

CC1	Gene name	Length (AA)	KEGG #	Annotation (Kegg GO and prokka)	Class	Type of variation
	<i>manB</i>	145	K02744	PTS-Aga-EIIA; PTS system, N-acetylglucosamine-specific IIA component [EC:2.7.1.1]	env	Gene absent
	<i>gcc11</i>	60		hypothetical protein		Point mutations
	<i>gcc12</i>	190		hypothetical protein		Gene absent
	<i>gcc13</i>	55		hypothetical protein		Gene absent
	<i>gcc14</i>	188		hypothetical protein		Gene absent
	<i>gcc15</i>	374		hypothetical protein		Gene absent
	<i>gcc16</i>	108		hypothetical protein		Gene absent
	<i>gcc17</i>	45		hypothetical protein		Gene absent
	<i>gcc18</i>	531		hypothetical protein		Gene absent
	<i>phd</i>	86	K19185	Antitoxin Phd		Gene absent
	<i>doc</i>	124	K07341	Toxin: death on curing protein		Gene absent
	<i>gcc19</i>	103		hypothetical protein		Gene absent
	<i>gcc110</i>	133		hypothetical protein		Gene absent
	<i>lyg</i>	469		hypothetical protein		Gene absent
	<i>gcc111</i>	176		hypothetical protein		Gene absent
	<i>gcc112</i>	65	K07729	Relative transcriptional regulator		Gene absent
	<i>gcc113</i>	134		hypothetical protein		Gene absent
	<i>Tn916</i>	284		hypothetical protein		Gene absent
	<i>xerD</i>	409		hypothetical protein		Gene absent
	<i>gcc114</i>	65		hypothetical protein		Gene absent
	<i>gcc115</i>	273		hypothetical protein		Gene absent
	<i>gcc116</i>	470		hypothetical protein		Gene absent
	<i>gcc117</i>	146		hypothetical protein		Gene absent
	<i>gcc118</i>	103		hypothetical protein		Gene absent
	<i>gcc119</i>	131		hypothetical protein		Gene absent
	<i>gcc120</i>	139		hypothetical protein		Gene absent
	<i>gcc121</i>	97		hypothetical protein		Gene absent
	<i>gcc122</i>	248		hypothetical protein		Gene absent
	<i>gcc123</i>	98		hypothetical protein		Gene absent
	<i>gcc124</i>	105		hypothetical protein		Gene absent
	<i>gcc125</i>	102		hypothetical protein		Gene absent
	<i>gcc126</i>	197		hypothetical protein		Gene absent
	<i>mif</i>	1166	K03723	mif: transcription-repair coupling factor (superfamily II helicase) [EC:3.6.4.1]		Point mutations
	<i>gcc127</i>	386		hypothetical protein		Gene absent
	<i>xre</i>	198		HTH-type transcriptional regulator Xre		Gene absent
	<i>gcc128</i>	62		hypothetical protein		Gene absent
	<i>gcc129</i>	201		hypothetical protein		Gene absent
	<i>gcc130</i>	151		hypothetical protein		Gene absent
	<i>gcc131</i>	111		hypothetical protein		Gene absent
	<i>gcc132</i>	74		hypothetical protein		Gene absent
	<i>gcc133</i>	64		hypothetical protein		Gene absent
	<i>gcc134</i>	91		hypothetical protein		Gene absent
	<i>gcc135</i>	465		hypothetical protein		Gene absent
	<i>gcc136</i>	96		hypothetical protein		Gene absent
	<i>gcc137</i>	186		hypothetical protein		Gene absent
	<i>gcc138</i>	163		hypothetical protein		Gene absent
	<i>gcc139</i>	126		hypothetical protein		Gene absent
	<i>gcc140</i>	98		hypothetical protein		Gene absent
	<i>gcc141</i>	116		hypothetical protein		Gene absent
	<i>acpP</i>	56	K02078	Acyl carrier protein	met	Point mutations
	<i>gcc142</i>	73		hypothetical protein		Truncated protein
CC10	<i>gcc101</i>	102		hypothetical protein		Truncated protein
	<i>gcc102</i>	113		hypothetical protein		Gene absent
	<i>gcc103</i>	687		putative IiABC operon regulator		Gene absent
	<i>gatB_1</i>	393	K02774	PTS-Gat-EIIB; PTS system, galactitol-specific IIB component [EC:2.7.1.200]	met/env	Gene absent
	<i>gatC_1</i>	446	K02775	PTS-Gat-EIIC; PTS system, galactitol-specific IIC component [EC:2.7.1.200]	met/env	Gene absent
	<i>rhaD</i>	277	K01629	Rhamnose-1-phosphate aldolase [EC:4.1.2.19]	met	Gene absent
	<i>gatA</i>	155	K02773	PTS-Gat-EIIA; PTS system, galactitol-specific IIA component [EC:2.7.1.200]	met/env	Gene absent
	<i>gatC_2</i>	444	K02775	PTS-Gat-EIIC; PTS system, galactitol-specific IIC component [EC:2.7.1.200]	met/env	Gene absent
	<i>gatB_2</i>	95	K02774	PTS-Gat-EIIB; PTS system, galactitol-specific IIB component [EC:2.7.1.200]	met/env	Gene absent
	<i>sovS</i>	277		Regulatory protein		Gene absent
	<i>araO</i>	426	K02027	ABC MS S: multiple sugar transport system substrate-binding protein		Gene absent
	<i>araF</i>	297	K02025	ABC MS P: multiple sugar transport system permease protein - Lactase transport system permease protein		Gene absent
	<i>araO</i>	278	K02026	ABC MS P1: multiple sugar transport system permease protein - L-arabinose transport system permease protein		Gene absent
	<i>gcc104</i>	734	K07407	E3.2.1.22B, alpha-galactosidase [EC:3.2.1.22]	met	Gene absent
	<i>galK</i>	391	K00849	Galactokinase [EC:2.7.1.5]	met	Gene absent
	<i>galT</i>	383	K00665	UDP-galucose-4-epimerase/UDP-glucose 4-epimerase [EC:2.7.1.2]	met	Gene absent
	<i>galE</i>	332	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]	met	Synonymous point mutations
	<i>galM</i>	334	K01785	Aldose 1-epimerase [EC:5.1.3.3]	met	Gene absent
	<i>cas2</i>	283	K19118	CRISPR-associated protein		Gene absent
	<i>cas4</i>	224	K07464	CRISPR-associated exonuclease		Gene absent
	<i>cas2</i>	98	K09951	CRISPR-associated protein		Gene absent
	<i>gcc105</i>	70		hypothetical protein		Gene absent
	<i>gcc106</i>	383		hypothetical protein		Truncated protein
	<i>galK_2</i>	317	K00849	Galactokinase [EC:2.7.1.5]	met	Gene absent
	<i>gcc107</i>	58		hypothetical protein		Gene absent
	<i>ydfK</i>	239	K07150	Putative membrane protein		Point mutations
	<i>phoE</i>	218		Phosphate regulon transcriptional regulatory protein		Gene absent
	<i>bacS</i>	447		Genal transcription halidine-protein kinase		Gene absent
	<i>gcc108</i>	176		hypothetical protein		Gene absent
	<i>gcc109</i>	1159		IgA FC receptor		Gene absent
	<i>gcc110</i>	341		hypothetical protein		Gene absent
	<i>gcc111</i>	303		hypothetical protein		Gene absent
	<i>gcc112</i>	501	K06919	Putative DNA primase/helicase		Gene absent
	<i>gcc113</i>	286		hypothetical protein		Gene absent
	<i>gcc114</i>	66		hypothetical protein		Gene absent
	<i>gcc115</i>	103		hypothetical protein		Gene absent
	<i>gcc116</i>	388		hypothetical protein		Point mutations
	<i>yeeL</i>	215		Regulatory protein		Point mutations
	<i>gcc117</i>	205	K07078	Regulatory protein		Synonymous point mutations
	<i>gcc118</i>	292		Z7-O-demethylfarnesyl SV methyltransferase		Truncated protein
	<i>lacC</i>	311	K00917	Taqotase 6-phosphate kinase [EC:2.7.1.144]	met	Truncated protein
CC19	<i>mifH</i>	411	K08152	MFS transporter, DHAT family, multidrug resistance protein B		Point mutations
	<i>nicC</i>	273	K03742	Nicotinamide nucleotide amidase - Putative competence-damage inducible protein [EC:3.5.1.42]	met	Point mutations
	<i>gcc191</i>	390		hypothetical protein		Point mutations
	<i>xerC</i>	235		Tyrosine recombinase		Gene absent
	<i>gcc192</i>	76		hypothetical protein		Gene absent
	<i>imrM</i>	75		HTH-type transcriptional regulator		Gene absent
	<i>gcc193</i>	122		hypothetical protein		Gene absent
	<i>gcc194</i>	96		hypothetical protein		Gene absent
	<i>zhaA</i>	710	K01534	Cd <sup>2+</sup> /Zn <sup>2+</sup> -exporting ATPase - putative cadmium-transporting ATPase [EC:3.6.3.3 3.6.3.5]		Gene absent
	<i>casC</i>	123	K21903	ArskA toxin transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein		Gene absent
	<i>gcc195</i>	100		hypothetical protein		Gene absent
	<i>gcc196</i>	263		hypothetical protein		Gene absent
	<i>gcc197</i>	199		hypothetical protein		Gene absent
	<i>gcc198</i>	69		hypothetical protein		Gene absent
	<i>copA</i>	158	K17686	Cu--exporting ATPase [EC:3.6.3.54]	env	Gene absent
	<i>gcc199</i>	130		hypothetical protein		Gene absent
	<i>gcc110</i>	76		hypothetical protein		Gene absent
	<i>gcc1911</i>	164		hypothetical protein		Gene absent
	<i>gcc1912</i>	184		hypothetical protein		Gene absent
	<i>gcc1913</i>	64		hypothetical protein		Gene absent
	<i>gcc1914</i>	197		hypothetical protein		Gene absent
	<i>gcc1915</i>	282		hypothetical protein		Gene absent
	<i>gcc1916</i>	934		N-acetylmuramoyl-L-alanine amidase domain-containing protein		Gene absent
	<i>gcc1917</i>	118		hypothetical protein		Gene absent
	<i>gcc1918</i>	285		hypothetical protein		Gene absent
	<i>gcc1919</i>	81		hypothetical protein		Gene absent
	<i>varD4</i>	606	K03205	Type IV secretion system protein	env	Gene absent
	<i>gcc1920</i>	163		hypothetical protein		Gene absent
	<i>gcc1921</i>	195		hypothetical protein		Gene absent
	<i>gcc1922</i>	79		hypothetical protein		Gene absent
	<i>spxA</i>	128		Regulatory protein		Gene absent
	<i>gcc1923</i>	143		hypothetical protein		Gene absent
	<i>hpaII</i>	452	K00558	DNMT1: DNA (cytosine-5)-methyltransferase 1 - Modification methylase [EC:2.1.1.37]	met	Gene absent
	<i>gcc1924</i>	273		hypothetical protein		Gene absent
	<i>gcc1925</i>	58		hypothetical protein		Gene absent
	<i>mmuP/rocE</i>	459	K16235	S-methylmethionine amino-acid permease		Point mutations
	<i>gcc1926</i>	186		hypothetical protein		Point mutations
	<i>sstA</i>	284	K07284	Sorbose A [EC:3.4.22.70]		Gene absent
	<i>gcc1927</i>	706		hypothetical protein		Gene absent
CC17	<i>gcc171</i>	89		hypothetical protein		Point mutations
	<i>phT</i>	491	K03305	Phenol-dependent oligopeptide transporter, POT family		Synonymous point mutations
	<i>manR</i>	363	K02529	HTH-type LacI family transcriptional regulator		Point mutations
	<i>phT</i>	458	K02445	MFS transporter, OPA family, glycerol-3-phosphate transporter	env	Point mutations
	<i>arpP</i>	269	K02030	ABC, polar amino acid transport system substrate-binding protein - Arginine-binding extracellular protein	env	Synonymous point mutations
	<i>gcc172</i>	115		hypothetical protein		Gene absent
	<i>gcc173</i>	147		hypothetical protein		Gene absent
	<i>gcc174</i>	68		hypothetical protein		Gene absent
	<i>fluC</i>	334	K02015	ABC, iron complex transport system permease protein - Iron-uptake system permease protein	env	Point mutations
	<i>ascY</i>	413	KV03076	Accessory Sec system protein translocase subunit	met/env/cell	Gene absent
	<i>asp1</i>	526	K12288	Accessory secretory protein Asp1	env	Gene absent
	<i>asp2</i>	530	K12269	Accessory secretory protein Asp2	env	Gene absent
	<i>asp3</i>	182	K12270	Accessory secretory protein Asp3	env	Gene absent
	<i>gfl1</i>	507		Glycosyltransferase		Gene absent
	<i>gfl2</i>	443		Glycosyltransferase-stabilizing protein		Gene absent
	<i>gcc174</i>	56		hypothetical protein		Gene absent
	<i>wbbJ</i>	332		Beta-1,6-galactofuranosyltransferase		Gene absent
	<i>gpaS</i>	571		Putative glycosyltransferase		Gene absent

<i>capA</i>	393	K07282	Gamma-polyglutamate biosynthesis protein - Capsule biosynthesis protein		Point mutations
<i>degV</i>	283		hypothetical protein (containing DegV domain)		Synonymous point mutations
<i>yleE</i>	66	K03828	Putative acetyltransferase [EC:2.3.1.-]		Point mutations
<i>efbB</i>	590	K18888	ATP-binding cassette, subfamily B, multistep efflux pump	env	Point mutations
<i>gph</i>	450	K03092	Glutamate dehydrogenase (NADP+ specific) [EC:1.4.1.41]	met	Point mutations
<i>yhcR</i>	691	K01081	5-nucleotidase [EC:3.1.3.5]	met	Point mutations
<i>glcA</i>	363	K00005	Glycerol dehydrogenase [EC:1.1.1.6]	met	Point mutations
<i>goc175</i>	163	K02755	PTS-Bot-EIIA, PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-]	env	Point mutations
<i>goc176</i>	435	K01992	ABC-2 type transport system permease protein	env	Point mutations
<i>goc177</i>	77		hypothetical protein		Truncated protein
<i>nasA</i>	108	K01990	ABC-2 type transport system ATP-binding protein	env	Point mutations
<i>dnbB</i>	830	K03722	ATP-dependent DNA helicase [EC:3.6.4.12]	met	Point mutations
<i>nikE</i>	133	K10524	Nickel transport system ATP-binding protein [EC:3.6.3.24]	env	Truncated protein
<i>nikD</i>	263	K15587	Nickel transport system ATP-binding protein [EC:3.6.3.24]	env	Point mutations
<i>gspA</i>	402		General stress protein A		Gene absent
<i>bsaA</i>	235		Putative transglycosylase		Synonymous point mutations
<i>lydN</i>	37		hypothetical protein		Point mutations
<i>goc178</i>	586	K00382	DLI, dihydroloipoamide dehydrogenase [EC:1.8.1.4]	met/cell	Synonymous point mutations
<i>polnC</i>	463	K00627	DLAT, pyruvate dehydrogenase E2 component (dihydroloipoamide acetyltransferase) [EC:2.3.1.12]	met	Point mutations
<i>acvA</i>	323	K00161	PDHA: pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	met/env	Synonymous point mutations
<i>glpD</i>	107	K00976	glpC: glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]	met/cell	Point mutations
<i>glpC</i>	380	K00975	Glucose-1-phosphate adenylyltransferase	met/cell	Point mutations
<i>metW</i>	245	K02071	Methionine import ATP-binding protein MetN	env	Point mutations
<i>goc179</i>	230		hypothetical protein		Truncated protein
<i>yhcW</i>	407	K08177	oxT, MFS transporter, OFA family, oxalate/formate antiporter	env	Point mutations
<i>luxA</i>	348		Alkanal monooxygenase alpha chain		Point mutations
<i>goc1710</i>	58		hypothetical protein		Gene absent
<i>goc1711</i>	65		hypothetical protein		Truncated protein
<i>goc1712</i>	134		hypothetical protein		Gene absent
<i>goc1713</i>	406		hypothetical protein		Gene absent
<i>goc1714</i>	359		hypothetical protein		Point mutations
<i>casR</i>	320		CdsA regulatory protein		Synonymous point mutations
<i>goc1715</i>	282		hypothetical protein		Gene absent
<i>goc1716</i>	415		hypothetical protein		Gene absent
<i>lacC</i>	270	K00917	1,4-lactose 6-phosphate kinase [EC:2.7.1.144]	met	Point mutations
<i>goc1717</i>	66		FAM-binding protein		Truncated protein
<i>dnbB</i>	370	K02346	DNA polymerase IV [EC:2.7.7.7]	met	Point mutations
<i>mta_2</i>	58		hypothetical protein		Point mutations
<i>glpF_1</i>	238	K02440	GLPF: glycerol uptake facilitator protein	env	Point mutations
<i>goc1718</i>	92		hypothetical protein		Gene absent
<i>endA</i>	118	K15051	DNA-entry nuclease		Gene absent
<i>goc1719</i>	67		hypothetical protein		Point mutations
<i>janE</i>	318	K00077	2-dehydropanoate 2-reductase [EC:1.1.1.169]	met	Gene absent
<i>goc1720</i>	235		hypothetical protein		Gene absent
<i>puuD</i>	230	K07010	Putative glutamine amidotransferase	met	Point mutations
<i>yleM_1</i>	278	K02030	ABC, polar amino acid transport system substrate-binding protein	env	Point mutations
<i>speG_1</i>	186		Spermidine N(1)-acetyltransferase		Gene absent
<i>cas3</i>	480	K07012	CRISPR-associated endonuclease/helicase [EC:3.1.-.3.6.4.-]	cell	Point mutations
<i>goc1721</i>	271		Putative phosphatase		Point mutations
<i>goc1722</i>	895	K01537	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]		Synonymous point mutations
<i>gpaA</i>	102		hypothetical protein		Synonymous point mutations
<i>goc1723</i>	205		hypothetical protein		Point mutations
<i>gpp1724</i>	288	K07052	hypothetical protein		Point mutations
<i>casS</i>	419		Sensor histidine kinase		Point mutations
<i>lysS</i>	834	K01869	LARS: leucyl-RNA synthetase [EC:6.1.1.4]	met	Point mutations
<i>pta</i>	331	K00625	Phosphate acetyltransferase [EC:2.3.1.8]	met	Point mutations
<i>ydgG</i>	197		NADP-dependent 3-hydroxy acid dehydrogenase		Truncated protein
<i>pyrB</i>	308	K00609	Aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]	met	Point mutations
<i>smc_1</i>	625		Chromosome partition protein Smc		Truncated protein
<i>goc1725</i>	177		hypothetical protein		Gene absent
<i>gpp1726</i>	159		hypothetical protein		Gene absent
<i>gpp1727</i>	136		hypothetical protein		Gene absent
<i>gpp1728</i>	89		hypothetical protein		Gene absent
<i>goc1729</i>	127		hypothetical protein		Gene absent
<i>lysS</i>	580	K07704	Two-component system, LysTR family, sensor histidine kinase [EC:2.7.13.3]	met/env	Point mutations
<i>lysR</i>	486		Transcriptional regulator LysR		Point mutations
<i>amx</i>	680		Acylamidase		Truncated protein
<i>pacB</i>	414	K19689	Aminopeptidase [EC:3.4.11.-]	met	Point mutations
<i>lvrB</i>	664	K03702	Exonuclease ABC subunit B - LvrABC system protein	met	Point mutations
<i>prp_2</i>	1386		PilI-type protease		Gene absent
<i>goc1730</i>	384		hypothetical protein		Gene absent
<i>mutT</i>	175	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.55]	met	Truncated protein
<i>goc1731</i>	56		hypothetical protein		Truncated protein
<i>sigA</i>	370	K03086	RNA polymerase primary sigma factor	met	Synonymous point mutations
<i>goc1732</i>	61		hypothetical protein		Gene absent
<i>lspB</i>	190	K03100	Signal peptidase I [EC:3.4.21.89]	met/cell	Gene absent
<i>intA_2</i>	1435		Interralin-A		Gene absent
<i>goc1733</i>	503		Fimbrial subunit type 1		Gene absent
<i>lypB</i>	305	K12987	Rhamnosyltransferase [EC:2.4.1.1]	met	Point mutations
<i>sapA</i>	457	K01361	C5a peptidase - lactocepin [EC:3.4.21.96]	met	Truncated protein
<i>strA</i>	292	K07284	Sortase A [EC:3.4.22.70]	met	Gene absent
<i>goc1734</i>	224		hypothetical protein		Gene absent
<i>ramH_1</i>	189		hypothetical protein		Point mutations
<i>goc1735</i>	282		putative NTE family protein		Point mutations
<b>CC23</b>					
<i>goc231</i>	207		hypothetical protein		Gene absent
<i>goc232</i>	86		hypothetical protein		Gene absent
<i>goc233</i>	368		hypothetical protein		Gene absent
<i>comR</i>	301	K20342	HTH-type transcriptional regulator, regulator for ComX	cell	Gene absent
<i>yvgN_2</i>	115		putative oxidoreductase		Point mutations
<i>goc234</i>	132		hypothetical protein		Truncated protein
<i>goc235</i>	369		hypothetical protein		Gene absent
<i>goc236</i>	173		hypothetical protein		Gene absent
<i>goc237</i>	95		hypothetical protein		Gene absent
<i>goc238</i>	285		hypothetical protein		Gene absent
<i>goc239</i>	97		hypothetical protein		Gene absent
<i>goc2310</i>	135		hypothetical protein		Gene absent
<i>goc2311</i>	119		hypothetical protein		Gene absent
<i>hasS</i>	462	K01154	Type I restriction enzyme, S subunit - EcoKI specificity protein [EC:3.1.21.3]	cell	Gene absent
<i>goc2312</i>	507		hypothetical protein		Point mutations
<i>goc2313</i>	107		hypothetical protein		Point mutations
<i>argH</i>	384		D-alanyl-D-alanine-carboxypeptidase/endorpeptidase		Point mutations
<i>fabG_1</i>	241	K00059	3-oxoacyl-(acyl-carrier protein) reductase [EC:1.1.1.100]	met	Synonymous point mutations
<i>cyfE</i>	868	K11052	Cyclic uncharacterised protein	env	Point mutations
<i>goc17</i>	318	K00605	Aminomethyltransferase [EC:2.1.2.10]	met	Point mutations
<i>fabF_1</i>	732	K09458	3-oxoacyl-(acyl-carrier-protein) synthase II [EC:2.3.1.179]	met	Point mutations
<i>goc2314</i>	460		hypothetical protein		Point mutations
<i>CyR</i>	192	K11056	Cyclic uncharacterised protein		Point mutations
<i>goc2315</i>	162		hypothetical protein		Point mutations
<i>fabA</i>	219	K02068	Putative ABC transport system ATP-binding protein - iron export	env	Synonymous point mutations
<i>goc2316</i>	65		hypothetical protein		Truncated protein
<i>yvgM</i>	652	K02004	Putative ABC transport system permease protein	env	Point mutations
<i>graS</i>	313		Sensor histidine kinase		Synonymous point mutations
<i>smc_2</i>	537		Chromosome partition protein		Point mutations
<i>goc2317</i>	143		hypothetical protein		Truncated protein
<i>mntH</i>	523	K03322	Manganese/divalent metal cation transport protein	env	Gene absent
<i>goc2318</i>	436		hypothetical protein		Gene absent
<i>cdtA</i>	263	K11045	cAMP factor	env	Gene absent
<i>dnbJ</i>	98	K07473	DNA-damage-inducible protein J	cell	Point mutations
<i>goc2319</i>	113		hypothetical protein		Gene absent
<i>goc2320</i>	123		hypothetical protein		Gene absent
<i>goc2321</i>	141		hypothetical protein		Gene absent
<i>xre_1</i>	113		HTH-type transcriptional regulator		Gene absent
<i>xre_2</i>	105		HTH-type transcriptional regulator		Gene absent
<i>goc2322</i>	47		hypothetical protein		Gene absent
<i>xre_3</i>	144		HTH-type transcriptional regulator		Gene absent
<i>goc2324</i>	104		hypothetical protein		Gene absent
<i>goc2325</i>	154		hypothetical protein		Gene absent
<i>goc2326</i>	88		hypothetical protein		Gene absent
<i>smc</i>	754		Chromosome partition protein		Gene absent
<i>goc2327</i>	126		hypothetical protein		Gene absent
<i>xre</i>	75		HTH-type transcriptional regulator		Truncated protein
<i>rsuR</i>	118		HTH-type transcriptional regulator		Gene absent
<i>goc2328</i>	834		hypothetical protein		Gene absent
<i>goc2329</i>	181		hypothetical protein		Gene absent
<i>goc2330</i>	125		Transcriptional regulator		Gene absent
<i>rip5</i>	272	K04783	Yersiniabactin salicyl-AMP ligase [EC:6.3.2.-]	met	Gene absent
<i>goc2331</i>	148		2-hydroxy-2-methyl-5-methyl-1-naphthoate-CoA ligase		Gene absent
<i>goc2332</i>	62		hypothetical protein		Point mutations
<i>goc2333</i>	135		hypothetical protein		Gene absent
<i>ftsT</i>	199	K16926	Energy-coupling factor transport system substrate-specific component	env	Gene absent
<i>goc17</i>	238	K16785	Energy-coupling factor transport system permease protein	env	Gene absent
<i>goc2334</i>	290	K08147	ABC-B-BAC, ATP-binding cassette, subfamily B	env	Gene absent
<i>msbA</i>	292	K06147	ABC-B-BAC, ATP-binding cassette, subfamily B - Lipid A export ATP-binding/permease protein	env	Gene absent
<i>ndvA</i>	574	K06147	ABC-B-BAC, ATP-binding cassette, subfamily B - Beta-1-2-galactan export ATP-binding/permease protein	env	Gene absent
<i>glpT</i>	488	K02445	MFS transporter, OFA family, glycerol-3-phosphate transporter	env	Point mutations
<i>goc2335</i>	168	K08940	uncharacterized protein		Point mutations
<i>goc2336</i>	676		hypothetical protein		Truncated protein
<i>vanYB</i>	251	K07260	Zinc D-Ala-D-Ala carboxypeptidase [EC:3.4.17.14]	met/env	Gene absent