ATP-binding domain (N-terminal)					19
b3487	yhiI	1068 3627558 3628625	- putative membrane protein					19
b3488	yhiJ	1623 3628991 3630613	- orf, hypothetical protein	1	1		1	8
b3489	yhiK	372 3630875 3631246	- orf, hypothetical protein	1	1		1	7
b3490	yhiL	1239 3631243 3632481	- orf, hypothetical protein	1	1		1	7
b3491	yhiM	1152 3632765 3633916	+ orf, hypothetical protein	1	1		1	7
b3492	yhiN	1203 3634231 3635433	- orf, hypothetical protein					21
b3493	pitA	1500 3635665 3637164	+ low-affinity phosphate transport					21
b3494	yhiO	336 3637408 3637743	- orf, hypothetical protein	1				21
b3495	uspA	435 3638134 3638568	+ universal stress protein; broad regulatory					21
b3496	yhiP	1470 3638885 3640354	+ putative transport					14
b3497	yhiQ	753 3640403 3641155	- orf, hypothetical protein					21
b3498	priC	2043 3641163 3643205	- oligopeptidase A					21
b3499	yhiR	843 3643408 3644250	+ orf, hypothetical protein					21
b3500	gor	1353 3644322 3645674	+ glutathione oxidoreductase					21
b3501	arsR	354 3646551 3646904	+ transcriptional repressor of chromosomal ars					13
b3502	arsB	1311 3646937 3648247	+ arsenical pump membrane protein					14
b3503	arsC	426 3648260 3648685	+ arsenate reductase					11
b3504	yhiS	783 3649314 3650096	+ orf, hypothetical protein	1	1		1	8
b3505	trs5_11	1017 3650205 3651221	- IS5 transposase	1	1		1	2
b3506	slp	600 3651951 3652550	+ outer membrane protein induced after carbon starvation		1		1	10
b3507	yhiF	531 3652706 3653236	+ orf, hypothetical protein	1	1		1	10
b3508	yhiD	648 3653278 3653925	- putative transport		1		1	16
b3509	hdeB	339 3653989 3654327	- orf, hypothetical protein	1	1		1	19
b3510	hdeA	333 3654431 3654763	- orf, hypothetical protein		1		1	10
b3511	hdeD	573 3655018 3655590	+ orf, hypothetical protein		1		1	14
b3512	yhiE	528 3656389 3656916	+ orf, hypothetical protein	1	1		1	10
b3513	yhiU	1158 3657255 3658412	+ putative membrane protein				1	8
b3514	yhiV	3114 3658437 3661550	+ putative transport system permease				1	8
b3515	yhiW	729 3661913 3662641	- putative ARAC-type regulatory protein	1	1		1	9
b3516	gadX	825 3663009 3663833	- putative ARAC-type regulatory protein	1	1		1	11

b3517	gadA	1401 3664203 3665603	- glutamate decarboxylase isozyme			1	9
b3518	yhjA	1398 3665814 3667211	- putative cytochrome C peroxidase			1	18
b3519	treF	1650 3667615 3669264	+ cytoplasmic trehalase			1	14
b3520	yhjB	603 3669315 3669917	- putative regulator	1		1	15
b3521	yhjC	972 3670365 3671336	+ putative transcriptional regulator LYSR-type			1	20
b3522	yhjD	1014 3671385 3672398	+ orf, hypothetical protein				21
b3523	yhjE	1323 3672809 3674131	+ putative transport				20
b3524	yhjG	2076 3674313 3676388	- orf, hypothetical protein				18
b3525	yhjH	771 3676443 3677213	- orf, hypothetical protein				20
b3526	kdgK	1149 3677223 3678371	+ ketodeoxygluconokinas	1			20
b3527	yhjJ	1497 3678467 3679963	- orf, hypothetical protein				21
b3528	dctA	1287 3680184 3681470	- uptake of C4-dicarboxylic acids				21
b3529	yhjK	1956 3681653 3683608	- orf, hypothetical protein				21
b3530	yhjL	3423 3683723 3687145	- putative oxidoreductase subunit				8
b3531	bcsC	1107 3687178 3688284	- endo-1,4-D-glucanase				16
b3532	yhjN	2340 3688291 3690630	- orf, hypothetical protein				15
b3533	yhjO	2667 3690641 3693307	- putative cellulose synthase				11
b3534	yhjQ	729 3693256 3693984	- orf, hypothetical protein			1	14
b3535	yhjR	189 3694020 3694208	- orf, hypothetical protein		1	1	14
b3536	yhjS	1572 3694481 3696052	+ conserved hypothetical protein	1		1	14
b3537	yhjT	189 3696052 3696240	+ orf, hypothetical protein				15
b3538	yhjU	1680 3696237 3697916	+ orf, hypothetical protein				15
b4453	ldrD	108 3698003 3698110	- small toxic polypeptide				10
b3539	yhjV	1272 3698586 3699857	+ putative transporter protein				19
b3540	dppF	1005 3699887 3700891	- putative ATP-binding component of dipeptide transport system				21
b3541	dppD	984 3700888 3701871	- putative ATP-binding component of dipeptide transport system				21
b3542	dppC	903 3701882 3702784	- dipeptide transport system permease				21
b3543	dppB	1020 3702794 3703813	- dipeptide transport system permease protein 2				21
b3544	dppA	1608 3704121 3705728	- dipeptide transport system permease protein 1				20
b3546	yhjW	77 3706639 3706715	- tRNA-Pro				18
b3547	yhjX	1725 3706807 3708531	- orf, hypothetical protein				21
b3548	yhjY	1209 3708822 3710030	- putative resistance				16
b3549	tag	705 3710259 3710963	- putative lipase				21
b3550	yiaC	564 3711115 3711678	+ 3-methyl-adenine DNA glycosylase I,	1			19
b3551	bisC	441 3711675 3712115	+ orf, hypothetical protein				21
b3552	yiaD	2220 3712084 3714303	- biotin sulfoxide				19
b3553	tkrA	660 3714570 3715229	+ putative outer membrane protein				20
b3554	yiaF	987 3715321 3716307	+ 2-ketoaldonate				20
b3555	yiaG	831 3716357 3717187	- orf, hypothetical protein	1			13
b3556	cspA	291 3717501 3717791	+ orf, hypothetical protein	1		1	21
b4455	hokA	213 3718072 3718284	+ cold shock protein 7.4, transcriptional activator of hns			1	6
b3557	yi5A	153 3718471 3718623	- small toxic membrane polypeptide			1	10
b3558	t150	522 3718703 3719224	+ IS150 hypothetical	1	1	1	14
b3559	glyS	852 3719221 3720072	+ IS150 putative transposase	1	1	1	21
b3560	glyQ	2070 3720351 3722420	- glycine tRNA synthetase, beta				21
b3561	yiaH	912 3722430 3723341	- glycine tRNA synthetase, alpha				19
b3562	yiaA	996 3723910 3724905	+ orf, hypothetical protein			1	18
b3563	yiaB	441 3724947 3725387	- orf, hypothetical protein	1	1	1	18
		354 3725430 3725783	- orf, hypothetical protein	1	1	1	18

b3564	xylB	1455 3725940 3727394	- xylulokinase					20
b3565	xylA	1323 3727466 3728788	- D-xylose isomerase			1		18
b3566	xylF	993 3729154 3730146	+ xylose binding protein			1		13
			transport system					
b3567	xylG	1542 3730224 3731765	+ putative ATP-binding			1		13
			protein of xylose					
			transport system					
b3568	xylH	1182 3731743 3732924	+ putative xylose					13
			transport, membrane					
b3569	xylR	1179 3733002 3734180	+ putative regulator of xyl					18
			operon					
b3570	bax	825 3734376 3735200	- putative ATP-binding	1				15
			protein					
b3571	malS	2031 3735520 3737550	+ alpha-amylase					17
b3572	avtA	1254 3737728 3738981	+ alanine-alpha-					19
			ketoisovalerate (or					
			valine-pyruvate)					
			transaminase.					
b3573	yiaI	474 3739132 3739605	- orf, hypothetical protein	1				20
b3574	yiaJ	849 3739707 3740555	- transcriptional					10
			repressor of the yiaK-S					
b3575	yiaK	999 3740756 3741754	+ putative dehydrogenase					10
b3576	yiaL	468 3741766 3742233	+ putative lipase	1	1			8
b3577	yiaM	474 3742351 3742824	+ orf, hypothetical protein	1	1		1	17
b3578	yiaN	1278 3742827 3744104	+ putative membrane				1	9
			protein					
b3579	yiaO	987 3744117 3745103	+ putative solute-binding				1	5
			transport protein					
b3580	lyxK	1497 3745107 3746603	+ L-xylulose kinase,					11
b3581	sgbH	663 3746600 3747262	+ probable 3-hexulose 6-					8
			phosphate synthase					
b3582	sgbU	894 3747222 3748115	+ 3-epimerase					12
b3583	sgbE	696 3748109 3748804	+ L-ribulose-5-phosphate					7
			4-epimerase					
b3584	yiaT	741 3749151 3749891	- putative outer				1	4
			membrane protein					
b3585	yiaU	975 3750015 3750989	+ putative transcriptional				1	4
			regulator LYSR-type					
b3586	yiaV	1137 3750986 3752122	- putative membrane				1	4
			protein					
b3587	yiaW	324 3752128 3752451	- orf, hypothetical protein				1	4
b3588	aldB	1629 3752996 3754624	- aldehyde					16
			dehydrogenase B					
			(lactaldehyde					
b3589	yiaY	1152 3754699 3755850	- putative oxidoreductase				1	18
b3590	selB	1845 3756040 3757884	- selenocysteinyl-tRNA-					18
			specific translation					
b3591	selA	1392 3757881 3759272	- selenocysteine					20
			synthase: L-seryl-tRNA					
			(Ser) selenium					
b3592	yibF	609 3759370 3759978	- putative S-transferase				1	15
b3593	rhsA	4134 3760206 3764339	+ rhsA protein in rhs	1	1		1	18
			element					
b3594	yibA	843 3764360 3765202	+ orf, hypothetical protein	1	1		1	3
b3595	yibJ	702 3765244 3765945	+ orf, hypothetical protein	1	1		1	
b3596	yibG	462 3766200 3766661	+ orf, hypothetical protein	1	1		1	6
b3597	yibH	1137 3768266 3769402	- putative membrane					9
			protein					
b3598	yibI	363 3769405 3769767	- orf, hypothetical protein	1				9
b3599	mtlA	1914 3770304 3772217	+ PTS system, mannitol-					19
			specific enzyme IIABC					
			components					
b3600	mtlD	1149 3772447 3773595	+ mannitol-1-phosphate					19
			dehydrogenase					
b3601	mtlR	588 3773595 3774182	+ repressor for mtl	1				18
b3602	yibL	363 3774688 3775050	+ orf, hypothetical protein					19
b3603	lldP	1656 3775422 3777077	+ L-lactate permease					16
b3604	lldR	777 3777077 3777853	+ transcriptional regulator					15
b3605	lldD	1191 3777850 3779040	+ L-lactate					21
b3606	yibK	474 3779238 3779711	+ orf, hypothetical protein					21
b3607	cysE	822 3779764 3780585	- serine acetyltransferase					21
b3608	gpsA	1020 3780665 3781684	- glycerol-3-phosphate					21
			dehydrogenase (NAD+)					

b3609	secB	468 3781684 3782151	- protein export; molecular chaperone; may bind to signal					21
b3610	grxC	252 3782214 3782465	- glutaredoxin 3					19
b3611	yibN	432 3782607 3783038	- orf, hypothetical protein					21
b3612	yibO	1545 3783283 3784827	+ putative 2,3- bisphosphoglycerate- independent phosphoglycerate putative membrane protein					19
b3613	yibP	1284 3784837 3786120	+ orf, hypothetical protein					21
b3614	yibQ	834 3786250 3787083	+ putative regulator	1			1	18
b3615	yibD	1035 3787070 3788104	- threonine				1	19
b3616	tdh	1026 3788343 3789368	- 2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)				1	21
b3617	kbl	1197 3789378 3790574	- involved in lipopolysaccharide biosynthesis	1	1		1	21
b3618	htrL	873 3790849 3791721	+ ADP-L-glycero-D- mannoheptose-6- epimerase			1	1	5
b3619	rfaD	933 3792010 3792942	+ ADP-heptose--lps heptosyltransferase II; lipopolysaccharide core biosynthesis			1	1	21
b3620	rfaF	1047 3792952 3793998	+ heptosyl transferase I; lipopolysaccharide core biosynthesis			1	1	21
b3621	rfaC	960 3794002 3794961	+ O-antigen ligase; lipopolysaccharide core biosynthesis	1	1		1	21
b3622	rfaL	1260 3794971 3796230	- probably hexose transferase; lipopolysaccharide core biosynthesis	1	1		1	8
b3623	rfaK	1074 3796262 3797335	- lipopolysaccharide core biosynthesis	1	1		1	2
b3624	rfaZ	852 3797368 3798219	- lipopolysaccharide core biosynthesis	1	1		1	8
b3625	rfaY	699 3798290 3798988	- lipopolysaccharide core biosynthesis	1	1		1	15
b3626	rfaJ	1017 3799006 3800022	- UDP-D- glucose:(galactosyl)lipo polysaccharide glucosyltransferase	1	1		1	16
b3627	rfaI	1020 3800062 3801081	- UDP-D- galactose:(glucosyl)lipo polysaccharide- alpha- 1,3-D-	1	1		1	16
b3628	rfaB	1110 3801081 3802190	- UDP-D- galactose:(glucosyl)lipo polysaccharide-1, 6- D- galactosyltransferase	1	1		1	10
b3629	rfaS	936 3802204 3803139	- lipopolysaccharide core biosynthesis	1	1		1	2
b3630	rfaP	798 3803176 3803973	- lipopolysaccharide core biosynthesis; phosphorylation of core heptose; attaches phosphate-containing substrate to LPS on glucosyltransferase I;	1	1		1	15
b3631	rfaG	1125 3803966 3805090	- lipopolysaccharide core biosynthesis	1	1		1	17
b3632	rfaQ	1035 3805087 3806121	- lipopolysaccharide core biosynthesis	1	1		1	21
b3633	kdtA	1278 3806563 3807840	+ 3-deoxy-D-manno- octulosonic-acid transferase (KDO transferase)					21
b3634	coaD	480 3807848 3808327	+ phosphopantetheine adenyltransferase					21

b3635	mutM	810 3808366 3809175	- formamidopyrimidine DNA glycosylase	21
b3636	rpmG	168 3809273 3809440	- 50S ribosomal subunit protein L33	21
b3637	rpmB	237 3809461 3809697	- 50S ribosomal subunit protein L28	20
b3638	radC	675 3809914 3810588	- DNA repair protein	20
b3639	dfp	1293 3810682 3811974	+ flavoprotein affecting synthesis of DNA and pantothenate	21
b3640	dut	456 3811955 3812410	+ deoxyuridinetriphosphat ase	21
b3641	ttk	639 3812475 3813113	+ putative transcriptional regulator	21
b3642	pyrE	642 3813150 3813791	- orotate phosphoribosyltransfera se	21
b3643	rph	687 3813886 3814572	- RNase PH	21
b3644	yicC	864 3814699 3815562	+ putative alpha helix	21
b3645	dinD	837 3815771 3816607	+ DNA-damage-inducible protein	10
b3646	yicG	672 3816843 3817514	+ orf, hypothetical protein	21
b3647	yicF	1689 3817511 3819199	- putative enzyme	17
b3648	gmk	624 3819451 3820074	+ guanylate kinase	21
b3649	rpoZ	276 3820129 3820404	+ RNA polymerase, omega subunit	21
b3650	spoT	2109 3820423 3822531	+ (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'- pyrophosphohydrolase	21
b3651	trmH	690 3822538 3823227	+ tRNA (Guanosine-2'-O-)methyltransferase	20
b3652	recG	2082 3823233 3825314	+ DNA helicase, resolution of Holliday junctions. branch	21
b3653	gltS	1206 3825483 3826688	- glutamate transport	20
b3654	yicE	1392 3826968 3828359	+ putative transport	21
b3655	yicH	1710 3828480 3830189	+ orf, hypothetical protein	21
b3656	yicI	2319 3830242 3832560	- orf, hypothetical protein	19
b3657	yicJ	1440 3832570 3834009	- putative permease	20
tRNA-Sec ¹	tRNA-Sec	95 3834245 3834339	+ tRNA-Sec	1
b3659	yicK	1185 3834976 3836160	+ two-module transport protein	16
b3660	yicL	924 3836271 3837194	+ putative permease transporter	12
b3661	nlpA	819 3837198 3838016	- lipoprotein-28	9
b3662	yicM	1356 3838572 3839927	- putative transport	16
b3663	yicN	480 3839973 3840452	- orf, hypothetical protein	19
b3664	yicO	1413 3840478 3841890	- orf, hypothetical protein	5
b3665	ade	1767 3841987 3843753	+ Mn-dependent adenine deaminase (cryptic)	10
b3666	uhpT	1392 3843799 3845190	- hexose phosphate transport protein	14
b3667	uhpC	1323 3845328 3846650	- regulator of uhpT	21
b3668	uhpB	1506 3846657 3848162	- sensor histidine protein kinase phosphorylates UhpA	19
b3669	uhpA	591 3848159 3848749	- response regulator, positive activator of uhpT transcription (sensor. uhpB)	19
b3670	ilvN	291 3848825 3849115	- acetolactate synthase I, valine sensitive, small subunit	20
b3671	ilvB	1689 3849119 3850807	- acetolactate synthase I, valine-sensitive, large subunit	20
b3672	ivbL	99 3850913 3851011	- ilvB operon leader	8
b3673	emrD	1191 3851939 3853129	+ 2-module integral membrane pump; multidrug resistance	15
b3674	yidF	498 3853137 3853634	- putative transcriptional regulator	15

b3675	yidG	363 3853631 3853993	- orf, hypothetical protein	1		15
b3676	yidH	348 3853983 3854330	- orf, hypothetical protein			14
b3677	yidI	450 3854438 3854887	+ orf, hypothetical protein	1		8
b3678	yidJ	1494 3854934 3856427	- putative sulfatase			14
b3679	yidK	1716 3856424 3858139	- putative cotransporter		1	12
b3680	yidL	924 3858276 3859199	+ putative ARAC-type regulatory protein	1	1	14
b3681	glvG	639 3859372 3860010	- probable 6-phospho-beta-glucosidase			7
b3682	glvB	486 3860010 3860495	- PTS system, arbutin-like IIB component			9
b3683	glvC	1368 3860520 3861887	- PTS system, arbutin-like IIC component	1		7
b3684	yidP	717 3861922 3862638	+ putative transcriptional regulator			16
b3685	yidE	1686 3862635 3864320	- putative transport			20
b3686	ibpB	435 3864492 3864926	- heat shock protein			20
b3687	ibpA	414 3865032 3865445	- heat shock protein			20
b3688	yidQ	408 3865676 3866083	+ orf, hypothetical protein	1		21
b3689	yidR	1251 3866085 3867335	- orf, hypothetical protein			18
b3690	yidS	1086 3867379 3868464	+ orf, hypothetical protein			9
b3691	dgoT	1338 3868461 3869798	- D-galactonate transport			10
b4478	dgoD	1149 3869873 3871021	- galactonate			19
b4477	dgoA	618 3871018 3871635	- 2-oxo-3-deoxygalactonate 6-			5
b3693	dgoK	879 3871619 3872497	- 2-oxo-3-deoxygalactonate			9
b4479	dgoR	690 3872494 3873183	- transcriptional repressor for galactonate utilization			9
b3696	yidX	657 3873461 3874117	+ putative replicase	1	1	14
b3697	yidA	813 3874163 3874975	- orf, hypothetical protein			19
b3698	yidB	408 3875090 3875497	- orf, hypothetical protein			10
b3699	gyrB	2415 3875728 3878142	- DNA gyrase subunit B, type II topoisomerase, ATPase activity			21
b3700	recF	1074 3878171 3879244	- ssDNA and dsDNA binding, ATP binding			21
b3701	dnaN	1101 3879244 3880344	- DNA polymerase III, beta-subunit			21
b3702	dnaA	1404 3880349 3881752	- DNA biosynthesis; initiation of chromosome replication: can be			20
b3703	rpmH	141 3882359 3882499	+ 50S ribosomal subunit protein L34			21
b3704	mpA	360 3882516 3882875	+ RNase P, protein component; protein C5	1		21
b3705	yidC	1647 3883099 3884745	+ 60 KD inner-membrane protein			21
b3706	trmE	1365 3884851 3886215	+ GTPase involved in synthesis of hypermodified nucleoside, tRNA 5-methylaminomethyl-2-thiouridine; involved in			21
b3707	tnaL	75 3886458 3886532	+ tryptophanase leader peptide		1	7
b3708	tnaA	1431 3886738 3888168	+ tryptophanase		1	8
b3709	tnaB	1248 3888259 3889506	+ low affinity tryptophan permease			9
b3710	yidY	1176 3889638 3890813	+ putative transport			21
b3711	yidZ	960 3890788 3891747	+ putative transcriptional regulator LYSR-type			12
b3712	yieE	762 3891892 3892653	+ orf, hypothetical protein	1		16
b3713	yieF	567 3892675 3893241	+ orf, hypothetical protein			13
b3714	yieG	1338 3893295 3894632	- putative membrane / transport protein			20
b3715	yieH	666 3894797 3895462	+ putative phosphatase			19
b3716	yieI	468 3895529 3895996	+ orf, hypothetical protein	1	1	7
b3717	yieJ	588 3896045 3896632	+ orf, hypothetical protein	1	1	2

b3718	yieK	723 3896694 3897416	- pyrimidine-specific nucleoside hydrolase			5
b3719	yieL	1203 3897431 3898633	- putative xylanase		1	6
b3720	yieC	1617 3898627 3900243	- putative receptor		1	7
b3721	bglB	1413 3900312 3901724	- phospho-beta-glucosidase B; cryptic		1	11
b3722	bglF	1878 3901743 3903620	- PTS system beta-glucosides, enzyme II, cryptic		1	8
b3723	bglG	837 3903754 3904590	- positive regulation of bgl operon	1	1	9
b3724	phoU	726 3904876 3905601	- negative regulator for pho regulon and putative enzyme in phosphate metabolism			21
b3725	pstB	774 3905616 3906389	- ATP-binding component of high-affinity phosphate-specific transport			21
b3726	pstA	891 3906572 3907462	- high-affinity phosphate-specific transport			21
b3727	pstC	960 3907462 3908421	- high-affinity phosphate-specific transport system, cytoplasmic membrane component			21
b3728	pstS	1041 3908508 3909548	- high-affinity phosphate-specific transport system; periplasmic phosphate-binding			21
b3729	glmS	1830 3909862 3911691	- L-glutamine:D-fructose-6-phosphate aminotransferase			21
b3730	glmU	1371 3911853 3913223	- N-acetyl glucosamine-1-phosphate uridylyltransferase			21
b3731	atpC	420 3913576 3913995	- membrane-bound ATP synthase, F1 sector, epsilon-subunit			21
b3732	atpD	1383 3914016 3915398	- membrane-bound ATP synthase, F1 sector, beta-subunit			21
b3733	atpG	864 3915425 3916288	- membrane-bound ATP synthase, F1 sector, gamma-subunit			21
b3734	atpA	1542 3916339 3917880	- membrane-bound ATP synthase, F1 sector, alpha-subunit			21
b3735	atpH	534 3917893 3918426	- membrane-bound ATP synthase, F1 sector, delta-subunit			21
b3736	atpF	471 3918441 3918911	- membrane-bound ATP synthase, F0 sector, subunit b			21
b3737	atpE	240 3918973 3919212	- membrane-bound ATP synthase, F0 sector, subunit c			21
b3738	atpB	816 3919259 3920074	- membrane-bound ATP synthase, F0 sector, subunit a			20
b3739	atpI	393 3920083 3920475	- membrane-bound ATP synthase, dispensable protein, affects expression of atoB	1	1	21
b3740	gidB	624 3921080 3921703	- glucose-inhibited division; chromosome			21
b3741	gidA	1890 3921767 3923656	- glucose-inhibited division; chromosome			21
b3742	mioC	444 3924035 3924478	- initiation of chromosome replication			21
b3743	asnC	459 3924568 3925026	- regulator for asnA, asnC and gidA			21
b3744	asnA	993 3925178 3926170	+ asparagine synthetase			21
b3745	yieM	1452 3926175 3927626	- orf, hypothetical protein			21

b3746	yieN	1521 3927620 3929140	- putative 2-component regulator	21
b3747	kup	1869 3929339 3931207	+ low affinity potassium transport system	20
b3748	rbsD	456 3931338 3931793	+ D-ribose high-affinity transport system; membrane-associated protein	20
b3749	rbsA	1506 3931801 3933306	+ ATP-binding component of D-ribose high-affinity transport	13
b3750	rbsC	966 3933311 3934276	+ D-ribose high-affinity transport system	20
b3751	rbsB	891 3934301 3935191	+ D-ribose periplasmic binding protein	16
b3752	rbsK	930 3935317 3936246	+ ribokinase	21
b3753	rbsR	993 3936250 3937242	+ regulator for rbs operon	16
b3754	yieO	1428 3937208 3938635	- putative transport protein (MFS family)	18
b3755	yieP	693 3938658 3939350	- orf, hypothetical protein	18
rrnC_16S	rrnC_16S	1542 3939831 3941372	+ rrnC_16S	
tRNA-Glu2	tRNA-Glu	76 3941458 3941533	+ tRNA-Glu	
rrnC_23S	rrnC_23S	2904 3941727 3944630	+ rrnC_23S	
rrnC_5S	rrnC_5S	120 3944723 3944842	+ rrnC_5S	
tRNA-Asp	tRNA-Asp	77 3944895 3944971	+ tRNA-Asp	
tRNA-Trp	tRNA-Trp	76 3944980 3945055	+ tRNA-Trp	
b4480	hdfR	840 3945151 3945990	- transcriptional regulator of the flhDC operon	21
b3764	yifE	339 3946109 3946447	+ orf, hypothetical protein	21
b3765	yifB	1551 3946472 3948022	- putative 2-component regulator	15
b3766	ilvL	99 3948345 3948443	+ ilvGEDA operon leader peptide	1
b4488	ilvG	1645 3948583 3950227	+ acetolactate synthase II, valine insensitive, large subunit	
b3769	ilvM	264 3950224 3950487	+ acetolactate synthase II, valine insensitive, small subunit	20
b3770	ilvE	930 3950507 3951436	+ branched-chain amino-acid aminotransferase	21
b3771	ilvD	1851 3951501 3953351	+ dihydroxyacid dehydratase	21
b3772	ilvA	1545 3953354 3954898	+ threonine deaminase (dehydratase)	21
b3773	ilvY	894 3954950 3955843	- positive regulator for	21
b3774	ilvC	1476 3955993 3957468	+ ketol-acid reductoisomerase	21
b3775	ppiC	282 3957555 3957836	- peptidyl-prolyl cis-trans isomerase C (rotamase C)	20
b3776	-	276 3958035 3958310	- orf, hypothetical protein	4
b3777	yifN	261 3958265 3958525	- orf, hypothetical protein	4
b3778	rep	2022 3958700 3960721	+ rep helicase, a single-stranded DNA dependent ATPase	21
b3779	gppA	1485 3960768 3962252	- guanosine pentaphosphatase; exopolyphosphatase	19
b3780	rhIB	1266 3962388 3963653	- putative ATP-dependent RNA	20
b3781	trxA	384 3963730 3964113	+ thioredoxin 1	21
b3782	rhoL	102 3964254 3964355	+ rho operon leader	10
b3783	rho	1260 3964440 3965699	+ transcription termination factor Rho; polarity suppressor	21
b3784	rfe	1104 3965939 3967042	+ UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase; synthesis of enterobacterial common antigen (ECA)	21

b3785	wzzE	1050 3967051 3968100	+ putative transport					21
b3786	wecB	1131 3968156 3969286	+ UDP-N-acetyl glucosamine -2- epimerase; synthesis of enterobacterial common antigen (ECA)					21
b3787	wecC	1263 3969283 3970545	+ UDP-N-acetyl-D- mannosaminuronic acid dehydrogenase; synthesis of enterobacterial common antigen (ECA)					21
b3788	rffG	1068 3970545 3971612	+ dTDP-glucose 4,6- dehydratase					20
b3789	rffH	882 3971631 3972512	+ glucose-1-phosphate thymidyltransferase					20
b3790	wecD	546 3972619 3973164	+ orf, hypothetical protein					21
b3791	wecE	1131 3973169 3974299	+ putative regulator					21
b3792	wzxE	1251 3974301 3975551	+ putative cytochrome					21
b4481	rffT	1080 3975548 3976627	+ TDP-Fuc4NAc:lipidII transferase	1				21
b3793	wecF	1353 3976624 3977976	+ TDP-Fuc4NAc:lipidII transferase; synthesis of enterobacterial common antigen (ECA)					21
b3794	wecG	741 3977979 3978719	+ probable UDP-N-acetyl- D-mannosaminuronic acid transferase; synthesis of enterobacterial putative amino acid/amine transport					21
b3795	yifK	1386 3978910 3980295	+ tRNA-Arg					21
tRNA-Arg7	tRNA-Arg	77 3980398 3980474	+ tRNA-His					
tRNA-His1	tRNA-His	77 3980532 3980608	+ tRNA-Leu					
tRNA-Leu	tRNA-Leu	87 3980629 3980715	+ tRNA-Pro					
tRNA-Pro3	tRNA-Pro	77 3980758 3980834	+ putative arylsulfatase regulator					18
b3800	aslB	1236 3980981 3982216	- arylsulfatase			1		6
b3801	aslA	1656 3982375 3984030	- a late step of protoheme IX synthesis					21
b3802	hemY	1197 3984709 3985905	- uroporphyrinogen III methylase					21
b3803	hemX	1182 3985908 3987089	- uroporphyrinogen III synthase					21
b3804	hemD	741 3987111 3987851	- porphobilinogen deaminase = hydroxymethylbilane synthase					21
b3805	hemC	942 3987848 3988789	+ adenylate cyclase					21
b3806	cyaA	2547 3989176 3991722	+ orf, hypothetical protein	1				7
b3808	yzcX	486 3991873 3992358	+ diaminopimelate epimerase					21
b3809	dapF	828 3992782 3993609	+ orf, hypothetical protein					21
b3810	yigA	708 3993606 3994313	+ site-specific recombinase, acts on cer sequence of ColE1, effects chromosome segregation at cell					21
b3811	xerC	897 3994310 3995206	+ putative phosphatase					21
b3812	yigB	717 3995206 3995922	+ DNA-dependent ATPase I and helicase					21
b3813	uvrD	2163 3996006 3998168	- orf, hypothetical protein	1				8
b4482	yigE	765 3998315 3999079	+ Mg2+ transport, system					21
b3816	corA	951 3999449 4000399	- orf, hypothetical protein	1	1		1	8
b3817	yigF	381 4000442 4000822	- orf, hypothetical protein	1	1		1	10
b3818	yigG	417 4000836 4001252	- orf, hypothetical protein				1	21
b3819	rarD	891 4001311 4002201	- orf, hypothetical protein					21
b3820	yigI	486 4002253 4002738	+ outer membrane phospholipase A					20
b3821	pIdA	870 4002885 4003754	+ ATP-dependent DNA helicase					21
b3822	recQ	1830 4003887 4005716	+ amino acid exporter (threonine)					20
b3823	rhtC	621 4005780 4006400						

b3824	rhtB	621 4006462 4007082	- amino acid exporter (homoserine, HSL)	1	21
b3825	pIdB	1023 4007193 4008215	+ lysophospholipase L(2)		21
b3826	yigL	801 4008223 4009023	+ conserved protein, phosphatase-like		21
b3827	yigM	900 4009099 4009998	+ orf, hypothetical protein		20
b3828	metR	954 4009886 4010839	- regulator for metE and metH		21
b3829	metE	2262 4011076 4013337	+ tetrahydropteroyltryglutamate methyltransferase		21
b3830	ysgA	816 4013377 4014192	- putative enzyme	1	19
b3831	udp	762 4014454 4015215	+ uridine phosphorylase		21
b3832	yigN	1428 4015356 4016783	+ putative alpha helix		21
b3833	ubiE	756 4016878 4017633	+ 2-octaprenyl-6-methoxy-1,4-benzoquinone --> 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone		21
b3834	yigP	606 4017647 4018252	+ orf, hypothetical protein		21
b3835	ubiB	1641 4018249 4019889	+ 2-octaprenylphenol hydroxylase of ubiquinone biosynthetic		21
b3836	tatA	312 4019926 4020237	+ component of Sec-independent		21
b3838	tatB	516 4020241 4020756	+ component of Sec-independent		21
b3839	tatC	777 4020759 4021535	+ component of Sec-independent		21
b4483	tatD	783 4021577 4022359	+ cytoplasmic Dnase		17
b3842	rfaH	489 4022356 4022844	- transcriptional activator affecting biosynthesis of lipopolysaccharide core. F pilin. and		21
b3843	ubiD	1494 4023011 4024504	+ 3-octaprenyl-4-hydroxybenzoate decarboxylase		21
b3844	fre	702 4024550 4025251	+ ferrisiderophore reductase; flavin reductase (NADPH:flavin		21
b3845	fadA	1164 4025632 4026795	- thiolase I; 3-ketoacyl-CoA thiolase; acetyl-CoA transferase		21
b3846	fadB	2190 4026805 4028994	- 4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxybutyryl-CoA epimerase; delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase; enoyl-CoA hydratase		20
b3847	pepQ	1332 4029184 4030515	+ proline dipeptidase		21
b3848	yigZ	618 4030512 4031129	+ orf, hypothetical protein		20
b3849	trkH	1452 4031168 4032619	+ potassium uptake, requires TrkE		20
b3850	hemG	546 4032631 4033176	+ protoporphyrin oxidase		21
rrnA_16S	rrnA_16S	1542 4033554 4035095	+ rrnA_16S		
tRNA-Ile5	tRNA-Ile	77 4035164 4035240	+ tRNA-Ile		
tRNA-Ala5	tRNA-Ala	76 4035283 4035358	+ tRNA-Ala		
rrnA_23S	rrnA_23S	2905 4035542 4038446	+ rrnA_23S		
rrnA_5S	rrnA_5S	120 4038540 4038659	+ rrnA_5S		
b3856	mobB	513 4038929 4039441	- molybdopterin-guanine dinucleotide biosynthesis protein B		21
b3857	mobA	585 4039438 4040022	- molybdopterin ---> molybdopterin-guanine dinucleotide, protein Ar	1	20
b3858	yihD	270 4040092 4040361	+ orf, hypothetical protein		20
b3859	yihE	987 4040438 4041424	+ orf, hypothetical protein	1	21

b3860	dsbA	627 4041441 4042067	+ protein disulfide isomerase I, essential for cytochrome c synthesis and formate-dependent reduction	1				21
b3861	yihF	1473 4042180 4043652	+ putative GTP-binding protein		1	1		7
b3862	yihG	933 4043693 4044625	- putative endonuclease			1		14
b3863	polA	2787 4044989 4047775	+ DNA polymerase I, 3' --> 5' polymerase, 5' --> 3' and 3' --> 5'			1		20
b3865	yihA	600 4048156 4048755	- GTPase essential for cell cycle					21
b3866	yihI	510 4049370 4049879	+ orf, hypothetical protein					21
b3867	hemN	1380 4050062 4051441	+ O2-independent coproporphyrinogen III oxidase					21
b3868	glnG	1410 4051892 4053301	- response regulator for gln (sensor glnL)					21
b3869	glnL	1050 4053313 4054362	- histidine protein kinase sensor for GlnG					21
b3870	glnA	1410 4054648 4056057	- glutamine synthetase					21
b3871	bipA	1824 4056430 4058253	+ GTP-binding protein					21
b3872	yihL	711 4058470 4059180	+ putative transcriptional regulator					12
b3873	yihM	981 4059188 4060168	+ orf, hypothetical protein				1	11
b3874	yihN	1266 4060270 4061535	+ putative resistance protein (transport)	1			1	13
b3875	yshA	693 4061626 4062318	- orf, hypothetical protein	1	1		1	19
b3876	yihO	1404 4062386 4063789	- putative permease	1			1	20
b3877	yihP	1407 4063832 4065238	- putative permease				1	20
b3878	yihQ	2037 4065263 4067299	- putative glycosidase				1	19
b3879	yihR	927 4067498 4068424	- putative aldose-1-epimerase					11
b3880	yihS	1257 4068538 4069794	- orf, hypothetical protein					8
b3881	yihT	879 4069796 4070674	- putative aldolase					15
b3882	yihU	897 4070698 4071594	- putative dehydrogenase					21
b3883	yihV	903 4071756 4072658	+ putative kinase					14
b3884	yihW	810 4072668 4073477	+ putative DEOR-type transcriptional regulator					14
b3885	yihX	621 4073555 4074175	+ putative phosphatase					21
b3886	rbn	873 4074169 4075041	+ tRNA processing exoribonuclease BN					18
b3887	dtd	438 4075038 4075475	+ D-Tyr-tRNA ^{Tyr} deacylase					21
b3888	yiiD	990 4075472 4076461	+ putative					21
b3889	yiiE	246 4077287 4077532	+ orf, hypothetical protein	1	1	1		13
b3890	yiiF	243 4077750 4077992	+ orf, hypothetical protein	1	1	1		13
b3891	fdhE	930 4078322 4079251	- affects formate dehydrogenase-N					21
b3892	fdol	636 4079248 4079883	- formate dehydrogenase, cytochrome B556					20
b3893	fdoH	903 4079880 4080782	- formate dehydrogenase-O, iron-					20
b3894	fdoG	3051 4080795 4083845	- formate dehydrogenase-O,					16
b3895	fdhD	834 4084039 4084872	+ affects formate dehydrogenase-N					21
b3896	yiiG	1056 4085025 4086080	+ orf, hypothetical protein				1	11
b3897	frvR	1749 4086130 4087878	- putative frv operon regulatory protein	1				14
b3898	frvX	1071 4087878 4088948	- frv operon protein					15
b3899	frvB	1458 4088938 4090395	- PTS system, fructose-like enzyme IIBC					8
b3900	frvA	447 4090400 4090846	- PTS system, fructose-specific IIA component				1	10
b3901	yiiL	315 4091147 4091461	- orf, hypothetical protein					20
b3902	rhaD	825 4091471 4092295	- rhamnulose-phosphate aldolase					18
b3903	rhaA	1260 4092746 4094005	- L-rhamnose isomerase					19

b3904	rhaB	1470 4094002 4095471	- rhamnulokinase			20
b3905	rhaS	837 4095759 4096595	+ positive regulator for rhaBAD operon			20
b3906	rhaR	939 4096579 4097517	+ positive regulator for rhaRS operon			19
b3907	rhaT	1035 4097514 4098548	- rhamnose transport			18
b3908	sodA	621 4098833 4099453	+ superoxide dismutase, manganese			21
b3909	kdgT	993 4099704 4100696	+ 2-keto-3-deoxy-D-gluconate transport system			16
b3910	yiiM	705 4100815 4101519	+ orf, hypothetical protein	1		16
b3911	cpxA	1374 4101625 4102998	- probable sensor protein (histidine protein kinase), acting on arcA transcriptional regulator in 2-component system			21
b3912	cpxR	699 4102995 4103693	- periplasmic repressor of cpx regulon by interaction with CpxA	1		21
b4484	cpxP	501 4103843 4104343	+ putative transport system permease			20
b3915	yiiP	903 4104492 4105394	+ 6-phosphofructokinase I			21
b3916	pfkA	963 4105575 4106537	+ periplasmic sulfate-binding protein			21
b3917	sbp	990 4106857 4107846	+ CDP-diacylglycerol phosphatidylhydrolase			19
b3918	cdh	756 4107953 4108708	- triosephosphate isomerase			21
b3919	tpiA	768 4108763 4109530	- orf, hypothetical protein			21
b3920	yiiQ	600 4109638 4110237	+ orf, hypothetical protein	1		18
b3921	yiiR	441 4110338 4110778	+ orf, hypothetical protein		1	10
b3922	yiiS	300 4110990 4111289	+ putative regulator	1	1	10
b3923	yiiT	429 4111316 4111744	- ferredoxin-NADP reductase			21
b3924	fpr	747 4111749 4112495	- unknown function in glycerol metabolism			19
b3925	glpX	1011 4112592 4113602	- glycerol kinase			20
b3926	glpK	1509 4113737 4115245	- facilitated diffusion of glycerol	1		21
b3927	glpF	846 4115268 4116113	+ orf, hypothetical protein			21
b3928	yiiU	246 4116538 4116783	- menaquinone biosynthesis, unknown			21
b3929	menG	486 4116868 4117353	- 1,4-dihydroxy-2-naphthoate --> dimethylmenaquinone			21
b3930	menA	927 4117446 4118372	- heat shock protein hslVU, ATPase subunit, homologous to chaperones			21
b3931	hslU	1332 4118439 4119770	- heat shock protein hslVU, proteasome-related peptidase			21
b3932	hslV	531 4119780 4120310	- essential cell division protein			21
b3933	ftsN	960 4120403 4121362	- regulator for deo operon, udp, cdd, tsx, nupC, and nupG			21
b3934	cytR	1026 4121454 4122479	- primosomal protein N'(= factor Y)(putative helicase)			21
b3935	priA	2199 4122635 4124833	+ 50S ribosomal subunit protein L31	1		20
b3936	rpmE	213 4125036 4125248	- orf, hypothetical protein			10
b3937	yiiX	609 4125309 4125917	- repressor of all met genes but metF			21
b3938	metJ	318 4126101 4126418	+ cystathionine gamma-synthase			19
b3939	metB	1161 4126695 4127855	+ aspartokinase II and homoserine dehydrogenase II			21
b3940	metL	2433 4127858 4130290				

b3941	metF	891 4130639 4131529	+ 5,10-methylenetetrahydrofolate reductase	21			
b3942	katG	2181 4131858 4134038	+ catalase; hydroperoxidase HPI(I)	19			
b3943	yijE	939 4134098 4135036	+ orf, hypothetical protein	9			
b3944	yijF	618 4135063 4135680	- orf, hypothetical protein	10			
b3945	gldA	1143 4135955 4137097	- glycerol dehydrogenase, (NAD)	15			
b3946	talC	663 4137069 4137731	- fructose-6-phosphate aldolase	20			
b3947	ptsA	2502 4137743 4140244	- PEP-protein phosphotransferase system enzyme I	14			
b3949	frwC	1080 4140553 4141632	+ PTS system, fructose-like enzyme II	16			
b3950	frwB	321 4141647 4141967	+ PTS system fructose-like IIB component 1	16			
b3951	pflD	2298 4142018 4144315	+ formate acetyltransferase 2	16			
b3952	pflC	879 4144281 4145159	+ probable pyruvate formate lyase activating	12			
b3953	frwD	342 4145161 4145502	+ PTS system fructose-like IIB component 2	16			
b3954	yijO	852 4145489 4146340	- putative ARAC-type regulatory protein	19			
b3955	yijP	1734 4146555 4148288	- protein required for invasion of brain microvascular endothelial cells	15			
b3956	ppc	2652 4148470 4151121	- phosphoenolpyruvate carboxylase	21			
b3957	argE	1152 4151719 4152870	- acetylornithine deacetylase	21			
b3958	argC	1005 4153024 4154028	+ N-acetyl-gamma-glutamylphosphate reductase	21			
b3959	argB	777 4154036 4154812	+ acetylglutamate kinase	21			
b3960	argH	1374 4154873 4156246	+ argininosuccinate lyase	21			
b3961	oxyR	918 4156513 4157430	+ activator, hydrogen peroxide-inducible	21			
b3962	udhA	1335 4157413 4158747	- soluble pyridine nucleotide	21			
b3963	yijC	705 4159090 4159794	+ orf, hypothetical protein	21			
b3964	yijD	360 4159794 4160153	+ orf, hypothetical protein	21			
b3965	trnA	1101 4160193 4161293	- tRNA (uracil-5)-methyltransferase	21			
b3966	btuB	1845 4161662 4163506	+ outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage	20			
b3967	murl	870 4163439 4164308	+ glutamate racemase, required for biosynthesis of D-glutamate and	21			
rrnB_16S	rrnB_16S	1542 4164682 4166223	+ rrnB_16S				
tRNA-Glu3	tRNA-Glu	76 4166395 4166470	+ tRNA-Glu				
rrnB_23S	rrnB_23S	2904 4166664 4169567	+ rrnB_23S				
rrnB_5S	rrnB_5S	120 4169660 4169779	+ rrnB_5S				
b3972	murB	1029 4170080 4171108	+ UDP-N-acetylenolpyruvoylglutamine reductase	21		1	
b3973	birA	966 4171105 4172070	+ biotin-[acetylCoA carboxylase] holoenzyme synthetase and biotin operon	21	1	1	
b3974	coaA	951 4172099 4173049	- pantothenate kinase			1	1
b3975	-	156 4173236 4173391	- orf, hypothetical protein	12	1	1	
tRNA-Thr3	tRNA-Thr	76 4173411 4173486	+ tRNA-Thr				1
tRNA-Tyr	tRNA-Tyr	85 4173495 4173579	+ tRNA-Tyr				1
tRNA-Gly3	tRNA-Gly	75 4173696 4173770	+ tRNA-Gly				1
tRNA-Thr	tRNA-Thr	76 4173777 4173852	+ tRNA-Thr				1

b3980	tufB	1185 4173967 4175151	+ protein chain elongation factor EF-Tu	20
b3981	secE	384 4175381 4175764	+ preprotein translocase	21
b3982	nusG	546 4175766 4176311	+ component in transcription antitermination	21
b3983	rplK	429 4176470 4176898	+ 50S ribosomal subunit protein L11	21
b3984	rplA	705 4176902 4177606	+ 50S ribosomal subunit protein L1, regulates synthesis of L1 and L11	21
b3985	rplJ	498 4178019 4178516	+ 50S ribosomal subunit protein L10	21
b3986	rplL	366 4178583 4178948	+ 50S ribosomal subunit protein L7/L12	21
b3987	rpoB	4029 4179268 4183296	+ RNA polymerase, beta subunit	21
b3988	rpoC	4224 4183373 4187596	+ RNA polymerase, beta prime subunit	21
b3989	htrC	540 4187809 4188348	+ heat shock protein htrC	5
b3990	thiH	1134 4188758 4189891	- thiamin (thiazole moiety) biosynthesis	21
b3991	thiG	771 4189888 4190658	- thiamin (thiazole moiety) biosynthesis	21
b4407	thiS	201 4190660 4190860	- sulfur carrier protein	15
b3992	thiF	738 4190844 4191581	- adenylyltransferase	20
b3993	thiE	636 4191592 4192227	- thiamin-phosphate synthase (thiamine-phosphate pyrophosphorylase)	21
b3994	thiC	1896 4192227 4194122	- thiamin (pyrimidine moiety) biosynthesis protein	21
b3995	rsd	477 4194355 4194831	- regulator of sigma D	20
b3996	nudC	774 4194926 4195699	+ NADH	21
b3997	hemE	1065 4195739 4196803	+ uroporphyrinogen decarboxylase	21
b3998	nfi	678 4196807 4197484	+ endonuclease V (deoxyinosine 3'endonuclease)	20
b3999	yjaG	591 4197527 4198117	+ orf, hypothetical protein	21
b4000	hupA	273 4198304 4198576	+ DNA-binding protein HU-alpha (HU-2)	21
b4001	yjaH	696 4198589 4199284	+ orf, hypothetical protein	21
b4002	zraP	567 4199286 4199852	- Zn-binding periplasmic protein	17
b4003	zraS	1398 4199949 4201346	+ sensor kinase of Zn/Pb responsive two-component regulatory system	17
b4004	zraR	1326 4201343 4202668	+ response regulator of Zn/Pb responsive two-component regulatory system	17
b4005	purD	1290 4202665 4203954	- phosphoribosylglycinamide synthetase = GAR synthetase	21
b4006	purH	1590 4203966 4205555	- phosphoribosylaminoimidazolecarboxamideformyltransferase = AICAR formyltransferase	20
rrnE_16S	rrnE_16S	1542 4206170 4207711	+ rrnE_16S	
tRNA-Glu4	tRNA-Glu	76 4207797 4207872	+ tRNA-Glu	
rrnE_23S	rrnE_23S	2904 4208066 4210969	+ rrnE_23S	
rrnE_5S	rrnE_5S	120 4211063 4211182	+ rrnE_5S	
b4011	yjaA	384 4211257 4211640	+ orf, hypothetical protein	10
b4012	yjaB	444 4211703 4212146	- orf, hypothetical protein	15
b4013	metA	930 4212303 4213232	+ homoserine transsuccinylase	20
b4014	aceB	1602 4213501 4215102	+ malate synthase A	18
b4015	aceA	1305 4215132 4216436	+ isocitrate lyase	20

b4016	aceK	1737 4216619 4218355	+ isocitrate dehydrogenase				17
b4017	arpA	2187 4218324 4220510	- regulator of acetyl CoA synthetase; ankyrin-like	1	1	1	5
b4018	iclR	864 4220827 4221690	- repressor of aceBA operon				20
b4019	metH	3684 4221851 4225534	+ B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of metF and				20
b4020	yjbB	1632 4225754 4227385	+ putative alpha helix				15
b4021	pepE	690 4227476 4228165	- peptidase E, a dipeptidase where amino-terminal residue				14
b4022	yjbC	873 4228377 4229249	+ orf, hypothetical protein				16
b4023	yjbD	273 4229382 4229654	- orf, hypothetical protein			1	18
b4024	lysC	1350 4229907 4231256	- aspartokinase III, lysine sensitive				21
b4025	pgi	1650 4231781 4233430	+ glucosephosphate isomerase				21
b4026	yjbE	243 4233929 4234171	+ orf, hypothetical protein	1		1	15
b4027	yjbF	669 4234255 4234923	+ orf, hypothetical protein				16
b4028	yjbG	738 4234920 4235657	+ orf, hypothetical protein				16
b4029	yjbH	2097 4235657 4237753	+ orf, hypothetical protein				16
b4030	yjbA	411 4238348 4238758	+ orf, hypothetical protein				20
b4031	xyIE	1476 4238802 4240277	- xylose-proton symport			1	8
b4032	malG	891 4240649 4241539	- part of maltose permease, inner				18
b4033	malF	1545 4241554 4243098	- part of maltose permease, periplasmic				18
b4034	malE	1191 4243252 4244442	- periplasmic maltose-binding protein; substrate recognition				18
b4035	malk	1116 4244807 4245922	+ ATP-binding component of transport system for maltose				18
b4036	lamB	1341 4245994 4247334	+ phage lambda receptor protein; maltose high-affinity receptor				18
b4037	malM	921 4247577 4248497	+ periplasmic protein of mal regulon				18
b4038	yjbI	1329 4248978 4250306	+ orf, hypothetical protein	1	1	1	7
b4039	ubiC	609 4250418 4251026	+ chorismate lyase	1		1	21
b4040	ubiA	873 4251039 4251911	+ 4-hydroxybenzoate-octaprenyltransferase				21
b4041	plsB	2484 4252066 4254549	- glycerol-3-phosphate acyltransferase				21
b4042	dgkA	369 4254660 4255028	+ diacylglycerol kinase				21
b4043	lexA	609 4255138 4255746	+ regulator for SOS(lexA) regulon				21
b4044	dinF	1380 4255765 4257144	+ DNA-damage-inducible protein F				16
b4045	yjbJ	210 4257260 4257469	+ orf, hypothetical protein				16
b4046	zur	576 4257511 4258086	- transcriptional repressor of Zn			1	21
b4047	yjbL	255 4258344 4258598	+ orf, hypothetical protein	1	1	1	7
b4048	yjbM	708 4258622 4259329	+ orf, hypothetical protein	1	1	1	8
b4049	yjbN	1038 4259692 4260729	+ orf, hypothetical protein			1	21
b4050	yjbO	453 4260653 4261105	+ orf, hypothetical protein	1			20
b4051	qor	984 4261271 4262254	- quinone oxidoreductase				21
b4052	dnaB	1416 4262337 4263752	+ replicative DNA helicase; part of				21
b4053	alr	1080 4263805 4264884	+ alanine racemase 1				21
b4054	tyrB	1194 4265137 4266330	+ tyrosine aminotransferase, tyrosine repressible				21
b4055	aphA	714 4267437 4268150	+ diadenosine tetraphosphatase			1	14
b4056	yjbQ	417 4268261 4268677	+ orf, hypothetical protein				16
b4057	yjbR	357 4268681 4269037	+ orf, hypothetical protein				19

b4058	uvrA	2823 4269072 4271894	- excision nuclease subunit A				21
b4059	ssb	537 4272148 4272684	+ ssDNA-binding protein				21
b4060	yjcB	351 4272783 4273133	- orf, hypothetical protein	1		1	13
b4061	yjcC	1587 4273494 4275080	+ orf, hypothetical protein	1		1	
b4062	soxS	324 4275083 4275406	- regulation of superoxide response regulon	1			14
b4063	soxR	465 4275492 4275956	+ redox-sensing activator of soxS				16
b4064	yjcD	1350 4276502 4277851	+ orf, hypothetical protein				20
b4065	yjcE	1650 4278003 4279652	+ orf, hypothetical protein				21
b4066	yjcF	1293 4279806 4281098	- orf, hypothetical protein	1	1	1	15
b4067	actP	1650 4281276 4282925	- acetate permease				20
b4068	yjcH	315 4282922 4283236	- orf, hypothetical protein				18
b4069	acs	1959 4283436 4285394	- acetyl-CoA synthetase				16
b4070	nrfA	1437 4285787 4287223	+ periplasmic cytochrome c(552): plays a role in nitrite reduction				15
b4071	nrfB	573 4287262 4287834	+ formate-dependent nitrite reductase; a penta-haeme				15
b4072	nrfC	672 4287831 4288502	+ formate-dependent nitrite reductase; Fe-S	1			15
b4073	nrfD	957 4288499 4289455	+ formate-dependent nitrate reductase complex:				15
b4074	nrfE	1659 4289535 4291193	+ formate-dependent nitrite reductase; possible assembly				15
b4075	nrfF	384 4291186 4291569	+ part of formate-dependent nitrite				15
b4076	nrfG	597 4291566 4292162	+ part of formate-dependent nitrite				15
b4077	gltP	1314 4292504 4293817	+ glutamate-aspartate symport protein				19
b4078	yjcO	690 4294459 4295148	- orf, hypothetical protein				21
b4079	fdhF	2148 4295242 4297389	- selenopolypeptide subunit of formate dehydrogenase H				14
b4080	yjcP	1467 4297587 4299053	- putative enzyme				8
b4081	yjcQ	1911 4299050 4300960	- putative enzyme				13
b4082	yjcR	1032 4301101 4302132	- putative membrane protein			1	13
b4083	yjcS	1998 4302635 4304632	- orf, hypothetical protein			1	11
b4084	alsK	930 4304893 4305822	- D-allose kinase	1			3
b4085	alsE	696 4305806 4306501	- D-allulose-6-phosphate 3-epimerase				3
b4086	alsC	981 4306512 4307492	- D-allose transport system permease				3
b4087	alsA	1533 4307471 4309003	- D-allose transport ATP-binding protein			1	3
b4088	alsB	936 4309130 4310065	- D-allose-binding periplasmic protein			1	3
b4089	rpiR	924 4310124 4311047	- transcriptional repressor of rpiB	1		1	12
b4090	rpiB	450 4311373 4311822	+ ribose 5-phosphate isomerase B				10
b4487	yjdP	330 4311891 4312220	+ conserved hypothetical protein	1	1		6
b4092	phnP	759 4312367 4313125	- phosphonate		1		13
b4093	phnO	435 4313127 4313561	- putative regulator, phn operon		1		13
b4094	phnN	558 4313548 4314105	- ATP-binding component of		1		12
b4095	phnM	1137 4314105 4315241	- phosphonate		1		13
b4096	phnL	681 4315238 4315918	- ATP-binding component of		1		13
b4097	phnK	759 4316029 4316787	- ATP-binding component of		1		13
b4098	phnJ	846 4316784 4317629	- phosphonate		1		13
b4099	phnI	1065 4317622 4318686	- phosphonate		1		13
b4100	phnH	585 4318686 4319270	- phosphonate		1		13
b4101	phnG	453 4319267 4319719	- phosphonate		1		12

b4102	phnF	726 4319720 4320445	- putative transcriptional regulator		1		12
b4103	-	222 4320466 4320687	- orf, hypothetical protein		1		13
b4104	phnE	621 4320684 4321304	- membrane channel protein component of Pn transporter	1	1		13
b4105	phnD	1017 4321359 4322375	- periplasmic binding protein component of Pn transporter		1		14
b4106	phnC	789 4322400 4323188	- ATP-binding component of		1		14
b4107	phnB	444 4323321 4323764	- orf, hypothetical protein		1		13
b4108	phnA	336 4324422 4324757	- orf, hypothetical protein		1		21
b4109	yjdA	2229 4325158 4327386	+ putative vimentin			1	8
b4110	yjcZ	846 4327416 4328261	+ orf, hypothetical protein	1			9
b4111	proP	1503 4328525 4330027	+ low-affinity transport system; proline permease II				20
b4112	basS	1092 4330204 4331295	- sensor protein for basR				20
b4113	basR	669 4331305 4331973	- transcriptional regulatory protein, member of 2-component regulatory protein				19
b4114	yjdB	1674 4331970 4333643	- orf, hypothetical protein				20
b4115	yjdE	1338 4333717 4335054	- putative amino acid/amine transport			1	19
b4116	adiY	762 4335191 4335952	- putative ARAC-type regulatory protein	1	1	1	15
b4117	adiA	2271 4336277 4338547	- biodegradative arginine decarboxylase				20
b4118	melR	909 4338743 4339651	- regulator of melibiose operon				14
b4119	melA	1356 4339934 4341289	+ alpha-galactosidase				15
b4120	melB	1410 4341404 4342813	+ melibiose permease II	1			20
b4121	yjdF	630 4342952 4343581	- orf, hypothetical protein				8
b4122	fumB	1647 4343703 4345349	- fumarate B= fumarate hydratase Class I; anaerobic isozyme				20
b4123	dcuB	1341 4345427 4346767	- anaerobic dicarboxylate transport			1	17
b4124	dcuR	720 4347338 4348057	- response regulator of fumarate two-component regulatory system	1		1	16
b4125	dcuS	1632 4348054 4349685	- sensor of fumarate two-component regulatory system			1	15
b4126	yjdI	231 4349866 4350096	+ orf, hypothetical protein	1		1	8
b4127	yjdJ	273 4350108 4350380	+ orf, hypothetical protein		1	1	8
b4128	yjdK	297 4350607 4350903	+ orf, hypothetical protein	1	1	1	5
b4129	lysU	1518 4351223 4352740	- lysine tRNA synthetase, inducible; heat shock protein			1	21
b4130	yjdL	1458 4352977 4354434	- putative peptide transporter			1	12
b4131	cadA	2148 4354493 4356640	- lysine decarboxylase 1			1	10
b4132	cadB	1335 4356720 4358054	- transport of lysine/cadaverine			1	12
b4133	cadC	1539 4358419 4359957	- transcriptional activator of cad operon	1	1	1	12
tRNA-Phe:tRNA-Phe		76 4360574 4360649	- tRNA-Phe				
b4135	yjdC	600 4360756 4361355	- orf, hypothetical protein				21
b4136	dsbD	1698 4361368 4363065	- thiol:disulfide interchange protein; divalent cation tolerance protein; cytochrome c				21
b4137	cutA	339 4363041 4363379	- anaerobic dicarboxylate transport	1			19
b4138	dcuA	1302 4363495 4364796	- aspartate ammonia-lyase (aspartase)				21
b4139	aspA	1482 4364914 4366395	- suppressor of F exclusion of				21
b4140	fxsA	378 4366786 4367163	+ putative transport				21
b4141	yjeH	1257 4367179 4368435	-				20

b4142	groS	294 4368711 4369004	+ GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase		21
b4143	groL	1647 4369048 4370694	+ GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein		21
b4144	yjeI	387 4370799 4371185	+ orf, hypothetical protein		21
b4145	yjeJ	870 4371388 4372257	- orf, hypothetical protein	1	14
b4146	yjeK	1029 4372652 4373680	- orf, hypothetical protein		21
b4147	efp	567 4373722 4374288	+ elongation factor P (EF-)		21
b4410	ecnA	126 4374340 4374465	+ entericidin A		13
b4411	ecnB	147 4374576 4374722	+ entericidin B		12
b4148	sugE	468 4374748 4375215	+ suppresses groEL, may be chaperone	1	19
b4149	blc	534 4375212 4375745	- outer membrane lipoprotein (lipocalin)		16
b4150	ampC	1134 4375834 4376967	- beta-lactamase; penicillin resistance	1	12
b4151	frdD	360 4377030 4377389	- fumarate reductase, anaerobic, membrane anchor polypeptide		21
b4152	frdC	396 4377400 4377795	- fumarate reductase, anaerobic, membrane anchor polypeptide		21
b4153	frdB	735 4377806 4378540	- fumarate reductase, anaerobic, iron-sulfur protein subunit		21
b4154	frdA	1809 4378533 4380341	- fumarate reductase, anaerobic, flavoprotein subunit		21
b4155	yjeA	1008 4380636 4381643	+ putative lysyl-tRNA synthetase		21
b4156	yjeM	1545 4381820 4383364	+ putative transport	1	11
b4157	yjeN	315 4383416 4383730	+ orf, hypothetical protein	1	5
b4158	yjeO	315 4383727 4384041	+ orf, hypothetical protein		9
b4159	yjeP	3324 4384070 4387393	- putative periplasmic binding protein		20
b4160	psd	969 4387415 4388383	- phosphatidylserine decarboxylase; phospholipid synthesis		21
b4161	yjeQ	1014 4388480 4389493	- orf, hypothetical protein		21
b4162	orn	615 4389558 4390172	+ oligoribonuclease		21
tRNA-Gly4 tRNA-Gly		76 4390383 4390458	+ tRNA-Gly		
tRNA-Gly5 tRNA-Gly		76 4390495 4390570	+ tRNA-Gly		
tRNA-Gly6 tRNA-Gly		76 4390606 4390681	+ tRNA-Gly		
b4166	yjeS	1140 4390951 4392090	- orf, hypothetical protein		21
b4167	yjeF	1548 4392089 4393636	+ orf, hypothetical protein		19
b4168	yjeE	462 4393608 4394069	+ orf, hypothetical protein		21
b4169	amiB	1338 4394088 4395425	+ N-acetylmuramoyl-L-alanine amidase II; a murein hydrolase		21
b4170	mutL	1848 4395435 4397282	+ enzyme in methyl-directed mismatch		21
b4171	miaA	951 4397275 4398225	+ delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	1	21
b4172	hfq	309 4398311 4398619	+ host factor I for bacteriophage Q beta replication, a growth-related protein		21
b4173	hflX	1281 4398695 4399975	+ GTP - binding subunit of protease specific for phage lambda cII		21
b4174	hflK	1260 4400061 4401320	+ repressor protease specific for phage lambda cII		21
b4175	hflC	1005 4401323 4402327	+ repressor protease specific for phage lambda cII		21
			repressor		

b4176	yjeT	198 4402409 4402606	+ orf, hypothetical protein				19
b4177	purA	1299 4402710 4404008	+ adenylosuccinate synthetase				21
b4178	yjeB	426 4404213 4404638	+ orf, hypothetical protein	1			21
b4179	rnr	2484 4404635 4407118	+ ribonuclease R				21
b4180	yjfH	732 4407298 4408029	+ orf, hypothetical protein				21
b4181	yjfl	402 4408156 4408557	+ orf, hypothetical protein	1	1	1	11
b4182	yjfJ	699 4408576 4409274	+ putative alpha helical protein			1	9
b4183	yjfK	660 4409325 4409984	+ orf, hypothetical protein			1	12
b4184	yjfl	399 4410002 4410400	+ orf, hypothetical protein	1	1	1	13
b4185	yjfm	639 4410410 4411048	+ orf, hypothetical protein	1		1	14
b4186	yjfC	1164 4411051 4412214	+ putative synthetase/amidase				14
b4187	aidB	1641 4412283 4413923	+ putative acyl coenzyme A dehydrogenase				18
b4188	yjfN	303 4414040 4414342	- orf, hypothetical protein				15
b4189	yjfO	429 4414464 4414892	- orf, hypothetical protein	1			20
b4190	yjfP	750 4414975 4415724	+ orf, hypothetical protein	1			19
b4191	yjfQ	756 4415721 4416476	- putative DEOR-type transcriptional regulator				15
b4192	yjfR	1071 4416584 4417654	- orf, hypothetical protein				21
b4193	sgaT	1455 4417946 4419400	+ orf, hypothetical protein		1		20
b4194	sgaB	306 4419416 4419721	+ orf, hypothetical protein		1		15
b4195	ptxA	465 4419731 4420195	+ putative PTS system enzyme II A component		1		21
b4196	sgaH	651 4420209 4420859	+ probable hexulose-6-phosphate synthase		1		15
b4197	sgaU	855 4420869 4421723	+ putative hexulose-6-phosphate isomerase		1		14
b4198	sgaE	687 4421723 4422409	+ putative epimerase/aldolase		1		14
b4199	yjfY	276 4422539 4422814	- orf, hypothetical protein	1			13
b4200	rpsF	396 4423141 4423536	+ 30S ribosomal subunit protein S6				21
b4201	priB	315 4423543 4423857	+ primosomal replication protein N	1			18
b4202	rpsR	228 4423862 4424089	+ 30S ribosomal subunit protein S18				21
b4203	rplI	450 4424131 4424580	+ 50S ribosomal subunit protein L9				21
b4204	yjfZ	795 4424651 4425445	- orf, hypothetical protein	1	1	1	5
b4205	ytfA	327 4425792 4426118	+ orf, hypothetical protein	1	1	1	8
b4206	ytfB	675 4426102 4426776	- orf, hypothetical protein				20
b4207	fkIB	780 4426799 4427578	+ FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase)	1			18
b4208	cycA	1413 4427887 4429299	+ transport of D-alanine, D-serine, and glycine				21
b4209	ytfE	663 4429344 4430006	- orf, hypothetical protein				20
b4210	ytfF	975 4430114 4431088	- putative transmembrane subunit				16
b4211	ytfG	861 4431187 4432047	- putative oxidoreductase				20
b4212	ytfH	471 4432046 4432516	+ orf, hypothetical protein				20
b4213	cpdB	1944 4432645 4434588	- 2':3'-cyclic-nucleotide 2'-phosphodiesterase				21
b4214	cysQ	741 4434778 4435518	+ affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis				21
b4215	ytfI	939 4435730 4436668	+ orf, hypothetical protein	1	1	1	7
b4216	ytfJ	555 4436731 4437285	- orf, hypothetical protein				21
b4217	ytfK	246 4437571 4437816	+ orf, hypothetical protein	1			20
b4218	ytfL	1344 4437895 4439238	- putative transport				21
b4219	msrA	639 4439561 4440199	- peptide methionine sulfoxide reductase				21
b4220	ytfM	1734 4440405 4442138	+ orf, hypothetical protein				21
b4221	ytfN	3780 4442135 4445914	+ orf, hypothetical protein				21
b4222	ytfP	342 4445917 4446258	+ orf, hypothetical protein				21
b4223	yzfA	270 4445999 4446268	- orf, hypothetical protein	1	1		5

b4224	chpS	258 4446464 4446721	+ suppressor of inhibitory function of ChpB, Peme-like, autoregulated	6
b4225	chpB	351 4446715 4447065	+ probable growth inhibitor, PemK-like,	8
b4226	ppa	531 4447145 4447675	- inorganic pyrophosphatase	21
b4227	ytfQ	957 4447985 4448941	+ putative LACI-type transcriptional regulator	13
b4485	ytfR	1503 4449081 4450583	+ putative sugar transport protein (ABC superfamily, atp bind)	14
b4230	ytfT	1026 4450594 4451619	+ putative transport system permease	15
b4231	yjfF	972 4451630 4452601	+ putative transport system permease	14
b4232	fbp	999 4452634 4453632	- fructose-1,6-bisphosphatase	21
b4233	mpl	1374 4453808 4455181	+ UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl- meso-diaminonimelate ligase	20
b4234	yjgA	552 4455337 4455888	- putative alpha helix	21
b4235	pmbA	1353 4455982 4457334	+ maturation of antibiotic MccB17, see tld genes	21
b4236	cybC	303 4457576 4457878	+ cytochrome b(562)	19
b4237	nrdG	465 4457923 4458387	- anaerobic ribonucleotide reductase activating anaerobic	21
b4238	nrdD	2139 4458545 4460683	- ribonucleoside-trehalase 6-P hydrolase	21
b4239	treC	1656 4461077 4462732	- PTS system enzyme II, trehalose specific	20
b4240	treB	1422 4462782 4464203	- repressor of treA,B,C	20
b4241	treR	948 4464322 4465269	+ Mg2+ transport ATPase, P-type 1	21
b4242	mgfA	2697 4465648 4468344	- orf, hypothetical protein	21
b4243	yjgF	426 4468550 4468975	- aspartate carbamoyltransferase, regulatory subunit	21
b4244	pyrI	462 4469009 4469470	- aspartate carbamoyltransferase, catalytic subunit	21
b4245	pyrB	936 4469483 4470418	- pyrBI operon leader peptide	14
b4246	pyrL	135 4470422 4470556	+ orf, hypothetical protein	7
b4247	yjgG	333 4470536 4470868	- orf, hypothetical protein	10
b4248	yjgH	396 4470837 4471232	- putative oxidoreductase	15
b4249	yjgI	714 4471363 4472076	+ orf, hypothetical protein	7
b4250	-	165 4472250 4472414	+ orf, hypothetical protein	14
b4251	yjgJ	255 4472486 4472740	+ orf, hypothetical protein	19
b4252	yjgK	462 4472876 4473337	+ orf, hypothetical protein	5
b4253	yjgL	1851 4473424 4475274	- ornithine carbamoyltransferase 1	21
b4254	argI	1005 4475330 4476334	+ orf, hypothetical protein	21
b4255	yjgD	417 4476496 4476912	- orf, hypothetical protein	19
b4256	yjgM	504 4477057 4477560	+ orf, hypothetical protein	19
b4257	yjgN	1197 4477753 4478949	- valine tRNA synthetase	21
b4258	valS	2856 4479005 4481860	- DNA polymerase III, chi subunit	21
b4259	holC	444 4481860 4482303	- aminopeptidase A/I	21
b4260	pepA	1512 4482463 4483974	+ orf, hypothetical protein	21
b4261	yjgP	1101 4484241 4485341	+ orf, hypothetical protein	14
b4262	yjgQ	1086 4485338 4486423	- orf, hypothetical protein	13
b4263	yjgR	1503 4486584 4488086	- L-idonate transcriptional regulator	7
b4264	idnR	999 4488164 4489162	- L-idonate transporter	11
b4265	idnT	1320 4489229 4490548	- 5-keto-D-gluconate 5-reductase	7
b4266	idnO	765 4490610 4491374	- L-idonate	7
b4267	idnD	1032 4491398 4492429	- L-idonate	7

b4268	idnK	564 4492646 4493209	+ gluconate kinase, thermosensitive glucokinase	1	1	1	12
b4269	yjgB	1062 4493213 4494274	- putative oxidoreductase				14
b4271	tRNA-Leu ³ tRNA-Leu	85 4494428 4494512	+ tRNA-Leu				
b4271	intB	1191 4494773 4495963	+ prophage P4 integrase	1	1		16
b4272	yi21_6	411 4496250 4496660	+ IS2 hypothetical protein	1	1	1	8
b4273	yi22_6	906 4496618 4497523	+ IS2 hypothetical protein	1	1		18
b4274	yjgW	336 4497622 4497957	+ orf, hypothetical protein	1			2
b4275	yjgX	447 4498066 4498512	- orf, hypothetical protein				3
b4276	yjgY	450 4498455 4498904	- orf, hypothetical protein	1			2
b4277	yjgZ	330 4499283 4499612	+ orf, hypothetical protein	1			11
b4278	yi41	1329 4500126 4501454	- IS4 hypothetical protein	1	1		11
b4279	yjhB	1278 4502021 4503298	+ putative transport	1	1	1	6
b4280	yjhC	1134 4503295 4504428	+ putative dehydrogenase	1	1	1	13
b4281	yjhD	375 4504649 4505023	- orf, hypothetical protein	1		1	2
b4282	yjhE	204 4504929 4505132	+ orf, hypothetical protein		1	1	2
b4283	yi91b	303 4505184 4505486	+ transposase insN for insertion sequence element IS911B	1	1	1	13
b4284	tra8_3	1152 4505489 4506640	- IS30 transposase	1	1		7
b4285	-	597 4506981 4507577	+ putative transposase	1			14
b4286	-	414 4507743 4508156	+ orf, hypothetical protein	1			3
b4287	fecE	768 4508713 4509480	- ATP-binding component of citrate- dependent iron(III) citrate-dependent iron transport, membrane- bound protein	1	1		6
b4288	fecD	957 4509481 4510437	- citrate-dependent iron(III) transport		1		6
b4289	fecC	999 4510434 4511432	- citrate-dependent iron(III) transport		1		6
b4290	fecB	909 4511429 4512337	- citrate-dependent iron transport, periplasmic protein		1		9
b4291	fecA	2325 4512376 4514700	- outer membrane receptor; citrate- dependent iron transport. outer regulator for fec operon,		1		19
b4292	fecR	954 4514787 4515740	- periplasmic probable RNA polymerase sigma		1		5
b4293	fecI	522 4515737 4516258	- IS1 protein InsA		1		6
b4294	insA_7	276 4516550 4516825	+ orf, hypothetical protein	1	1		15
b4295	yjhU	801 4517361 4518161	- putative transport	1		1	6
b4296	yjhF	1350 4518694 4520043	- system permease putative dehydratase				2
b4297	yjhG	1968 4520150 4522117	- putative lyase/synthase			1	2
b4298	yjhH	960 4522128 4523087	- putative regulator		1	1	4
b4299	yjhI	789 4523038 4523826	- putative DEOR-type transcriptional regulator	1	1	1	2
b4300	sgcR	783 4524129 4524911	- putative epimerase	1			7
b4301	sgcE	633 4524928 4525560	- putative PTS system	1			7
b4302	sgcA	432 4525572 4526003	- enzyme II A component putative nucleoside triphosphatase				7
b4303	sgcQ	807 4526134 4526940	- putative PTS system enzyme IIC component putative lyase/synthase				15
b4304	sgcC	1314 4526953 4528266	- putative putative				15
b4305	sgcX	1152 4528553 4529704	- orf, hypothetical protein	1	1	1	8
b4306	yjhP	747 4530460 4531206	- orf, hypothetical protein	1	1	1	2
b4307	yjhQ	546 4531262 4531807	- putative frameshift suppressor	1	1	1	8
b4308	yjhR	1017 4533038 4534054	+ orf, hypothetical protein	1	1	1	9
b4309	yjhS	981 4534637 4535617	- orf, hypothetical protein	1	1	1	17
b4310	yjhT	1215 4535682 4536896	- orf, hypothetical protein	1	1	1	19
b4311	yjhA	726 4536808 4537533	- recombinase involved in phase variation; regulator for fimA	1	1	1	13
b4312	fimB	603 4538980 4539582	+ recombinase involved in phase variation; regulator for fimA	1	1	1	8
b4313	fimE	597 4540060 4540656	+ recombinase involved in phase variation; regulator for fimA	1	1	1	8

b4314	fimA	549 4541138 4541686	+ major type 1 subunit fimbrin (pilin)		1	1	8
b4315	fimI	648 4541643 4542290	+ fimbrial protein	1	1	1	12
b4316	fimC	726 4542327 4543052	+ periplasmic chaperone, required for type 1 fimbriae	1	1	1	16
b4317	fimD	2637 4543119 4545755	+ outer membrane protein; export and assembly of type 1 fimbriae. interrupted	1	1	1	14
b4318	fimF	531 4545765 4546295	+ fimbrial morphology	1	1		8
b4319	fimG	504 4546308 4546811	+ fimbrial morphology	1	1		13
b4320	fimH	903 4546831 4547733	+ minor fimbrial subunit, D-mannose specific	1	1		8
b4321	gntP	1344 4547976 4549319	- gluconate transport system permease 3				11
b4322	uxuA	1185 4549659 4550843	+ mannonate hydrolase				20
b4323	uxuB	1461 4550924 4552384	+ D-mannonate oxidoreductase				15
b4324	uxuR	774 4552599 4553372	+ regulator for uxu operon				20
b4325	yjiC	831 4553513 4554343	- orf, hypothetical protein	1	1	1	7
b4326	yjiD	402 4555007 4555408	+ orf, hypothetical protein	1		1	11
b4327	yjiE	912 4555401 4556312	- putative transcriptional regulator LYSR-type				13
b4328	iadA	1173 4556377 4557549	- isoaspartyl dipeptidase				13
b4329	yjiG	462 4557562 4558023	- orf, hypothetical protein				13
b4330	yjiH	696 4558020 4558715	- orf, hypothetical protein				13
b4331	kptA	657 4558851 4559507	+ 2'-phosphotransferase	1			8
b4332	yjiJ	1179 4559520 4560698	- putative transport	1			17
b4333	yjiK	972 4560766 4561737	- orf, hypothetical protein	1	1		10
b4334	yjiL	774 4561945 4562718	- putative enzyme				6
b4335	yjiM	1173 4562722 4563894	- orf, hypothetical protein				6
b4336	yjiN	1281 4563989 4565269	- orf, hypothetical protein				11
b4337	yjiO	1233 4565310 4566542	- putative transport				10
b4338	yjiP	312 4567021 4567332	+ orf, hypothetical protein	1			2
b4339	yjiQ	561 4567381 4567941	+ orf, hypothetical protein	1			2
b4340	yjiR	1413 4568185 4569597	- putative regulator			1	6
b4341	yjiS	165 4569774 4569938	+ orf, hypothetical protein	1	1	1	9
b4342	yjiT	1566 4570389 4571954	+ orf, hypothetical protein	1	1	1	7
b4486	yjiV	2721 4572158 4574878	+ conserved hypothetical protein	1	1		7
b4345	mcrC	1047 4574935 4575981	- component of McrBC 5- methylcytosine restriction system, expands range of	1	1	1	5
b4346	mcrB	1398 4575981 4577378	- component of McrBC 5- methylcytosine restriction system	1	1	1	6
b4347	yjiW	399 4577522 4577920	- orf, hypothetical protein		1	1	10
b4348	hsdS	1395 4578091 4579485	- specificity determinant for hsdM and hsdR	1	1	1	15
b4349	hsdM	1590 4579482 4581071	- host modification; DNA methylase M		1		14
b4350	hsdR	3567 4581272 4584838	- host restriction; endonuclease R		1		12
b4351	mrr	915 4584972 4585886	+ restriction of methylated adenine		1		6
b4352	yjiA	855 4585932 4586786	- orf, hypothetical protein				16
b4353	yjiX	204 4586899 4587102	- orf, hypothetical protein				20
b4354	yjiY	2166 4587152 4589317	- putative carbon starvation protein			1	20
b4355	tsr	1656 4589680 4591335	+ methyl-accepting chemotaxis protein I, serine sensor receptor			1	17
b4356	yjiZ	1362 4591384 4592745	- putative transport protein, cryptic, orf, joins former yjiZ and			1	11
b4357	yjiM	915 4592960 4593874	- orf, hypothetical protein	1		1	10
b4358	yjiN	1038 4593998 4595035	+ putative oxidoreductase			1	10
b4359	mdoB	2253 4595173 4597425	- phosphoglycerol transferase I				15
b4360	yjiA	498 4597718 4598215	- putative glycoprotein/receptor				19

b4361	dnaC	738 4598261 4598998	- chromosome replication; initiation and chain elongation				15
b4362	dnaT	540 4599001 4599540	- DNA biosynthesis; primosomal protein i				15
b4363	yjjB	327 4599647 4599973	- orf, hypothetical protein		1		20
b4364	yjjP	834 4600111 4600944	- putative structural	1		1	18
b4365	yjjQ	726 4601500 4602225	+ putative regulator	1	1	1	15
b4366	bgIJ	678 4602183 4602860	+ 2-component transcriptional regulator	1	1	1	13
b4367	fhuF	789 4602898 4603686	- orf, hypothetical protein	1			20
tRNA-Leu4	tRNA-Leu	88 4604101 4604188	- tRNA-Leu				
tRNA-Leu5	tRNA-Leu	87 4604223 4604309	- tRNA-Leu				
tRNA-Leu6	tRNA-Leu	87 4604338 4604424	- tRNA-Leu				
b4371	rsmC	1032 4604692 4605723	- 16S rRNA m2G1207 methylase				21
b4372	holD	414 4605826 4606239	+ DNA polymerase III, psi subunit				20
b4373	rimI	447 4606208 4606654	+ acyltransferase for 30S ribosomal subunit protein S18; acetylation of N-terminal alanine				21
b4374	yjjG	678 4606669 4607346	+ putative phosphatase				20
b4375	prfC	1590 4607437 4609026	+ peptide chain release factor RF-3				21
b4376	osmY	606 4609419 4610024	+ hyperosmotically inducible periplasmic				20
b4377	yjjU	1074 4610434 4611507	+ orf, hypothetical protein				20
b4378	yjjV	636 4611648 4612283	+ orf, hypothetical protein				21
b4379	yjjW	864 4612703 4613566	- putative activating				15
b4380	yjjI	1551 4613538 4615088	- orf, hypothetical protein				15
b4381	deoC	780 4615346 4616125	+ 2-deoxyribose-5-phosphate aldolase				21
b4382	deoA	1323 4616252 4617574	+ thymidine				18
b4383	deoB	1224 4617626 4618849	+ phosphopentomutase				21
b4384	deoD	720 4618906 4619625	+ purine-nucleoside phosphorylase				21
b4385	yjjJ	1332 4619792 4621123	+ orf, hypothetical protein				4
b4386	lplA	1017 4621124 4622140	- lipoate-protein ligase A				17
b4387	smP	645 4622168 4622812	- orf, hypothetical protein				21
b4388	serB	969 4622918 4623886	+ 3-phosphoserine phosphatase				21
b4389	sms	1383 4623935 4625317	+ probable ATP-dependent protease				21
b4390	nadR	1254 4625317 4626570	+ probable nadAB transcriptional regulator				20
b4391	yjjK	1668 4626878 4628545	- putative ATP-binding component of a transport system				19
b4392	slt	1965 4628729 4630693	+ soluble lytic murein transglycosylase				21
b4393	trpR	327 4630783 4631109	+ regulator for trp operon and aroH; trp aporepressor				21
b4394	yjjX	522 4631256 4631777	- orf, hypothetical protein				17
b4395	gpmB	648 4631820 4632467	+ phosphoglyceromutase				21
b4396	rob	870 4632464 4633333	- right origin-binding				21
b4397	creA	474 4633544 4634017	+ orf, hypothetical protein				21
b4398	creB	690 4634030 4634719	+ catabolic regulation response regulator				19
b4399	creC	1425 4634719 4636143	+ catabolite repression sensor kinase for PhoB; alternative sensor for pho regulon				18
b4400	creD	1353 4636201 4637553	+ tolerance to colicin E2				18
b4401	arcA	717 4637613 4638329	- negative response regulator of genes in aerobic pathways, (sensors. ArcB and				21
b4402	yjjY	141 4638425 4638565	+ orf, hypothetical protein	1	1		14
b4403	lasT	687 4638965 4639651	+ orf, hypothetical protein			1	16

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- a) Start and end positions and direction of coding sequence.
 - b) Phage and fimbria-related genes are colored by purple and yellow, respectively.
 - c) Horizontally acquired genes suggested by Nakamura et al. (2004) is marked by 1 and colored.
 - d) Horizontally acquired genes proposed by Lawrence and Ochman (2004) is marked by 1 and colored.
 - e) H-NS associated genes in Supplementary Table 1 is marked by 1 and colored.
 - f) Number of species in which ortholog gene was identified among 21 complete genome sequences of Enterobacteriaceae. Ortholog gene table was created according to MBGD (<http://mbgd.genome.ad.jp/>).
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