

Table S2. Genes regulated with a statistical reliability ( $|fold\ change| \geq 2.0$ ;  $p\text{-value} \leq 0.05$ ) under the effect of iodine-containing complexes at least at one condition.

1 - upregulation; -1 - downregulation;

Locus tag in <i>E. coli</i> BAA-196	Locus tag in <i>S. aureus</i> BAA-39	Gene	<i>E. coli</i> BAA-196						<i>S. aureus</i> BAA-39						Annotation
			IPC25		IPC33		IPC51		IPC25		IPC33		IPC51		
			Lag	Log	Lag	Log	Lag	Log	Lag	Log	Lag	Log	Lag	Log	
BAA196NC_0001	HMPRNC0000_0001	<i>dnaA</i>							-1						Chromosomal replication initiation protein
BAA196NC_0054	HMPRNC0000_1766	<i>spoT</i>			1		1								Bifunctional (p)ppGpp synthetase II/ guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase
BAA196NC_0056	HMPRNC0000_1263	<i>gmk</i>					1								Guanylate kinase
BAA196NC_0065	HMPRNC0000_1265	<i>dfp</i>						1			1				Bifunctional phosphopantothencysteine decarboxylase/phosphopantothenate synthase
BAA196NC_0066	HMPRNC0000_1785	<i>yciR</i>					-1								DNA repair protein RadC
BAA196NC_0089	HMPRNC0000_0594	<i>kbl</i>							-1						2-amino-3-ketobutyrate coenzyme A ligase
BAA196NC_0094	HMPRNC0000_0864	<i>gpml</i>							1	1	1	1			Phosphoglyceromutase
BAA196NC_0098	HMPRNC0000_1589	<i>gpsA</i>	-1				-1	-1		1	1	1			NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
BAA196NC_0120	HMPRNC0000_0169	<i>aldB</i>						-1		1	1	1			Aldehyde dehydrogenase B
BAA196NC_0145	HMPRNC0000_2772	<i>xyiB</i>												-1	Xylulokinase
BAA196NC_0158	HMPRNC0000_0955	<i>tiaE</i>							-1						2-ketoaldonate reductase/glyoxylate reductase B
BAA196NC_0170	HMPRNC0000_1025	<i>dppD</i>						-1							Dipeptide transporter
BAA196NC_0249	HMPRNC0000_0035	<i>zntA</i>	1		1				1	1	1	1			Zinc, cobalt and lead efflux system
BAA196NC_0271	HMPRNC0000_0224	<i>ggt</i>	1				-1		1	1					Gamma-glutamyltranspeptidase periplasmic precursor
BAA196NC_0316	HMPRNC0000_1928	<i>pck</i>	1				-1		-1	-1					Phosphoenolpyruvate carboxykinase
BAA196NC_0318	HMPRNC0000_0538	<i>hslO</i>							1	1	1	1			Hsp33-like chaperonin
BAA196NC_0353	HMPRNC0000_2659	<i>nirB</i>						1	-1	-1					Nitrite reductase, large subunit, NAD(P)H-binding
BAA196NC_0359	HMPRNC0000_0787	<i>pabA</i>			1										Para-aminobenzoate synthase component II
BAA196NC_0360	HMPRNC0000_0987	<i>argD</i>							-1	-1					Bifunctional acetylornithine aminotransferase/ succinyladiaminopimelate aminotransferase
BAA196NC_0378	HMPRNC0000_0588	<i>rpsL</i>							1	1					30S ribosomal protein S12
BAA196NC_0379	HMPRNC0000_0589	<i>rpsG</i>							1	1					30S ribosomal protein S7
BAA196NC_0380	HMPRNC0000_0590	<i>fusA</i>	1						1	1					Elongation factor EF-2
BAA196NC_0400	HMPRNC0000_2462	<i>rplC</i>	1												50S ribosomal protein L3
BAA196NC_0402	HMPRNC0000_2460	<i>rplW</i>						-1	1	1	1	1			50S ribosomal protein L23
BAA196NC_0404	HMPRNC0000_2458	<i>rpsS</i>						-1							30S ribosomal protein S19
BAA196NC_0405	HMPRNC0000_2457	<i>rplV</i>												-1	50S ribosomal protein L22
BAA196NC_0407	HMPRNC0000_2455	<i>rplP</i>	1						1	1					50S ribosomal protein L16
BAA196NC_0408	HMPRNC0000_2454	<i>rpmC</i>			1				1	1	-1	1			50S ribosomal protein L29
BAA196NC_0409	HMPRNC0000_2453	<i>rpsQ</i>							1	1					30S ribosomal protein S17
BAA196NC_0411	HMPRNC0000_2451	<i>rplX</i>						-1							50S ribosomal protein L24
BAA196NC_0412	HMPRNC0000_2450	<i>rplE</i>							1	1					50S ribosomal protein L5
BAA196NC_0414	HMPRNC0000_2449	<i>rpsH</i>	1						-1	-1					30S ribosomal protein S8
BAA196NC_0415	HMPRNC0000_2448	<i>rplF</i>						-1	1	1					50S ribosomal protein L6
BAA196NC_0416	HMPRNC0000_2447	<i>rplR</i>	1						1	1					50S ribosomal protein L18
BAA196NC_0418	HMPRNC0000_2445	<i>rpmD</i>	1		1				1	1	1	1			50S ribosomal protein L30
BAA196NC_0419	HMPRNC0000_2444	<i>rplO</i>	1												50S ribosomal protein L15
BAA196NC_0420	HMPRNC0000_2443	<i>secY</i>							1	1					Protein translocase subunit SecY
BAA196NC_0424	HMPRNC0000_1859	<i>rpsD</i>							-1	-1					30S ribosomal protein S4
BAA196NC_0425	HMPRNC0000_2437	<i>rpoA</i>						-1						-1	DNA-directed RNA polymerase subunit alpha
BAA196NC_0428	HMPRNC0000_0064	<i>zntR</i>							1						Zinc-responsive transcriptional regulator
BAA196NC_0430	HMPRNC0000_1447	<i>mscL</i>						1							Large-conductance mechanosensitive channel
BAA196NC_0432	HMPRNC0000_1274	<i>rsmB</i>							1	1					16S rRNA m5C967 methyltransferase, S-adenosyl-L-methionine-dependent
BAA196NC_0458	HMPRNC0000_1651	<i>accC</i>						-1							Acetyl-CoA carboxylase
BAA196NC_0459	HMPRNC0000_1652	<i>accB</i>					1								Acetyl-CoA carboxylase
BAA196NC_0461	HMPRNC0000_2623	<i>yhdH</i>	1												Predicted oxidoreductase, Zn-dependent and NAD(P)-binding
BAA196NC_0477	HMPRNC0000_2889	<i>mdh</i>	1										1		Malate dehydrogenase
BAA196NC_0482	HMPRNC0000_2432	<i>rplM</i>						-1							50S ribosomal protein L13
BAA196NC_0498	HMPRNC0000_0488	<i>gltD</i>	1						1	1	1	1			Glutamate synthase, 4Fe-4S protein, small subunit
BAA196NC_0499	HMPRNC0000_0487	<i>gltB</i>	1		1				1	1	1	1			Glutamate synthase, large subunit
BAA196NC_0507	HMPRNC0000_0852	<i>yhbJ</i>	-1						1	1	1	1			Hypothetical protein
BAA196NC_0525	HMPRNC0000_1584	<i>ispB</i>							-1					-1	Octaprenyl diphosphate synthase
BAA196NC_0526	HMPRNC0000_1780	<i>rplU</i>						1							50S ribosomal protein L21
BAA196NC_0527	HMPRNC0000_1778	<i>rpmA</i>													50S ribosomal protein L27
BAA196NC_0533	HMPRNC0000_1728	<i>yhbY</i>						-1							Predicted RNA-binding protein
BAA196NC_0535	HMPRNC0000_0537	<i>ftsH</i>							1	1					Protease, ATP-dependent zinc-metallo
BAA196NC_0546	HMPRNC0000_1339	<i>rpsO</i>						-1							30S ribosomal protein S15
BAA196NC_0548	HMPRNC0000_1340	<i>pnp</i>												-1	Polynucleotide phosphorylase/polyadenylase
BAA196NC_0552	HMPRNC0000_1755	<i>yhbW</i>							1	1	1	1			Luciferase-like monooxygenase
BAA196NC_0594	HMPRNC0000_1548	<i>tdcB</i>	-1		-1			-1							Threonine dehydratase
BAA196NC_0606	HMPRNC0000_2583	<i>yhaH</i>												1	Predicted inner membrane protein
BAA196NC_0646	HMPRNC0000_2227	<i>ygjD</i>							1						O-sialoglycoprotein endopeptidase
BAA196NC_0706	HMPRNC0000_2568	<i>yghA</i>						1			-1		-1		Oxidoreductase
BAA196NC_0737	HMPRNC0000_2616	<i>lctP</i>												-1	L-lactate permease
BAA196NC_0749	HMPRNC0000_2047	<i>mutY</i>						-1							Adenine DNA glycosylase
BAA196NC_0764	HMPRNC0000_1706	<i>yggJ</i>							1	1		1			Hypothetical protein
BAA196NC_0768	HMPRNC0000_1927	<i>metK</i>	1					1							S-adenosylmethionine synthetase
BAA196NC_0782	HMPRNC0000_0861	<i>pgk</i>							1	1		1			Phosphoglycerate kinase
BAA196NC_0785	HMPRNC0000_0893	<i>argO</i>										1			Arginine exporter protein

BAA196NC_0804	HMPRNC0000_1665	<i>gcvT</i>																	Glycine cleavage system aminomethyltransferase T
BAA196NC_0805	HMPRNC0000_0904	<i>gcvH</i>	1	1	1														Glycine cleavage system protein H
BAA196NC_0810	HMPRNC0000_2386	<i>yqfA</i>			-1														Predicted oxidoreductase, inner membrane subunit
BAA196NC_0818	HMPRNC0000_0838	<i>prfB</i>				1	1												Peptide chain release factor 2
BAA196NC_0883	HMPRNC0000_1536	<i>thyA</i>				-1													Thymidylate synthase
BAA196NC_0921	HMPRNC0000_2778	<i>gudP</i>				-1													Predicted D-glucarate transporter
BAA196NC_0930	HMPRNC0000_2324	<i>pyrG</i>					1	1											CTP synthetase
BAA196NC_0946	HMPRNC0000_2912	<i>cysI</i>				1													Sulfite reductase, alpha subunit, flavoprotein
BAA196NC_0976	HMPRNC0000_0769	<i>ygbI</i>				1	1	1	1										Predicted DNA-binding transcriptional regulator
BAA196NC_1014	HMPRNC0000_1351	<i>recA</i>																	Recombinase A
BAA196NC_1016	HMPRNC0000_1749	<i>alaS</i>		1															Alanyl-tRNA synthetase
BAA196NC_1034	HMPRNC0000_0809	<i>nrdF</i>																	Ribonucleotide-diphosphate reductase beta subunit
BAA196NC_1048	HMPRNC0000_2892	<i>gabT</i>				1	1												4-aminobutyrate aminotransferase
BAA196NC_1090	HMPRNC0000_1711	<i>grpE</i>				1	1	1	1	1									Heat shock protein
BAA196NC_1093	HMPRNC0000_1301	<i>ffh</i>									1	1							Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)
BAA196NC_1096	HMPRNC0000_1306	<i>trmD</i>									1								tRNA (guanine-N(1)-)-methyltransferase
BAA196NC_1107	HMPRNC0000_1249	<i>rluD</i>									1	1							23S rRNA pseudouridine synthase
BAA196NC_1108	HMPRNC0000_1237	<i>yfiH</i>									1								Hypothetical protein
BAA196NC_1109	HMPRNC0000_1008	<i>clpB</i>				1	1	1	1	1									Protein disaggregation chaperone
BAA196NC_1165	HMPRNC0000_1148	<i>suhB</i>									1								Inositol monophosphatase
BAA196NC_1169	HMPRNC0000_0939	<i>iscU</i>				1													Scaffold protein
BAA196NC_1181	HMPRNC0000_1583	<i>ndk</i>					1												Nucleoside diphosphate kinase
BAA196NC_1185	HMPRNC0000_1762	<i>hisS</i>		-1															Histidyl-tRNA synthetase
BAA196NC_1191	HMPRNC0000_0434	<i>guaB</i>	1	1															Inositol-5-monophosphate dehydrogenase
BAA196NC_1192	HMPRNC0000_0435	<i>guaA</i>	1	1															Bifunctional GMP synthase/glutamine amidotransferase protein
BAA196NC_1200	HMPRNC0000_1110	<i>purN</i>									1								Phosphoribosylglycinamide formyltransferase
BAA196NC_1201	HMPRNC0000_1109	<i>purM</i>	1	1															Phosphoribosylaminoimidazole synthetase
BAA196NC_1202	HMPRNC0000_2304	<i>upp</i>																	Phosphoribosyltransferase
BAA196NC_1203	HMPRNC0000_1252	<i>uraA</i>				1													Uracil transporter
BAA196NC_1220	HMPRNC0000_2041	<i>bcp</i>					1												Thioredoxin-dependent thiol peroxidase
BAA196NC_1222	HMPRNC0000_1502	<i>dapA</i>																	Dihydrodipicolinate synthase
BAA196NC_1224	HMPRNC0000_1101	<i>purC</i>	1	1															Phosphoribosylaminoimidazole-succinocarboxamide synthase
BAA196NC_1230	HMPRNC0000_1030	<i>yffB</i>																	Hypothetical protein
BAA196NC_1231	HMPRNC0000_2477	<i>acrD</i>																	Aminoglycoside/multidrug efflux system
BAA196NC_1236	HMPRNC0000_1439	<i>tktB</i>				1													Transketolase 2, thiamin-binding
BAA196NC_1272	HMPRNC0000_0204	<i>murP</i>																	N-acetylmuramic acid phosphotransfer permease
BAA196NC_1273	HMPRNC0000_0203	<i>yfeU</i>																	N-acetylmuramic acid-6-phosphate etherase
BAA196NC_1289	HMPRNC0000_2088	<i>ligA</i>																	NAD-dependent DNA ligase LigA
BAA196NC_1298	HMPRNC0000_0571	<i>glxX</i>																	Glutamyl-tRNA synthetase
BAA196NC_1303	HMPRNC0000_0341	<i>nupC</i>																	Nucleoside (except guanosine) transporter
BAA196NC_1304	HMPRNC0000_1146	<i>mntH</i>																	Manganese transport protein MntH
BAA196NC_1377	HMPRNC0000_1501	<i>usg</i>																	Putative beta-semialdehyde dehydrogenase
BAA196NC_1378	HMPRNC0000_2433	<i>truA</i>																	tRNA pseudouridine synthase A
BAA196NC_1380	HMPRNC0000_1833	<i>accD</i>																	Acetyl-CoA carboxylase subunit beta
BAA196NC_1381	HMPRNC0000_1787	<i>folC</i>									1	1	1	1					Bifunctional folypolyglutamate synthase/ dihydrofolate synthase
BAA196NC_1384	HMPRNC0000_1106	<i>purF</i>	1	1															Amidophosphoribosyltransferase
BAA196NC_1392	HMPRNC0000_0857	<i>yfcH</i>																	Conserved protein with NAD(P)-binding Rossmann-fold domain
BAA196NC_1393	HMPRNC0000_0541	<i>folX</i>																	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase
BAA196NC_1400	HMPRNC0000_1846	<i>ackA</i>																	Acetate kinase
BAA196NC_1433	HMPRNC0000_1074	<i>menD</i>																	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase
BAA196NC_1459	HMPRNC0000_0989	<i>glpQ</i>																	Periplasmic glycerophosphodiester phosphodiesterase
BAA196NC_1467	HMPRNC0000_1455	<i>gyrA</i>																	DNA gyrase subunit A
BAA196NC_1474	HMPRNC0000_0394	<i>atoB</i>																	Acetyl-CoA acetyltransferase
BAA196NC_1600	HMPRNC0000_2283	<i>thiM</i>																	Hydroxyethylthiazole kinase
BAA196NC_1601	HMPRNC0000_2284	<i>thiD</i>																	Phosphomethylpyrimidine kinase
BAA196NC_1608	HMPRNC0000_2322	<i>gatY</i>																	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit
BAA196NC_1615	HMPRNC0000_0269	<i>gatD</i>																	Galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding
BAA196NC_1625	HMPRNC0000_1744	<i>yegQ</i>																	Predicted peptidase
BAA196NC_1672	HMPRNC0000_0128	<i>rfbX</i>																	Predicted polisoprenol-linked O-antigen transporter
BAA196NC_1683	HMPRNC0000_2982	<i>hisI</i>																	Bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein
BAA196NC_1684	HMPRNC0000_2983	<i>hisF</i>																	Imidazole glycerol phosphate synthase subunit HisF
BAA196NC_1685	HMPRNC0000_2984	<i>hisA</i>																	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase
BAA196NC_1686	HMPRNC0000_2985	<i>hisH</i>																	Imidazole glycerol phosphate synthase subunit HisH
BAA196NC_1688	HMPRNC0000_0800	<i>hisC</i>																	Histidinol-phosphate aminotransferase
BAA196NC_1689	HMPRNC0000_2989	<i>hisD</i>																	Histidinol dehydrogenase
BAA196NC_1696	HMPRNC0000_2220	<i>yeeE</i>																	Predicted inner membrane protein
BAA196NC_1697	HMPRNC0000_2219	<i>yeeD</i>																	Hypothetical protein
BAA196NC_1737	HMPRNC0000_0595	<i>hchA</i>																	Chaperone protein HchA
BAA196NC_1780	HMPRNC0000_2676	<i>fliY</i>																	Cystine transporter subunit
BAA196NC_1782	HMPRNC0000_2675	<i>yecS</i>																	Predicted transporter subunit: membrane component of ABC superfamily
BAA196NC_1783	HMPRNC0000_2003	<i>yecC</i>																	Predicted transporter subunit: ATP-binding component of ABC superfamily
BAA196NC_1787	HMPRNC0000_1194	<i>uvrC</i>																	Excinuclease ABC subunit C
BAA196NC_1792	HMPRNC0000_2078	<i>ftnA</i>																	Ferritin-like protein 2

BAA196NC_1819	HMPRNC0000_0666	<i>argS</i>	1	1					Arginyl-tRNA synthetase
BAA196NC_1829	HMPRNC0000_1761	<i>aspS</i>			-1				Aspartyl-tRNA synthetase
BAA196NC_1836	HMPRNC0000_0691	<i>znuB</i>			-1	-1			High-affinity zinc transporter membrane component
BAA196NC_1844	HMPRNC0000_1624	<i>zwf</i>					1		Glucose-6-phosphate 1-dehydrogenase
BAA196NC_1866	HMPRNC0000_1857	<i>yebR</i>		1					Hypothetical protein
BAA196NC_1920	HMPRNC0000_1815	<i>gapA</i>			-1	-1			Glyceraldehyde-3-phosphate dehydrogenase
BAA196NC_1928	HMPRNC0000_0658	<i>ydjG</i>					1		Predicted oxidoreductase
BAA196NC_1936	HMPRNC0000_2467	<i>topB</i>		-1					DNA topoisomerase III
BAA196NC_1938	HMPRNC0000_0988	<i>gdhA</i>			-1	-1			Glutamate dehydrogenase
BAA196NC_1949	HMPRNC0000_0994	<i>ydjX</i>						-1	Predicted inner membrane protein
BAA196NC_1963	HMPRNC0000_2410	<i>chbC</i>	-1		-1	-1	-1		N,N'-diacetylchitobiose-specific enzyme IIC component of PTS
BAA196NC_1977	HMPRNC0000_2415	<i>pfkB</i>			-1	-1			6-phosphofructokinase II
BAA196NC_1980	HMPRNC0000_1811	<i>thrS</i>				1	1		Threonyl-tRNA synthetase
BAA196NC_1982	HMPRNC0000_1808	<i>rpmI</i>	-1						50S ribosomal protein L35
BAA196NC_1984	HMPRNC0000_1185	<i>pheS</i>					-1		Phenylalanyl-tRNA synthetase alpha subunit
BAA196NC_1998	HMPRNC0000_0253	<i>menE</i>					-1	-1	Long-chain-fatty-acid--CoA ligase
BAA196NC_2006	HMPRNC0000_0254	<i>ydiF</i>					-1	1	Fused predicted acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit/beta
BAA196NC_2008	HMPRNC0000_1729	<i>ydiB</i>						-1	subunit
BAA196NC_2022	HMPRNC0000_0938	<i>sufS</i>						-1	Quinate/shikimate 5-dehydrogenase, NAD(P)-binding
BAA196NC_2039	HMPRNC0000_1912	<i>ribC</i>					1		Selenocysteine lyase
BAA196NC_2052	HMPRNC0000_0986	<i>nemaA</i>	1	1	1	1	1		Riboflavin synthase subunit alpha
BAA196NC_2055	HMPRNC0000_0756	<i>ydhF</i>						-1	N-ethylmaleimide reductase, FMN-linked
BAA196NC_2092	HMPRNC0000_1996	<i>fumC</i>			-1	-1			Predicted oxidoreductase
BAA196NC_2163	HMPRNC0000_2754	<i>ydfG</i>					1		Fumarate hydratase
BAA196NC_2253	HMPRNC0000_2406	<i>yncB</i>			1	1			L-allo-threonine dehydrogenase, NAD(P)-binding
BAA196NC_2276	HMPRNC0000_0376	<i>rimL</i>					1		Predicted oxidoreductase, Zn-dependent and NAD(P)-binding
BAA196NC_2288	HMPRNC0000_2317	<i>aldA</i>	1	1					Ribosomal-protein-L7/L12-serine acetyltransferase
BAA196NC_2291	HMPRNC0000_0226	<i>azoR</i>	1	1	1	1			Aldehyde dehydrogenase A, NAD-linked
BAA196NC_2361	HMPRNC0000_0093	<i>abgA</i>							Acyl carrier protein phosphodiesterase
BAA196NC_2361	HMPRNC0000_1505	.						-1	Predicted peptidase, aminobenzoyl-glutamate utilization protein
BAA196NC_2376	HMPRNC0000_1849	<i>tpx</i>					1		N-acetyl-L,L-diaminopimelate deacetylase
BAA196NC_2385	HMPRNC0000_0232	<i>ycjS</i>					-1		Thiol peroxidase
BAA196NC_2412	HMPRNC0000_1044	<i>fabI</i>					1		Predicted oxidoreductase, NADH-binding
BAA196NC_2420	HMPRNC0000_1257	<i>pyrF</i>				1	1		Enoyl-(acyl carrier protein) reductase
BAA196NC_2425	HMPRNC0000_1449	<i>acnA</i>	1		-1	-1			Orotidine 5'-phosphate decarboxylase
BAA196NC_2428	HMPRNC0000_1315	<i>topA</i>					1	1	Aconitate hydratase
BAA196NC_2440	HMPRNC0000_1473	<i>trpB</i>	1	1		-1	-1		DNA topoisomerase I
BAA196NC_2441	HMPRNC0000_1474	<i>trpA</i>	1	1		-1	-1	-1	Tryptophan synthase subunit beta
BAA196NC_2454	HMPRNC0000_1022	<i>oppF</i>					-1	-1	Tryptophan synthase subunit alpha
BAA196NC_2455	HMPRNC0000_1021	<i>oppD</i>	1		-1	-1	-1	-1	Oligopeptide transporter subunit
BAA196NC_2456	HMPRNC0000_1020	<i>oppC</i>			-1	-1	-1	-1	Oligopeptide transporter ATP-binding component
BAA196NC_2457	HMPRNC0000_1019	<i>oppB</i>			-1	-1	-1	-1	Oligopeptide transporter subunit
BAA196NC_2458	HMPRNC0000_1023	<i>oppA</i>	1		-1	-1	-1	-1	Oligopeptide permease ABC transporter membrane protein
BAA196NC_2473	HMPRNC0000_2652	<i>narH</i>			-1	-1	-1		Oligopeptide transporter subunit
BAA196NC_2474	HMPRNC0000_2655	<i>narG</i>	1	1	1	1	1		Nitrate reductase 1, beta (Fe-S) subunit
BAA196NC_2475	HMPRNC0000_2644	<i>narK</i>			1	-1	-1		Nitrate reductase 1, alpha subunit
BAA196NC_2478	HMPRNC0000_2068	<i>narL</i>							Nitrate/nitrite transporter
BAA196NC_2497	HMPRNC0000_0517	<i>ispE</i>	-1		1			-1	DNA-binding response regulator in two-component regulatory system with NarX (or NarQ)
BAA196NC_2502	HMPRNC0000_0407	<i>ychF</i>					1		4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
BAA196NC_2565	HMPRNC0000_1825	<i>icd</i>	1	1	-1	-1			Translation-associated GTPase
BAA196NC_2568	HMPRNC0000_1753	<i>trmU</i>					1		Isocitrate dehydrogenase
BAA196NC_2589	HMPRNC0000_0525	<i>mfd</i>					1	1	trNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
BAA196NC_2594	HMPRNC0000_0966	<i>ndh</i>					1		Transcription-repair coupling factor
BAA196NC_2610	HMPRNC0000_1292	<i>acpP</i>	-1	1					Respiratory NADH dehydrogenase 2/cupric reductase
BAA196NC_2611	HMPRNC0000_1290	<i>fabG</i>	-1					1	Acyl carrier protein
BAA196NC_2612	HMPRNC0000_1289	<i>fabD</i>					1	1	3-oxoacyl-[acyl-carrier-protein] reductase
BAA196NC_2613	HMPRNC0000_1015	<i>fabH</i>					1	1	Acyl carrier protein S-malonyltransferase
BAA196NC_2682	HMPRNC0000_0380	<i>ycdB</i>					1		3-oxoacyl-(acyl carrier protein) synthase
BAA196NC_2685	HMPRNC0000_2087	<i>putP</i>					-1		Hypothetical protein
BAA196NC_2710	HMPRNC0000_1509	<i>cspG</i>			-1	-1		-1	Proline:sodium symporter
BAA196NC_2731	HMPRNC0000_1511	<i>yccX</i>					1		DNA-binding transcriptional regulator
BAA196NC_2755	HMPRNC0000_2876	<i>pyrD</i>					-1		Predicted acylphosphatase
BAA196NC_2766	HMPRNC0000_0177	<i>ssuC</i>					1	1	Dihydroxyacetate dehydrogenase
BAA196NC_2767	HMPRNC0000_0175	<i>ssuB</i>					1	1	Alkanesulfonate transporter subunit
BAA196NC_2773	HMPRNC0000_1674	<i>ycbL</i>					1	1	Alkanesulfonate transporter subunit
BAA196NC_2786	HMPRNC0000_2045	<i>msbA</i>					1	1	Predicted metal-binding enzyme
BAA196NC_2796	HMPRNC0000_2662	<i>focA</i>					-1	-1	Fused lipid transporter subunits of ABC superfamily: membrane component/ATP-binding component
BAA196NC_2797	HMPRNC0000_0241	<i>pfIB</i>	-1						Formate transporter
BAA196NC_2808	HMPRNC0000_1758	<i>ycal</i>						-1	Pyruvate formate lyase I
BAA196NC_2812	HMPRNC0000_0851	<i>trxB</i>					1	1	Recombination protein
BAA196NC_2828	HMPRNC0000_2817	<i>poxB</i>	1				-1	-1	Thioredoxin reductase, FAD/NAD(P)-binding
BAA196NC_2842	HMPRNC0000_1142	<i>potI</i>					-1		Pyruvate dehydrogenase
BAA196NC_2850	HMPRNC0000_0426	<i>nfsA</i>					1		Putrescine transporter subunit: membrane component of ABC superfamily
BAA196NC_2882	HMPRNC0000_1497	<i>ybiT</i>					1		Nitroreductase A, NADPH-dependent, FMN-dependent
BAA196NC_2890	HMPRNC0000_2340	<i>dps</i>	-1	-1	1	1	1	1	Fused predicted transporter subunits of ABC superfamily: ATP-binding components
									DNA protection during starvation conditions

BAA196NC_2917	HMPRNC0000_2490	<i>moaE</i>				1	1	1	Molybdopterin synthase, large subunit	
BAA196NC_2919	HMPRNC0000_2494	<i>moaC</i>		1					Molybdenum cofactor biosynthesis protein C	
BAA196NC_2920	HMPRNC0000_2495	<i>moaB</i>		1	1				Molybdopterin biosynthesis protein B	
BAA196NC_2921	HMPRNC0000_2486	<i>moaA</i>	1			1	1	1	Molybdenum cofactor biosynthesis protein A	
BAA196NC_2923	HMPRNC0000_0842	<i>uvrB</i>						-1	Excinuclease ABC subunit B	
BAA196NC_2928	HMPRNC0000_2696	<i>bioA</i>						-1	Adenosylmethionine--8-amino-7-oxononanoate transaminase	
BAA196NC_3009	HMPRNC0000_2679	<i>gpmA</i>				1			Phosphoglyceromutase	
BAA196NC_3012	HMPRNC0000_2350	<i>zitB</i>				1	1	1	1	Zinc transporter ZitB
BAA196NC_3025	HMPRNC0000_1124	<i>cydA</i>					1	1	Cytochrome d terminal oxidase, subunit I	
BAA196NC_3030	HMPRNC0000_1313	<i>sucD</i>	1			-1		-1	Succinyl-CoA synthetase subunit alpha	
BAA196NC_3031	HMPRNC0000_1312	<i>sucC</i>	1	-1	-1	-1		-1	Succinyl-CoA synthetase subunit beta	
BAA196NC_3032	HMPRNC0000_1519	<i>sucB</i>	1	-1	-1	-1		-1	Dihydrolipoamide acetyltransferase	
BAA196NC_3033	HMPRNC0000_1520	<i>sucA</i>	1		-1	-1		-1	Alpha-ketoglutarate decarboxylase	
BAA196NC_3034	HMPRNC0000_1198	<i>sdhB</i>	1		-1	-1		-1	Succinate dehydrogenase, FeS subunit	
BAA196NC_3035	HMPRNC0000_1197	<i>sdhA</i>	1	1	-1	-1		-1	Succinate dehydrogenase flavoprotein subunit	
BAA196NC_3037	HMPRNC0000_1195	<i>sdhC</i>			-1	-1			Succinate dehydrogenase cytochrome b556 large membrane subunit	
BAA196NC_3046	HMPRNC0000_1739	<i>ybgK</i>	1						Predicted enzyme subunit	
BAA196NC_3047	HMPRNC0000_1740	<i>ybgJ</i>		1					Predicted enzyme subunit	
BAA196NC_3050	HMPRNC0000_0760	<i>phr</i>				-1		-1	Deoxyribodipyrimidine photolyase, FAD-binding	
BAA196NC_3061	HMPRNC0000_2263	<i>kdpB</i>						-1	1 Potassium-transporting ATPase subunit B	
BAA196NC_3062	HMPRNC0000_2262	<i>kdpC</i>						-1	1 Potassium-transporting ATPase subunit C	
BAA196NC_3064	HMPRNC0000_2267	<i>kdpE</i>						-1	DNA-binding response regulator in two-component regulatory system with KdpD	
BAA196NC_3080	HMPRNC0000_2816	<i>nagE</i>							-1 Fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB , and IIA components	
BAA196NC_3088	HMPRNC0000_1359	<i>miaB</i>		1					Isopentenyl-adenosine A37 tRNA methylthiolase	
BAA196NC_3098	HMPRNC0000_0263	<i>rihA</i>		-1					Ribonucleoside hydrolase 1	
BAA196NC_3107	HMPRNC0000_1903	<i>leuS</i>					1	1	Leucyl-tRNA synthetase	
BAA196NC_3115	HMPRNC0000_2703	<i>mrdB</i>				-1		-1	Cell wall shape-determining protein	
BAA196NC_3126	HMPRNC0000_1509	<i>cspE</i>	-1			-1		-1	-1 Cold shock protein E	
BAA196NC_3143	HMPRNC0000_0424	<i>ahpF</i>		1					1 Alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding	
BAA196NC_3160	HMPRNC0000_0710	<i>fepD</i>				1			Iron-enterobactin transporter subunit	
BAA196NC_3162	HMPRNC0000_0708	<i>fepC</i>				1	1		Iron-enterobactin transporter subunit	
BAA196NC_3175	HMPRNC0000_2797	<i>nfnB</i>					1	1	1 Dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive	
BAA196NC_3229	HMPRNC0000_0573	<i>cysS</i>		1			1		CysteinyI-tRNA synthetase	
BAA196NC_3230	HMPRNC0000_0984	<i>ppiB</i>				1	1		-1 Peptidyl-prolyl cis-trans isomerase B (rotamase B)	
BAA196NC_3232	HMPRNC0000_1099	<i>purE</i>				-1	-1	-1	-1 Phosphoribosylaminoimidazole carboxylase catalytic subunit	
BAA196NC_3233	HMPRNC0000_1100	<i>purK</i>		-1		-1		-1	Phosphoribosylaminoimidazole carboxylase	
BAA196NC_3241	HMPRNC0000_2704	<i>glxK</i>							-1 Glycerate kinase II	
BAA196NC_3243	HMPRNC0000_1254	<i>allB</i>				-1	1	-1	1 Allantoinase	
BAA196NC_3262	HMPRNC0000_2727	<i>ybbM</i>					-1	-1	putative iron export permease protein FetB	
BAA196NC_3269	HMPRNC0000_2838	<i>capA</i>	1	1	1	1	1	1	1 Copper transporter	
BAA196NC_3285	HMPRNC0000_1767	<i>apt</i>					1		Adenine phosphoribosyltransferase	
BAA196NC_3314	HMPRNC0000_1588	<i>hupB</i>			-1		-1	-1	1 HU, DNA-binding transcriptional regulator, beta subunit	
BAA196NC_3317	HMPRNC0000_0856	<i>clpP</i>					1	1	1 ATP-dependent Clp protease proteolytic subunit	
BAA196NC_3324	HMPRNC0000_1094	<i>cyoB</i>	1	1		-1			Cytochrome o ubiquinol oxidase subunit I	
BAA196NC_3327	HMPRNC0000_1158	<i>cyoE</i>	1	1					Protoheme IX farnesyltransferase	
BAA196NC_3349	HMPRNC0000_1770	<i>tgt</i>					1	1	Queuine tRNA-ribosyltransferase	
BAA196NC_3354	HMPRNC0000_0191	<i>brnQ</i>				-1		-1	Predicted branched chain amino acid transporter (LIV-II)	
BAA196NC_3356	HMPRNC0000_1610	<i>phoB</i>		1			-1		DNA-binding response regulator in two-component regulatory system with PhoR (or CreC)	
BAA196NC_3366	HMPRNC0000_1666	<i>arol</i>				-1	-1	-1	-1 Shikimate kinase II	
BAA196NC_3387	HMPRNC0000_1796	<i>hemB</i>		1	1				Delta-aminolevulinic acid dehydratase	
BAA196NC_3399	HMPRNC0000_2275	<i>frmR</i>				1			Regulator protein that represses frmRAB operon	
BAA196NC_3423	HMPRNC0000_1826	<i>prpC</i>				-1		-1	1 2-methylcitrate synthase	
BAA196NC_3442	HMPRNC0000_2404	<i>betT</i>		1					-1 Choline transporter of high affinity	
BAA196NC_3444	HMPRNC0000_2903	<i>betB</i>						-1	Betaine aldehyde dehydrogenase, NAD-dependent	
BAA196NC_3459	HMPRNC0000_2315	<i>ykgM</i>		1		-1			50S ribosomal protein L31	
BAA196NC_3510	HMPRNC0000_2080	<i>dinB</i>					1	1	DNA polymerase IV	
BAA196NC_3522	HMPRNC0000_2205	<i>yafV</i>					1	1	Predicted C-N hydrolase family amidase, NAD(P)-binding	
BAA196NC_3536	HMPRNC0000_0477	<i>metN</i>					1	1	DL-methionine transporter subunit	
BAA196NC_3537	HMPRNC0000_0478	<i>metI</i>					1	1	DL-methionine transporter subunit	
BAA196NC_3538	HMPRNC0000_0479	<i>metQ</i>					1	1	DL-methionine transporter subunit	
BAA196NC_3541	HMPRNC0000_1327	<i>proS</i>					1	1	Prolyl-tRNA synthetase	
BAA196NC_3556	HMPRNC0000_2291	<i>fabZ</i>		1	1				(3R)-hydroxymyristoyl ACP dehydratase	
BAA196NC_3565	HMPRNC0000_1323	<i>frr</i>				-1			Ribosome releasing factor	
BAA196NC_3566	HMPRNC0000_1322	<i>pyrH</i>		1		-1		-1	Uridylate kinase	
BAA196NC_3571	HMPRNC0000_2072	<i>map</i>							-1 Methionine aminopeptidase	
BAA196NC_3582	HMPRNC0000_0965	<i>yadR</i>		1		1	1	1	Hypothetical protein	
BAA196NC_3604	HMPRNC0000_2886	<i>panB</i>				1	1		3-methyl-2-oxobutanoate hydroxymethyltransferase	
BAA196NC_3605	HMPRNC0000_2885	<i>panC</i>				1	1		Pantoate--beta-alanine ligase	
BAA196NC_3633	HMPRNC0000_1433	<i>guaC</i>						-1	Guanosine 5'-monophosphate oxidoreductase	
BAA196NC_3634	HMPRNC0000_1816	<i>coaE</i>				1	1	1	Dephospho-CoA kinase	
BAA196NC_3647	HMPRNC0000_1154	<i>ftsW</i>	-1		-1				Integral membrane protein involved in stabilizing FtsZ ring during cell division	
BAA196NC_3648	HMPRNC0000_1232	<i>murD</i>				-1		-1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	
BAA196NC_3649	HMPRNC0000_1231	<i>mraY</i>				-1		-1	Phospho-N-acetylmuramoyl-pentapeptide- transferase	
BAA196NC_3650	HMPRNC0000_2269	<i>murF</i>						-1	UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D- alanine ligase	

BAA196NC_3651	HMPRNC0000_1053	<i>murE</i>										UDP-N-acetylmuramoylanyl-D-glutamate--2, 6-diaminopimelate ligase
BAA196NC_3654	HMPRNC0000_1229	<i>mraW</i>										S-adenosyl-methyltransferase
BAA196NC_3655	HMPRNC0000_1228	<i>mraZ</i>										Hypothetical protein
BAA196NC_3658	HMPRNC0000_2233	<i>ilvI</i>										Acetolactate synthase III large subunit
BAA196NC_3660	HMPRNC0000_2236	<i>leuA</i>										2-isopropylmalate synthase
BAA196NC_3661	HMPRNC0000_2239	<i>leuB</i>										3-isopropylmalate dehydrogenase
BAA196NC_3662	HMPRNC0000_2240	<i>leuC</i>										Isopropylmalate isomerase large subunit
BAA196NC_3684	HMPRNC0000_0515	<i>ksgA</i>										Dimethyladenosine transferase
BAA196NC_3688	HMPRNC0000_1043	<i>kefC</i>										Glutathione-regulated potassium-efflux system protein
BAA196NC_3703	HMPRNC0000_1256	<i>carB</i>										Carbamoyl-phosphate synthase large subunit
BAA196NC_3704	HMPRNC0000_1255	<i>carA</i>										Carbamoyl-phosphate synthase small subunit
BAA196NC_3712	HMPRNC0000_1716	<i>rpsT</i>										30S ribosomal protein S20
BAA196NC_3720	HMPRNC0000_1708	<i>dnaJ</i>										Chaperone Hsp40, co-chaperone with DnaK
BAA196NC_3731	HMPRNC0000_1425	<i>thrB</i>										Homoserine kinase
BAA196NC_3740	HMPRNC0000_0892	<i>ytjC</i>										Phosphoglycerate mutase
BAA196NC_3744	HMPRNC0000_0794	<i>yjjK</i>										Fused predicted transporter subunits of ABC superfamily: ATP-binding components
BAA196NC_3752	HMPRNC0000_2339	<i>deoD</i>										Purine nucleoside phosphorylase
BAA196NC_3753	HMPRNC0000_0135	<i>deoB</i>										Phosphopentomutase
BAA196NC_3783	HMPRNC0000_0463	<i>yjiA</i>										Predicted GTPase
BAA196NC_3845	HMPRNC0000_2771	<i>yjhF</i>										KpLE2 phage-like element; predicted transporter
BAA196NC_3880	HMPRNC0000_1788	<i>valS</i>										Valyl-tRNA synthetase
BAA196NC_3891	HMPRNC0000_1253	<i>pyrB</i>										Aspartate carbamoyltransferase catalytic subunit
BAA196NC_3893	HMPRNC0000_0519	<i>yjgF</i>										Ketoacid-binding protein
BAA196NC_3896	HMPRNC0000_2632	<i>treB</i>										Fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component
BAA196NC_3897	HMPRNC0000_0491	<i>treC</i>										Trehalose-6-P hydrolase
BAA196NC_3898	HMPRNC0000_2908	<i>nrdD</i>										Anaerobic ribonucleoside triphosphate reductase
BAA196NC_3903	HMPRNC0000_1885	<i>murC</i>										UDP-N-acetylmuramate--L-alanine ligase
BAA196NC_3926	HMPRNC0000_2710	<i>cycA</i>										D-alanine/D-serine/glycine transporter
BAA196NC_3938	HMPRNC0000_0619	<i>ulaD</i>										3-keto-L-gulonate 6-phosphate decarboxylase
BAA196NC_3954	HMPRNC0000_0575	<i>rlmB</i>										23S rRNA (Gm2251)-methyltransferase
BAA196NC_3955	HMPRNC0000_0870	<i>rrn</i>										Exoribonuclease R, RNase R
BAA196NC_3957	HMPRNC0000_0018	<i>purA</i>										Adenylosuccinate synthetase
BAA196NC_3961	HMPRNC0000_1373	<i>hflX</i>										Predicted GTPase
BAA196NC_3977	HMPRNC0000_1197	<i>frdA</i>										Fumarate reductase
BAA196NC_3978	HMPRNC0000_1198	<i>frdB</i>										Fumarate reductase (anaerobic), Fe-S subunit
BAA196NC_3986	HMPRNC0000_1654	<i>efp</i>										Elongation factor P
BAA196NC_3990	HMPRNC0000_2200	<i>groL</i>										Chaperonin GroEL
BAA196NC_3991	HMPRNC0000_2201	<i>groS</i>										Co-chaperonin GroES
BAA196NC_4003	HMPRNC0000_0543	<i>lysU</i>										Lysine tRNA synthetase, inducible
BAA196NC_4006	HMPRNC0000_2794	<i>yjdJ</i>										Predicted acyltransferase with acyl-CoA N-acyltransferase domain
BAA196NC_4026	HMPRNC0000_2879	<i>phnB</i>										Hypothetical protein
BAA196NC_4057	HMPRNC0000_2640	<i>gltP</i>										Glutamate/aspartate:proton symporter
BAA196NC_4065	HMPRNC0000_1877	<i>acs</i>										Acetyl-coenzyme A synthetase
BAA196NC_4078	HMPRNC0000_0843	<i>uvrA</i>										Excinuclease ABC subunit A
BAA196NC_4095	HMPRNC0000_1436	<i>lexA</i>										LexA repressor
BAA196NC_4104	HMPRNC0000_0229	<i>malE</i>										Maltose ABC transporter periplasmic protein
BAA196NC_4106	HMPRNC0000_0231	<i>malG</i>										Maltose transporter subunit
BAA196NC_4128	HMPRNC0000_1111	<i>purH</i>										Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP
BAA196NC_4129	HMPRNC0000_1112	<i>purD</i>										cyclohydrolase
BAA196NC_4134	HMPRNC0000_1588	<i>hupA</i>										Phosphoribosylamine--glycine ligase
BAA196NC_4137	HMPRNC0000_1977	<i>hemE</i>										HU, DNA-binding transcriptional regulator, alpha subunit
BAA196NC_4141	HMPRNC0000_2282	<i>thiE</i>										Uroporphyrinogen decarboxylase
BAA196NC_4148	HMPRNC0000_0585	<i>rpoB</i>										Thiamine-phosphate pyrophosphorylase
BAA196NC_4150	HMPRNC0000_0582	<i>rplJ</i>										DNA-directed RNA polymerase subunit beta
BAA196NC_4151	HMPRNC0000_0581	<i>rplA</i>										50S ribosomal protein L10
BAA196NC_4152	HMPRNC0000_0580	<i>rplK</i>										50S ribosomal protein L1
BAA196NC_4153	HMPRNC0000_0579	<i>nusG</i>										50S ribosomal protein L11
BAA196NC_4168	HMPRNC0000_0990	<i>argH</i>										Transcription antitermination protein NusG
BAA196NC_4171	HMPRNC0000_2193	<i>dapE</i>										Argininosuccinate lyase
BAA196NC_4188	HMPRNC0000_0476	<i>metB</i>										Acetylornithine deacetylase
BAA196NC_4192	HMPRNC0000_1267	<i>priA</i>										Cystathionine gamma-synthase
BAA196NC_4195	HMPRNC0000_1317	<i>hslV</i>										Primosome assembly protein PriA
BAA196NC_4196	HMPRNC0000_1318	<i>hslU</i>										ATP-dependent protease peptidase subunit
BAA196NC_4197	HMPRNC0000_1072	<i>menA</i>										ATP-dependent protease ATP-binding subunit
BAA196NC_4200	HMPRNC0000_1366	<i>glpF</i>										1,4-dihydroxy-2-naphthoate octaprenyltransferase
BAA196NC_4201	HMPRNC0000_1367	<i>glpK</i>										Glycerol facilitator
BAA196NC_4208	HMPRNC0000_0863	<i>tpiA</i>										Glycerol kinase
BAA196NC_4216	HMPRNC0000_2578	<i>yjiM</i>										Triosephosphate isomerase
BAA196NC_4218	HMPRNC0000_1682	<i>sodA</i>										Hypothetical protein
BAA196NC_4229	HMPRNC0000_2729	<i>frvX</i>										Superoxide dismutase, Mn
BAA196NC_4232	HMPRNC0000_2501	<i>fdhD</i>										Predicted endo-1,4-beta-glucanase
BAA196NC_4259	HMPRNC0000_1379	<i>glnA</i>										Formate dehydrogenase accessory protein
BAA196NC_4265	HMPRNC0000_1801	<i>yihA</i>										Glutamine synthetase
BAA196NC_4267	HMPRNC0000_1818	<i>polA</i>										GTP-binding protein
BAA196NC_4295	HMPRNC0000_0398	<i>metE</i>										DNA polymerase I
												5-methyltetrahydropteroyltryglutamate-- homocysteine methyltransferase

BAA196NC_4301	HMPRNC0000_0795	<i>recQ</i>		-1	1				ATP-dependent DNA helicase
BAA196NC_4309	HMPRNC0000_2089	<i>uvrD</i>		-1					DNA-dependent ATPase I and helicase II
BAA196NC_4318	HMPRNC0000_1798	<i>hemC</i>			1	1	1		Porphobilinogen deaminase
BAA196NC_4335	HMPRNC0000_2303	<i>rffE</i>			-1				UDP-N-acetyl glucosamine-2-epimerase
BAA196NC_4340	HMPRNC0000_1193	<i>trxA</i>	1		1			1	Thioredoxin
BAA196NC_4349	HMPRNC0000_2231	<i>ilvD</i>			1		1		Dihydroxy-acid dehydratase
BAA196NC_4357	HMPRNC0000_2597	<i>hsrA</i>						1	Predicted multidrug or homocysteine efflux system
BAA196NC_4359	HMPRNC0000_0289	<i>rbsK</i>		-1					Ribokinase
BAA196NC_4363	HMPRNC0000_0290	<i>rbsD</i>	-1	-1					Predicted cytoplasmic sugar-binding protein
BAA196NC_4370	HMPRNC0000_3027	<i>gidA</i>			1	1		1	Glucose-inhibited division protein A
BAA196NC_4373	HMPRNC0000_2301	<i>atpB</i>			-1				F0F1 ATP synthase subunit A
BAA196NC_4375	HMPRNC0000_2299	<i>atpF</i>	1		-1		-1		F0F1 ATP synthase subunit B
BAA196NC_4377	HMPRNC0000_2297	<i>atpA</i>	1		-1		-1		F0F1 ATP synthase subunit alpha
BAA196NC_4378	HMPRNC0000_2296	<i>atpG</i>	1						F0F1 ATP synthase subunit gamma
BAA196NC_4379	HMPRNC0000_2295	<i>atpD</i>	1					-1	F0F1 ATP synthase subunit beta
BAA196NC_4380	HMPRNC0000_2294	<i>atpC</i>			-1		-1		F0F1 ATP synthase subunit epsilon
BAA196NC_4381	HMPRNC0000_0521	<i>glmU</i>						1	Bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase
BAA196NC_4387	HMPRNC0000_1486	<i>phoU</i>	1						Negative regulator of PhoR/PhoB two-component regulator
BAA196NC_4405	HMPRNC0000_3029	<i>trmE</i>			1	1	1	1	TRNA modification GTPase
BAA196NC_4478	HMPRNC0000_2586	.						-1	Sodium/glutamate symporter
BAA196NC_0005	NA	<i>yidB</i>			1				Hypothetical protein
BAA196NC_0017	NA	<i>ibpA</i>	1		1				Heat shock chaperone
BAA196NC_0018	NA	<i>ibpB</i>			1				Heat shock chaperone
BAA196NC_0034	NA	<i>uhpA</i>			-1				DNA-binding response regulator in two-component regulatory system with UhpB
BAA196NC_0055	NA	<i>rpoZ</i>			1				DNA-directed RNA polymerase subunit omega
BAA196NC_0060	NA	<i>yicC</i>		-1		1			Hypothetical protein
BAA196NC_0067	NA	<i>rpmB</i>		-1	-1				50S ribosomal protein L28
BAA196NC_0077	NA	.						-1	Lipopolysaccharide 1,6-galactosyltransferase
BAA196NC_0090	NA	<i>tdh</i>	1	1	1				L-threonine 3-dehydrogenase
BAA196NC_0106	NA	<i>mtlR</i>		-1					DNA-binding repressor
BAA196NC_0139	NA	<i>bax</i>						1	Hypothetical protein
BAA196NC_0155	NA	<i>cspA</i>	-1	-1	-1	-1	-1	-1	Major cold shock protein
BAA196NC_0156	NA	<i>yiaG</i>						1	Predicted transcriptional regulator
BAA196NC_0157	NA	<i>yiaF</i>		-1				1	Hypothetical protein
BAA196NC_0164	NA	<i>yhjX</i>					-1		Predicted transporter
BAA196NC_0188	NA	<i>kdgK</i>						1	Ketodeoxygluconokinase
BAA196NC_0198	NA	<i>gadX</i>		-1				1	DNA-binding transcriptional dual regulator
BAA196NC_0201	NA	<i>gadW</i>		-1					DNA-binding transcriptional activator
BAA196NC_0203	NA	<i>mdtE</i>	1		-1				Multidrug resistance efflux transporter
BAA196NC_0205	NA	<i>gadE</i>						1	DNA-binding transcriptional activator
BAA196NC_0206	NA	<i>hdeD</i>						1	Acid-resistance membrane protein
BAA196NC_0208	NA	<i>hdeB</i>		-1				1	Acid-resistance protein
BAA196NC_0209	NA	<i>yhiD</i>		-1					Predicted Mg(2+) transport ATPase inner membrane protein
BAA196NC_0211	NA	<i>slp</i>						1	Outer membrane lipoprotein
BAA196NC_0217	NA	<i>gorA</i>			1				Glutathione reductase
BAA196NC_0223	NA	<i>yhiO</i>						1	Universal stress protein UspB
BAA196NC_0226	NA	<i>yhiM</i>						1	Conserved inner membrane protein
BAA196NC_0257	NA	<i>rpoH</i>			1			1	RNA polymerase sigma factor
BAA196NC_0281	NA	<i>yhhW</i>	1	1	1	1	1	1	Quercetin 2,3-dioxygenase
BAA196NC_0282	NA	<i>gntR</i>			1				DNA-binding transcriptional repressor
BAA196NC_0290	NA	<i>glgA</i>						-1	Glycogen synthase
BAA196NC_0302	NA	<i>malQ</i>						-1	4-alpha-glucanotransferase (amylomaltase)
BAA196NC_0322	NA	<i>nudE</i>						1	ADP-ribose diphosphatase
BAA196NC_0329	NA	<i>aroK</i>						1	Shikimate kinase I
BAA196NC_0358	NA	<i>fic</i>						-1	Stationary-phase protein, cell division
BAA196NC_0363	NA	<i>yhfA</i>						1	Hypothetical protein
BAA196NC_0381	NA	<i>tufA</i>			-1				Protein chain elongation factor EF-Tu (duplicate of tufB)
BAA196NC_0384	NA	<i>bfr</i>		-1	-1	-1			Bacterioferritin, iron storage and detoxification protein
BAA196NC_0427	NA	<i>yhdN</i>						1	Hypothetical protein
BAA196NC_0429	NA	<i>yhdL</i>						1	Hypothetical protein
BAA196NC_0454	NA	<i>dusB</i>	-1					-1	tRNA-dihydrouridine synthase B
BAA196NC_0464	NA	<i>mreC</i>						-1	Cell wall structural complex MreBCD transmembrane component MreC
BAA196NC_0474	NA	<i>yhcO</i>		-1					Predicted barnase inhibitor
BAA196NC_0475	NA	<i>yhcN</i>						1	Hypothetical protein
BAA196NC_0514	NA	<i>kdsC</i>						-1	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
BAA196NC_0519	NA	<i>yrbD</i>			1				Predicted ABC-type organic solvent transporter
BAA196NC_0523	NA	<i>murA</i>						1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
BAA196NC_0528	NA	<i>yhbE</i>						1	Conserved inner membrane protein
BAA196NC_0532	NA	<i>greA</i>						1	Transcription elongation factor GreA
BAA196NC_0538	NA	<i>secG</i>						1	Protein-export membrane protein
BAA196NC_0547	NA	<i>rpsO</i>			1				30S ribosomal protein S15
BAA196NC_0550	NA	<i>deaD</i>						-1	ATP-dependent RNA helicase
BAA196NC_0558	NA	<i>yhbP</i>						1	Hypothetical protein
BAA196NC_0582	NA	<i>yhaV</i>		-1		-1			Hypothetical protein
BAA196NC_0589	NA	<i>yhaC</i>						-1	Uncharacterized protein
BAA196NC_0593	NA	<i>tdcA</i>						-1	DNA-binding transcriptional activator
BAA196NC_0595	NA	<i>tdcC</i>						-1	L-threonine/L-serine transporter

BAA196NC_0596	NA	<i>tdcD</i>		-1	-1	Propionate kinase/acetate kinase C, anaerobic
BAA196NC_0597	NA	<i>tdcE</i>		-1	-1	Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase
BAA196NC_0598	NA	<i>tdcF</i>			-1	Predicted L-PSP (mRNA) endoribonuclease
BAA196NC_0601	NA	<i>yhaM</i>		1	-1	Hypothetical protein
BAA196NC_0608	NA	<i>yqjF</i>	1		1	Predicted quinol oxidase subunit
BAA196NC_0610	NA	<i>yqjE</i>		1		Conserved inner membrane protein
BAA196NC_0623	NA	<i>yqjR</i>		-1	-1	Predicted NAD(P)-binding dehydrogenase
BAA196NC_0629	NA	<i>fadH</i>		-1	-1	2,4-dienoyl-CoA reductase, NADH and FMN-linked
BAA196NC_0643	NA	<i>rpoD</i>	1	1		RNA polymerase sigma factor
BAA196NC_0644	NA	<i>dnaG</i>			1	DNA primase
BAA196NC_0645	NA	<i>rpsU</i>		-1	1	30S ribosomal protein S21
BAA196NC_0664	NA	<i>glgS</i>		-1		Glycogen synthesis protein GlgS
BAA196NC_0671	NA	<i>yqiC</i>		-1	-1	Hypothetical protein
BAA196NC_0675	NA	<i>zupT</i>		1	1	Predicted dioxygenase
BAA196NC_0684	NA	<i>ygiN</i>		-1		Quinol monoxygenase
BAA196NC_0689	NA	<i>ygiV</i>			1	Predicted transcriptional regulator
BAA196NC_0700	NA	<i>yqhD</i>	1	1		Alcohol dehydrogenase, NAD(P)-dependent
BAA196NC_0704	NA	<i>exbB</i>			1	Membrane spanning protein in TonB-ExbB-ExbD complex
BAA196NC_0708	NA	<i>yghZ</i>			-1	Aldo-keto reductase
BAA196NC_0713	NA	<i>hybO</i>			-1	Hydrogenase 2, small subunit
BAA196NC_0714	NA	<i>hybA</i>			-1	Hydrogenase 2 4Fe-4S ferredoxin-type component
BAA196NC_0716	NA	<i>hybC</i>			-1	Hydrogenase 2, large subunit
BAA196NC_0732	NA	<i>glcD</i>	1			Glycolate oxidase subunit, FAD-linked
BAA196NC_0733	NA	<i>glcE</i>	1	1		Glycolate oxidase FAD binding subunit
BAA196NC_0734	NA	<i>glcF</i>	1	1		Glycolate oxidase iron-sulfur subunit
BAA196NC_0735	NA	<i>glcG</i>	1			Hypothetical protein
BAA196NC_0736	NA	<i>glcB</i>	1	1		Malate synthase
BAA196NC_0746	NA	<i>nupG</i>			1	Nucleoside transporter
BAA196NC_0751	NA	<i>yggL</i>		-1		Hypothetical protein
BAA196NC_0753	NA	<i>ansB</i>		-1	-1	Periplasmic L-asparaginase II
BAA196NC_0762	NA	<i>yqgE</i>			1	Hypothetical protein
BAA196NC_0774	NA	<i>tktA</i>	1			Transketolase 1, thiamin-binding
BAA196NC_0784	NA	<i>mscS</i>			1	Mechanosensitive channel
BAA196NC_0786	NA	<i>yggE</i>	1		1	Hypothetical protein
BAA196NC_0798	NA	<i>gcvH</i>	1	1	1	Glycine cleavage system protein H
BAA196NC_0801	NA	<i>pepP</i>			-1	Proline aminopeptidase P II
BAA196NC_0802	NA	<i>ubiH</i>	1			2-octaprenyl-6-methoxyphenyl hydroxylase
BAA196NC_0803	NA	<i>visC</i>			-1	Hypothetical protein
BAA196NC_0807	NA	<i>yjff</i>			-1	Predicted NAD(P)-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain
BAA196NC_0811	NA	<i>yjzZ</i>		1	1	Putative global regulator
BAA196NC_0839	NA	<i>ygeV</i>			-1	Predicted DNA-binding transcriptional regulator
BAA196NC_0876	NA	<i>ygdR</i>		-1	-1	Hypothetical protein
BAA196NC_0889	NA	<i>recC</i>			-1	Exonuclease V (RecBCD complex), gamma chain
BAA196NC_0890	NA	<i>ptr</i>			1	Protease III
BAA196NC_0899	NA	<i>ygdI</i>		-1	1	Hypothetical protein
BAA196NC_0900	NA	<i>fucK</i>		-1		L-fuculokinase
BAA196NC_0913	NA	<i>sdaC</i>			1	Predicted serine transporter
BAA196NC_0914	NA	<i>ygdH</i>			-1	Hypothetical protein
BAA196NC_0927	NA	<i>chpR</i>			1	Antitoxin of the ChpA-ChpR toxin-antitoxin system
BAA196NC_0959	NA	<i>cysD</i>		1		Sulfate adenyllyltransferase subunit 2
BAA196NC_0966	NA	<i>truD</i>	1			tRNA pseudouridine synthase D
BAA196NC_0969	NA	<i>nlpD</i>	1	1		Predicted outer membrane lipoprotein
BAA196NC_0970	NA	<i>rpoS</i>	1		1	RNA polymerase sigma factor
BAA196NC_0983	NA	<i>hypD</i>			-1	Protein required for maturation of hydrogenases
BAA196NC_0985	NA	<i>hypB</i>			-1	GTP hydrolase involved in nickel liganding into hydrogenases
BAA196NC_1004	NA	<i>norR</i>			1	Anaerobic nitric oxide reductase transcription regulator
BAA196NC_1017	NA	<i>csrA</i>		-1	-1	Carbon storage regulator
BAA196NC_1031	NA	<i>proX</i>	1			Glycine betaine transporter subunit
BAA196NC_1040	NA	<i>ygaW</i>			1	Predicted inner membrane protein
BAA196NC_1044	NA	<i>yqaE</i>			1	Predicted membrane protein
BAA196NC_1046	NA	<i>csiR</i>			1	DNA-binding transcriptional dual regulator
BAA196NC_1049	NA	<i>gabD</i>			-1	Succinate-semialdehyde dehydrogenase I, NADP-dependent
BAA196NC_1051	NA	<i>ygaT</i>	1			Hypothetical protein
BAA196NC_1082	NA	<i>yjff</i>	-1	-1		Uncharacterized protein
BAA196NC_1104	NA	<i>pheA</i>			1	Fused chorismate mutase P/prephenate dehydratase
BAA196NC_1105	NA	<i>yfiA</i>		-1	-1	Cold shock protein associated with 30S ribosomal subunit
BAA196NC_1113	NA	<i>yfiQ</i>			-1	Fused predicted acyl-CoA synthetase: NAD(P)-binding subunit/ATP-binding subunit
BAA196NC_1115	NA	<i>trxC</i>			1	Thioredoxin 2
BAA196NC_1118	NA	<i>yfiD</i>	-1	-1	-1	Pyruvate formate lyase subunit
BAA196NC_1124	NA	<i>rpoE</i>			1	RNA polymerase, sigma 24 (sigma E) factor
BAA196NC_1126	NA	<i>rseB</i>		1		Periplasmic negative regulator of sigmaE
BAA196NC_1133	NA	<i>pdxI</i>			1	Pyridoxal phosphate biosynthetic protein
BAA196NC_1137	NA	<i>yfhB</i>			1	Hypothetical protein
BAA196NC_1141	NA	<i>purl</i>		-1		Phosphoribosylformylglycinamide synthase
BAA196NC_1145	NA	<i>glnB</i>			1	Regulatory protein P-II for glutamine synthetase
BAA196NC_1168	NA	<i>iscS</i>	1	1		Cysteine desulfurase
BAA196NC_1175	NA	<i>pepB</i>		1		Aminopeptidase B
BAA196NC_1223	NA	<i>nlpB</i>	1			Lipoprotein

BAA196NC_1237	NA	<i>talA</i>	1			Transaldolase A
BAA196NC_1238	NA	<i>maeB</i>	1	1		Malic enzyme
BAA196NC_1261	NA	<i>eutC</i>			-1	Ethanolamine ammonia-lyase small subunit
BAA196NC_1275	NA	<i>ucpA</i>		-1	-1	Short chain dehydrogenase
BAA196NC_1300	NA	<i>yfeC</i>			-1	Predicted DNA-binding transcriptional regulator
BAA196NC_1318	NA	<i>yfdY</i>			1	Predicted inner membrane protein
BAA196NC_1325	NA	<i>evgS</i>	-1		-1	Hybrid sensory histidine kinase in two-component regulatory system with EvgA
BAA196NC_1351	NA	<i>yfcZ</i>	-1		-1	Hypothetical protein
BAA196NC_1352	NA	<i>yfcY</i>			-1	Acetyl-CoA acetyltransferase
BAA196NC_1354	NA	<i>sixA</i>			1	Phosphohistidine phosphatase
BAA196NC_1364	NA	<i>yfcN</i>	-1			Hypothetical protein
BAA196NC_1372	NA	<i>fabB</i>			1	3-oxoacyl-(acyl carrier protein) synthase
BAA196NC_1375	NA	<i>flk</i>			-1	Predicted flagella assembly protein
BAA196NC_1383	NA	<i>cvpA</i>	1	1		Membrane protein required for colicin V production
BAA196NC_1399	NA	<i>pta</i>		1	-1	Phosphate acetyltransferase
BAA196NC_1401	NA	<i>yfbV</i>	-1		-1	Hypothetical protein
BAA196NC_1402	NA	<i>yfbU</i>			1	Hypothetical protein
BAA196NC_1404	NA	<i>yfbS</i>			-1	Predicted transporter
BAA196NC_1407	NA	<i>irhA</i>	-1		1	DNA-binding transcriptional repressor of flagellar, motility and chemotaxis genes
BAA196NC_1411	NA	<i>nuoC</i>			-1	NADH:ubiquinone oxidoreductase, chain C,D
BAA196NC_1412	NA	<i>nuoE</i>			-1	NADH dehydrogenase subunit E
BAA196NC_1414	NA	<i>nuoG</i>			-1	NADH dehydrogenase subunit G
BAA196NC_1431	NA	<i>elaB</i>	-1	-1	-1	Hypothetical protein
BAA196NC_1432	NA	<i>menF</i>			-1	Menaquinone-specific isochorismate synthase
BAA196NC_1437	NA	<i>menE</i>			-1	O-succinylbenzoic acid--CoA ligase
BAA196NC_1438	NA	<i>pmrD</i>			-1	Polymyxin resistance protein B
BAA196NC_1483	NA	<i>rcsD</i>			-1	Phosphotransfer intermediate protein in two-component regulatory system with RcsBC
BAA196NC_1485	NA	<i>ompC</i>	-1		-1	Outer membrane porin protein C
BAA196NC_1495	NA	<i>napA</i>			-1	Nitrate reductase, periplasmic, large subunit
BAA196NC_1496	NA	<i>napG</i>			-1	Quinol dehydrogenase periplasmic component
BAA196NC_1499	NA	<i>napC</i>			-1	Nitrate reductase, cytochrome c-type, periplasmic
BAA196NC_1524	NA	<i>spr</i>			1	Predicted peptidase, outer membrane lipoprotein
BAA196NC_1560	NA	<i>cdd</i>	-1			Cytidine deaminase
BAA196NC_1575	NA	<i>yehX</i>			-1	Predicted transporter subunit: ATP-binding component of ABC superfamily
BAA196NC_1609	NA	<i>gatZ</i>	-1		-1	D-tagatose 1,6-bisphosphate aldolase 2, subunit
BAA196NC_1634	NA	<i>yegK</i>			1	Uncharacterized protein
BAA196NC_1635	NA	<i>yegJ</i>			1	Uncharacterized protein
BAA196NC_1667	NA	<i>galF</i>			1	Predicted subunit with GalU
BAA196NC_1669	NA	<i>rfbD</i>	-1			DTDP-4-dehydrorhamnose reductase subunit, NAD(P)-binding, of dTDP-L-rhamnose synthase
BAA196NC_1702	NA	<i>yeeX</i>			-1	Hypothetical protein
BAA196NC_1709	NA	<i>flu</i>			-1	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter
BAA196NC_1733	NA	<i>yedY</i>			1	Hypothetical protein
BAA196NC_1745	NA	<i>yodC</i>			1	Hypothetical protein
BAA196NC_1749	NA	<i>yodD</i>	-1		-1	Hypothetical protein
BAA196NC_1750	NA	<i>dsrB</i>	-1		-1	Hypothetical protein
BAA196NC_1791	NA	<i>yecH</i>	-1		1	Hypothetical protein
BAA196NC_1821	NA	<i>cutC</i>	-1		-1	Copper homeostasis protein
BAA196NC_1824	NA	<i>yecP</i>			-1	Predicted S-adenosyl-L-methionine-dependent methyltransferase
BAA196NC_1826	NA	<i>yecN</i>	-1			Predicted inner membrane protein
BAA196NC_1827	NA	<i>yecE</i>			-1	Hypothetical protein
BAA196NC_1830	NA	<i>nudB</i>			1	DATP pyrophosphohydrolase
BAA196NC_1832	NA	<i>ruvC</i>			1	Holliday junction resolvase
BAA196NC_1847	NA	<i>purT</i>			1	Phosphoribosylglycinamide formyltransferase 2
BAA196NC_1848	NA	<i>yebG</i>			-1	Conserved protein regulated by LexA
BAA196NC_1850	NA	<i>yebE</i>			1	Hypothetical protein
BAA196NC_1862	NA	<i>yebV</i>	-1			Hypothetical protein
BAA196NC_1869	NA	<i>htpX</i>	1	1	1	Heat shock protein HtpX
BAA196NC_1875	NA	<i>yobF</i>	-1	-1	-1	Hypothetical protein
BAA196NC_1876	NA	<i>cspC</i>	-1		-1	Stress protein, member of the CspA-family
BAA196NC_1882	NA	<i>manX</i>			-1	Fused mannose-specific PTS enzymes: IIA component/IIIB component
BAA196NC_1886	NA	<i>sdaA</i>			-1	L-serine deaminase I
BAA196NC_1890	NA	<i>yaaC</i>	-1		-1	Hypothetical protein
BAA196NC_1893	NA	<i>yaaZ</i>			-1	Predicted peptidase
BAA196NC_1895	NA	<i>fadD</i>			-1	Acyl-CoA synthase
BAA196NC_1896	NA	<i>rmd</i>			1	Ribonuclease D
BAA196NC_1905	NA	<i>yaaQ</i>			1	Conserved inner membrane protein
BAA196NC_1913	NA	<i>yaaJ</i>			1	Predicted diguanylate cyclase
BAA196NC_1915	NA	<i>yaaH</i>			-1	Hypothetical protein
BAA196NC_1916	NA	<i>yaaG</i>			-1	Conserved protein with nucleoside triphosphate hydrolase domain
BAA196NC_1917	NA	<i>mipA</i>	1	1		Scaffolding protein for murein synthesizing machinery
BAA196NC_1953	NA	<i>astA</i>			-1	Arginine succinyltransferase
BAA196NC_1954	NA	<i>astD</i>			-1	Succinylglutamic semialdehyde dehydrogenase
BAA196NC_1955	NA	<i>astB</i>			-1	Succinylarginine dihydrolase
BAA196NC_1956	NA	<i>astE</i>			-1	Succinylglutamate desuccinylase



BAA196NC_1962	NA	<i>chbB</i>	-1	-1			N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	
BAA196NC_1971	NA	<i>ydjN</i>			1		Predicted transporter	
BAA196NC_1974	NA	<i>yniB</i>	-1				Predicted inner membrane protein	
BAA196NC_1976	NA	<i>ydjZ</i>	1			1	Hypothetical protein	
BAA196NC_1986	NA	<i>ihfA</i>	-1	-1			Integration host factor subunit alpha	
BAA196NC_1989	NA	<i>btuD</i>				-1	Vitamin B12-transporter ATPase	
BAA196NC_1997	NA	<i>pps</i>	1	1	1		Phosphoenolpyruvate synthase	
BAA196NC_2021	NA	<i>sufD</i>				-1	Component of SufBCD complex	
BAA196NC_2025	NA	<i>lpp</i>	-1	-1	-1	1	-1	Murein lipoprotein
BAA196NC_2027	NA	<i>fumD</i>	-1	-1			Fumarase D	
BAA196NC_2043	NA	<i>purR</i>				1	DNA-binding transcriptional repressor, hypoxanthine-binding	
BAA196NC_2053	NA	<i>ydhM</i>					1	Predicted DNA-binding transcriptional regulator
BAA196NC_2061	NA	<i>slyB</i>			1	1	Outer membrane lipoprotein	
BAA196NC_2084	NA	<i>hadA</i>					1	7-alpha-hydroxysteroid dehydrogenase
BAA196NC_2085	NA	<i>uidR</i>					-1	DNA-binding transcriptional repressor
BAA196NC_2100	NA	<i>pntA</i>	1					NAD(P) transhydrogenase subunit alpha
BAA196NC_2101	NA	<i>pntB</i>	1					Pyridine nucleotide transhydrogenase
BAA196NC_2105	NA	<i>ydgD</i>					1	Predicted peptidase
BAA196NC_2118	NA	<i>ynfC</i>	-1					Hypothetical protein
BAA196NC_2139	NA	<i>relB</i>					1	Qin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin system/ transcriptional repressor
BAA196NC_2141	NA	<i>hokD</i>					1	Qin prophage; small toxic polypeptide
BAA196NC_2146	NA	<i>cspB</i>					-1	Qin prophage; cold shock protein
BAA196NC_2164	NA	<i>dcp</i>	1				1	Dipeptidyl carboxypeptidase II
BAA196NC_2167	NA	<i>ydeH</i>			1			Hypothetical protein
BAA196NC_2170	NA	<i>marB</i>		1				Hypothetical protein
BAA196NC_2171	NA	<i>marA</i>					1	DNA-binding transcriptional dual activator of multiple antibiotic resistance
BAA196NC_2186	NA	<i>lsrB</i>			-1	-1		AI2 transporter
BAA196NC_2188	NA	<i>lsrC</i>	-1	-1				AI2 transporter
BAA196NC_2189	NA	<i>lsrA</i>		-1	-1			Fused AI2 transporter subunits of ABC superfamily: ATP-binding components
BAA196NC_2211	NA	<i>yddV</i>			-1			Predicted diguanylate cyclase
BAA196NC_2221	NA	<i>sra</i>	-1	-1				30S ribosomal subunit protein S22
BAA196NC_2233	NA	<i>narZ</i>					-1	Nitrate reductase 2 (NRZ), alpha subunit
BAA196NC_2234	NA	<i>narY</i>					-1	Nitrate reductase 2 (NRZ), beta subunit
BAA196NC_2250	NA	<i>yncE</i>			1			Hypothetical protein
BAA196NC_2261	NA	<i>ydcT</i>					-1	Predicted spermidine/putrescine transporter subunit
BAA196NC_2262	NA	<i>ydcS</i>					-1	Predicted spermidine/putrescine transporter subunit
BAA196NC_2266	NA	<i>tehB</i>	1	1	1			Putative S-adenosyl-L-methionine-dependent methyltransferase
BAA196NC_2277	NA	<i>ydchH</i>	-1				-1	Hypothetical protein
BAA196NC_2279	NA	<i>ydcl</i>			-1			Hypothetical protein
BAA196NC_2287	NA	<i>ydbD</i>	-1				-1	Uncharacterized protein
BAA196NC_2325	NA	<i>hslJ</i>			-1			Heat-inducible protein
BAA196NC_2326	NA	<i>ydbJ</i>	-1					Hypothetical protein
BAA196NC_2328	NA	<i>ydbK</i>		1				Fused predicted pyruvate-flavodoxin oxidoreductase: conserved protein/conserved protein/FeS binding protein
BAA196NC_2331	NA	<i>uspF</i>			-1	1		Stress-induced protein, ATP-binding protein
BAA196NC_2355	NA	<i>dbpA</i>					-1	ATP-dependent RNA helicase, specific for 23S rRNA
BAA196NC_2359	NA	<i>ycjY</i>			1			Putative hydrolase
BAA196NC_2365	NA	<i>fnr</i>					1	DNA-binding transcriptional dual regulator, global regulator of anaerobic growth
BAA196NC_2392	NA	<i>pspE</i>		1				Thiosulfate:cyanide sulfurtransferase (rhodanese)
BAA196NC_2415	NA	<i>gmr</i>					1	Modulator of Rnase II stability
BAA196NC_2418	NA	<i>osmB</i>	-1		-1			Lipoprotein
BAA196NC_2424	NA	<i>ribA</i>	-1		1			GTP cyclohydrolase II protein
BAA196NC_2429	NA	<i>yciN</i>	-1					Hypothetical protein
BAA196NC_2442	NA	<i>yciG</i>	-1					Hypothetical protein
BAA196NC_2443	NA	<i>yciF</i>					1	Hypothetical protein
BAA196NC_2444	NA	<i>yciE</i>					1	Hypothetical protein
BAA196NC_2445	NA	<i>ompW</i>					-1	Outer membrane protein W
BAA196NC_2464	NA	<i>hns</i>	-1	-1				Global DNA-binding transcriptional dual regulator H-NS
BAA196NC_2465	NA	<i>galU</i>					1	Glucose-1-phosphate uridylyltransferase
BAA196NC_2467	NA	<i>rssA</i>	-1				1	Hypothetical protein
BAA196NC_2477	NA	<i>narX</i>					1	Sensory histidine kinase in two-component regulatory system with NarL
BAA196NC_2500	NA	<i>ychH</i>	-1	-1	-1			Predicted inner membrane protein
BAA196NC_2512	NA	<i>ymgE</i>					1	Predicted inner membrane protein
BAA196NC_2518	NA	<i>dadX</i>	1	1				
BAA196NC_2529	NA	<i>ycgI</i>					1	Hypothetical protein
BAA196NC_2569	NA	<i>hflD</i>	-1				-1	Hypothetical protein
BAA196NC_2576	NA	<i>ycfP</i>			1	1		Probably esterase of a salvage cluster
BAA196NC_2580	NA	<i>potD</i>	1					Spermidine/putrescine ABC transporter periplasmic substrate-binding protein
BAA196NC_2591	NA	<i>ycfR</i>			1	1	1	Hypothetical protein
BAA196NC_2642	NA	<i>pyrC</i>	1	1				Dihydroorotase
BAA196NC_2644	NA	<i>yceP</i>			-1			Hypothetical protein
BAA196NC_2652	NA	<i>msyB</i>	1	1		1		Hypothetical protein
BAA196NC_2653	NA	<i>yceK</i>					1	Predicted lipoprotein
BAA196NC_2654	NA	<i>mdoH</i>		1				Glucosyltransferase MdoH

BAA196NC_2687	NA	<i>putA</i>	1			Fused DNA-binding transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase
BAA196NC_2725	NA	<i>hyaD</i>	-1	-1		Protein involved in processing of HyaA and HyaB proteins
BAA196NC_2727	NA	<i>hyaB</i>		-1		Hydrogenase 1, large subunit
BAA196NC_2728	NA	<i>hyaA</i>		-1		Hydrogenase 1, small subunit
BAA196NC_2746	NA	<i>fabA</i>		1		3-hydroxydecanoyl-ACP dehydratase
BAA196NC_2747	NA	<i>rmf</i>	-1			Ribosome modulation factor
BAA196NC_2748	NA	<i>ymbA</i>		1		Hypothetical protein
BAA196NC_2751	NA	<i>uup</i>		-1		Fused predicted transporter subunits of ABC superfamily: ATP-binding components
BAA196NC_2753	NA	<i>ycbX</i>		-1		Predicted 2Fe-2S cluster-containing protein
BAA196NC_2771	NA	<i>ompF</i>	-1	-1	-1	Outer membrane porin 1a (Ia;b;F)
BAA196NC_2772	NA	<i>aspC</i>		1		Aspartate aminotransferase, PLP-dependent
BAA196NC_2794	NA	<i>ycaP</i>		1		Conserved inner membrane protein
BAA196NC_2802	NA	<i>ycaD</i>		1		Putative MFS family transporter protein
BAA196NC_2803	NA	<i>ycaC</i>		1		Predicted hydrolase
BAA196NC_2804	NA	<i>dmsC</i>		-1		Dimethyl sulfoxide reductase, anaerobic, subunit C
BAA196NC_2806	NA	<i>dmsA</i>		-1		Dimethyl sulfoxide reductase, anaerobic, subunit A
BAA196NC_2811	NA	<i>lrp</i>		-1		DNA-binding transcriptional dual regulator, leucine-binding
BAA196NC_2819	NA	<i>cspD</i>	-1			Cold shock protein homolog
BAA196NC_2829	NA	<i>ltaE</i>	1	1		L-allo-threonine aldolase, PLP-dependent
BAA196NC_2833	NA	<i>ybjQ</i>			1	Hypothetical protein
BAA196NC_2863	NA	<i>dacC</i>		-1		D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)
BAA196NC_2865	NA	<i>ylil</i>		1		Predicted dehydrogenase
BAA196NC_2866	NA	<i>yltH</i>		-1	-1	Hypothetical protein
BAA196NC_2883	NA	<i>ybiS</i>		1		L,D-transpeptidase ldtB
BAA196NC_2886	NA	<i>rhlE</i>	-1	-1		RNA helicase
BAA196NC_2888	NA	<i>ompX</i>	-1			Outer membrane protein X
BAA196NC_2891	NA	<i>glnH</i>		-1		Glutamine ABC transporter periplasmic protein
BAA196NC_2892	NA	<i>glnP</i>	1			Glutamine ABC transporter permease protein
BAA196NC_2893	NA	<i>glnQ</i>	1	-1		Glutamine ABC transporter ATP-binding protein
BAA196NC_2896	NA	<i>ybiM</i>			1	Hypothetical protein
BAA196NC_2897	NA	<i>fiu</i>		1		Predicted iron outer membrane transporter
BAA196NC_2900	NA	<i>ybiJ</i>		1	1	Hypothetical protein
BAA196NC_2907	NA	<i>ybhG</i>		-1		Hypothetical protein
BAA196NC_2911	NA	<i>ybhQ</i>		1		Predicted inner membrane protein
BAA196NC_2938	NA	<i>ynfO-1</i>			1	Qin prophage protein
BAA196NC_2947	NA	<i>ninH</i>		-1		Uncharacterized phage protein
BAA196NC_2951	NA	<i>ninB</i>		-1		Phage DNA recombination
BAA196NC_2975	NA	<i>ybhl</i>	-1			Inner membrane protein
BAA196NC_3007	NA	<i>galK</i>		-1		Galactokinase
BAA196NC_3013	NA	<i>pnuC</i>			1	Predicted nicotinamide mononucleotide transporter
BAA196NC_3015	NA	<i>ybgF</i>	-1			Hypothetical protein
BAA196NC_3018	NA	<i>tolA</i>		1		Cell envelope integrity inner membrane protein TolA
BAA196NC_3024	NA	<i>cydB</i>		-1		Cytochrome d terminal oxidase, subunit II
BAA196NC_3036	NA	<i>sdhD</i>		-1	-1	Succinate dehydrogenase cytochrome b556 small membrane subunit
BAA196NC_3038	NA	<i>gltA</i>	1			Citrate synthase
BAA196NC_3058	NA	<i>ybfA</i>	-1	-1		Hypothetical protein
BAA196NC_3060	NA	<i>kdpA</i>			-1	Potassium-transporting ATPase subunit A
BAA196NC_3063	NA	<i>kdpD</i>			-1	Fused sensory histidine kinase in two-component regulatory system with KdpE: signal sensing protein
BAA196NC_3072	NA	<i>seqA</i>		1		Regulatory protein for replication initiation
BAA196NC_3075	NA	<i>fldA</i>	1	1		Flavodoxin 1
BAA196NC_3093	NA	<i>hscC</i>			-1	Hsp70 family chaperone Hsc62, binds to RpoD and inhibits transcription
BAA196NC_3117	NA	<i>dacA</i>		1	-1	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)
BAA196NC_3118	NA	<i>ybeD</i>	-1			Hypothetical protein
BAA196NC_3122	NA	<i>tatE</i>	-1	-1		Twin arginine translocase protein E
BAA196NC_3128	NA	<i>dcuC</i>		-1		Anaerobic C4-dicarboxylate transport
BAA196NC_3142	NA	<i>uspG</i>		1	1	Universal stress protein UP12
BAA196NC_3144	NA	<i>ahpC</i>	1	1	1	Alkyl hydroperoxide reductase, C22 subunit
BAA196NC_3152	NA	<i>cstA</i>	1			Carbon starvation protein
BAA196NC_3155	NA	<i>entB</i>	1			Isochorismatase
BAA196NC_3189	NA	<i>appY</i>			1	DLP12 prophage; DNA-binding transcriptional activator
BAA196NC_3248	NA	<i>allR</i>		1	1	DNA-binding transcriptional repressor
BAA196NC_3293	NA	<i>ybaJ</i>			1	Hypothetical protein
BAA196NC_3296	NA	<i>ylaC</i>		-1		Predicted inner membrane protein
BAA196NC_3297	NA	<i>ylaB</i>	-1			Conserved inner membrane protein
BAA196NC_3299	NA	<i>ybaX</i>	1		-1	7-cyano-7-deazaguanine synthase
BAA196NC_3313	NA	<i>ppiD</i>			1	Peptidyl-prolyl cis-trans isomerase (rotamase D)
BAA196NC_3318	NA	<i>tig</i>	-1	-1	-1	Trigger factor
BAA196NC_3320	NA	<i>bolA</i>	-1			Regulator of penicillin binding proteins and beta lactamase transcription (morphogene)
BAA196NC_3323	NA	<i>cyoA</i>	1		-1	Cytochrome o ubiquinol oxidase subunit II
BAA196NC_3325	NA	<i>cyoC</i>			-1	Cytochrome o ubiquinol oxidase subunit III
BAA196NC_3326	NA	<i>cyoD</i>			-1	Cytochrome o ubiquinol oxidase subunit IV
BAA196NC_3329	NA	<i>yajQ</i>			1	Nucleotide-binding protein
BAA196NC_3336	NA	<i>yajO</i>	-1			Predicted oxidoreductase, NAD(P)-binding
BAA196NC_3337	NA	<i>pgpA</i>			-1	Phosphatidylglycerophosphatase A
BAA196NC_3339	NA	<i>nusB</i>			1	Transcription antitermination protein NusB

BAA196NC_3355	NA	<i>phoR</i>		1			Sensory histidine kinase in two-component regulatory system with PhoB
BAA196NC_3361	NA	<i>rdgC</i>			1		Recombination associated protein
BAA196NC_3365	NA	<i>yaiA</i>	-1	-1			Hypothetical protein
BAA196NC_3370	NA	<i>psiF</i>	-1				Hypothetical protein
BAA196NC_3371	NA	<i>phoA</i>				1	Bacterial alkaline phosphatase
BAA196NC_3372	NA	<i>yaiB</i>				1	Hypothetical protein
BAA196NC_3400	NA	<i>frmA</i>		1	1	1	Alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase
BAA196NC_3419	NA	<i>codA</i>	1		1	-1	Cytosine deaminase
BAA196NC_3420	NA	<i>codB</i>			1		Cytosine transporter
BAA196NC_3424	NA	<i>prpB</i>				1	2-methylisocitrate lyase
BAA196NC_3426	NA	<i>yahO</i>	-1				Hypothetical protein
BAA196NC_3452	NA	<i>ykgC</i>				1	Pyridine nucleotide-disulfide oxidoreductase
BAA196NC_3460	NA	<i>ykgO</i>				1	RpmJ (L36) paralog
BAA196NC_3472	NA	<i>yagR</i>	-1			-1	Predicted oxidoreductase with molybdenum-binding domain
BAA196NC_3515	NA	<i>dinJ</i>	-1				Predicted antitoxin of YafQ-DinJ toxin-antitoxin system
BAA196NC_3521	NA	<i>ivy</i>			1		Inhibitor of vertebrate C-lysozyme
BAA196NC_3526	NA	<i>dnaQ</i>				1	DNA polymerase III subunit epsilon
BAA196NC_3530	NA	<i>mltD</i>	-1	-1		1	Predicted membrane-bound lytic murein transglycosylase D
BAA196NC_3546	NA	<i>yaeP</i>				1	Hypothetical protein
BAA196NC_3547	NA	<i>rof</i>				1	Modulator of Rho-dependent transcription termination
BAA196NC_3550	NA	<i>ldcC</i>				-1	Lysine decarboxylase 2, constitutive
BAA196NC_3551	NA	<i>accA</i>		-1			Acetyl-CoA carboxylase subunit alpha
BAA196NC_3555	NA	<i>lpxA</i>			1		UDP-N-acetylglucosamine acyltransferase
BAA196NC_3558	NA	<i>hlpA</i>			-1		Periplasmic chaperone
BAA196NC_3577	NA	<i>degP</i>	1	1			Serine endoprotease (protease Do), membrane-associated
BAA196NC_3579	NA	.		-1			5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
BAA196NC_3583	NA	<i>clcA</i>	-1				Chloride channel protein
BAA196NC_3588	NA	<i>fhuA</i>				1	Ferrichrome outer membrane transporter
BAA196NC_3592	NA	<i>sfsA</i>	-1	-1			Sugar fermentation stimulation protein A
BAA196NC_3593	NA	<i>dksA</i>	-1	-1			DNA-binding transcriptional regulator of rRNA transcription, DnaK suppressor protein
BAA196NC_3615	NA	<i>cueO</i>	1	1	1	1	Multicopper oxidase (laccase)
BAA196NC_3620	NA	<i>acnB</i>			1		Aconitate hydratase
BAA196NC_3623	NA	<i>aceF</i>			1	-1	Dihydrolipoamide acetyltransferase
BAA196NC_3645	NA	<i>murC</i>				1	UDP-N-acetylmuramate--L-alanine ligase
BAA196NC_3652	NA	<i>ftsI</i>			1	-1	Transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3)
BAA196NC_3682	NA	<i>surA</i>				-1	Peptidyl-prolyl cis-trans isomerase (PPIase)
BAA196NC_3716	NA	<i>nhaA</i>				1	PH-dependent sodium/proton antiporter
BAA196NC_3721	NA	<i>dnaK</i>				-1	Molecular chaperone DnaK
BAA196NC_3734	NA	<i>arcA</i>				1	DNA-binding response regulator in two-component regulatory system with ArcB or CpxA
BAA196NC_3761	NA	<i>osmY</i>	1		1	1	Periplasmic protein
BAA196NC_3773	NA	<i>dnaT</i>			-1		Primosomal protein I
BAA196NC_3781	NA	<i>yjiY</i>	1	1	-1		Predicted inner membrane protein
BAA196NC_3785	NA	<i>hsdR</i>				-1	Endonuclease R
BAA196NC_3824	NA	<i>fimA</i>			1		Major type 1 subunit fimbrin (piliin)
BAA196NC_3878	NA	<i>pepA</i>			1		Leucyl aminopeptidase
BAA196NC_3879	NA	<i>holC</i>	1				DNA polymerase III subunit chi
BAA196NC_3883	NA	<i>yjgD</i>				-1	Hypothetical protein
BAA196NC_3889	NA	<i>yjgI</i>		1	1	1	Predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain
BAA196NC_3892	NA	<i>pyrI</i>	1		1		Aspartate carbamoyltransferase regulatory subunit
BAA196NC_3894	NA	<i>mgfA</i>				1	Magnesium transporter
BAA196NC_3901	NA	<i>pmbA</i>			-1		Predicted peptidase required for the maturation and secretion of the antibiotic peptide MccB17
BAA196NC_3908	NA	<i>ytfQ</i>				1	Predicted sugar transporter subunit: periplasmic-binding component of ABC superfamily
BAA196NC_3909	NA	<i>ppa</i>				1	Inorganic pyrophosphatase
BAA196NC_3933	NA	<i>priB</i>			1		Primosomal replication protein N
BAA196NC_3945	NA	<i>yjfO</i>	-1	-1	-1	-1	Hypothetical protein
BAA196NC_3946	NA	<i>yjfN</i>	-1		-1	-1	Hypothetical protein
BAA196NC_3962	NA	<i>hfq</i>			-1		RNA-binding protein Hfq
BAA196NC_3982	NA	<i>blc</i>				1	Outer membrane lipoprotein (lipocalin)
BAA196NC_3984	NA	<i>ecnB</i>	-1		-1		Entericidin B membrane lipoprotein
BAA196NC_3994	NA	<i>aspA</i>	-1	-1		-1	Aspartate ammonia-lyase
BAA196NC_3995	NA	<i>dcuA</i>			-1	-1	C4-dicarboxylate antiporter
BAA196NC_4070	NA	<i>yjcD</i>	1		1		Predicted permease
BAA196NC_4072	NA	<i>yjbQ</i>		-1			Uncharacterized protein
BAA196NC_4075	NA	<i>yjcC</i>	-1				Predicted signal transduction protein (EAL domain containing protein)
BAA196NC_4079	NA	<i>yjbR</i>	-1		-1		Hypothetical protein
BAA196NC_4087	NA	<i>qor</i>				1	Quinone oxidoreductase, NADPH-dependent
BAA196NC_4092	NA	<i>zur</i>	-1				DNA-binding transcriptional repressor, Zn(II)-binding
BAA196NC_4093	NA	<i>yjbJ</i>	-1			1	Predicted stress response protein
BAA196NC_4102	NA	<i>lamB</i>				-1	Maltoporin precursor
BAA196NC_4103	NA	<i>malk</i>				-1	Fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein

BAA196NC_4119	NA	<i>metH</i>				-1			B12-dependent methionine synthase
BAA196NC_4122	NA	<i>aceK</i>			1	-1			Bifunctional isocitrate dehydrogenase kinase/phosphatase protein
BAA196NC_4123	NA	<i>aceA</i>	1		1				Isocitrate lyase
BAA196NC_4124	NA	<i>aceB</i>	1		1	-1			Malate synthase
BAA196NC_4136	NA	<i>nfi</i>						-1	Endonuclease V
BAA196NC_4140	NA	<i>thiC</i>						-1	Thiamine biosynthesis protein ThiC
BAA196NC_4142	NA	<i>thiF</i>						-1	Thiamine biosynthesis protein ThiF
BAA196NC_4145	NA	<i>thiH</i>						-1	Thiamine biosynthesis protein ThiH
BAA196NC_4164	NA	<i>fabR</i>			1				DNA-binding transcriptional repressor
BAA196NC_4189	NA	<i>metJ</i>				-1			Transcriptional repressor protein MetJ
BAA196NC_4191	NA	<i>rpmE</i>	-1	-1	-1	-1			50S ribosomal subunit protein L31
BAA196NC_4194	NA	<i>ftsN</i>						1	Essential cell division protein
BAA196NC_4198	NA	<i>rraA</i>	-1						Ribonuclease activity regulator protein RraA
BAA196NC_4204	NA	<i>yjiT</i>						1	Stress-induced protein
BAA196NC_4205	NA	<i>yjiS</i>						1	Hypothetical protein
BAA196NC_4210	NA	<i>sbp</i>	1	1				1	Sulfate transporter subunit
BAA196NC_4213	NA	<i>cpxP</i>						1	Periplasmic protein combats stress
BAA196NC_4234	NA	<i>fdoG</i>	1	1				-1	Formate dehydrogenase-O, large subunit
BAA196NC_4235	NA	<i>fdoH</i>						-1	Formate dehydrogenase-O, Fe-S subunit
BAA196NC_4236	NA	<i>fdoI</i>	1						Formate dehydrogenase-O, cytochrome b556 subunit
BAA196NC_4237	NA	<i>fahE</i>						-1	Formate dehydrogenase accessory protein FdhE
BAA196NC_4260	NA	<i>glnL</i>			1				Sensory histidine kinase in two-component regulatory system with GlnG
BAA196NC_4261	NA	<i>glnG</i>						-1	Fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator/sigma54 interaction protein
BAA196NC_4272	NA	<i>yihE</i>						1	Predicted kinase
BAA196NC_4273	NA	<i>yihD</i>						-1	Hypothetical protein
BAA196NC_4285	NA	<i>tatD</i>						-1	DNase, magnesium-dependent
BAA196NC_4287	NA	<i>tatB</i>						-1	Sec-independent translocase
BAA196NC_4316	NA	<i>cyaY</i>						-1	Fratxin-like protein
BAA196NC_4317	NA	<i>cyaA</i>	-1		-1				Adenylate cyclase
BAA196NC_4322	NA	<i>hemC</i>	-1					-1	Porphobilinogen deaminase
BAA196NC_4336	NA	<i>wzzE</i>						-1	Enterobacterial Common Antigen (ECA) polysaccharide chain length modulation protein
BAA196NC_4341	NA	<i>rhlB</i>	-1						ATP-dependent RNA helicase
BAA196NC_4342	NA	<i>gpp</i>						1	Guanosine pentaphosphate/exopolysphatase
BAA196NC_4367	NA	<i>asnA</i>						1	Asparagine synthetase AsnA
BAA196NC_4383	NA	<i>pstS</i>	1		1			1	Phosphate transporter subunit
BAA196NC_4404	NA	<i>tnaA</i>						-1	Tryptophanase/L-cysteine desulfhydrase, PLP-dependent
BAA196NC_4428	NA	<i>aph3</i>						-1	Aminoglycoside 3'-phosphotransferase
BAA196NC_4442	NA	<i>aacA6</i>	-1		-1				Aminoglycoside N(6)-acetyltransferase
BAA196NC_4447	NA	.						-1	S-(hydroxymethyl)glutathione dehydrogenase
BAA196NC_4471	NA	<i>terD</i>						1	Tellurium resistance protein TerD
BAA196NC_4472	NA	<i>terE</i>						1	Tellurium resistance cAMP binding protein TerE
NA	HMPRNC0000_0008	<i>hutH</i>						-1	Histidine ammonia-lyase
NA	HMPRNC0000_0014	.						-1	Hypothetical protein
NA	HMPRNC0000_0015	.						1	Cyclic-di-AMP phosphodiesterase GdpP
NA	HMPRNC0000_0023	<i>yycH</i>						1	Two-component system YycFG regulatory protein YycH
NA	HMPRNC0000_0026	.						1	Zn-dependent hydrolase YycJ/WalJ
NA	HMPRNC0000_0027	<i>sasH</i>						-1	Virulence-associated cell-wall-anchored protein SasH (LPXTG motif), 5'-nucleotidase
NA	HMPRNC0000_0034	<i>cadC</i>						1	Cadmium efflux system accessory protein
NA	HMPRNC0000_0037	.						1	Cadmium resistance protein
NA	HMPRNC0000_0038	.						1	DNA repair protein RadC
NA	HMPRNC0000_0045	<i>mecA</i>						-1	Penicillin-binding protein PBP2a, methicillin resistance determinant MecA, transpeptidase
NA	HMPRNC0000_0052	.						1	ctRNA
NA	HMPRNC0000_0053	.						1	Uncharacterized ncRNA
NA	HMPRNC0000_0054	<i>pre</i>						1	Plasmid recombination enzyme type 3
NA	HMPRNC0000_0055	<i>tet</i>						1	Tetracycline resistance, MFS efflux pump -> Tet(K)
NA	HMPRNC0000_0102	.						-1	Protein A, von Willebrand factor binding protein Spa
NA	HMPRNC0000_0121	.						1	Hypothetical protein
NA	HMPRNC0000_0123	<i>budC</i>						1	2,3-butanediol dehydrogenase, S-alcohol forming, (R)-acetoin-specific / Acetoin (diacetyl) reductase
NA	HMPRNC0000_0129	<i>sodA</i>						1	Superoxide dismutase (Mn), Superoxide dismutase (Fe)
NA	HMPRNC0000_0173	.						1	Hypothetical protein
NA	HMPRNC0000_0176	.						1	Hypothetical protein
NA	HMPRNC0000_0178	.						1	Acyl-CoA dehydrogenase, short-chain specific
NA	HMPRNC0000_0182	.						-1	Polyketide synthase
NA	HMPRNC0000_0194	<i>ipdC</i>						-1	Pyruvate decarboxylase, Alpha-keto-acid decarboxylase
NA	HMPRNC0000_0207	<i>hsdR</i>						-1	Type I restriction-modification system, restriction subunit R
NA	HMPRNC0000_0234	.						-1	Inosose isomerase
NA	HMPRNC0000_0246	.						1	Hypothetical protein
NA	HMPRNC0000_0248	<i>fadA</i>						-1	3-ketoacyl-CoA thiolase (fadN-fadA-fadE operon)
NA	HMPRNC0000_0249	<i>fadB</i>						-1	3-hydroxyacyl-CoA dehydrogenase/Enoyl-CoA hydratase
NA	HMPRNC0000_0261	<i>ldhA</i>						-1	L-lactate dehydrogenase
NA	HMPRNC0000_0284	<i>lrgB</i>						1	LrgA-associated membrane protein LrgB
NA	HMPRNC0000_0299	.						-1	Hypothetical protein
NA	HMPRNC0000_0301	.						-1	Hypothetical protein
NA	HMPRNC0000_0307	<i>esxA</i>						-1	6 kDa early secretory antigenic target ESAT-6 (EsxA)

NA	HMPRNC0000_0312	<i>essC</i>		-1			FtsK/SpoIIIE family protein, putative EssC/YukB component of Type VII secretion system
NA	HMPRNC0000_0334	<i>brnQ</i>			1		Branched-chain amino acid transport system carrier protein
NA	HMPRNC0000_0337	<i>lolD</i>		-1		-1	ABC transporter, ATP-binding protein
NA	HMPRNC0000_0338	<i>pfoR</i>			-1		Perfringolysin O regulator protein PfoR
NA	HMPRNC0000_0347	.		-1			N-acetylmannosamine kinase
NA	HMPRNC0000_0348	.			1		Sialic acid utilization regulator, RpiR family
NA	HMPRNC0000_0351	<i>lip2</i>		-1	-1	-1	Lipase precursor
NA	HMPRNC0000_0363	.		-1			Putative sugar-specific permease, SgaT/UlaA
NA	HMPRNC0000_0364	.		-1	-1		PTS system, IIB component
NA	HMPRNC0000_0370	<i>glpT</i>		-1	-1		Glycerol-3-phosphate transporter
NA	HMPRNC0000_0371	<i>gloA</i>		1			Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
NA	HMPRNC0000_0372	.		1			Luciferase-like monooxygenase YhbW
NA	HMPRNC0000_0373	.		1	1	1	FMN reductase
NA	HMPRNC0000_0388	.				1	Transcriptional regulator, Xre family
NA	HMPRNC0000_0417	.		-1	-1		hypothetical protein
NA	HMPRNC0000_0418	.			1		Hypothetical protein
NA	HMPRNC0000_0419	.		-1	-1	-1	Hypothetical protein
NA	HMPRNC0000_0427	.		1	1		L-cystine uptake protein TcyP, sodium:anion symporter family
NA	HMPRNC0000_0431	.		-1	-1		hypothetical protein
							Putative transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 protein
NA	HMPRNC0000_0467	.				-1 -1	
NA	HMPRNC0000_0471	.		1	1		PAP2 family phosphatase/haloperoxidase
NA	HMPRNC0000_0472	.		1			Esterase/lipase family protein
NA	HMPRNC0000_0474	.		1	1		Sodium-dependent transporter
NA	HMPRNC0000_0480	<i>sle</i>				-1	Autolysin precursor
NA	HMPRNC0000_0482	.		1			Hypothetical protein
NA	HMPRNC0000_0483	.		1			Acetyltransferase, GNAT family
							PTS system, trehalose-specific IIB component / PTS system, trehalose-specific IIC component
NA	HMPRNC0000_0490	<i>treP</i>		1	1	-1	
NA	HMPRNC0000_0492	<i>treR</i>		1	1	-1	Trehalose operon transcriptional repressor
NA	HMPRNC0000_0493	.		-1	-1	-1	Bacterial signal recognition particle RNA
NA	HMPRNC0000_0495	<i>dnaX</i>		1	1		DNA polymerase III subunits gamma and tau
NA	HMPRNC0000_0504	.		-1	-1		nitrogen regulatory protein P-II (GLNB)
NA	HMPRNC0000_0516	.		-1	-1	-1 -1	Veg protein
NA	HMPRNC0000_0518	<i>purR</i>		1	1	1	Pur operon repressor PurR
							Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 protein)
NA	HMPRNC0000_0530	.		1			
NA	HMPRNC0000_0531	.			1		Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage
NA	HMPRNC0000_0532	.				-1	RNA binding protein, contains ribosomal protein S1 domain
NA	HMPRNC0000_0539	<i>cysK</i>		1	1		Cysteine synthase
							Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing), synthase subunit
NA	HMPRNC0000_0561	.		-1	-1		
							Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing), glutaminase subunit
NA	HMPRNC0000_0562	<i>pdxT</i>		-1	-1		
NA	HMPRNC0000_0563	.		-1			Pyrimidine nucleoside transporter NupC/NucG family
NA	HMPRNC0000_0564	.		-1	-1	-1	Pyrimidine nucleoside transporter NupC/NucG family
NA	HMPRNC0000_0565	<i>ctsR</i>		1	1	1	Transcriptional regulator CtsR
NA	HMPRNC0000_0566	.		1	1	1	1
NA	HMPRNC0000_0567	.		1	1	1	1
NA	HMPRNC0000_0568	<i>clpC</i>		1	1	1	1
NA	HMPRNC0000_0572	<i>cysE</i>		1			Serine acetyltransferase
NA	HMPRNC0000_0574	.		1			Mini-ribonuclease III
NA	HMPRNC0000_0576	<i>yacP</i>		1	1		Uncharacterized protein
NA	HMPRNC0000_0584	.				-1	16S rRNA (guanine(1207)-N(2))-methyltransferase
NA	HMPRNC0000_0587	<i>rplL3</i>				-1	Firmicutes ribosomal L7Ae family protein
NA	HMPRNC0000_0592	.		1			N-acetyl-L,L-diaminopimelate deacetylase
NA	HMPRNC0000_0597	<i>tdh</i>		-1	-1		L-threonine 3-dehydrogenase
NA	HMPRNC0000_0606	<i>sdrC</i>				-1	Adhesin SdrC
NA	HMPRNC0000_0608	<i>sdrD</i>		-1			Adhesin SdrD
NA	HMPRNC0000_0609	<i>sdrE</i>				-1	Adhesin SdrE
NA	HMPRNC0000_0613	.		1			GTP cyclohydrolase I type 2
NA	HMPRNC0000_0614	.		1	1		GTP cyclohydrolase I type 2
NA	HMPRNC0000_0615	<i>bshB2</i>		1			N-acetylglucosaminyl-L-malate N-acetyl hydrolase
NA	HMPRNC0000_0616	<i>yojF</i>			1		Uncharacterized protein
NA	HMPRNC0000_0625	<i>vraB</i>			-1		3-ketoacyl-CoA thiolase and Acetyl-CoA acetyltransferase
NA	HMPRNC0000_0638	.		1	1		Octanoyl-(GcvH):protein N-octanoyltransferase
NA	HMPRNC0000_0643	.		1			DUF1450 superfamily protein
NA	HMPRNC0000_0644	<i>merA2</i>		1	1	1	1
NA	HMPRNC0000_0645	.		1	1	1	1
NA	HMPRNC0000_0645	.		1	1	1	1
NA	HMPRNC0000_0645	.		1	1	1	1
NA	HMPRNC0000_0662	.		1	1	1	dNTP triphosphohydrolase, broad substrate specificity
NA	HMPRNC0000_0673	.		-1	-1	-1	Hypothetical protein
NA	HMPRNC0000_0689	.		1	1	1	1
NA	HMPRNC0000_0690	<i>sitC</i>		-1	-1		Manganese ABC transporter, periplasmic-binding protein SitA
NA	HMPRNC0000_0692	.		-1	-1	-1 -1	Manganese ABC transporter, ATP-binding protein SitB
NA	HMPRNC0000_0693	<i>sirR</i>				-1	Mn-dependent transcriptional regulator MntR
NA	HMPRNC0000_0704	<i>lmrA</i>			1		Efflux ABC transporter, permease/ATP-binding protein
NA	HMPRNC0000_0712	<i>fhuG</i>			1		Ferrichrome transport system permease protein FhuG

NA	HMPRNC0000_0716	.				1	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase, subunit DhaM, DHA-specific IIA component	
NA	HMPRNC0000_0717	.		1	1		Hypothetical protein	
NA	HMPRNC0000_0718	.		1	1		Hypothetical protein	
NA	HMPRNC0000_0723	.	1				Hypothetical protein	
NA	HMPRNC0000_0729	.		1	1		Putative low-affinity inorganic phosphate transporter	
NA	HMPRNC0000_0730	<i>amiD7</i>	-1	-1	-1		Secretory antigen precursor SsaA	
NA	HMPRNC0000_0738	.	1				Hypothetical protein	
NA	HMPRNC0000_0739	.	1	1	1		Catabolite control protein E (CcpE), LysR family	
NA	HMPRNC0000_0750	.		-1	-1		hypothetical protein	
NA	HMPRNC0000_0751	<i>uppP</i>	-1		-1		Undecaprenyl-diphosphatase	
NA	HMPRNC0000_0754	<i>mgrA</i>	-1				Transcriptional regulator MgrA (Regulator of autolytic activity)	
NA	HMPRNC0000_0771	<i>pfkB2</i>	1	1	1	1	1-phosphofructokinase	
NA	HMPRNC0000_0772	<i>fruA</i>	1	1	1	1	PTS system, fructose-specific IIA/IIB/IIC component	
NA	HMPRNC0000_0778	<i>saeR</i>	-1	-1	-1		Response regulator SaeR, exoprotein expression protein R	
NA	HMPRNC0000_0779	.		-1	-1	1	Hypothetical protein	
NA	HMPRNC0000_0780	.				1	Hypothetical protein	
NA	HMPRNC0000_0829	.	1				Protein co-occurring with transport systems	
NA	HMPRNC0000_0837	<i>secA</i>		1	1		Protein translocase subunit SecA	
NA	HMPRNC0000_0839	.				1	LysM domain protein	
NA	HMPRNC0000_0859	<i>cggR</i>		1	1	-1	-1	Central glycolytic regulator
NA	HMPRNC0000_0860	<i>gapA1</i>	1				-1	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase
NA	HMPRNC0000_0877	<i>clfA</i>	-1	-1	-1	-1	Clumping factor ClfA, fibrinogen-binding protein	
NA	HMPRNC0000_0883	<i>cspA2</i>	-1			-1	Cold shock protein of CSP family	
NA	HMPRNC0000_0898	.			1		Putative nitroreductase family protein	
NA	HMPRNC0000_0903	.	-1				Glutathione-dependent thiol reductase	
NA	HMPRNC0000_0909	.	-1				Uncharacterized ncRNA	
NA	HMPRNC0000_0910	<i>metN2</i>	1		1		Methionine ABC transporter ATP-binding protein	
NA	HMPRNC0000_0911	.	1		1		Methionine ABC transporter permease protein	
NA	HMPRNC0000_0912	<i>metQ</i>			1		Methionine ABC transporter substrate-binding protein	
NA	HMPRNC0000_0916	<i>sei</i>	-1				Exotoxin, phage associated	
NA	HMPRNC0000_0924	.			1		Hypothetical protein	
NA	HMPRNC0000_0931	.	1				Putative terminase, superantigen-encoding pathogenicity islands SaPI	
NA	HMPRNC0000_0942	.		-1	-1		hemolysin	
NA	HMPRNC0000_0947	.				-1	UPF0721 transmembrane protein YunE	
NA	HMPRNC0000_0948	.		1	1		5'-nucleotidase family protein	
NA	HMPRNC0000_0958	<i>dltB</i>				1	D-alanyl transfer protein DltB	
NA	HMPRNC0000_0960	<i>dltD</i>				1	Poly(glycerophosphate chain) D-alanine transfer protein DltD	
NA	HMPRNC0000_0964	.	1				DUF1450 superfamily protein	
NA	HMPRNC0000_0969	.	1	1	1	1	Histidine permease YuiF	
NA	HMPRNC0000_0978	<i>mnhD</i>		1	1		Na(+) H(+) antiporter subunit D	
NA	HMPRNC0000_0981	<i>mnhA</i>				-1	Na(+) H(+) antiporter subunit A	
NA	HMPRNC0000_0985	.				-1	General stress protein 13	
NA	HMPRNC0000_0991	<i>argG</i>	1		1		Argininosuccinate synthase	
NA	HMPRNC0000_0997	<i>addB</i>	1		1		ATP-dependent helicase/nuclease AddAB, subunit B	
NA	HMPRNC0000_1001	<i>fahA</i>	-1	-1	-1		Fumarylacetoacetate hydrolase family protein	
NA	HMPRNC0000_1005	<i>yitU</i>			1		Haloacid dehalogenase hydrolase	
NA	HMPRNC0000_1010	.	1	1			Transcriptional regulator, LysR family	
NA	HMPRNC0000_1013	.				1	Hypothetical protein	
NA	HMPRNC0000_1014	.				1	Hypothetical protein	
NA	HMPRNC0000_1031	<i>mecA2</i>	1		1		Negative regulator of genetic competence, sporulation and motility	
NA	HMPRNC0000_1033	<i>pepF</i>	-1				Oligoendopeptidase F	
NA	HMPRNC0000_1040	<i>ppnK</i>				1	NAD kinase	
NA	HMPRNC0000_1041	<i>yjbO</i>			1		Ribosomal large subunit pseudouridine synthase D	
NA	HMPRNC0000_1050	.	-1	-1	-1	-1	2H phosphoesterase superfamily protein Bsu1186 (yjcG)	
NA	HMPRNC0000_1063	.		-1	-1	1	Hypothetical protein	
NA	HMPRNC0000_1086	<i>atl</i>	-1	-1	-1		N-acetylmuramoyl-L-alanine amidase / Endo-beta-N-acetylglucosaminidase and Bifunctional autolysin Atl	
NA	HMPRNC0000_1089	.				-1	Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily F2	
NA	HMPRNC0000_1093	<i>qoxD</i>	-1	-1	-1		Cytochrome aa3-600 menaquinol oxidase subunit IV	
NA	HMPRNC0000_1095	<i>qoxA</i>				-1	Cytochrome aa3-600 menaquinol oxidase subunit II	
NA	HMPRNC0000_1098	<i>folD</i>	-1	-1	-1	-1	Methylenetetrahydrofolate cyclohydrolase / Methylenetetrahydrofolate dehydrogenase (NADP+)	
NA	HMPRNC0000_1103	<i>purS</i>				-1	Phosphoribosylformylglycinamide synthase, PurS subunit	
NA	HMPRNC0000_1104	<i>purQ</i>	-1	-1			Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit	
NA	HMPRNC0000_1105	<i>purL</i>	-1	-1		-1	Phosphoribosylformylglycinamide synthase, synthetase subunit	
NA	HMPRNC0000_1113	.	-1	-1	-1		Duplicated ATPase component YkoD	
NA	HMPRNC0000_1114	.	-1	-1	-1	-1	Substrate-specific component YkoE of thiamin-regulated ECF transporter for HydroxyMethylPyrimidine	
NA	HMPRNC0000_1126	<i>ktrA</i>	1				KtrCD potassium uptake system, peripheral membrane component KtrC	
NA	HMPRNC0000_1127	.		1	1		Ribonuclease J1 (endonuclease and 5' exonuclease)	
NA	HMPRNC0000_1145	.	1				Hypothetical protein	
NA	HMPRNC0000_1149	.				1	Hypothetical protein	
NA	HMPRNC0000_1153	.	1			1	UPF0358 protein YlaN	
NA	HMPRNC0000_1191	.	1	1			DNA polymerase X family	
NA	HMPRNC0000_1192	<i>mutS3</i>	1	1			Recombination inhibitory protein MutS2	

NA	HMPRNC0000_1195	<i>sdhC</i>							Succinate dehydrogenase cytochrome b558 subunit	
NA	HMPRNC0000_1203	.			1	1			Hypothetical protein	
NA	HMPRNC0000_1206	<i>fib</i>						1	Extracellular fibrinogen-binding protein Efb	
NA	HMPRNC0000_1207	<i>scn</i>			1				Fibrinogen-binding prophage protein	
NA	HMPRNC0000_1210	<i>hly</i>						1	Cytolytic pore-forming protein -> Alpha-hemolysin	
NA	HMPRNC0000_1227	<i>bshC</i>			1	1	1	1	Glucosaminyl-malate:cysteine ligase	
									Cell division protein FtsI (Peptidoglycan synthetase) and Penicillin-binding protein 2B	
NA	HMPRNC0000_1230	<i>pbpl</i>			-1					
NA	HMPRNC0000_1233	<i>divlB</i>			-1	-1			Cell division protein FtsQ	
NA	HMPRNC0000_1234	<i>ftsA</i>			-1	-1			Cell division protein FtsA	
NA	HMPRNC0000_1243	.						-1	Cell division initiation protein DivIVA	
NA	HMPRNC0000_1251	<i>upp2</i>			-1				Pyrimidine operon regulatory protein PyrR	
NA	HMPRNC0000_1258	<i>pyrE</i>						1	Orotate phosphoribosyltransferase	
NA	HMPRNC0000_1261	<i>fbpA</i>				1	1		Fibronectin/fibrinogen-binding protein	
NA	HMPRNC0000_1269	.			-1				Hypothetical protein	
NA	HMPRNC0000_1271	.			-1	-1			hypothetical protein	
NA	HMPRNC0000_1277	<i>prkC</i>				1	1		Serine/threonine protein kinase PrkC, regulator of stationary phase	
									LSU ribosomal protein L28p and LSU ribosomal protein L28p, zinc-independent	
NA	HMPRNC0000_1281	<i>rpmB</i>			-1	-1	-1			
NA	HMPRNC0000_1283	.			-1				Dihydroxyacetone kinase	
NA	HMPRNC0000_1287	.				1	1		Transcription factor FapR	
NA	HMPRNC0000_1321	<i>tsf</i>				1	1		Translation elongation factor Ts	
NA	HMPRNC0000_1328	<i>polC</i>				1	1		DNA polymerase III polC-type	
									Putative nucleic-acid-binding protein implicated in transcription termination	
NA	HMPRNC0000_1332	.			1					
NA	HMPRNC0000_1341	.				1	1		Ribonuclease J2 (endoribonuclease in RNA processing)	
NA	HMPRNC0000_1347	.				1	1		ACT domain protein	
NA	HMPRNC0000_1352	<i>cvfA</i>						1	Ribonuclease Y	
NA	HMPRNC0000_1356	<i>porB</i>					1		2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, beta subunit	
NA	HMPRNC0000_1368	<i>glpD</i>						1	Aerobic glycerol-3-phosphate dehydrogenase	
									FemC, factor involved in methicillin resistance / Glutamine synthetase repressor	
NA	HMPRNC0000_1377	<i>glnR</i>			-1					
NA	HMPRNC0000_1421	.			-1	-1			Hypothetical protein	
NA	HMPRNC0000_1423	<i>thrA</i>				1	1		Homoserine dehydrogenase	
NA	HMPRNC0000_1424	<i>thrC</i>				1			Threonine synthase	
NA	HMPRNC0000_1438	.						-1	Hypothetical protein	
NA	HMPRNC0000_1448	<i>opuD2</i>			-1	1	-1	1	Glycine betaine transporter OpuD	
NA	HMPRNC0000_1463	<i>msrR</i>			-1	-1			Peptide methionine sulfoxide reductase regulator MsrR	
NA	HMPRNC0000_1472	<i>trpF</i>				-1	-1	-1	Phosphoribosylanthranilate isomerase	
NA	HMPRNC0000_1483	<i>pepF</i>			-1				Oligoendopeptidase F	
NA	HMPRNC0000_1512	.						-1	5-bromo-4-chloroindolyl phosphate hydrolysis protein XpaC	
NA	HMPRNC0000_1514	<i>brnQ</i>				1			Branched-chain amino acid transport system carrier protein	
NA	HMPRNC0000_1515	.				1	1	1	Nitric oxide reductase activation protein NorD	
NA	HMPRNC0000_1541	.						-1	Surface anchored protein	
NA	HMPRNC0000_1543	<i>ebh</i>				1	1	-1	Surface anchored protein	
NA	HMPRNC0000_1550	.					-1		DNA polymerase I 5'-3' exonuclease domain	
NA	HMPRNC0000_1552	.			-1				Bsub YpbR	
NA	HMPRNC0000_1553	.			-1				Iron-regulated membrane protein, Iron-uptake factor PiuB	
NA	HMPRNC0000_1554	.						-1	23S rRNA (guanine(2445)-N(2))-methyltransferase	
NA	HMPRNC0000_1555	.			-1	-1	-1	-1	Bacterial RNase P class B	
NA	HMPRNC0000_1559	<i>recU</i>			-1	1	-1	1	RecU Holliday junction resolvase	
									Multimodular transpeptidase-transglycosylase / Penicillin-binding protein 1A/1B (PBP1)	
NA	HMPRNC0000_1560	<i>pbp</i>				1	1			
NA	HMPRNC0000_1563	.				1			Hypothetical protein	
NA	HMPRNC0000_1576	.				1			Hypothetical protein	
NA	HMPRNC0000_1577	.					1		Hypothetical protein	
NA	HMPRNC0000_1578	.					1		TPR-repeat-containing protein	
NA	HMPRNC0000_1591	<i>rpsA</i>			-1				SSU ribosomal protein S1p	
NA	HMPRNC0000_1597	<i>recQ</i>						-1	ATP-dependent DNA helicase RecS (RecQ family)	
NA	HMPRNC0000_1608	<i>srrB</i>						-1	Respiratory response protein SrrB	
NA	HMPRNC0000_1618	<i>nudF</i>			-1				ADP-ribose pyrophosphatase	
									Glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	
NA	HMPRNC0000_1631	.						-1		
									Glycine dehydrogenase (decarboxylating) (glycine cleavage system P2 protein)	
NA	HMPRNC0000_1662	<i>gcvP2</i>			-1	-1				
									Glycine dehydrogenase (decarboxylating) (glycine cleavage system P1 protein)	
NA	HMPRNC0000_1663	<i>gcvP</i>			-1	-1				
NA	HMPRNC0000_1679	<i>fthC</i>						1	5-formyltetrahydrofolate cyclo-ligase	
NA	HMPRNC0000_1681	<i>pbp3</i>					-1		Conserved protein Pbp3	
NA	HMPRNC0000_1691	<i>dnaG</i>				1	1		DNA primase	
NA	HMPRNC0000_1694	<i>glyS</i>				-1	-1		Glycyl-tRNA synthetase	
NA	HMPRNC0000_1704	.						-1	Hypothetical protein	
NA	HMPRNC0000_1707	<i>prmA</i>				1	1	1	1	Ribosomal protein L11 methyltransferase
NA	HMPRNC0000_1710	<i>dnaK</i>				1	1	1	1	Chaperone protein DnaK
NA	HMPRNC0000_1713	<i>hrcA</i>				1	1	1	1	Heat-inducible transcription repressor HrcA
NA	HMPRNC0000_1735	.			-1				Metal ion transporter YcsG, Mn(2+)/Fe(2+) NRAMP family	
NA	HMPRNC0000_1737	<i>accC</i>					-1		Biotin carboxylase	
NA	HMPRNC0000_1745	.				1			Protease small subunit YrrN	
NA	HMPRNC0000_1759	.						1	HesA/MoeB/ThiF family protein	
NA	HMPRNC0000_1760	.			-1	-1	-1	1	6S / SsrS RNA	

NA	HMPRNC0000_1772	<i>queA</i>				-1	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
NA	HMPRNC0000_1777	<i>cgtA</i>	1	1	1		GTP-binding protein Obg
NA	HMPRNC0000_1790	.			1		3'UTR
NA	HMPRNC0000_1802	<i>clpX</i>		1	1		ATP-dependent Clp protease ATP-binding subunit ClpX
NA	HMPRNC0000_1804	<i>tig</i>		1	1	1	Cell division trigger factor
NA	HMPRNC0000_1805	.				-1	Hypothetical protein
NA	HMPRNC0000_1809	<i>infC</i>	1				Translation initiation factor 3
NA	HMPRNC0000_1812	<i>dnal</i>		1	1		Helicase loader Dnal
NA	HMPRNC0000_1827	<i>cycA2</i>	-1			-1	D-serine/D-alanine/glycine transporter
NA	HMPRNC0000_1834	<i>maeB</i>	-1				NADP-dependent malic enzyme
NA	HMPRNC0000_1836	.				-1	3'-to-5' oligoribonuclease A
NA	HMPRNC0000_1839	.	-1	-1	-1	1	1 Universal stress protein family
NA	HMPRNC0000_1842	.	-1	-1			Transcript
NA	HMPRNC0000_1843	<i>ald</i>	-1	-1		1	Alanine dehydrogenase
NA	HMPRNC0000_1845	.		-1	-1	1	1 Universal stress protein family
NA	HMPRNC0000_1858	.			-1	1	Transcript
NA	HMPRNC0000_1863	.			1		Phosphoserine aminotransferase, putative
NA	HMPRNC0000_1864	<i>serA</i>	1	1			D-3-phosphoglycerate dehydrogenase
NA	HMPRNC0000_1868	.			-1	1	Serine protease, DegP/HtrA
NA	HMPRNC0000_1875	<i>fhs</i>	-1	-1			Formate-tetrahydrofolate ligase
NA	HMPRNC0000_1876	<i>acsA2</i>	-1	-1			Acetyl-CoA synthetase
NA	HMPRNC0000_1879	<i>acuC</i>				-1	NAD-independent protein deacetylase AcuC
NA	HMPRNC0000_1881	<i>aroF</i>				1	Chorismate mutase I / 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta
NA	HMPRNC0000_1882	.		-1	-1		hypothetical protein
NA	HMPRNC0000_1883	.		-1	-1		hypothetical protein
NA	HMPRNC0000_1884	.		-1	-1		hypothetical protein
NA	HMPRNC0000_1902	.	1				Rhodanese-like domain protein
NA	HMPRNC0000_1906	.	1				Putative rRNA methylase YtqB
NA	HMPRNC0000_1907	<i>rot</i>	-1	-1			Repressor of toxins Rot
NA	HMPRNC0000_1909	<i>putA</i>	-1	-1	-1	-1	Proline dehydrogenase
NA	HMPRNC0000_1911	<i>ribB</i>				1	3,4-dihydroxy-2-butanone 4-phosphate synthase / GTP cyclohydrolase II
NA	HMPRNC0000_1914	.				-1	Hypothetical protein
NA	HMPRNC0000_1935	.	-1	-1			Hypothetical protein
NA	HMPRNC0000_1936	.	-1	-1			Hypothetical protein
NA	HMPRNC0000_1937	.	-1	-1			Hypothetical protein
NA	HMPRNC0000_1939	.	-1	-1			Hypothetical protein
NA	HMPRNC0000_1947	.			-1		Type I restriction-modification system, specificity subunit S
NA	HMPRNC0000_1980	.				-1	ABC transporter, ATP-binding protein EcsA
NA	HMPRNC0000_1982	.		-1	-1		Hypothetical protein
NA	HMPRNC0000_1984	<i>prsA2</i>	-1	-1			Foldase protein PrsA precursor and Foldase clustered with pyrimidine conversion
NA	HMPRNC0000_2004	.	1	1			ABC transporter/substrate-binding protein/ABC transporter, permease protein
NA	HMPRNC0000_2049	<i>yfhP</i>				1	conserved membrane protein YfhP
NA	HMPRNC0000_2062	.	-1				Acyl-CoA hydrolase
NA	HMPRNC0000_2066	.	-1	-1	-1		Hypothetical protein
NA	HMPRNC0000_2067	<i>yihY</i>	-1				Inner membrane protein YihY, formerly thought to be RNase BN
NA	HMPRNC0000_2069	<i>vraS</i>				-1	Sensor histidine kinase VraS
NA	HMPRNC0000_2075	.	1	1			Putative amidotransferase similar to cobyrinic acid synthase
NA	HMPRNC0000_2076	<i>murE</i>	1	1			Putative amino acid ligase found clustered with an amidotransferase
NA	HMPRNC0000_2084	<i>gatB</i>		1	1		Aspartyl-tRNA(Asn) amidotransferase subunit B and Glutamyl-tRNA(Gln) amidotransferase subunit B
NA	HMPRNC0000_2086	<i>gatC</i>				-1	Aspartyl-tRNA(Asn) amidotransferase subunit C and Glutamyl-tRNA(Gln) amidotransferase subunit C
NA	HMPRNC0000_2092	<i>purB</i>	-1	-1			Adenylosuccinate lyase and SAICAR lyase
NA	HMPRNC0000_2104	<i>sdcS</i>	-1				Sodium-dependent anion transporter family
NA	HMPRNC0000_2128	<i>mapW2</i>		-1	-1		Extracellular adherence protein of broad specificity Eap/Map
NA	HMPRNC0000_2132	<i>scn</i>	1				Fibrinogen binding phage associated protein
NA	HMPRNC0000_2135	<i>lytN</i>	1				Phage lysin, N-acetylmuramoyl-L-alanine amidase
NA	HMPRNC0000_2191	.				1	Cytolytic pore-forming protein S component -> Leukocidin LukS-PV
NA	HMPRNC0000_2202	.	-1	-1			Hypothetical protein
NA	HMPRNC0000_2204	.	1	1			Nitroreductase family protein
NA	HMPRNC0000_2229	<i>yeaZ</i>				-1	TRNA threonylcarbamoyladenosine biosynthesis protein TsaB
NA	HMPRNC0000_2235	<i>iivC</i>	1	1			Ketol-acid reductoisomerase (NADP(+))
NA	HMPRNC0000_2243	.				1	Mobile element protein
NA	HMPRNC0000_2268	<i>deaD</i>		1	1		DEAD-box ATP-dependent RNA helicase DeaD
NA	HMPRNC0000_2280	<i>yidC</i>			-1		Inner membrane protein translocase and chaperone YidC
NA	HMPRNC0000_2285	<i>tenA</i>	-1	-1			Thiaminease II involved in salvage of thiamine pyrimidine moiety
NA	HMPRNC0000_2300	<i>atpE</i>	-1	-1			ATP synthase F0 sector subunit c
NA	HMPRNC0000_2302	.	-1	-1			Uncharacterized ncRNA
NA	HMPRNC0000_2306	<i>ywlG</i>	-1	-1	-1		UPF0340 protein YwlG
NA	HMPRNC0000_2319	.	1	1			Transcriptional regulator, HxlR family
NA	HMPRNC0000_2332	.	1	1			Hypothetical protein
NA	HMPRNC0000_2349	<i>czrA</i>	1	1	1		Zn(II) or Co(II)-specific transcriptional repressor protein
NA	HMPRNC0000_2351	.				-1	Lytic regulatory protein
NA	HMPRNC0000_2358	<i>mtlA</i>				1	PTS system, mannitol-specific IIC component / PTS system, mannitol-specific IIB component



NA	HMPRNC0000_2363	<i>fmtB1</i>				1	FmtB (Mrp) protein involved in methicillin resistance and cell wall biosynthesis
NA	HMPRNC0000_2370	<i>rocF</i>	-1				Arginase
NA	HMPRNC0000_2384	<i>sepA</i>				-1	Uncharacterized ncRNA
NA	HMPRNC0000_2387	.				-1	N-acetylglucosamine-1-phosphate uridylyltransferase eukaryotic
NA	HMPRNC0000_2389	.				1	Hypothetical protein
NA	HMPRNC0000_2401	<i>asp</i>	-1	-1		-1	Alkaline shock protein 23
NA	HMPRNC0000_2403	.				-1	Hypothetical protein
							Bifunctional protein: zinc-containing alcohol dehydrogenase, quinone oxidoreductase (NADPH:quinone reductase), Similar to arginate lyase
NA	HMPRNC0000_2405	.	1			1	
NA	HMPRNC0000_2407	.				1	Cell surface hydrolase (putative)
NA	HMPRNC0000_2409	<i>lacG</i>	-1			-1	6-phospho-beta-galactosidase
NA	HMPRNC0000_2471	<i>glcU</i>	1				Glucose:proton symporter GlcU
NA	HMPRNC0000_2473	.				-1	Hypothetical protein
NA	HMPRNC0000_2485	<i>sarV</i>	1			1	Transcriptional regulator SarV (accessory regulator V)
NA	HMPRNC0000_2528	<i>ssaA</i>	-1			-1	Secretory antigen precursor SsaA
NA	HMPRNC0000_2538	.				-1	hypothetical protein
NA	HMPRNC0000_2539	<i>yjgC</i>				-1	putative oxidoreductase YjgC
NA	HMPRNC0000_2545	.	1			1	Transcriptional regulator, DeoR family
NA	HMPRNC0000_2547	.	-1			-1	Protein of pXO2-46
NA	HMPRNC0000_2564	.	1				Hypothetical protein
NA	HMPRNC0000_2566	.				-1	hypothetical protein
NA	HMPRNC0000_2569	<i>hipO</i>	1				N-acetyl-L,L-diaminopimelate deacetylase
NA	HMPRNC0000_2570	<i>hutI</i>	-1			-1	Imidazolonepropionase
NA	HMPRNC0000_2572	<i>hutU</i>	-1			-1	Urocanate hydratase
NA	HMPRNC0000_2574	<i>hutG</i>				-1	Formiminoglutamase
NA	HMPRNC0000_2581	.	-1				ABC-type Na+ efflux pump, permease component
NA	HMPRNC0000_2582	.	-1				ABC transporter, ATP-binding protein
NA	HMPRNC0000_2615	.				-1	Uncharacterized ncRNA
NA	HMPRNC0000_2633	.	-1	-1		-1	1 Putative type II DNA modification enzyme
NA	HMPRNC0000_2660	<i>cbiX</i>	-1	-1		-1	Sirohydrochlorin ferrochelatase SirB
NA	HMPRNC0000_2669	.				1	Hypothetical protein
NA	HMPRNC0000_2673	.	1	1		1	L-cystine ABC transporter, ATP-binding protein TcyC
NA	HMPRNC0000_2674	.				1	Transcript
NA	HMPRNC0000_2685	<i>sbi</i>	1			1	1 IgG-binding protein SBI
NA	HMPRNC0000_2687	<i>hlgA</i>	1	-1		1	Cytolytic pore-forming protein S component -> Gamma-hemolysin HlgA
NA	HMPRNC0000_2689	<i>lukS</i>				1	Cytolytic pore-forming protein S component -> Gamma-hemolysin HlgC
NA	HMPRNC0000_2691	<i>hlgB</i>	1	-1		1	Cytolytic pore-forming protein F component -> Gamma-hemolysin HlgB
NA	HMPRNC0000_2708	.	1				Hypothetical protein
NA	HMPRNC0000_2711	.				1	Na+/H+ antiporter
NA	HMPRNC0000_2714	.	1				Hypothetical protein
NA	HMPRNC0000_2715	.	1				Uncharacterized ncRNA
NA	HMPRNC0000_2717	.	1			1	MFS-type transporter
NA	HMPRNC0000_2722	<i>proV</i>				1	Choline ABC transport system, ATP-binding protein OpuBA
NA	HMPRNC0000_2724	.	1	1		1	Amino acid-proton symporter YbeC
NA	HMPRNC0000_2725	<i>pnbA</i>	-1	-1		-1	Carboxylesterase, type B
NA	HMPRNC0000_2756	.				-1	hypothetical protein
NA	HMPRNC0000_2759	<i>pgm</i>	-1			-1	Phosphoglucosamine mutase / Phosphomannomutase
NA	HMPRNC0000_2765	<i>sasG</i>				-1	1 Virulence-associated cell-wall-anchored protein SasG
NA	HMPRNC0000_2769	<i>fnbB</i>	1			1	Fibronectin binding protein FnbB
NA	HMPRNC0000_2770	<i>fnbA</i>	1	1		1	Fibronectin binding protein FnbA
NA	HMPRNC0000_2774	.				-1	Transcriptional regulator, MerR family
NA	HMPRNC0000_2776	.				-1	hypothetical protein
NA	HMPRNC0000_2786	.	-1				Efflux ABC transporter, ATP-binding protein
NA	HMPRNC0000_2787	.	-1			-1	Putative membrane-spanning protein
NA	HMPRNC0000_2791	.	1			1	Phospholipase/carboxylesterase
NA	HMPRNC0000_2792	.	1			1	Glyoxalase family protein
NA	HMPRNC0000_2793	.	1			1	Transcriptional regulator, MarR family
NA	HMPRNC0000_2795	.	1			1	Glyoxalase family protein
NA	HMPRNC0000_2804	<i>srtA</i>	1				LPXTG specific sortase A
NA	HMPRNC0000_2814	.	1			1	Thioredoxin
NA	HMPRNC0000_2815	.	1			1	Hypothetical protein
NA	HMPRNC0000_2824	<i>mvaS</i>				-1	Hydroxymethylglutaryl-CoA synthase
NA	HMPRNC0000_2828	<i>clpL</i>				-1	ClpE family protein
NA	HMPRNC0000_2834	<i>rocA</i>	-1			-1	Delta-1-pyrroline-5-carboxylate dehydrogenase
NA	HMPRNC0000_2839	<i>copZ</i>	1				Copper(I) chaperone CopZ
NA	HMPRNC0000_2842	<i>crtN</i>	-1				-1 Dehydroisqualene desaturase
NA	HMPRNC0000_2843	<i>crtM</i>				-1	-1 Dehydroisqualene synthase
NA	HMPRNC0000_2844	.	-1	-1		-1	4,4'-diaponeurosporenoate glycosyltransferase
NA	HMPRNC0000_2846	<i>crtI</i>	-1				Diapycopene oxygenase
NA	HMPRNC0000_2849	.				-1	Acyltransferase
NA	HMPRNC0000_2852	<i>isaA</i>				-1	Immunodominant antigen A precursor
NA	HMPRNC0000_2856	.	1	1		1	Hypothetical protein
NA	HMPRNC0000_2857	.	1	1		1	1 Hypothetical protein
NA	HMPRNC0000_2865	.				-1	-1 Putative hydrolase/acyltransferase

NA	HMPRNC0000_2891	.		1	1	-1	-1	Amino acid permease, GabP family
NA	HMPRNC0000_2898	.		-1		-1		hypothetical protein
NA	HMPRNC0000_2918	.		-1				ABC transporter sensor linked response regulator
NA	HMPRNC0000_2924	.				-1		Cardiolipin synthetase
NA	HMPRNC0000_2926	<i>clfB</i>		-1	-1	-1	-1	Clumping factor ClfB, fibrinogen binding protein
NA	HMPRNC0000_2942	<i>manA</i>				-1		PTS system, mannose-specific IIB/IIC/IIA component
NA	HMPRNC0000_2949	<i>sraP</i>			1			Putative cell-wall-anchored protein SasF (LPXAG motif)
NA	HMPRNC0000_2966	.		-1		-1		hypothetical protein
NA	HMPRNC0000_2986	<i>hisB</i>			1			Imidazoleglycerol-phosphate dehydratase
NA	HMPRNC0000_2987	<i>hisC</i>		1	1			Histidinol-phosphate aminotransferase
NA	HMPRNC0000_2990	<i>hisG</i>		1	1			ATP phosphoribosyltransferase -> HisGs
NA	HMPRNC0000_2991	<i>hisZ</i>		1	1			ATP phosphoribosyltransferase regulatory subunit
NA	HMPRNC0000_2996	.			1			Duplicated ATPase component MtsB of energizing module of methionine-regulated ECF transporter
NA	HMPRNC0000_2999	.			1			Hypothetical protein
NA	HMPRNC0000_3011	.					1	Hypothetical protein
NA	HMPRNC0000_3019	<i>cspB</i>					-1	Cold shock protein of CSP family
NA	HMPRNC0000_3025	.		1	1		1	Chromosome (plasmid) partitioning protein ParB-2