

# SUPPLEMENTAL TABLES

## Details of modularized genes from *E.coli* data

Module	Gene #	Systematic name	Common name	TIGR annotation	Linked genes	Assigned color	
Module 1	1	b0012	htgA	transcriptional activator for sigma H (sigma 32) promoters, permitting growth at high temperature	4	Black	
	2	b1474	fdnG	formate dehydrogenase-N, alpha subunit, nitrate-inducible	4	Red	
	3	b2939	yqgB	unknown CDS	4	Gray10	
	4	b3138	agaB	PTS family enzyme IIB component I, N-acetylgalactosamine-specific	1 2 3	Red	
Module 2	5	b0173	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	6	Red	
	6	b2142	yohK	putative transmembrane protein	5 7 8	Red	
	7	b2246	yfaV	putative transport protein (MFS family)	6 8 9 10	Red	
	8	b2322	yfcJ	putative transport protein (MFS family)	6 7	Red	
	9	b2546	yphD	putative sugar transport protein (ABC superfamily, membrane)	7 10	Red	
	10	b2547	yphE	multimodular; putative sugar transport protein (ABC superfamily, atp_bind)	7 9	Red	
	Module 3	11	b1155	ymfS	e14 prophage	14 22 12 15 16 19	Gray10
		12	b1156	tfaE	e14 prophage; putative tail fiber assembly	13 14 22 11 15	Gray10
		13	b0223	yafJ	conserved protein with N-terminal nucleophile aminohydrolase domain	12 21	Gray10
		14	b0224	yafK	conserved protein of unknown function	22 11 12 15 17	Gray10
15		b2353	tfaK	CPS-53 (KpLE1) prophage	14 22 11 12 16 19	Gray10	
16		b2354	yfaK	CPS-53 (KpLE1) prophage; putative tail fiber assembly	22 11 15 19	Gray10	
17		b2499	purM	phosphoribosylaminoimidazole synthetase (AIR synthetase)	14	Red	
18		b3777	yifN	conserved protein of unknown function	21	Gray10	
19		b4016	aceK	isocitrate dehydrogenase kinase/phosphatase	22 11 15 16	Red	
20		b0413	ybaD	conserved protein of unknown function	21	Gray10	
21		b4248	yjgH	putative translation factor	13 20 22 18	Gray10	
22		b0827	moeA	molybdopterin biosynthesis protein, molybdenum incorporation step	14 11 12 15 16 19 21	Red	
Module 4		23	b0254	perR	CP4-6 prophage; putative transcriptional repressor of peroxide resistance (LysR family)	25 24	Red
		24	b2786	barA	multimodular; hybrid sensory histidine kinase in two-component regulatory system with UvrY	23 25	Red
	25	b0318	yahD	putative regulator with ankyrin repeat	23 24	Red	
	26	b1331	yi52_4	IS5 protein	33 34 27 29	Red	
	27	b1370	yi52_5	Rac prophage; IS5 protein	30 26 28	Red	
Module 5	28	b2030	yi52_7	IS5 protein	27 29 31	Red	
	29	b2192	yi52_8	IS5 protein	33 34 26 28	Red	
	30	b0259	yi52_1	CP4-6 prophage; IS5 protein I	34 27 32	Red	
	31	b2982	yi52_9	IS5 protein	28 32	Red	
	32	b3218	yi5210	IS5 protein 10	30 31	Red	
	33	b0552	yi52_2	DLP12 prophage; IS 5 protein	34 26 29	Red	
	34	b0656	yi52_3	IS5 protein	30 33 26 29	Red	
	Module 6	35	b2364	dsrC	transcriptional regulator of D-serine dehydratase (deaminase) (LysR family)	37 43 36 38 39 40 41 42	Red
		36	b2596	b2596	unknown CDS	37 43 35 38 39 40 41 42	Gray10
		37	b0276	yagJ	CP4-6 prophage	35 36 38 39 40 41 42	Gray10
38		b2849	yqeK	unknown CDS	37 43 35 36 38 39 40 41 42	Gray10	
39		b2853	ygeI	unknown CDS	37 43 35 36 38 40 41 42	Gray10	
40		b3119	tdcR	transcriptional activator for threonine dehydratase	37 43 35 36 38 39 41 42	Red	
41		b3263	yhdU	unknown CDS	37 43 35 36 38 39 40 42	Gray10	
42		b4313	fimE	tyrosine recombinase, regulator of fimA	37 43 35 36 38 39 40 41	Black	
43		b0989	cspH	cold shock-like protein, nucleic acid-binding domain	35 36 38 39 40 41 42	Gray10	
Module 7		44	b2089	insF5	putative transposase for IS3	45 46	Red
		45	b0299	insF1	putative IS transposase	46 44	Red
		46	b0541	insF3	DLP12 prophage; putative transposase for insertion sequence IS3	45 44	Red
Module 8	47	b1746	astD	succinylglutamic semialdehyde dehydrogenase	56 48	Red	
	48	b1748	astC	succinylornithine transaminase, also has acetylornithine transaminase activity, PLP-dependent	56 47 51	Red	
	49	b1971	yedY	putative reductase with Sulfite oxidase, middle catalytic domain	52 55	Red	
	50	b1988	nac	transcriptional repressor of histidine utilization/nitrogen assimilation (LysR family)	54 56 53	Red	
	51	b3268	yhdW	putative amino acid transport protein (ABC superfamily, peri_bind)	48	Red	
	52	b0359	b0359	putative acyl transferase with trimeric LpxA-like domain	55 49	Red	
	53	b3869	glnL	sensory kinase (soluble) in two-component regulatory system with GlnG, nitrogen regulation (nitrogen regulator II, NRII)	54 50	Red	
	54	b0450	glnK	regulatory protein (P-II 2) for nitrogen assimilation, regulates GlnL (NRII), GlnE (ATase), and AmtB (ammonium transporter)	56 50 53	Red	
	55	b1006	ycdG	putative uracil transport protein (NCS2 family)	52 56 49	Red	
	56	b1011	ycdL	putative enzyme with cysteine hydrolase domain	54 55 47 48 50	Red	
Module 9	57	b1493	gadB	glutamate decarboxylase, PLP-dependent, isozyme beta	60 59	Red	
	58	b3506	slp	outer membrane protein, induced after carbon starvation	60	Lavender	
	59	b3517	gadA	glutamate decarboxylase A, isozyme, PLP-dependent	60 57	Red	
	60	b0485	ybaS	putative glutaminase/carboxypeptidase with beta-Lactamase/D-ala carboxypeptidase domain	57 58 59	Red	
Module 10	61	b1114	mfd	transcription-repair ATP-dependent coupling factor	63	Black	
	62	b2893	dsbC	protein disulfide isomerase II, activated by N-terminal of DsbD	63	Black	
	63	b3210	arcB	multimodular; hybrid sensory histidine kinase in two-component regulatory system with ArcA, regulates respiration and fermentation, senses oxidized quinones	64 66 61 62	Red	
	64	b0495	ybbA	putative transport protein (ABC superfamily, atp_bind)	65 66 63	Red	
Module 11	65	b0644	ybeQ	conserved protein with protein prenyltransferase domain	64	Gray10	
	66	b0769	ybhH	conserved protein of unknown function	64 63	Gray10	
	67	b1161	ycgX	putative phage protein	73 68 69 70 71 72	Gray10	
	68	b1575	dicB	Qin prophage; inhibitor of cell division	73 67 69 70 72	Gray10	
	69	b1979	b1979	putative transport protein	73 67 68 70 72	Gray10	
	70	b2238	yfaH	conserved protein with periplasmic binding protein-like II domain	73 67 68 69 72	Gray10	
	71	b2856	b2856	unknown CDS	67 72	Gray10	
	72	b2857	b2857	unknown CDS	73 67 68 69 70 71	Gray10	
	73	b0533	sfmH	fimbrial assembly protein with adhesin domain	67 68 69 70 72	Red	
	74	b0543	emrE	DLP12 prophage; auxiliary multidrug transport protein, methylviologen and ethidium resistance (SMR family)	75 76	Red	
Module 12	75	b0544	ybcK	DLP12 prophage; putative recombinase	74 76	Gray10	
	76	b0561	ybcX	DLP12 prophage; putative tail fiber assembly gene	74 75	Gray10	
	77	b0614	citX	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	78	Gray10	
	78	b0622	crcA	palmitoyl transferase for Lipid A, outer membrane integral protein	77 80	Gray10	
	79	b0629	ybeF	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	80	Gray10	
	80	b0645	ybeR	conserved protein of unknown function	78 79	Gray10	
	Module 14	81	b1048	mdoG	periplasmic glucans biosynthesis protein	82 167 192 310 381	Black
		82	b1049	mdoH	glycosyltransferase, synthesis of membrane-derived oligosaccharide/synthesis of osmoregulated periplasmic glucans	387 81	Black
		83	b1051	msyB	acidic protein suppresses mutants lacking function of protein export	285	Black
		84	b0104	guaC	GMP reductase	112 125 144 383 394 401 415 419 421 86 93 105 111 123 135 165 167 181 194 217 218 247 252 258 272 338 342	LimeGreen
85		b1060	yceP	conserved protein of unknown function	209	Gray10	
86		b1062	pyrC	dihydroorotase	84 125 147 383 388 414 421 93 105 108 111 135 148 167	LimeGreen	

					181 189 192 194 195 199 214 217 218 239 246 270 290 292 306 331 334 338	
87	b1088	yceD	conserved protein of unknown function		170 347 256 265 326 340	Gray10
88	b1090	plsX	fatty acid/phospholipid synthesis protein, methyltransferase domain		292	LimeGreen
89	b1094	acpP	acyl carrier protein		165	LimeGreen
90	b1109	ndh	respiratory NADH dehydrogenase 2; cupric reductase		186 223 325 346 377	LimeGreen
91	b1123	potD	spermidine/putrescine transport protein (ABC superfamily, peri_bind)		383 232 247 321 322 323 325	LimeGreen
92	b1128	yefD	putative enzyme with RmlC-like domain		144 401 191 245	Gray10
93	b1131	purB	adenylosuccinate lyase		84 112 125 144 147 383 401 414 415 418 421 86 105 135 167 181 191 192 194 195 214 217 246 247 258 260 290 306 338 343 363	LimeGreen
94	b1136	icdA	e14 prophage: isocitrate dehydrogenase, specific for NADP+		97 109 286 339	LimeGreen
95	b0114	aceE	pyruvate dehydrogenase, decarboxylase subunit, thiamin-binding		96	LimeGreen
96	b0115	aceF	pyruvate dehydrogenase, dihydrolipoyltransacetylase subunit		95 320	LimeGreen
97	b0116	lpdA	dihydrolipoamide dehydrogenase, FAD/NAD(P)-binding, component of the 2-oxoglutarate dehydrogenase and the pyruvate dehydrogenase complexes		94 275	LimeGreen
98	b1188	ycgB	conserved protein of unknown function		119 397 127 299 302	Gray10
99	b1189	dadA	D-amino acid dehydrogenase subunit		100 228 366	Red
100	b1190	dadX	alanine racemase 2, PLP-binding, catabolic		99	Red
101	b1205	ychH	conserved protein of unknown function		125 402 212 228 365 366	Gray10
102	b1207	prsA	phosphoribosylpyrophosphate synthetase		135 217	LimeGreen
103	b0119	yacl	conserved protein of unknown function		243	Gray10
104	b0121	speE	spermidine synthase (putrescine aminopropyltransferase)		128 253 286	LimeGreen
105	b1232	purU	formyltetrahydrofolate hydrolase		84 383 402 414 86 93 135 167 192 194 195 306 338	LimeGreen
106	b1275	cysB	transcriptional regulator of biosynthesis of L-cysteine and regulator of sulfur assimilation (LysR family)		381	Lavender
107	b1286	rnb	RNase II, mRNA degradation		325	Lavender
108	b1287	yciW	conserved protein of unknown function		86	Gray10
109	b1300	aldH	aldehyde dehydrogenase, prefers NADP over NAD		94 218	LimeGreen
110	b0129	yadI	putative PTS family enzyme IIA component		398 410 212 228 296 361 365 366	Lavender
111	b1324	tpx	lipid hydroperoxide peroxidase		84 393 86 135 239 290 338	Black
112	b0131	panD	aspartate 1-decarboxylase		84 125 144 401 419 421 93 123 131 165 194 214 217 218 219 220 239 247 252 258 272 290 314 318 342 357	LimeGreen
113	b1338	abgA	indole-3-acetyl-L-aspartic acid hydrolase, p-aminobenzoyl-glutamate utilization (strain BN101)		309 120 143 352	Lavender
114	b1341	b1341	conserved protein with PYP-like sensor domain		143	Gray10
115	b0133	panC	pantothenate synthetase		391	LimeGreen
116	b1376	ynaF	putative electron transfer flavoprotein with adenine nucleotide-binding domain		300	Lavender
117	b1406	yubC	putative oxidoreductase, NAD(P)-binding domain		397 411 422 158 198 212 228 365 366 373 374 385	Red
118	b1447	ydcZ	putative transport protein		121 248 333	Gray10
119	b0146	sfsA	transcriptional regulator of maltose metabolism		397 98 127 302 385 386	Red
120	b1471	yddK	putative glycoprotein with ribonuclease inhibitor domain		309 392 113 141 143 154 156 172 178 240 307 311 327 352 353 358	Red
121	b1507	hipA	transcriptional repressor which interacts with HipB		122 420 118 350	Lavender
122	b0153	fluB	multimodular: hydroxamate-dependent iron transport protein (ABC superfamily, membrane)		420 121 141 178 197 229 350 356	LimeGreen
123	b1637	tyrS	tyrosine tRNA synthetase		84 112 360 367 252 258 272	Red
124	b0165	b0165	unknown CDS		226 141 178 205 358	Gray10
125	b0166	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase		84 112 134 348 383 402 414 417 418 419 86 93 101 131 135 181 194 199 214 217 246 247 252 258 314 338 357 363 372	Lavender
126	b1658	purR	transcriptional repressor for de novo purine nucleotide synthesis (GalR/LacI family)		148 182	LimeGreen
127	b1678	ynhG	putative ATP synthase subunit with LysM domain		119 397 416 98 136 232 300 302	Gray10
128	b0169	rpsB	30S ribosomal subunit protein S2		104 383 203 253 260 261 266 269 270 271 273 286	Red
129	b0170	tsf	protein chain elongation factor EF-Ts		383 261 264 270 271 322 325 364	Red
130	b1715	pheM	phenylalanyl-tRNA synthetase (pheST) operon leader peptide		399 141	Red
131	b1716	rpIT	50S ribosomal subunit protein L20, also postranslational autoregulator		112 125 132 165 181 202 217 218 220 246 252 258 259 260 272 273 275 278 314 341 342 369	Red
132	b1717	rpmI	50S ribosomal subunit protein A		131 165 218 246 252 259 260 261 266 268 269 271 273 275 276 282 286 314 339 341 342 369	Red
133	b1725	yniA	conserved protein with protein kinase-like domain		398 297	Gray10
134	b0177	yaef	putative outer membrane antigen		125 384 217	Gray10
135	b1779	gapA	glyceraldehyde-3-phosphate dehydrogenase A		236 84 125 147 383 393 394 400 402 414 86 93 102 105 111 181 192 194 195 214 217 218 222 239 246 247 252 258 260 270 271 290 306 321 338 341 342 363 381	LimeGreen
136	b1783	yeaG	conserved protein with nucleotide triphosphate hydrolase domain		382 397 411 416 127 232 235 239 291 300	Gray10
137	b0179	lpxD	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase		394	Black
138	b1805	fadD	acyl-CoA synthetase (long-chain-fatty-acid-CoA ligase)		411 300	Red
139	b1809	yoaB	conserved protein with YjgF-like domain		247	Gray10
140	b1810	b1810	conserved protein of unknown function		251 153 354	Gray10
141	b1815	b1815	conserved protein of unknown function		122 124 226 309 120 130 156 166 172 178 229 294 352 358	Gray10
142	b0185	accA	acetylCoA carboxylase, carboxytransferase subunit alpha		396 230	LimeGreen
143	b1933	b1933	unknown CDS		309 113 114 120 311 352 353	Gray10
144	b0194	proS	proline tRNA synthetase		84 112 355 383 394 401 415 419 92 93 167 191 192 194 217 241 246 252 258 259 273 362	Red
145	b1947	flhO	flagellar biosynthesis		257 307	Red
146	b1953	yodD	unknown CDS		424 299	Gray10
147	b0197	metQ	D-methionine transport protein (ABC superfamily, peri_bind)		383 393 400 402 414 86 93 135 167 189 192 194 195 214 217 218 220 246 247 258 260 264 270 271 292 306 322 323 325 338 341 343 363	Gray10
148	b1983	yeeN	conserved protein with YebC-like domain		86 126	Gray10

	149	b2023	hisH	glutamine amidotransferase, subunit with HisF (imidazole glycerol phosphate synthase holoenzyme)	182 185 222 246	Lavender
	150	b2029	gnd	gluconate-6-phosphate dehydrogenase, decarboxylating	194	LimeGreen
	151	b2039	rfbA	dTDP-glucose pyrophosphorylase	347	LimeGreen
	152	b0211	mltD	lytic murein transglycosylase C, membrane-bound	414 214	LimeGreen
	153	b2080	yegP	conserved protein of unknown function	251 406 424 140 232 354	Gray10
	154	b2108	yehA	conserved protein with adhesin-like domain	309 120 156 178	Red
	155	b2115	molR_1	split molybdate metabolism regulator, fragment 1 of 3	178 352	Lavender
	156	b2122	yehQ	conserved protein of unknown function	226 309 120 141 154 157 159 166 172 178 229 311 327 352	Gray10
	157	b2136	yohD	putative integral membrane protein	156 159 166 172 178 327	Gray10
	158	b2137	yohF	putative oxidoreductase with NAD(P)-binding domains	117	Red
	159	b2158	yehH	putative membrane protein	156 157 160 162 163 164 166 168 178 327	Gray10
	160	b2165	yehN	conserved protein of unknown function	159 162 163 164 166	Gray10
	161	b2171	yehP	putative elongation factor	162	Red
	162	b2173	yehR	putative enzyme with 3 nucleoside triP hydrolase domains	159 160 161 163 166 168	Gray10
	163	b2174	yehU	putative phosphatase	159 160 162 166 168 225	Gray10
	164	b2178	yehB	putative oligopeptide transport protein (ABC superfamily, membrane)	159 160	Gray10
	165	b2185	rplY	50S ribosomal subunit protein L25	84 112 383 393 415 89 131 132 202 218 220 239 246 252 258 259 260 272 273 275 286 314 338 339 341 342 357 369 370 378 379	Red
	166	b2186	yehK	nucleotide associated protein, present in spermidine nucleoids	141 156 157 159 160 162 163 172 178 327	Gray10
	167	b2188	yehM	putative phosphatase/sulphatase	237 84 144 147 383 401 415 81 86 93 105 187 191 192 194 195 214 218 220 246 247 252 258 259 260 261 269 270 271 273 279 282 292 306 328 338 341 342 343 362 363 364	Gray10
	168	b2226	b2226	conserved protein of unknown function	159 162 163	Gray10
	169	b2234	nrdA	ribonucleoside diphosphate reductase 1, alpha subunit	321	LimeGreen
	170	b0023	rpsT	30S ribosomal subunit protein S20	360 87 234 256 326	Red
	171	b2265	menF	isochorismate synthase (isochorismate hydroxymutase 2), menaquinone biosynthesis	220 252 370	LimeGreen
	172	b2269	elaD	putative enzyme with cysteine proteinase domain	120 141 156 157 166 178 327 352 358	Gray10
	173	b0235	b0235	unknown CDS	216	Gray10
	174	b2312	purF	amidophosphoribosyltransferase (PRPP amidotransferase)	195	LimeGreen
	175	b2313	cvpA	membrane protein required for colicin V production	324	Black
	176	b2319	usg	putative dehydrogenase with NAD(P)-binding domain and Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain	254	Gray10
	177	b2329	aroC	chorismate synthase	348 402 414 418 186	Lavender
	178	b2339	b2339	putative fimbrial-like adhesin protein	122 124 226 309 120 141 154 155 156 157 159 166 172 229 294 327 352 358	Red
	179	b2373	yfdU	putative oxalyl-CoA decarboxylase with Thiamin diphosphate-binding fold (THDP-binding) and DHS-like NAD/FAD-binding domain	399 294	Gray10
	180	b2384	b2384	putative endoglucanase with Zn-dependent exopeptidase domain	221 225	Gray10
	181	b2414	cysK	subunit of cysteine synthase A and O-acetylserine sulphydrylase A, PLP-dependent enzyme	84 125 383 86 93 131 135 194 202 210 214 217 218 239 246 252 258 260 270 271 290 306 314 338 342 363 372	Lavender
	182	b2421	cysM	cysteine synthase B (O-acetylserine sulphydrylase B)	126 149	Lavender
	183	b2426	ucpA	putative oxidoreductase, NAD(P)-binding domain	410 293	Red
	184	b0025	ribF	bifunctional: flavokinase; FAD synthetase	295 330	Gray10
	185	b2472	dapE	N-succinyl-diaminopimelate deacylase	149	Lavender
	186	b2478	dapA	dihydrodipicolinate synthase	402 90 177 306	Lavender
	187	b2491	hyfR	transcriptional activator for expression of hydrogenase 4 genes, interacts with sigma 54 (EBP family)	425 167	Gray10
	188	b2496	hda	regulatory factor involved in inactivation of DnaA	315 316	Lavender
	189	b2498	upp	uracil phosphoribosyltransferase	147 383 421 86 195 218 220 232 253 380	LimeGreen
	190	b2500	purN	phosphoribosylglycinamide formyltransferase 1	334 344	LimeGreen
	191	b2502	ppx	exopolysphatase	144 92 93 167 192 280 304	LimeGreen
	192	b2508	guaB	IMP dehydrogenase	237 144 147 383 402 414 81 86 93 105 135 167 191 194 195 214 246 247 260 270 271 292 306 319 322 325 338 343 362 363 381	LimeGreen
	193	b2509	xseA	exonuclease VII, large subunit	318 357	Black
	194	b2514	hisS	histidine tRNA synthetase	84 112 125 144 147 383 401 402 414 86 93 105 135 150 167 181 192 214 217 218 239 246 247 260 270 290 292 306 338 363	Red
	195	b2551	glyA	serine hydroxymethyltransferase	147 383 86 93 105 135 167 174 189 192 246 260 261 269 270 271 288 289 306 322 325 338	Lavender
	196	b2569	lepA	GTP-binding elongation factor	318	Red
	197	b2577	yfiE	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	122	Gray10
	198	b2584	yfiQ	multimodular putative acyl-CoA synthetase: NAD(P)-binding protein (N-terminal); ATP-binding protein (C-terminal)	117 212 228 365 366	Gray10
	199	b2595	yfiO	putative lipoprotein with tetratricopeptide repeats (TPR) domain	125 86 214	Gray10
	200	b2597	yfiA	ribosome associated factor, stabilizes ribosomes against dissociation	398 411 232 361	Gray10
	201	b2606	rplS	50S ribosomal subunit protein L19	219	Red
	202	b2607	trmD	tRNA (guanine-1-)-methyltransferase	383 415 131 165 181 203 218 220 239 252 253 258 260 261 269 270 271 272 273 286 314 338 339 341 342 364 369 380	Red
	203	b2609	rpsP	30S ribosomal subunit protein S16	128 383 202 253 259 260 261 266 269 270 271 273 276 279 282 286 289 341 342 369	Red
	204	b2639	b2639	CP4-57 prophage; putative arsenical pump protein	312	Lavender
	205	b2641	b2641	CP4-57 prophage	124	Gray10
	206	b2665	ygau	conserved protein with LysM domain	208 227 285 359	Gray10
	207	b2667	b2667	conserved protein with winged-helix DNA-binding domain	225	Gray10
	208	b2672	ygam	conserved protein of unknown function	206 285 359	Gray10
	209	b2696	csrA	carbon storage regulator, post-translational activator of flhDC expression, regulates biofilm formation, RNA-binding	424 85 232	Red
	210	b2752	cysD	ATP-sulfurylase, subunit 2 (ATP:sulfate adenylyltransferase)	181	LimeGreen
	211	b2779	eno	enolase	223	LimeGreen
	212	b2800	fucA	L-fuculose-1-phosphate aldolase	110 403 410 101 117 198 228 365 366 373	Red

	213	b2810	csdA	cysteine sulfinate desulfinate	215 225	Gray10
	214	b2821	ptrA	protease III	112 125 147 152 348 383 414 419 86 93 135 167 181 192 194 199 217 218 220 239 246 247 252 258 260 290 292 338 343 363	Black
	215	b2866	xdhA	putative xanthine dehydrogenase subunit, molybdenum cofactor-binding domain	213 225	Gray10
	216	b0295	ykgL	unknown CDS	404 173 226 231 399 294	Gray10
	217	b2891	prfB	peptide chain release factor RF-2	84 112 125 134 144 147 348 383 401 402 414 418 419 86 93 102 131 135 181 194 214 218 239 246 247 252 258 259 260 270 272 273 290 292 314 321 338 341 342 357 363	Red
	218	b2903	gecP	glycine cleavage complex protein P, glycine decarboxylase, PLP-dependent	236 84 112 147 383 393 400 415 86 109 131 132 135 165 167 181 189 194 202 214 217 220 232 239 246 247 249 250 252 253 258 259 260 261 264 266 269 270 271 272 273 275 279 282 286 287 299 314 321 323 338 339 341 342 357 363 369 380	Lavender
	219	b2904	gecH	glycine cleavage complex protein H, carrier of aminomethyl moiety via covalently bound lipoyl cofactor	112 201 247 252	LimeGreen
	220	b2907	ubiH	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding	112 147 274 383 131 165 167 171 189 202 214 218 239 246 247 252 253 258 260 261 269 273 282 286 314 334 339 341 342 344 369	LimeGreen
	221	b2923	argO	arginine transport protein (LYSE family)	180 225	Gray10
	222	b2925	ftaA	fructose-bisphosphate aldolase, class II	135 149 223	LimeGreen
	223	b2926	pgk	phosphoglycerate kinase	90 211 222	LimeGreen
	224	b2927	epd	D-erythrose 4-phosphate dehydrogenase	425	LimeGreen
	225	b2944	sprT	conserved protein of unknown function	163 180 207 213 215 221	Gray10
	226	b0303	ykgI	unknown CDS	404 124 216 399 405 141 156 178 229 294 358	Gray10
	227	b3000	b3000	conserved protein of unknown function	206 354	Gray10
	228	b3001	yghZ	aldo-keto reductase	110 99 101 117 198 212 365 366 373	Gray10
	229	b3014	yqhH	putative outer membrane lipoprotein	122 226 141 156 178 294	Gray10
	230	b3017	sufI	repressor protein for FtsI with three cupredoxin-like domains	142 396	Gray10
	231	b0309	b0309	unknown CDS	216	Gray10
	232	b3049	glgS	glycogen biosynthesis, rpoS-dependent	397 411 416 424 91 127 136 153 189 200 209 218 239 302 325	Red
	233	b3050	b3050	conserved protein of unknown function	238	Gray10
	234	b3065	rpsU	30S ribosomal subunit protein S21	170 258 326	Red
	235	b3073	yggG	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent	136	Red
	236	b0004	thrC	threonine synthase	383 135 218 246 249 252 260 261 270 271 273 338 341 342	Lavender
	237	b0031	dapB	dihydropicolinate reductase	383 167 192 260 271 273 345	Lavender
	238	b3128	garD	(D)-galactarate dehydrogenase	425 233	Gray10
	239	b3135	agaA	N-acetylglucosamine 6-phosphate deacetylase, gene fragment	112 383 393 421 86 111 135 136 165 181 194 202 214 217 218 220 232 246 252 260 286 290 314 329 334 338 339 342 357	Gray10
	240	b3142	yraH	putative fimbrial-like adhesin protein	120 284 307 311	Red
	241	b3168	infB	multimodular: protein chain initiation factor IF-2	144 242 272 287	Red
	242	b3169	nusA	transcription pausing; L factor	241 259	Lavender
	243	b3175	secG	preprotein translocase, membrane component, transport across inner membrane (General Secretory Pathway)	103 247 344	Black
	244	b3177	folP	7,8-dihydropterotate synthase	315 317	LimeGreen
	245	b3185	rpmA	50S ribosomal subunit protein L27	389 92	Red
	246	b3186	rplU	50S ribosomal subunit protein L21	236 125 144 147 348 383 393 400 402 414 86 93 131 132 135 149 165 167 181 192 194 195 214 217 218 220 239 247 252 258 259 260 261 262 264 269 270 271 273 282 283 286 292 306 314 321 322 323 325 338 339 341 342 363 369 372 381	Red
	247	b3189	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	84 112 125 147 348 383 394 400 401 402 414 91 93 135 139 167 192 194 214 217 218 219 220 243 246 252 258 259 260 273 299 302 314 321 323 334 338 341 342 362 363 369	LimeGreen
	248	b3206	ptsO	NPr, phosphocarrier protein (HPr-like), nitrogen-related	118 333	Lavender
	249	b3212	glfB	glutamate synthase, large subunit	236 393 218 250 298	LimeGreen
	250	b3213	glfD	glutamate synthase, small subunit, nucleotide-binding, 4Fe-4S protein	393 218 249 339	LimeGreen
	251	b0329	yahO	conserved protein of unknown function	423 140 153	Gray10
	252	b3230	rpsI	30S ribosomal subunit protein S9	236 84 112 125 144 274 383 393 401 415 123 131 132 135 165 167 171 181 202 214 217 218 219 220 239 246 247 258 259 260 261 268 269 271 272 273 275 278 281 282 286 287 299 314 318 339 341 342 357 363 369 370 379	Red
	253	b3231	rplM	50S ribosomal subunit protein L13	104 128 383 415 189 302 203 218 220 260 261 269 270 271 273 282 286 314 325 339 364 369 380	Red
	254	b3251	mreB	actin-like protein involved in cell shape regulation, chromosome movement and segregation, associated with mecillinam resistance	176 308	Black
	255	b3260	dusB	rRNA-dihydrouridine synthase B	289	Gray10
	256	b3261	fis	DNA-binding protein for site-specific recombination and inversion, transcription of rRNA and tRNA operons, and DNA replication	170 87	Lavender
	257	b3264	envR	transcriptional repressor for multiple drug efflux pump (TetR/AcrR family)	145 311 312	Gray10
	258	b3294	rplQ	50S ribosomal subunit protein L17	84 112 125 144 147 383 394 400 401 415 93 123 131 135 165 167 181 202 214 217 218 220 234 246 247 252 259 260 261 268 269 270 271 272 273 275 278 279 281 282 287 299	Red

	259	b3295	rpoA	RNA polymerase, alpha subunit	314 321 339 341 342 363 369 144 383 401 415 131 132 165 167 203 217 218 242 246 247 252 258 260 261 266 268 269 270 271 272 273 275 278 279 281 282 286 287 321 339 341 342 362 369	Lavender
	260	b3296	rpsD	30S ribosomal subunit protein S4	236 237 128 147 383 393 400 415 93 131 132 135 165 167 181 192 194 195 202 203 214 217 218 220 239 246 247 252 253 258 259 261 262 264 266 268 269 270 271 272 273 275 276 278 279 281 282 283 286 287 299 306 314 321 322 323 325 338 339 341 342 363 364 369	Red
	261	b3297	rpsK	30S ribosomal subunit protein S11	236 128 129 383 400 132 167 195 202 203 218 220 246 252 253 258 259 260 262 264 266 268 269 270 271 273 276 278 279 280 281 282 283 286 287 288 289 298 314 320 321 322 323 325 339 341 342 363 364 369	Red
	262	b3298	rpsM	30S ribosomal subunit protein S13	400 246 260 261 269 270 271 276 278 280 282 283 320 321 322 341	Red
	263	b3299	rpmJ	50S ribosomal subunit protein X	265	Red
	264	b3300	secY	preprotein translocase, membrane component, transport across inner membrane (General Secretory Pathway)	129 147 383 393 400 218 246 260 261 269 270 271 273 276 282 283 286 288 322 323 325 338 339 341 364 369	Black
	265	b3302	rpmD	50S ribosomal subunit protein L30	87 263 268 272 275 287 368 370	Red
	266	b3303	rpsE	30S ribosomal subunit protein S5	128 132 203 218 259 260 261 267 268 269 270 271 273 276 278 279 282 286 287 339 341 342 369	Red
	267	b3304	rplR	50S ribosomal subunit protein L18	266 268 269 276 277 279 280 282	Red
	268	b3305	rplF	50S ribosomal subunit protein L6	132 252 258 259 260 261 265 266 267 269 272 273 275 276 278 279 280 281 282 286 287 339 341 369 370	Red
	269	b3306	rpsH	30S ribosomal subunit protein S8, and regulator	128 383 400 415 132 167 195 202 203 218 220 246 252 253 258 259 260 261 262 264 266 267 268 270 271 272 273 276 278 279 280 281 282 283 286 287 288 289 322 323 325 339 341 342 369	Red
	270	b3307	rpsN	30S ribosomal subunit protein S14	236 128 129 147 383 393 400 86 135 167 181 192 194 195 202 203 217 218 246 253 258 259 260 261 262 264 266 269 271 273 278 279 282 283 286 288 292 298 306 314 322 323 325 338 339 341 342 363 364 369	Red
	271	b3308	rplE	50S ribosomal subunit protein L5	236 237 128 129 147 383 393 400 415 132 135 167 181 192 195 202 203 218 246 252 253 258 259 260 261 262 264 266 269 270 273 276 279 280 282 283 286 287 288 289 298 306 322 323 338 339 341 342 363 364 369	Red
	272	b3309	rplX	50S ribosomal subunit protein L24	84 112 383 394 401 415 123 131 165 202 217 218 241 252 258 259 260 265 268 269 273 275 278 281 286 287 299 339 341 342 368 369 370	Red
	273	b3310	rplN	50S ribosomal subunit protein L14	236 237 128 144 274 383 400 401 415 131 132 165 167 202 203 217 218 220 246 247 252 253 258 259 260 261 264 266 268 269 270 271 272 275 276 278 279 280 281 282 283 286 287 289 299 314 322 323 339 341 342 363 364 369	Red
	274	b0337	codA	cytosine deaminase	421 220 252 273 379 380	LimeGreen
	275	b3313	rplP	50S ribosomal subunit protein L16	97 393 131 132 165 218 252 258 259 260 265 268 272 273 278 281 286 287 339 341 342 369 370	Red
	276	b3314	rpsC	30S ribosomal subunit protein S3	132 203 260 261 262 264 266 267 268 269 271 273 278 279 280 281 282 283 286 287 320 322 339 341 369	Red
	277	b3315	rplV	50S ribosomal subunit protein L22	267 280	Red
	278	b3316	rpsS	30S ribosomal subunit protein S19	131 252 258 259 260 261 262 266 268 269 270 272 273 275 276 279 280 281 282 286 287 320 341 369	Red
	279	b3317	rplB	50S ribosomal subunit protein L2	383 415 167 203 218 258 259 260 261 266 267 268 269 270 271 273 276 278 280 281 282 286 287 289 339 341 342 369	Red
	280	b3318	rplW	50S ribosomal subunit protein L23	191 261 262 267 268 269 271 273 276 277 278 279 281 282 283 287 289 322 341	Red
	281	b3319	rplD	50S ribosomal subunit protein L4, regulates expression of S10 operon	252 258 259 260 261 268 269 272 273 275 276 278 279 280 282 283 287 341 369	Red
	282	b3320	rplC	50S ribosomal subunit protein L3	383 415 132 167 203 218 220 246 252 253 258 259 260 261 262 264 266 267 268 269 270 271 273 276 278 279 280 281 283 286 287 288 289 320 322	Red

	283	b3321	rpsJ	30S ribosomal subunit protein S10	323 339 341 342 369 383 400 246 260 261 262 264 269 270 271 273 276 280 281 282 289 320 322 323 324 325 341 381	Red
	284	b3334	gspM	putative protein exporter, transport across outer membrane (General Secretary Pathway)	240 307	Gray10
	285	b3336	bfr	bacterioferritin, an iron storage homoprotein	83 206 208 359	Lavender
	286	b3339	tufA	protein chain elongation factor EF-Tu (duplicate of tufB)	104 128 383 393 415 94 132 165 202 203 218 220 239 246 252 253 259 260 261 264 266 268 269 270 271 272 273 275 276 278 279 282 287 298 314 338 339 341 342 369 378	Red
	287	b3340	fusA	protein chain elongation factor EF-G, GTP-binding	415 218 241 252 258 259 260 261 265 266 268 269 271 272 273 275 276 278 279 280 281 282 286 339 341 342 369	Red
	288	b3341	rpsG	30S ribosomal subunit protein S7, initiates assembly	391 195 261 264 269 270 271 282 289 322 325	Red
	289	b3342	rpsL	30S ribosomal subunit protein S12	195 203 255 261 269 271 273 279 280 282 283 288 322	Red
	290	b3347	fkpA	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	112 383 421 86 93 111 135 181 194 214 217 239 334 338	Red
	291	b3362	yhfG	conserved protein of unknown function	397 416 136 299 302	Gray10
	292	b3390	aroK	shikimate kinase I	147 383 402 86 88 167 192 194 214 217 246 270 325 330 338 343 363	Lavender
	293	b3403	pckA	phosphoenolpyruvate carboxykinase	183	Red
	294	b3409	feoB	multimodular; ferrous iron transport protein B (FeoB family)	216 226 399 141 178 179 229	Black
	295	b3424	glpG	putative membrane protein, member of glp regulon	184 366	LimeGreen
	296	b3426	glpD	sn-glycerol-3-phosphate dehydrogenase FAD/NAD(P)-binding (aerobic)	110 335 336	Red
	297	b3430	glcC	glucose-1-phosphate adenylyltransferase	398 133 361	Red
	298	b3433	asd	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	249 261 270 271 286 339	Lavender
	299	b3448	yhhA	conserved protein of unknown function	383 393 416 98 146 218 247 252 258 260 272 273 291 302 339 341 342 369	Gray10
	300	b3453	ugpB	sn-glycerol 3-phosphate transport protein (ABC superfamily, peri_bind)	382 397 411 116 127 136 138 385	Lavender
	301	b3477	nikB	nickel transport protein (ABC superfamily, membrane)	312	Lavender
	302	b3494	uspB	universal stress protein B	119 383 397 416 98 127 232 247 291 299 371	Gray10
	303	b3528	dctA	citrate and C4-dicarboxylic acids transport protein (DAACS family)	403	Lavender
	304	b3536	yhjS	conserved protein of unknown function	191	Gray10
	305	b3538	yhjU	putative membrane protein	309 333	Gray10
	306	b3553	tkrA	2-keto-D-gluconate reductase (2-ketoaldonate reductase)	147 383 414 86 93 105 135 167 181 186 192 194 195 246 260 270 271 322 325 338 364 381	Gray10
	307	b3558	yi5B	IS150 transposase	120 145 240 284 311	Black
	308	b3572	avtA	valine-pyruvate aminotransferase	402 414 254	Lavender
	309	b0363	yaiP	putative enzyme in polysaccharide metabolism with nucleotide-diphospho-sugar transferase domain	420 113 120 141 143 154 156 178 305 311 349 352 353 358	Lavender
	310	b3621	rfaC	ADP-heptose: LPS heptosyl transferase I	81	LimeGreen
	311	b3628	rfaB	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase	309 392 420 120 143 156 240 257 307 352 353 358	Red
	312	b3634	coaD	CMP-deoxy-D-manno-octulosonate-lipid A transferase (phosphopantetheine adenylyltransferase)	204 257 301	Lavender
	313	b3636	rpmG	50S ribosomal subunit protein L33	314	Red
	314	b3637	rpmB	50S ribosomal subunit protein L28	112 125 383 131 132 165 181 202 217 218 220 239 246 247 252 253 258 260 261 270 273 286 313 318 341 342	Red
	315	b3639	dfp	multimodular: 4'-phosphopantothencysteine decarboxylase (N-terminal); phosphopantothencysteine synthetase, FMN-binding (C-terminal)	407 188 244 317 327	Lavender
	316	b3643	rph	RNase PH	188	Lavender
	317	b3649	rpoZ	RNA polymerase, omega subunit	244 315 340	Lavender
	318	b3651	spoU	putative tRNA/rRNA methyltransferase	112 193 196 252 314 357	Gray10
	319	b3652	recG	DNA helicase, ATP-dependent resolution of Holliday junctions, branch migration	192	Lavender
	320	b3732	atpD	membrane-bound ATP synthase, F1 sector, beta-subunit	96 400 261 262 276 278 282 283 321 322 323	LimeGreen
	321	b3734	atpA	membrane-bound ATP synthase, F1 sector, alpha-subunit	383 400 91 135 169 217 218 246 247 258 259 260 261 262 320 322 323 341 381	LimeGreen
	322	b3735	atpH	membrane-bound ATP synthase, F1 sector, delta-subunit	129 147 383 400 91 192 195 246 260 261 262 264 269 270 271 273 276 280 282 283 288 289 306 320 321 323 324 325 341	LimeGreen
	323	b3736	atpF	membrane-bound ATP synthase, F0 sector, subunit b	147 383 400 91 218 246 247 260 261 264 269 270 271 273 282 283 320 321 322 325 341 363	LimeGreen
	324	b3737	atpE	membrane-bound ATP synthase, F0 sector, subunit c	175 283 322 325	LimeGreen
	325	b3738	atpB	membrane-bound ATP synthase, F0 sector, subunit a, important for FO assembly	129 147 383 90 91 107 192 195 232 246 253 260 261 264 269 270 283 288 292 306 322 323 324 343 363	LimeGreen
	326	b3739	atpI	membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase	170 87 234	LimeGreen
	327	b3740	gidB	glucose-inhibited division protein with S-adenosyl-L-methionine-dependent methyltransferase domain	408 120 156 157 159 166 172 178 315 352	Gray10
	328	b3741	gidA	glucose-inhibited division protein, oxidoreductase-like with FAD/NAD(P)-binding domain	167	Gray10
	329	b3774	ilvC	ketol-acid reductoisomerase, NAD(P)-binding	239	Lavender
	330	b3780	rlhB	putative ATP-dependent helicase with nucleoside triP hydrolase domain	184 402 292 332 365	Gray10
	331	b3783	rho	transcription termination factor Rho; polarity suppressor	86 338	Lavender
	332	b3806	cyaA	adenylate cyclase	402 330 346	Black
	333	b3823	rlhC	threonine efflux protein (RhlB family)	118 248 305	Gray10
	334	b3871	typA	GTP-binding elongation factor family protein with P-loop containing nucleoside triphosphate hydrolase domain	86 190 220 239 247 290	Gray10
	335	b3926	glpK	glycerol kinase	296 336	Red
	336	b3927	glpF	MIP channel, glycerol diffusion, uptake of As(3+) and Sb(3+)	296 335	Lavender
	337	b3955	yjiP	putative membrane protein	344	Gray10
	338	b3956	ppc	phosphoenolpyruvate carboxylase	236 84 125 147 383 393 400 402 86 93 105 111 135 165 167 181 192 194 195 202 214 217 218 239 246 247 260 264 270 271 286 290 292 306 331 339 342 363 364	Lavender
	339	b3980	tufB	protein chain elongation factor EF-Tu; possible GTP-binding factor (duplicate of tufA)	383 393 415 94 132 165 202	Red

					218 220 239 246 250 252 253 258 259 260 261 264 266 268 269 270 271 272 273 275 276 279 282 286 287 298 299 338 341 342 369 370 378	
	340	b3982	nusG	component in transcription antitermination	87 317	Lavender
	341	b3984	rplA	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11	236 147 383 400 415 131 132 135 165 167 202 203 217 218 220 246 247 252 258 259 260 261 262 264 266 268 269 270 271 272 273 275 276 278 279 280 281 282 283 286 287 299 314 321 322 323 339 342 363 369	Red
	342	b3985	rplJ	50S ribosomal subunit protein L10	236 84 112 383 393 415 131 132 135 165 167 181 202 203 217 218 220 239 246 247 252 258 259 260 261 266 269 270 271 272 273 275 279 282 286 287 299 314 338 339 341 363 369	Red
	343	b4005	purD	phosphoribosylglycinamide synthetase (GAR synthetase)	147 383 93 167 192 214 292 325 363	LimeGreen
	344	b4021	pepE	(alpha)-aspartyl dipeptidase	190 220 243 337	LimeGreen
	345	b4024	lysC	aspartokinase III, lysine sensitive	237	Lavender
	346	b4025	pgi	glucosephosphate isomerase	413 90 332	LimeGreen
	347	b0406	tgt	tRNA-guanine transglycosylase	87 151	Red
	348	b0407	yajC	preprotein translocase, auxiliary membrane component (General Secretory Pathway)	125 402 412 414 418 177 214 217 246 247 363	Gray10
	349	b4066	yjcF	conserved protein of unknown function	309 351 352 356	Gray10
	350	b4070	nrfA	nitrite reductase, periplasmic cytochrome c(552)	122 420 121	LimeGreen
	351	b4083	yjcS	putative enzyme with 2 metallo-hydrolase/oxidoreductase domains, 2 TPR-like domains, sterol carrier protein domain	349	Gray10
	352	b4086	alsC	allose transport protein (ABC superfamily, membrane)	309 392 420 113 120 141 143 155 156 172 178 311 327 349 353 358	Lavender
	353	b4103	b4103	putative C-terminal of split phnE gene (b4103)	309 120 143 311 352	Gray10
	354	b4107	phnB	conserved protein with glyoxalase and dihydroxybiphenyl dioxygenase domain	140 153 227	Gray10
	355	b0415	ribH	riboflavin synthase, beta chain	144	LimeGreen
	356	b4128	yjdK	unknown CDS	122 349	Gray10
	357	b4129	lysU	lysine tRNA synthetase, inducible; heat shock protein	112 125 165 193 217 218 239 252 318	Red
	358	b4131	cadA	lysine decarboxylase I	124 226 309 120 141 172 178 311 352	LimeGreen
	359	b4135	yjdC	putative regulator with homeodomain-like DNA binding domain with homeodomain-like DNA binding domain (TetR/AcrR family)	409 206 208 285	Gray10
	360	b0416	nusB	transcription termination; L factor	170 123	Lavender
	361	b4139	aspA	aspartate ammonia-lyase (aspartase)	398 110 200 297	Red
	362	b4147	efp	elongation factor P (EF-P)	144 167 192 247 259 381	Red
	363	b4175	hflC	with HflK, part of modulator for protease specific for FtsH phage lambda cII repressor	125 147 348 383 393 400 402 414 93 135 167 181 192 194 214 217 218 246 247 252 258 260 261 270 271 273 292 323 325 338 341 342 343 381	LimeGreen
	364	b4177	purA	adenylosuccinate synthetase	129 383 167 202 253 260 261 264 270 271 273 306 338	LimeGreen
	365	b4188	yjfN	conserved protein of unknown function	110 402 410 422 101 117 198 212 228 330 366 373 374	Gray10
	366	b4189	yjfO	conserved protein of unknown function	110 402 410 422 99 101 117 198 212 228 295 365 373	Gray10
	367	b0421	ispA	geranyltransferase (=farnesyl diphosphate synthase)	123	LimeGreen
	368	b4201	priB	primosomal replication protein N	265 272 370	Lavender
	369	b4202	rpsR	30S ribosomal subunit protein S18	383 393 415 131 132 165 202 203 218 220 246 247 252 253 258 259 260 261 264 266 268 269 270 271 272 273 275 276 278 279 281 282 286 287 299 339 341 342 370	Red
	370	b4203	rplI	50S ribosomal subunit protein L9	165 171 252 265 268 272 275 339 368 369	Red
	371	b4214	cysQ	protein that acts on 3'-phosphoadenosine-5'-phosphosulfate with sugar phosphatase domain	302	Red
	372	b4226	ppa	inorganic pyrophosphatase	125 181 246	LimeGreen
	373	b4227	ytfQ	putative D-ribose transport protein with periplasmic binding protein domain (ABC superfamily, peri_bind)	422 117 212 228 365 366 374	Gray10
	374	b4228	ytfR	putative sugar transport protein (ABC superfamily, atp_bind)	117 365 373 375 376	Lavender
	375	b4229	ytfS	putative sugar transport protein with P-loop containing nucleoside triphosphate hydrolase domain	374	Lavender
	376	b4230	ytfT	putative sugar transport protein (ABC superfamily, membrane)	374	Lavender
	377	b4233	mpl	UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	387 90	Gray10
	378	b4243	yjgF	conserved protein with YjgF-like domain	165 286 339 379 380	Gray10
	379	b4244	pyrI	aspartate carbamoyltransferase, regulatory subunit (allosteric regulation)	274 165 252 378 380	LimeGreen
	380	b4245	pyrB	aspartate carbamoyltransferase, catalytic subunit	274 383 421 189 202 218 253 378 379	LimeGreen
	381	b4258	valS	valine tRNA synthetase	400 81 106 135 192 246 283 306 321 362 363	Red
	382	b0435	bolA	transcriptional activator of morphogenic pathway (BoLA family), important in general stress response	397 136 300	Lavender
	383	b0436	tig	peptidyl-prolyl cis/trans isomerase (trigger factor), molecular chaperone involved in cell division	236 237 84 125 128 129 144 147 393 400 402 415 86 91 93 105 135 165 167 181 189 192 194 195 202 203 214 217 218 220 239 246 247 252 253 258 259 260 261 264 269 270 271 272 273 279 282 283 286 290 292 299 302 306 314 321 322 323 325 338 339 341 342 343 363 364 369 380	Black
	384	b0441	ppiD	peptidyl-prolyl cis-trans isomerase, for periplasmic folding of outer membrane proteins	134 417	Gray10
	385	b4401	arcA	response regulator in two-component regulatory system with ArcB (or CpxA), regulates respiratory and fermentative metabolism (OmpR family)	119 397 117 300 386	Red
	386	b4402	yjiY	unknown CDS	119 385	Gray10
	387	b0463	acrA	component of acridine efflux pump	390 396 82 377	Black
	388	b0469	apt	adenine phosphoribosyltransferase	421 86	LimeGreen
	389	b0471	ybaB	conserved protein of unknown function	245	Gray10
	390	b0051	ksgA	S-adenosylmethionine-6-N'-adenosyl (rRNA) dimethyltransferase, kasugamycin resistance	387	Lavender
	391	b0529	folD	bifunctional: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase	115 288	LimeGreen
	392	b0558	ybcV	DLP12 prophage; putative envelope protein	120 311 352	Red

	393	b0565	ompT	DLP12 prophage; protease VII, outer membrane protein 3b (a), putative porin	147 383 400 111 135 165 218 239 246 249 250 252 260 264 270 271 275 286 299 338 339 342 363 369	Black
	394	b0578	nfnB	dihydropteridine reductase; oxygen-insensitive NAD(P)H nitroreductase, also anaerobic azo reductase	84 137 144 400 401 419 135 247 258 272	Black
	395	b0591	ybdA	putative transport protein (POT family)	399	Gray10
	396	b0642	leuS	leucine tRNA synthetase	142 387 230	Red
	397	b0643	ybeL	conserved protein of unknown function	119 382 411 416 98 117 127 136 232 291 300 302 385	Gray10
	398	b0665	yabl	putative integral membrane protein	110 133 200 297 361	Gray10
	399	b0693	speF	ornithine decarboxylase isozyme, inducible	404 216 226 395 130 179 294	LimeGreen
	400	b0741	pal	required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA	147 383 393 394 135 218 246 247 258 260 261 262 264 269 270 271 273 283 320 321 322 323 338 341 363 381	Black
	401	b0742	ybgF	putative periplasmic protein with protein prenyltransferase domain	84 112 144 394 415 419 92 93 167 194 217 247 252 258 259 272 273	Gray10
	402	b0754	aroG	3-deoxy-D-arabinohexulosonate-7-phosphate synthase (DAHPS synthetase, phenylalanine-repressible)	125 147 348 383 414 418 101 105 135 177 186 192 194 217 246 247 292 308 330 332 338 363 365 366	Lavender
	403	b0765	modC	molybdate transport protein (ABC superfamily, atp_bind)	410 212 303	Gray10
	404	b0076	leuO	putative transcriptional regulator of leucine biosynthesis with periplasmic binding protein domain (LysR family)	216 226 399	Lavender
	405	b0790	ybhP	putative DNase with DNase I-like domain	226	Gray10
	406	b0812	dps	stress response DNA-binding protein with ferritin-like domain	153	Lavender
	407	b0817	mntR	transcriptional regulator of mntH, Mn(2+) responsive	315	Gray10
	408	b0852	rimK	ribosomal protein S6 modification protein	327	Red
	409	b0865	ybjP	conserved protein of unknown function	359	Gray10
	410	b0879	macB	multimodular: macrolide transport protein (ABC superfamily, atp_bind (N-terminal), membrane (C-terminal))	110 403 422 183 212 365 366	Lavender
	411	b0880	cspD	DNA replication inhibitor, nucleic acid-binding domain	397 117 136 138 200 232 300	Black
	412	b0889	lrp	transcriptional regulator of lrp regulon and for high-affinity branched-chain amino acid transport system (AsnC family)	348	Lavender
	413	b0903	pflB	pyruvate formate lyase I, induced anaerobically	346	LimeGreen
	414	b0907	serC	3-phosphoserine/phosphohydroxythreonine aminotransferase	125 147 152 348 402 418 86 93 105 135 177 192 194 214 217 246 247 306 308 363	Lavender
	415	b0911	rpsA	30S ribosomal subunit protein S1	84 144 383 401 421 93 165 167 202 218 252 253 258 259 260 269 271 272 273 279 282 286 287 339 341 342 369	Red
	416	b0925	ycbB	putative carboxypeptidase with PGDB-like domain	397 127 136 232 291 299 302	Gray10
	417	b0928	aspC	aspartate aminotransferase, PLP-dependent	125 384	Lavender
	418	b0930	asnS	asparagine tRNA synthetase	125 348 402 414 93 177 217	Red
	419	b0931	pncB	nicotinate phosphoribosyltransferase	84 112 125 144 394 401 214 217	LimeGreen
	420	b0941	ycbT	putative fimbrial-like adhesin protein	122 309 121 311 350 352	Red
	421	b0945	pyrD	dihydroorotate oxidase, FMN-linked	84 112 274 388 415 86 93 189 239 290 380	LimeGreen
	422	b1002	agp	glucose-1-phosphatase, also has inositol phosphatase activity	410 117 365 366 373	Red
	423	b1003	yccJ	unknown CDS	251 424	Gray10
	424	b1004	wrbA	flavodoxin-like protein, trp repressor-binding protein	423 146 153 209 232	Red
	425	b1013	ycdC	putative transcriptional repressor with homeodomain-like DNA binding domain (TetR/AcrR family)	187 224 238	Gray10
Mdoule 15	426	b2680	b2680	putative resistance protein, possible transport protein	428 427	Gray10
	427	b3874	yihN	putative transport protein (MFS family)	428 426	Red
	428	b0913	ycal	putative recombination protein with metallo-hydrolase domain	426 427	Gray10
Module 16	429	b1072	flgA	flagellar biosynthesis; assembly of basal-body periplasmic P ring	437	Red
	430	b1073	flgB	flagellar biosynthesis; cell-proximal portion of basal-body rod	431 432 433 434 435 436 444 445 446 447	Red
	431	b1074	flgC	flagellar biosynthesis; cell-proximal portion of basal-body rod	430 432 433 434 435 436 445 446 447	Red
	432	b1075	flgD	flagellar biosynthesis; initiation of hook assembly	430 431 433 435 446 447	Red
	433	b1076	flgE	flagellar biosynthesis; hook protein	430 431 432 434 435 445 446 447	Red
	434	b1077	flgF	flagellar biosynthesis; cell-proximal portion of basal-body rod	430 431 433 435 436 445 446 447	Red
	435	b1078	flgG	flagellar biosynthesis; cell-distal portion of basal-body rod	430 431 432 433 434 436 445 446 447	Red
	436	b1079	flgH	flagellar biosynthesis; basal-body outer-membrane L (lipopolysaccharide layer) ring protein	430 431 434 435 446 447	Red
	437	b1081	flgJ	flagellar biosynthesis; muramidase	429 447	Red
	438	b1082	flgK	flagellar biosynthesis; hook-filament junction protein 1	439 441 442 444	Red
	439	b1083	flgL	flagellar biosynthesis; hook-filament junction protein	438	Red
	440	b1194	ycgR	putative regulator (TetR/AcrR family)	441 444	Gray10
	441	b1921	fliZ	putative regulator of FliA	438 440 444	Lavender
	442	b1922	fliA	sigma F (sigma 28) factor of RNA polymerase, transcription of late flagellar genes (class 3a and 3b operons)	438 443 444	Lavender
	443	b1923	fliC	flagellar biosynthesis; flagellin, filament structural protein	442	Lavender
	444	b1924	fliD	flagellar biosynthesis; filament capping protein, enables filament assembly	430 438 440 441 442	Lavender
	445	b1943	fliK	flagellar hook-length control protein	430 431 433 434 435 446 447	Lavender
	446	b1944	fliL	flagellar biosynthesis	430 431 432 433 434 435 436 445 447	Lavender
	447	b1945	fliM	flagellar biosynthesis; component of motor switch and energizing	430 431 432 433 434 435 436 437 445 446	Lavender
Module 17	448	b1095	fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	449 450	Red
	449	b3255	accB	acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit	448 450	Red
	450	b3256	accC	acetyl CoA carboxylase, biotin carboxylase subunit	448 449	Red
Module 18	451	b1119	ycfX	putative transcriptional regulator with ATPase domain (NagC/XylR (ROK) family)	496 501 502 453 454 456 457 463 464 470	Red
	452	b1139	lit	e14 prophage; like phage T4 late gene expression	459 464 470 472 475	Yellow
	453	b1162	ycgE	putative transcriptional repressor with DNA-binding domain (MerR family)	451 454	Red
	454	b1284	yciT	putative transcriptional regulator with DNA-binding Winged helix domain (DeoR family)	496 451 453 456 463	Red
	455	b1303	pspF	transcriptional activator of phage shock proteins (EBP family)	458 459	Red
	456	b1328	ycjZ	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	496 501 502 451 454 457 460 463 464 470 477 485 487	Red
	457	b1339	ahgR	putative transcriptional regulator of p-aminobenzoyl-glutamate utilization with periplasmic binding protein domain (LysR family)	479 496 501 502 451 456 460 463 464 467 470 471 477 482 484	Red
	458	b1345	intR	Rac prophage; putative transposase/integrase	455	Gray10
	459	b1351	racC	Rac prophage; contains recE and oriJ	499 452 455 475	Yellow
	460	b1384	feaR	transcriptional activator of 2-phenylethylamine catabolism (AraC/XylS family)	502 456 457 463 467 470 477 484	Red
	461	b1479	sfcA	NAD-linked malate dehydrogenase	481 478 483	LimeGreen

462	b0150	fhuA	outer membrane protein; transports ferrichrome, albomycin, rifamycin; receptor for colicin M, microcinJ25, phages T1, T5, phi80, and UC1	493 465 473	Black	
463	b1618	uidR	transcriptional repressor for glucuronide metabolism (TetR/AcrR family)	451 454 456 457 460 464 466 470	Red	
464	b1659	ydhB	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	501 451 452 456 457 463 466 467 470 471 475 478	Red	
465	b1835	yebU	putative methyltransferase with S-adenosyl-L-methionine-dependent methyltransferase domain	462 473	Gray10	
466	b2015	yeeY	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	463 464 467 470 471 472 475 478	Red	
467	b2061	wzb	protein-tyrosine-phosphatase, colanic acid export	457 460 464 466 470 471 472 475 477 478 484 487	Red	
468	b2062	wza	putative polysaccharide export protein, outer membrane	501	Gray10	
469	b2299	b2299	putative enzyme (Nudix hydrolase)	471	Red	
470	b2382	ypdC	putative transcriptional regulator with homeodomain-like DNA binding domain (AraC/XylS family)	501 502 451 452 456 457 460 463 464 466 467 471 472 475 477 478 484 487	Red	
471	b2409	yfeR	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	501 457 464 466 467 469 470 475 478	Red	
472	b2412	zipA	cell division protein involved in FisK recruitment to Z ring	452 466 467 470 475 478 484 487	Black	
473	b2428	yfeU	conserved protein with phosphosugar-binding domain	462 465 484 487	Red	
474	b0252	yafZ	CP4-6 prophage	499 495	Gray10	
475	b2537	hcaR	transcriptional activator of hca cluster (LysR family)	452 459 464 466 467 470 471 472 478 487	Red	
476	b2622	intA	CP4-57 prophage; integrase	486 490	Yellow	
477	b2698	recX	regulatory protein, inhibitor of RecA recombinase and coprotease activities	501 502 456 457 460 467 470 482 484	Red	
478	b2735	ygbI	putative transcriptional repressor with DNA-binding Winged helix domain (DeoR family)	461 464 466 467 470 471 472 475 484 487	Red	
479	b0288	ykgJ	putative ferredoxin	457	Gray10	
480	b2847	yqel	putative transcriptional regulator with C-terminal, effector domain of the bipartite response regulator	496 485 490 491	Red	
481	b0291	yagX	putative aromatic compound dioxygenase	498 461 483	Gray10	
482	b2921	ygfI	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	502 457 477	Red	
483	b3018	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	481 493 461	Black	
484	b3025	qseB	response regulator in two-component regulatory system with QseC, regulates flagella and motility by quorum sensing (OmpR family)	457 460 467 470 472 473 477 478 487	Red	
485	b3105	yhaJ	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	496 501 502 456 480 489	Red	
486	b3226	nanR	transcriptional repressor of sialic acid metabolism (GntR family)	476	Red	
487	b3375	yhrR	putative transcriptional repressor with DNA-binding Winged helix domain (GntR family)	456 467 470 472 473 475 478 484	Red	
488	b3432	glgB	1,4-alpha-glucan branching enzyme	494	Black	
489	b3440	yhhX	putative NAD(P)-binding dehydrogenase with NAD(P)-binding domain	485	Red	
490	b3520	yhbB	putative response regulator in two-component regulatory system	476 480 491	Red	
491	b3684	yidP	putative transcriptional repressor with DNA-binding Winged helix domain (GntR family)	496 480 490	Red	
492	b3706	trmE	GTPase involved in tRNA modification and in thiophene and furan oxidation	494	Black	
493	b0379	yaiY	putative membrane protein	494 462 483	Gray10	
494	b0039	caiA	crotonobetaine reductase subunit II, FAD-binding	493 488 492	Red	
495	b4182	yjJ	conserved protein of unknown function	474	Gray10	
496	b0603	ybdO	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	497 501 502 451 454 456 457 480 485 491	Red	
497	b0620	dpiA	response regulator in two-component regulatory system with DpiB, regulation of citrate fermentation and of plasmid inheritance (OmpR family)	496 501	Red	
498	b0731	mngA	multimodular: PTS family enzyme IIA (N-terminal); enzyme IIB (middle); enzyme IIC (C-terminal), induction of ompC, 2-O-alpha-mannosyl-D-glycerate specific	481	Black	
499	b0738	tolR	tol protein, role in outer membrane integrity, uptake of group A colicins (TonB-independent), and phage DNA	474 500 459	Yellow	
500	b0740	tolB	required for outer membrane integrity, uptake of group A colicins, and translocation of phage DNA	499	Yellow	
501	b0933	ssuB	alkanesulfonate transport protein (ABC superfamily, atp_bind)	496 497 502 451 456 457 464 468 470 471 477 485	Yellow	
502	b0986	ymcC	putative synthetase	496 501 451 456 457 460 470 477 482 485	Red	
Module 19	503	b1321	ycjX	conserved protein with nucleotide triphosphate hydrolase domain	504 505	Gray10
	504	b3686	ibpB	small heat shock protein	503 505	Black
	505	b4152	frdC	fumarate reductase, anaerobic, membrane anchor polypeptide	503 504	Red
Module 20	506	b1379	hsJ	heat shock protein hsJ	507 508	Black
	507	b4319	fimG	minor fimbrial subunit, type 1 fimbriae	506 508	Red
	508	b4320	fimH	minor fimbrial subunit, type 1 fimbriae	506 507	Red
Module 21	509	b1558	csfP	Qin prophage; cold shock protein	510 511 512	Red
	510	b2823	ppdC	prepilin peptidase-dependent protein C, possibly in type IV pilin biogenesis	509 511 512	Gray10
	511	b3718	yieK	putative hexosamine-P deaminase/isomerase	509 510 512	Gray10
	512	b4306	yjhP	KpLE2 phage-like element; putative methyltransferase with S-adenosyl-L-methionine-dependent methyltransferase domain	509 510 511	Gray10
Module 22	513	b1143	ymfI	eI4 prophage	519	Gray10
	514	b1273	yciN	conserved protein of unknown function	519	Gray10
	515	b1559	ydfI	Qin prophage; putative antitermination protein Q	516	Gray10
	516	b2449	b2449	CPZ-55 prophage	515 517 518 519	Gray10
	517	b2910	ygfE	conserved protein of unknown function	516	Gray10
	518	b2960	yggH	tRNA (m7G46) methyltransferase, SAM-dependent	516	Gray10
	519	b3199	yrbK	conserved protein of unknown function	520 513 514 516	Gray10
	520	b0460	hha	hemolysin expression modulator	519	Red
Module 23	521	b1610	tus	replication termination protein	522	Red
	522	b1961	dcm	DNA cytosine methylase	521 523 524	Red
	523	b2218	rcsC	multimodular: hybrid sensory histidine kinase in two-component regulatory system with RcsB and YojN, regulates capsule biosynthesis, cell division genes, OsmC expression, fhDC operon	522 524	Red
Module 24	524	b4317	fimD	split gene (fragment 1 and 2), outer membrane protein, export and assembly of type 1 fimbriae	522 523	Gray10
	525	b1668	b1668	putative oxidoreductase with NAD(P)/FAD-binding domain	527	Gray10
	526	b2057	wcaC	putative glycosyl transferase, colanic acid synthesis with UDP-Glycosyltransferase/glycogen phosphorylase domain	527 528 530	Gray10
	527	b2060	wzc	tyrosine-protein kinase, phosphorylates Ugd and Wzc, colanic acid export	525 526	Gray10
	528	b2081	yegQ	putative protease	526 529	Gray10
	529	b2099	yegU	putative glycohydrolase	528	Gray10
	530	b2102	yegX	putative hydrolase, with (trans)glycosidase domain	526	Gray10
Module 25	531	b1066	rimJ	acetylation of N-terminal alanine of 30S ribosomal subunit protein S5	635 706	Purple
	532	b1087	yceF	conserved protein with Maf/Ham1 domain	814	Gray10
	533	b1099	holB	DNA polymerase III, delta prime subunit	776 803 549 564 574 595 610 685 710 716	Yellow
	534	b0111	ampE	putative transmembrane protein, putative protease	550 612 627 741	Yellow
	535	b0112	aroP	aromatic amino acid transport protein (APC family)	778 608 592 737	Red
	536	b1148	ymfM	eI4 prophage	587 614 681 733 746	Gray10
	537	b1201	dhaR	putative transcriptional regulator in two-component regulatory system with P-loop containing nucleoside triphosphate hydrolase and PYP-like sensor domains (EBP family)	776 552 616 632 678	Gray10
	538	b1213	b1213	putative transcriptional regulator	539 563 579 695	Gray10
	539	b1214	ychA	putative transcriptional regulator with tetratricopeptide repeats (TPR) domain	538 561	Gray10

540	b1220	ychP	conserved protein of unknown function, invasin-like	700 573	Gray10
541	b1226	narJ	nitrate reductase 1, delta subunit, chaperone required for molybdenum cofactor assembly	564	Red
542	b1240	b1240	unknown CDS	545 662 665 696 769	Gray10
543	b0124	gcd	glucose dehydrogenase	734 612 644	Red
544	b1268	yciQ	putative membrane protein	560 699 708 762	Gray10
545	b1289	ycjD	conserved protein with restriction endonuclease-like domain	542 557	Gray10
546	b1296	ycjJ	putative transport protein (APC family)	666 670 789 565 755 774	Red
547	b1312	ycjP	putative transport protein (ABC superfamily, membrane)	810 812 565 631	Red
548	b1317	pgmB	putative beta phosphoglucomutase, contains a phosphatase-like domain	551 559	Red
549	b1318	ycjV	putative sugar transport protein (ABC superfamily, atp_bind)	803 804 533 564 637 716	Red
550	b1320	ycjW	putative transcriptional repressor with periplasmic binding protein domain (GalR/LacI family)	534 666 670 734 779 573 612 627 638 644 689 693 718 741 760	Gray10
551	b1322	ycjF	putative membrane protein	548	Gray10
552	b1359	ydU	Rac prophage	537	Gray10
553	b0134	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	815 803 724	Red
554	b1364	b1364	Rac prophage	670 662	Gray10
555	b1369	b1369	Rac prophage; putative outer membrane protein	562 572 711	Gray10
556	b0136	yadK	putative fimbrial-like adhesin protein	809 813 693 760	Lavender
557	b1373	ynaC	Rac prophage; putative tail fiber assembly	545 586	Gray10
558	b1395	paaH	3-hydroxybutyryl-CoA dehydrogenase, phenylacetic acid degradation	648	Gray10
559	b1399	paaX	transcriptional repressor for phenylacetic acid degradation	548 561	Gray10
560	b1403	yi21_2	IS21 protein 2	810 544 636 637 662 669 688 699 708 714 762 764 768	Gray10
561	b1410	b1410	putative methylase with S-adenosyl-L-methionine-dependent methyltransferase domain and alpha/beta-hydrolase domain	539 559	Gray10
562	b1436	yncJ	unknown CDS	815 602 808 555 709 754	Gray10
563	b1458	b1458	conserved protein of unknown function	538 579	Gray10
564	b1467	narY	nitrate reductase 2, beta subunit	799 803 533 541 549 637 662	Red
565	b1483	ddpF	putative dipeptide transport protein (ABC superfamily, atp_bind)	670 810 546 547 693 718 755	Red
566	b1496	yddA	multimodular: putative transport protein (ABC superfamily, membrane (N-terminal), atp_bind (C-terminal))	589 624 643	Red
567	b1497	ydeM	putative regulator	697	Gray10
568	b0151	fluC	hydroxamate-dependent iron transport protein (ABC superfamily, atp_bind)	740	Red
569	b1505	ydeT	putative outer membrane protein	606 805 609 630 642 663 673 740	Gray10
570	b0152	fluD	hydroxamate-dependent iron transport protein (ABC superfamily, peri_bind)	589 590	Red
571	b1522	b1522	putative membrane protein	773	Gray10
572	b1556	essQ	Qin prophage	555	Gray10
573	b1581	rspA	putative dehydratase, starvation-sensing protein, member of enolase family	666 700 807 540 550 612 627 760 765	Yellow
574	b1582	ynfA	putative transmembrane protein	776 783 812 533 616 679 702 708 716 724 764	Gray10
575	b1584	speG	spermidine N1-acetyltransferase	604 813 625	Red
576	b1615	uidC	membrane-associated protein	795 805 634	Lavender
577	b1620	mall	transcriptional repressor of maltose regulon (GalR/LacI family)	794	Yellow
578	b0164	yaeI	conserved protein with metallo-dependent phosphatase domain	693	Gray10
579	b1644	ydhJ	putative multidrug resistance membrane protein	797 538 563 580 583 585	Gray10
580	b1645	ydhK	putative enzyme with PLP-dependent transferase domain	579 583 585	Gray10
581	b1648	ydhL	unknown CDS	587 681	Gray10
582	b1650	nemA	N-ethylmaleimide reductase, FMN-linked	717 594 691 767	Red
583	b1657	b1657	putative transport protein (MFS family)	797 579 580 585 766	Red
584	b1662	ribE	riboflavin synthase, alpha chain	748	Red
585	b1663	ydhE	multidrug transport protein (MATE family)	797 579 580 583	Red
586	b1672	b1672	conserved protein of unknown function	557	Gray10
587	b1673	ydhV	putative aldehyde ferridoxin oxidoreductase	811 536 581 614 646 655 673 681 703 733 746	Gray10
588	b1676	pykF	pyruvate kinase I (formerly F), fructose-stimulated	599 600	Red
589	b1690	ydiM	putative transport protein (MFS family)	794 570 566 590 694	Red
590	b1691	ydiN	putative transport protein (MFS family)	570 589 682 731	Red
591	b1697	ydiQ	putative electron transfer flavoprotein with ETFP adenine nucleotide-binding domain-like	659	Red
592	b1738	celA	PTS family enzyme IIB, cellobiose/arbutin/salicin sugar-specific	535	Red
593	b1745	astB	succinylarginine dihydrolase	784 616 676 764	Gray10
594	b1758	ynjF	putative transferase	582 601	Red
595	b1763	topB	DNA topoisomerase III, type 1	776 533 610 702 751	Yellow
596	b1785	yeal	putative membrane protein	733	Gray10
597	b1821	yebN	putative membrane protein, terpenoid synthase-like	730	Gray10
598	b1834	yebT	putative membrane protein	693	Gray10
599	b1852	zwf	glucose-6-phosphate dehydrogenase	588 600 621 691	Red
600	b1854	pykA	pyruvate kinase II, glucose-stimulated	588 599 621	Red
601	b1873	torY	cytochrome c-type protein in TMAO system II with TorZ	594 624 643 654 656 661	Red
602	b0189	rof	modulator of Rho-dependent transcription termination	808 813 562 620 625 626 760	Gray10
603	b1894	insA_5	IS1 protein InsA	617 645 652 657 713 756 772	Tan
604	b0190	yaeQ	conserved protein of unknown function	575	Gray10
605	b0191	yaeJ	conserved protein with RF2 (polypeptide chain release factor 2) domain	610 616 626 676 687 702 736 739 764 774	Gray10
606	b0020	nhaR	transcriptional activator of cation transport (LysR family)	781 805 569 609 630 639 642 671 677	Red
607	b0198	metI	D- and L-methionine transport protein (ABC superfamily, membrane)	795 611 766	Red
608	b0199	metN	D- and L-methionine transport protein (ABC superfamily, atp_bind)	778 535 802 805 639 671 729 737	Red
609	b1999	yeeP	CP4-44 prophage; putative GTP-binding factor	606 805 569 642	Gray10
610	b2005	yeeV	CP4-44 prophage; toxin component of toxin-antitoxin protein pair (YeeV-YeeU)	809 605 799 803 533 595 626 679 687 702 709 710 711 739 749 764 768	Gray10
611	b2027	wzzB	regulator of length of O-antigen component of lipopolysaccharide chains	607 766 767	Red
612	b2043	wcaM	putative colanic acid biosynthesis protein with pectin lyase-like domain	534 543 734 550 573 626 760	Gray10
613	b2098	yegT	putative transport protein (MFS family)	731	Red
614	b2132	bgIX	beta-D-glucoside glucosyltransferase, periplasmic	536 587 622 673 681 697 703 733	Red
615	b2134	pbpG	D-alanyl-D-alanine endopeptidase; penicillin-binding proteins 7 and 8	666 780	Red
616	b2138	yohG	putative outer membrane protein	776 605 780 784 799 810 812 537 574 593 632 662 676 679 687 702 716 762 764	Gray10
617	b0022	insA_1	IS1 protein InsA	645 652 785 603 713 727 772	Tan
618	b2161	yefI	putative transport protein (NUP family)	707	Red
619	b2168	fruK	fructose-1-phosphate kinase	659	Red
620	b2182	bcr	bicyclomyacin/multidrug transport protein (MFS family)	777 602	Yellow
621	b2194	ccmH	putative heme lyase subunit with protein prenyltransferase domain, cytochrome c-type biogenesis	599 600	Red
622	b2252	ais	protein induced by aluminum, contains phosphoglycerate mutase-like domain	614	Gray10
623	b2276	nuoN	NADH dehydrogenase I chain N, membrane subunit	654 659	Red
624	b2277	nuoM	NADH dehydrogenase I chain M, membrane subunit	566 601 643	Red
625	b2311	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	602 783 813 575 649 693 715 742	Gray10

626	b2315	folC	bifunctional: folylpolyglutamate synthase; dihydrofolate synthase	602 605 610 612 687 739	Red
627	b2321	div	cell division protein	534 666 779 550 573 735	Black
628	b2324	yfcK	multimodular; conserved protein of unknown function (N-terminal); protein with FAD/NAD(P)-binding domain (C-terminal)	676	Yellow
629	b2326	yfcM	conserved protein of unknown function	761	Red
630	b2327	yfcA	putative membrane protein	606 805 569 663	Lavender
631	b2336	yfcS	putative periplasmic pilin chaperone similar to PapD	812 547 679	Gray10
632	b2338	yfcU	putative outer membrane protein	776 800 812 537 616 676	Gray10
633	b2362	b2362	CPS-53 (KpLE1) prophage	675 724	Gray10
634	b2406	xapB	xanthosine permease (MFS family)	788 795 798 576	Red
635	b2419	yfcK	conserved protein of unknown function	531 637 699 706 708 716 724	Gray10
636	b2447	b2447	CPZ-55 prophage	560 709 764	Gray10
637	b2459	eutT	putative cobalamin adenosyltransferase with winged helix domain, in ethanolamine utilization	792 803 810 549 560 564 635 687 699 708 714 716 762	Gray10
638	b2470	acrD	aminoglycoside/multidrug efflux pump (RND family)	550	Yellow
639	b2477	nlpB	lipoprotein-34	606 608 781 786 795 801 805 677	Lavender
640	b2483	hyfC	hydrogenase 4, C (membrane) subunit	661	Red
641	b2485	hyfE	hydrogenase 4, E (membrane) subunit	723	Red
642	b2506	b2506	conserved protein of unknown function	606 805 569 609	Gray10
643	b2552	hmpA	multimodular; nitric oxide dioxygenase (N-terminal); dihydropteridine reductase 2 (C-terminal)	750 566 601 624	Red
644	b2570	rseC	regulator of sigma E (sigma 24) factor	543 734 550 647	Gray10
645	b0265	insA_2	CP4-6 prophage; IS1 protein InsA 2	617 652 785 603 713 772	Tan
646	b2587	kgtP	alpha-ketoglutarate permease (MFS family)	587 733	Red
647	b2626	yfjJ	CP4-57 prophage	644	Gray10
648	b2651	b2651	unknown CDS	558 681 746	Gray10
649	b2657	b2657	putative glycosyltransferase with (trans)glycosidase domain	783 625	Gray10
650	b2663	gabP	gamma-aminobutyrate transport protein, RpoS-dependent (APC family)	663 673 683 703 705 720	Red
651	b2678	proW	glycine betaine/proline transport protein (ABC superfamily, membrane)	680	Red
652	b0275	insA_3	CP4-6 prophage; IS1 protein InsA	617 645 785 603 713 772	Tan
653	b2719	hycG	hydrogenase-3, subunit	658 661	Red
654	b2722	hycD	hydrogenase 3, membrane subunit (part of FHL complex)	601 623 659 690 691	Red
655	b2723	hycC	hydrogenase 3, membrane subunit (part of FHL complex)	587	Red
656	b2724	hycB	hydrogenase-3, Fe-S subunit (part of FHL complex)	601 661 684	Red
657	b2725	hycA	regulatory protein for HycE (part of the FHL complex)	670 603 755	Red
658	b2729	hypD	hydrogenase expression/formation protein	653	Red
659	b2730	hypE	hydrogenase 3 maturation protein	591 619 623 654	Red
660	b2740	ygbN	putative transport protein (GntP family)	700	Gray10
661	b2769	ygcQ	putative electron transfer flavoprotein, NAD/FAD-binding domain and ETPP adenine nucleotide-binding domain-like	601 640 653 656	Gray10
662	b2791	truC	pseudouridine synthase	810 812 542 554 560 564 616 676 708 764	Gray10
663	b2801	fucP	fucose transport protein (MFS family)	805 569 630 650 673 683 703 705 733	Red
664	b2805	fucR	transcriptional activator for L-fucose utilization (DeoR family)	731	Red
665	b2812	ygdL	putative Molybdenum cofactor biosynthesis protein MoeB, NAD(P)-binding	542	Gray10
666	b0290	yagW	conserved protein of unknown function	546 550 573 615 627	Gray10
667	b2839	lysR	transcriptional activator for lysine biosynthesis (LysR family)	776 780	Red
668	b2841	araE	low-affinity L-arabinose/proton symporter (MFS family)	683 720	Red
669	b2861	yi21_4	IS2 protein	719 799 810 560 688 768	Tan
670	b0293	yagZ	conserved protein of unknown function	810 546 550 554 565 657 672 693 718	Tan
671	b2879	ssnA	putative protein with metallo-dependent hydrolase domain, commonly a deaminase	606 608 805 673 703 737	Lavender
672	b2894	xerD	site-specific tyrosine recombinase	670	Yellow
673	b2933	cmtA	PTS family enzyme IICB, mannitol-specific, cryptic	805 569 587 614 650 663 671 683 703 705 733 737	Red
674	b2934	cmtB	PTS family enzyme IIA, mannitol-specific, cryptic	799 679	Red
675	b2945	endA	DNA-specific endonuclease I	633	Yellow
676	b2950	yggR	putative transport protein with P-loop containing nucleoside triphosphate hydrolase domain	605 784 810 812 593 616 628 632 662 755 764	Gray10
677	b2954	yggV	dITP/dXTP pyrophosphatase	606 781 639	Lavender
678	b2956	yggM	conserved protein of unknown function	537 758	Gray10
679	b2968	yghD	putative secretion pathway protein	809 799 803 810 812 574 610 616 631 674 708 716 722 724 726 764	Gray10
680	b2970	yghF	putative protein exporter (General Secretory Pathway)	651 683 694	Gray10
681	b2973	yghJ	conserved protein of unknown function	811 536 581 587 614 648 703 733 746	Gray10
682	b2975	glcA	glycolate permease (LctP family)	590	Red
683	b2987	pitB	low-affinity phosphate transport protein (PIT family)	650 663 668 673 680 703 705 720	Red
684	b2992	hybE	putative hydrogenase	656	Red
685	b2993	hybD	putative processing element for hydrogenase-2 with HybD-like domain	799 533	Red
686	b2995	hybB	putative cytochrome Ni/Fe component of hydrogenase-2	690 759	Red
687	b3010	yqhC	putative transcriptional regulator with homeodomain-like DNA binding domain (AraC/XylS family)	605 783 810 610 616 626 637 702 723 736 764	Gray10
688	b3044	yi21_5	IS2 protein	719 810 560 669	Tan
689	b3046	yqiG	putative outer membrane usher protein	550	Gray10
690	b3061	tdA	L-tartrate dehydratase, alpha subunit	654 686 691	Red
691	b3062	tdB	L-tartrate dehydratase, beta subunit	582 599 654 690	Red
692	b0314	betT	high-affinity choline transport protein (BCCT family)	811	Red
693	b3074	ygiH	putative tRNA synthetase	556 578 670 779 810 813 550 565 598 625 713 718 742 760	Purple
694	b3075	ebgR	transcriptional repressor for ebg operon, beta-galactoside utilization (GalR/LacI family)	589 680	Red
695	b3079	ygiJ	unknown CDS	538	Gray10
696	b3090	ygiV	putative membrane protein	799 542 709 769	Gray10
697	b3110	yhaO	putative transport protein (HAAAP family)	567 614	Red
698	b3116	tdcC	L-threonine/L-serine permease, anaerobically inducible (HAAAP family)	704	Red
699	b3146	yral	putative enzyme with Cobalt precorrin-4 methyltransferase domain	792 791 812 544 560 635 637 708 773	Gray10
700	b0322	null	785 540 573 660 772	Gray10	
701	b3166	truB	tRNA pseudouridine 5S synthase	779 763	Purple
702	b3167	rbfA	30S ribosome-binding factor, role in processing of 16S rRNA	776 605 574 595 610 616 687	Purple
703	b3258	panF	sodium/pantothenate symporter (SSS family)	805 587 614 650 663 671 673 681 683 705 733 737 771	Red
704	b3269	yhdX	putative amino acid transport protein (ABC superfamily, membrane)	698 707	Red
705	b3290	trkA	potassium transport protein, NAD(P)-binding (Trk family)	650 663 673 683 703 733 775	Red
706	b3329	gspH	putative protein exporter, transport across outer membrane (General Secretory Pathway)	531 635	Red
707	b3370	yhiM	putative methionine transport protein (APC family)	618 704 731 732	Red
708	b3373	yhiP	conserved protein with Xylose isomerase-like domain	792 810 812 544 560 574 635 637 662 679 699 716 724 764	Gray10
709	b3382	yhiY	conserved protein with PTS-regulatory domain	562 610 636 696 723 749 764 768	Gray10
710	b3386	rpe	D-ribulose-5-phosphate 3-epimerase	803 533 610	Red
711	b3404	envZ	sensory histidine kinase (phosphorylase) in two-component regulatory system with OmpR	555 610 739 749	Black

				regulates ompF and ompC expression, senses osmolarity (OmpR family)		
	712	b3419	yhgJ	RNA 3'-terminal phosphate cyclase (with b3420)	773	Gray10
	713	b3444	insA_6	IS1 protein InsA	617 814 645 652 785 603 693 727 772	Tan
	714	b3459	yhhK	putative acyltransferase	560 637	Gray10
	715	b3463	ftsE	cell division protein for septal ring assembly and stability	813 625 747	Gray10
	716	b3478	nikC	nickel transport protein (ABC superfamily, membrane)	776 784 799 803 804 533 549 574 616 635 637 679 708 764	Red
	717	b0357	yaiN	conserved protein of unknown function	582	Gray10
	718	b3534	yhjQ	putative cell division protein, nucleotide triphosphate hydrolase domain	670 550 565 693 755 756 760	Gray10
	719	b0360	yt21_1	IS21 protein I	815 669 688 724 768	Tan
	720	b3567	xyjG	multimodular: D-xylose transport protein (ABC superfamily, atp_bind)	798 802 650 668 683	Red
	721	b3579	yiaO	putative periplasmic component of transport system	755 756 761	Red
	722	b3580	lyxK	3-keto-L-gulonate kinase	679	Red
	723	b3581	sgbH	3-keto-L-gulonate 6-phosphate decarboxylase	641 687 709 748 764	Red
	724	b3584	yiaT	putative outer membrane protein	815 553 719 803 810 574 633 635 679 708 753 764	Gray10
	725	b0036	caiD	crotonobetainyl-CoA hydratase	809	Red
	726	b3605	lldD	L-lactate dehydrogenase, FMN-linked	679	Red
	727	b3625	rfaY	putative enzyme with protein kinase-like domain in lipopolysaccharide core biosynthesis; modification of heptose region of the core	617 713 772	Red
	728	b3633	kdtA	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	761	Red
	729	b3644	yicC	conserved protein of unknown function	793 608	Gray10
	730	b3663	yicN	conserved protein with DHS-like NAD/FAD-binding domain	597 742	Gray10
	731	b3679	yidK	putative myo-inositol transport protein (SSS family)	590 613 664 707 732	Red
	732	b3685	yidE	putative transport protein	707 731	Red
	733	b3722	bgfF	multimodular: PTS family enzyme IIBC (N-terminal); enzyme IIA (C-terminal), beta-glucosidase-specific, regulates BglG by reversible phosphorylation	536 587 596 614 646 663 673 681 703 705 737 746	Red
	734	b0378	yaiW	conserved protein of unknown function	543 550 612 644 760	Gray10
	735	b3784	wecA	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	627	Red
	736	b3811	xerC	site-specific tyrosine recombinase	605 687	Black
	737	b3832	yigN	conserved protein of unknown function	793 535 608 671 673 703 733 746	Gray10
	738	b0388	aroL	shikimate kinase II	779	Red
	739	b3886	rnb	tRNA processing exoribonuclease BN	809 605 796 610 626 711 749 764 774	Purple
	740	b3899	frvB	multimodular: PTS family enzyme IIB (N-terminal); enzyme IIC (C-terminal), fructose-specific	568 787 569	Red
	741	b3924	fpr	ferredoxin-NADP reductase	534 550	Red
	742	b3940	metL	multimodular: aspartokinase II (N-terminal); homoserine dehydrogenase II (C-terminal), methionine sensitive	779 625 693 730	Red
	743	b3965	trmA	tRNA (uracil-5-)-methyltransferase	814	Purple
	744	b3996	yjaD	conserved protein of unknown function, MuTf-like	749	Gray10
	745	b4003	zraS	sensory histidine kinase in two-component regulatory system with ZraR, regulates zraP expression, senses Zn	756	Red
	746	b4004	zraR	multimodular: response regulator in two-component regulatory system with ZraS, regulates zraP expression (EBP family)	811 536 587 648 681 733 737 757	Red
	747	b4041	plsB	glycerolphosphate acyltransferase	715 754	Red
	748	b4043	lexA	transcriptional repressor for SOS response (signal peptidase of LexA family)	584 723 774	Gray10
	749	b4049	dusA	tRNA-dihydrouridine synthase A	610 709 711 739 744	Gray10
	750	b0408	secD	preprotein translocase, auxiliary membrane component (General Secretory Pathway)	643	Red
	751	b4056	yjbQ	cell division protein	595	Gray10
	752	b4058	uvrA	DNA excision repair enzyme subunit, with UvrBC	811	Yellow
	753	b4074	nrfE	formate-dependent nitrite reductase; involved in attachment of haem c to cytochrome c552	809 724	Red
	754	b4075	nrfF	part of formate-dependent nitrite reductase complex; involved in attachment of haem c to cytochrome c552	813 562 747	Red
	755	b4105	phnD	phosphonate transport protein (ABC superfamily, peri_bind)	546 565 657 676 718 721 756	Red
	756	b4106	phnC	phosphonate transport protein (ABC superfamily, atp_bind)	603 718 721 745 755	Red
	757	b4117	adiA	arginine decarboxylase, inducible by acid, catabolic	746	Red
	758	b4149	blc	outer membrane lipoprotein (lipocalin)	678	Red
	759	b4156	yjeM	putative amino-acid transport protein (APC family)	686	Red
	760	b4168	yjeE	putative enzyme with nucleoside triP hydrolase domain	556 602 734 550 573 612 693 718 764	Gray10
	761	b4169	amiB	N-acetylmuramoyl-L-alanine amidase II, a murein hydrolase	629 721 728	Lavender
	762	b4197	sgaU	L-xylulose 5-phosphate 3-epimerase	776 544 560 616 637 764	Red
	763	b4207	fkIB	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase)	779 701	Purple
	764	b4212	ytfH	putative transcriptional regulator with DNA-binding Winged helix domain	605 783 810 560 574 593 610 616 636 662 676 679 687 708 709 716 723 724 739 760 762	Gray10
	765	b4215	ytfI	conserved protein of unknown function	573	Gray10
	766	b4256	yjgM	putative acyltransferase	607 583 611 767 770	Gray10
	767	b4257	yjgN	putative membrane protein, transport	582 611 766	Gray10
	768	b4272	b4272	KpLE2 phage-like element; IS21 protein 3	719 810 560 610 669 709	Gray10
	769	b4275	yjgX	KpLE2 phage-like element; putative transmembrane protein	812 542 696 773	Gray10
	770	b4276	yjgY	KpLE2 phage-like element	766	Gray10
	771	b4291	fecA	KpLE2 phage-like element; outer membrane porin, receptor for ferric citrate, in multi-component regulatory system with cytoplasmic FecI (sigma factor) and membrane-bound FecR	703	Red
	772	b4294	insA_7	KpLE2 phage-like element; IS1 protein InsA	617 814 645 652 700 785 603 713 727	Tan
	773	b4307	yjhQ	KpLE2 phage-like element; conserved protein of unknown function	571 699 712 769	Gray10
	774	b4337	yjiO	multidrug transport protein (MFS family)	605 546 739 748	Red
	775	b4364	yjiP	putative transmembrane protein	705	Lavender
	776	b0045	yaaU	putative transport protein (MFS family)	780 784 803 533 537 574 595 616 632 667 702 716 762	Red
	777	b0046	yabF	putative quinone oxidoreductase, flavoprotein subunit for the KefC K+ efflux system	813 620	Red
	778	b0047	kefC	K+ efflux antiporter, glutathione-regulated, NAD(P)-binding (CPA2 family)	535 608	Red
	779	b0472	recR	gap repair protein with type I DNA topoisomerase domain, part of RecFOR complex that targets RecA to ssDNA-dsDNA junction	738 550 627 693 701 742 763	Yellow
	780	b0478	ybaL	putative transport protein with NAD(P)-binding Rossmann-fold domain (CPA2 family)	776 782 788 789 790 615 616 667	Red
	781	b0503	ybbB	selenophosphate-dependent tRNA 2-selenouridine synthase with Rhodanese domain	606 639 677	Lavender
	782	b0522	purK	AIR carboxylase converting aminoimidazole ribonucleotide (AIR) to N5-carboxyaminoimidazole ribonucleotide (NS-CAIR), ATP and HCO3- requiring	780	Red
	783	b0548	ninE	DLP12 prophage; similar to phage 82 and lambda proteins	810 574 625 649 687 764	Tan
	784	b0549	ybcO	DLP12 prophage	776 593 616 676 716	Gray10
	785	b0554	essD	DLP12 prophage; putative lysis protein S, homolog of Rz of phage PA-2	617 645 652 700 713 772	Gray10
	786	b0576	pheP	phenylalanene transport protein (APC family)	795 639	Red
	787	b0584	fepA	outer membrane porin, receptor for ferric enterobactin and colicins B and D	740	Red
	788	b0587	fepE	regulator of length of O-antigen component of lipopolysaccharide chains	780 790 634	Red
	789	b0589	fepG	ferric enterobactin transport protein (ABC superfamily, membrane)	780 790 546	Red
	790	b0592	fepB	ferric enterobactin transport protein (ABC superfamily, peri_bind)	780 788 789	Red
	791	b0596	entA	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	699	Red
	792	b0061	araD	L-ribulose-5-phosphate 4-epimerase	637 699 708	Red
	793	b0007	yaaJ	putative alanine/glycine transport protein (AGCS family)	729 737	Red
	794	b0063	araB	L-ribulokinase	577 589	Red
	795	b0633	rlpA	a minor lipoprotein	607 786 798 802 576 634 639	Lavender

	796	b0635	mrDA	cell elongation-specific transpeptidase of penicillin-binding protein 2 (peptidoglycan synthetase)	739	Black
	797	b0652	glTL	glutamate/aspartate transport protein (ABC superfamily, atp_bind)	579 583 585	Red
	798	b0653	glTK	glutamate/aspartate transport protein (ABC superfamily, membrane)	795 634 720	Red
	799	b0654	glJU	glutamate/aspartate transport protein (ABC superfamily, membrane)	809 803 810 812 564 610 616 669 674 679 685 696 716	Red
	800	b0067	thiP	multimodular: thiamin transport protein (ABC superfamily, membrane)	632	Red
	801	b0688	pgm	phosphoglucomutase	639	Red
	802	b0692	potE	putrescine:ornithine antiporter (APC family)	608 795 720	Red
	803	b0708	phrB	deoxyribodipyrimidine photolyase (photoreactivation), FAD-binding	776 815 553 799 533 549 564 610 637 679 710 716 724	Yellow
	804	b0764	modB	molybdate transport protein (ABC superfamily, membrane)	549 716	Red
	805	b0780	ybhK	putative phosphatase/sulfatase with NAD(P)-binding domain	606 806 608 569 576 609 630 639 642 663 671 673 703	Lavender
	806	b0082	mraW	S-adenosyl-dependent methyl transferase	805	Gray10
	807	b0834	ylfF	conserved protein of unknown function	573	Gray10
	808	b0846	ybjK	putative transcriptional regulator with homeodomain-like DNA binding domain (TetR family)	602 562	Gray10
	809	b0084	ftsI	cell division-specific transpeptidase, penicillin-binding protein 3	725 556 799 610 679 739 753	Gray10
	810	b0895	dmsB	anaerobic dimethyl sulfoxide (DMSO) reductase, catalytic subunit B	670 783 799 812 547 560 565 616 637 662 669 676 679 687 688 693 708 724 764 768	Red
	811	b0960	yccS	putative efflux transport protein (PET family)	692 587 681 746 752	Gray10
	812	b0977	hyaF	nickel incorporation into hydrogenase-1 proteins	799 810 547 574 616 631 632 662 676 679 699 708 769	Red
	813	b0982	yccY	putative protein-tyrosine-phosphatase	777 556 602 575 625 693 715 754	Gray10
	814	b0100	b0100	unknown CDS	532 713 743 772	Gray10
	815	b0101	yacG	conserved protein of unknown function	553 719 803 562 724	Gray10
Module 26	816	b1857	znuA	high-affinity Zn transport protein (ABC superfamily, peri_bind)	817 818	Gray10
	817	b1973	yodA	metal-binding protein, cadmium-induced	816 818	Gray10
	818	b1974	yodB	putative cytochrome	816 817	Gray10
Module 27	819	b2150	mglB	galactose transport protein (ABC superfamily, peri_bind)	822 823	Red
	820	b4033	malF	maltose transport protein (ABC superfamily, membrane)	823	Red
	821	b4034	malE	maltose transport protein, chemotaxis (ABC superfamily, peri_bind)	822 823	Red
	822	b4035	malK	multimodular: maltose transport protein (ABC superfamily, atp_bind) (N-terminal); phenotypic repressor of mal operon (C-terminal)	819 821 823	Red
	823	b4036	lamB	maltoporin, high-affinity receptor for maltose and maltoseoligosaccharides; phage lambda receptor	819 820 821 822	Red
Module 28	824	b2128	yehW	putative glycine betaine/choline transport protein, osmoprotection (ABC superfamily, membrane)	827	Red
	825	b2365	dsdX	transport protein (Gnt family)	826	Red
	826	b2775	yqcE	putative transport protein (MFS family)	825 827 829	Red
	827	b3195	yrbF	putative transport protein (ABC superfamily, atp_bind)	824 826	Red
	828	b3402	yhgE	putative membrane protein	829	Red
	829	b3473	yhhS	putative transport protein (MFS family)	826 828	Red
Module 29	830	b1526	yneJ	putative transcriptional regulator with periplasmic binding protein domain (LysR family)	833	Gray10
	831	b1571	ydfA	Qin prophage	832 833 834	Gray10
	832	b1957	b1957	unknown CDS	831 834	Gray10
	833	b2489	hyfI	hydrogenase 4, Fe-S subunit	830 831	Red
	834	b2744	surE	putative acid phosphatase, survival protein	831 832 837	Black
	835	b2964	nupG	nucleoside transport protein (MFS family)	836 837	Red
	836	b3425	glpE	thiosulfate:cyanide sulfurtransferase (rhodanese)	835	Red
	837	b3733	atpG	membrane-bound ATP synthase, F1 sector, gamma-subunit	834 835	Red
Module 30	838	b3540	dppF	dipeptide transport protein (ABC superfamily, atp_bind)	839 840	Red
	839	b3542	dppC	dipeptide transport protein 2 (ABC superfamily, membrane)	838 840	Red
	840	b3543	dppB	dipeptide transport protein 1 (ABC superfamily, membrane)	838 839	Red