

Appendix

Table A.3.01 Manual functional annotation of the Methanogenic archaeon isolate ISO4-H5 predicted open reading frames. Table excludes hypothetical proteins.

AMINO ACID METABOLISM

Glutamate/glutamine

AR505_0145 glutamate dehydrogenase GdhA
AR505_0091 glutamine synthase alpha subunit GlnA

Arginine

AR505_0671 argininosuccinate lyase ArgH
AR505_0672 argininosuccinate synthase ArgG
AR505_0673 *N*-acetyl-gamma-glutamyl-phosphate reductase
ArgC
AR505_0674 bifunctional ornithine acetyltransferase/*N*-acetylglutamate synthase protein ArgJ
AR505_0675 acetylglutamate kinase ArgB
AR505_0676 acetylornithine aminotransferase ArgD
AR505_1401 ornithine carbamoyltransferase ArgF

General

AR505_1429 aspartate aminotransferase Ast1
AR505_1666 aspartate aminotransferase Ast2

Alanine

AR505_1199 alanine aminotransferase Alt

Aspartate/asparagine

AR505_0736 asparagine synthase (glutamine-hydrolyzing)
AsnB1
AR505_1303 asparagine synthase (glutamine-hydrolyzing) AsnB2

Lysine

AR505_0160 aspartate kinase LysC
AR505_0157 L,L-diaminopimelate aminotransferase DapL
AR505_0158 diaminopimelate epimerase DapF
AR505_0159 diaminopimelate decarboxylase LysA
AR505_0161 dihydrodipicolinate synthase DapA
AR505_0491 aspartate-semialdehyde dehydrogenase Asd
AR505_0728 dihydrodipicolinate reductase DapB
AR505_1120 aspartokinase with LysC domain

Pyrrolysine

AR505_1322 pyrrolysine synthase PylD
AR505_1323 (2R,3R)-3-methylornithyl-N⁶-lysine synthase PylC
AR505_1324 methylornithine synthase PylB
AR505_1325 pyrrolysine--tRNA ligase PylS

Methionine

AR505_0293 homoserine dehydrogenase MetL
AR505_0694 homoserine *O*-succinyltransferase MetA
AR505_0738 *O*-acetylhomoserine/*O*-acetylserine sulfhydrylase
MetZ/CysK3

SAM cycle

AR505_0547 *S*-adenosyl-L-homocysteine hydrolase AhcY1
AR505_1788 *S*-adenosyl-L-homocysteine hydrolase AhcY2
AR505_0467 *S*-adenosylmethionine synthetase MetK1
AR505_0579 *S*-adenosylmethionine synthetase MetK2
AR505_1118 *S*-adenosylhomocystein nucleosidase

Threonine

AR505_0610 homoserine kinase ThrB
AR505_0611 threonine synthase ThrC

Chorismate

AR505_1148 triose-phosphate isomerase TpiA
AR505_0508 fructose 1,6-bisphosphate aldolase Fba
AR505_0509 3-dehydroquinate synthase AroB
AR505_0510 shikimate 5-dehydrogenase AroE
AR505_0511 shikimate kinase AroL
AR505_0512 3-phosphoshikimate 1-carboxyvinyltransferase
AroA
AR505_1449 chorismate synthase AroC

Tryptophan

AR505_1158 anthranilate synthase component I TrpE
AR505_1159 anthranilate synthase component II TrpG
AR505_1160 anthranilate phosphoribosyltransferase TrpD
AR505_1161 indole-3-glycerol phosphate synthase TrpC
AR505_1162 phosphoribosylanthranilate isomerase TrpF
AR505_1163 tryptophan synthase beta subunit TrpB
AR505_1164 tryptophan synthase alpha subunit TrpA
AR505_1151 tryptophan synthase beta subunit truncated TrpB

Phenylalanine/tyrosine

AR505_0490 chorismate mutase AroH
AR505_1450 chorismate mutase AroH
AR505_1745 prephenate dehydrogenase TyrA
AR505_0515 prephenate dehydratase PheA

Proline

AR505_0108 glutamate-5-semialdehyde dehydrogenase ProA
AR505_0109 glutamate 5-kinase ProB
AR505_1634 pyrroline-5-carboxylate reductase ProC

Histidine

AR505_0486 bifunctional phosphoribosyl-ATP
pyrophosphatase/phosphoribosyl-AMP
cyclohydrolase HisI
AR505_0487 imidazoleglycerol phosphate synthase HisF
AR505_0488 imidazoleglycerol-phosphate dehydratase HisB
AR505_0494 ATP phosphoribosyl transferase
AR505_0495 histidinol-phosphate aminotransferase HisC
AR505_0496 imidazole glycerol phosphate synthase HisH
AR505_0497 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide ribonucleotide isomerase HisA
AR505_1073 histidinal dehydrogenase HisD
AR505_1770 histidinol-phosphate phosphatase HisK

Serine

AR505_1664 phosphoglycerate dehydrogenase SerA
AR505_1665 phosphoserine amidotransferase SerC
AR505_0073 phosphoserine phosphatase SerB1
AR505_0757 phosphoserine phosphatase SerB2

Cysteine

AR505_1192 serine acetyltransferase CysE
AR505_0799 cysteine synthase CysK1
AR505_0800 cysteine synthase CysM
AR505_0695 cysteine synthase CysK2

Isoleucine/leucine/valine

AR505_0152 acetolactate synthase large subunit IlvB1
AR505_0153 acetolactate synthase large subunit IlvB2
AR505_0542 acetolactate synthase large subunit IlvB3
AR505_1768 acetolactate synthase small subunit IlvN
AR505_1767 branched-chain-amino-acid aminotransferase IlvE

AR505_0150	ketol-acid reductoisomerase IlvC
AR505_1452	dihydroxy-acid dehydratase IlvD
AR505_0631	2-isopropylmalate/homocitrate/citramalate synthase LeuA/CimA
AR505_0632	3-isopropylmalate dehydratase large subunit LeuC
AR505_0633	3-isopropylmalate dehydratase small subunit LeuD
AR505_0634	3-isopropylmalate dehydrogenase LeuB
Polyamines	
AR505_1607	arginase/agmatinase family protein SpeB
AR505_0376	<i>N</i> -carbamoyl-D-amino acid amidohydrolase AguB
AR505_0268	pyruvoyl-dependent arginine decarboxylase PdaD
Salvage- general	
AR505_0999	indolepyruvate ferredoxin oxidoreductase alpha subunit IorA
AR505_0998	indolepyruvate ferredoxin oxidoreductase beta subunit IorB

CELL CYCLE

Cell division

AR505_0446	cell division control protein Cdc48
AR505_0854	cell division control protein Cdc48
AR505_1412	cell division ATPase MinD
AR505_0975	cell division protein FtsZ1
AR505_1792	cell division protein FtsZ2

Chromosome replication

AR505_1277	ATP-dependent DNA ligase DnII
AR505_0001	orc1/cdc6 family replication initiation protein
AR505_1205	cdc6 family replication initiation protein Cdc6
AR505_0130	DNA polymerase family B PolB
AR505_0374	DNA polymerase III PolC
AR505_1037	DNA polymerase IV
AR505_1438	DNA polymerase II large subunit DP2 PolD2
AR505_1816	DNA polymerase II small subunit DP1 PolD1
AR505_0009	DNA primase small subunit PriA
AR505_1142	DNA primase DnaG
AR505_1782	DNA primase large subunit PriB
AR505_1668	OB fold nucleic acid binding domain-containing protein
AR505_0828	replication factor C large subunit RfcL
AR505_1209	replication factor C small subunit
AR505_0018	replicative DNA helicase Mcm
AR505_0209	ribonuclease HII RnhB
AR505_0420	ribonuclease H
AR505_0461	flap endonuclease Fen
AR505_0603	DNA-binding protein
AR505_0125	replication-associated recombination protein A

Genome segregation

AR505_0033	DNA gyase B subunit GyrB
AR505_0034	DNA gyase A subunit GyrA
AR505_1609	chromosome segregation and condensation protein ScpB
AR505_1610	chromosome segregation and condensation protein ScpA
AR505_1611	chromosome segregation protein SMC
AR505_0388	DNA topoisomerase VI subunit A
AR505_0389	DNA topoisomerase VI subunit B
AR505_1299	DNA topoisomerase I TopA

CELL ENVELOPE

Cell surface proteins

AR505_0005	adhesin-like protein
------------	----------------------

AR505_0061	adhesin-like protein
AR505_0353	adhesin-like protein
AR505_0354	adhesin-like protein
AR505_0355	adhesin-like protein
AR505_0407	adhesin-like protein
AR505_0594	adhesin-like protein
AR505_0614	adhesin-like protein
AR505_0646	adhesin-like protein
AR505_0654	adhesin-like protein
AR505_0657	adhesin-like protein
AR505_0658	adhesin-like protein
AR505_0660	adhesin-like protein
AR505_0664	adhesin-like protein
AR505_0666	adhesin-like protein
AR505_0668	adhesin-like protein
AR505_0670	adhesin-like protein
AR505_0704	adhesin-like protein
AR505_0744	adhesin-like protein
AR505_0807	adhesin-like protein
AR505_0851	adhesin-like protein
AR505_0874	adhesin-like protein
AR505_0993	adhesin-like protein
AR505_0985	adhesin-like protein
AR505_0991	adhesin-like protein
AR505_0992	adhesin-like protein
AR505_1032	adhesin-like protein
AR505_1033	adhesin-like protein
AR505_1155	adhesin-like protein
AR505_1173	adhesin-like protein
AR505_1290	adhesin-like protein
AR505_1509	adhesin-like protein
AR505_1521	adhesin-like protein
AR505_1524	adhesin-like protein
AR505_1532	adhesin-like protein
AR505_1534	adhesin-like protein
AR505_1547	adhesin-like protein
AR505_1549	adhesin-like protein
AR505_1559	adhesin-like protein
AR505_1560	adhesin-like protein
AR505_1561	adhesin-like protein
AR505_1707	adhesin-like protein
AR505_1715	adhesin-like protein
AR505_1741	adhesin-like protein
AR505_1761	adhesin-like protein

Expolysaccharide synthesis

AR505_0539	polysaccharide biosynthesis protein
AR505_0540	cell wall biosynthesis protein glycosyltransferase family
AR505_0543	CDP-glucose 4,6-dehydratase RfbG
AR505_0549	glucose-1-phosphate cytidylyltransferase RfbF
AR505_0550	glycosyl transferase GT2 family
AR505_0551	UDP-galactopyranose mutase Glf
AR505_0552	glucose-1-phosphate thymidylyltransferase RfbA
AR505_0553	dTDP-glucose 4,6-dehydratase RfbB
AR505_0554	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC
AR505_0555	polysaccharide/polyol phosphate ABC transporter permease protein
AR505_0556	polysaccharide/polyol phosphate ABC transporter ATP-binding protein
AR505_0558	LPS biosynthesis protein LICD family
AR505_0559	glycosyl transferase GT8 family
AR505_0561	glycosyl transferase GT2 family
AR505_1106	dolichol kinase (7 TMs)
AR505_1754	D-sedoheptuloase 7-phosphate isomerase
AR505_1763	glycosyl transferase GT2 family
AR505_1770	D-glycerol-D-manno-heptose-7-phosphate kinase
AR505_1771	D-glycerol-D-manno-heptose 1,7-bisphosphate 7-phosphatase
AR505_1772	D-glycerol-D-manno-heptose 1-phosphate guanylyltransferase
AR505_1778	glycosyl transferase GT2 family
AR505_1786	glycosyl transferase family protein
AR505_1787	glycosyl transferase family protein

Cell envelope phospholipid biosynthesis			
AR505_0081	UDP-glucose 4-epimerase	GalE	
AR505_0123	phosphoglucosamine mutase	GlmM	
AR505_0361	cell wall biosynthesis protein	Mur ligase family	
AR505_0541	NAD-dependent epimerase/dehydratase		
AR505_0542	acetolactate synthase large subunit	IlvB	
AR505_1608	phosphoglucosamine mutase	GlmM	

CELLULAR PROCESSES

Oxidative stress response			
AR505_0212	CoA-disulfide reductase cdr		
AR505_0263	glycolate oxidase D subunit	GlcD	
AR505_0630	desulfoferredoxin	Dfx	
AR505_0700	rubredoxin		
AR505_0766	peroxiredoxin	AhpC	
AR505_1047	rubredoxin		
AR505_1353	rubrerythrin	Rbr	
AR505_0047	thioredoxin	TrxA	
AR505_0048	thioredoxin-disulfide reductase	TrxB1	

Stress response			
AR505_1343	universal stress protein	UspA	
AR505_0443	universal stress protein	UspA	
AR505_0294	universal stress protein	UspA	

CENTRAL CARBON METABOLISM

Acetate			
AR505_0429	pyruvate ferredoxin oxidoreductase gamma subunit	PorC	
AR505_0430	pyruvate ferredoxin oxidoreductase delta subunit	PorD	
AR505_0431	pyruvate ferredoxin oxidoreductase alpha subunit	PorA	
AR505_0432	pyruvate ferredoxin oxidoreductase beta subunit	PorB	
AR505_1282	acetyl-CoA synthetase	AcsA	

Aromatic ccompounds			
AR505_1280	carboxymuconolactone decarboxylase family protein		

Bicarbonate			
AR505_0752	nitrate/sulfonate/bicarbonate ATPase	NtrD	ABC transporter
AR505_0753	nitrate/sulfonate/bicarbonate permease protein	NtrB	ABC transporter
AR505_0754	nitrate/sulfonate/bicarbonate substrate-binding protein		ABC transporter
AR505_1245	carbonic anhydrase	Cab	

Gluconeogenesis			
AR505_1769	bifunctional isomerase	phosphoglucose/phosphomannose	
AR505_0154	glyceraldehyde-3-phosphate dehydrogenase	Gap	
AR505_0155	phosphoglycerate kinase	Pgk	
AR505_0427	phosphoenolpyruvate synthase	PpsA	
AR505_0470	phosphopyruvate hydratase	Eno	
AR505_0474	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	ApgM	
AR505_0560	bifunctional isomerase	phosphoglucose/phosphomannose	
AR505_0942	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	GpmA	
AR505_1104	phosphoenolpyruvate synthase	PpsA	
AR505_1148	triose-phosphate isomerase	TpiA	
AR505_1149	fructose 1,6-bisphosphatase	Fbp	
AR505_0082	aldose 1-epimerase		
AR505_0932	fructose-bisphosphate aldolase	Fba	

Glycolate salvage pathway		
AR505_0753	phosphoglycolate/pyridoxal phosphate	phosphatase family
AR505_0604	phosphoglycolate	phosphatase
AR505_0762	glycolate oxidase subunit	GlcD

PRPP synthesis		
AR505_1513	ribose 5-phosphate isomerase A	RpiA
AR505_1685	ribose-phosphate diphosphokinase	Prs

Ribulose monophosphate pathway		
AR505_0014	bifunctional synthase/ribonuclease regulator	hexulose-6-phosphate
AR505_0177	6-phospho 3-hexuloisomerase	hxlB
AR505_1785	ribokinase	RbsK
AR505_1648	transketolase subunit	B
AR505_1649	transketolase subunit	A
AR505_1647	fructose-6-phosphate aldolase	Fsa
AR505_0461	ribulose-phosphate 3-epimerase	Rpe
AR505_1604	ribulose-5-phosphate 4-epimerase and epimerases and aldolases	related

Tricarboxylic cycle		
AR505_0022	fumarate hydratase	FumA
AR505_0023	fumarate hydratase	FumB
AR505_1780	malate dehydrogenase	Mdh
AR505_0592	aconitate hydratase 1	AcnA
AR505_0678	citrate synthase	
AR505_0531	isopropylmalate/isohomocitrate	dehydrogenases
	LeuB	

ENERGY METABOLISM

Electron transfer		
AR505_0289	NADPH-dependent FMN reductase	
AR505_0446	flavodoxin	
AR505_0451	ferredoxin	
AR505_0452	ferredoxin	
AR505_0627	NADPH-dependent FMN reductase	
AR505_0681	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_0692	anaerobic sulfatase maturase	
AR505_0725	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_0763	electron transfer flavoprotein beta subunit	
AR505_0764	electron transfer flavoprotein alpha subunit	
AR505_0775	NADPH-dependent FMN reductase	
AR505_0825	flavodoxin	
AR505_0902	Fe-S oxidoreductase	
AR505_0915	NADPH-dependent FMN reductase	
AR505_0953	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_0976	NADPH-dependent FMN reductase	
AR505_0978	flavodoxin-like protein	
AR505_1039	NADPH-dependent FMN reductase	
AR505_1068	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_1189	flavoredoxin family protein	
AR505_1320	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_1338	NADPH-dependent FMN reductase	
AR505_1410	NADPH-dependent FMN reductase	
AR505_1434	Ferredoxin	
AR505_1512	4Fe-4S-binding-domain containing ATP-binding protein	
AR505_1579	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	
AR505_1818	A ₁ A ₀ archaeal ATP synthase subunit	D
AR505_1819	A ₁ A ₀ archaeal ATP synthase subunit	B
AR505_1820	A ₁ A ₀ archaeal ATP synthase subunit	A
AR505_1821	A ₁ A ₀ archaeal ATP synthase subunit	F
AR505_1822	A ₁ A ₀ archaeal ATP synthase subunit	C
AR505_1823	A ₁ A ₀ archaeal ATP synthase subunit	E

AR505_1824	A ₁ A ₀ archaeal ATP synthase subunit K
AR505_1825	A ₁ A ₀ archaeal ATP synthase subunit I
AR505_1826	A ₁ A ₀ archaeal ATP synthase subunit H
Alcohol metabolism	
AR505_0483	NADP-dependent alcohol dehydrogenase Adh
H₂ metabolism	
AR505_1476	methyl-viologen-reducing hydrogenase alpha subunit MvhA
AR505_1477	methyl-viologen-reducing hydrogenase gamma subunit MvhG
AR505_1478	methyl-viologen-reducing hydrogenase delta subunit MvD
Methanogenesis pathway	
AR505_0040	CoB--CoM heterodisulfide reductase subunit D HdrD
AR505_0168	CoB--CoM heterodisulfide reductase subunit D HdrD
AR505_0273	CoB--CoM heterodisulfide reductase subunit C HdrC
AR505_0274	CoB--CoM heterodisulfide reductase subunit B HdrB
AR505_0679	CoB--CoM heterodisulfide reductase subunit B HdrB
AR505_1479	CoB--CoM heterodisulfide reductase subunit A HdrA
AR505_0949	methanol-cobalamin methyltransferase B subunit MtaB2
AR505_0950	methanol corrinoid protein MtaC2
AR505_0951	methanol-cobalamin methyltransferase B subunit MtaB1
AR505_0952	methanol corrinoid protein MtaC1
AR505_1064	methyltransferase cognate corrinoid protein
AR505_1066	methylcobalamin:coenzyme M methyltransferase MtsA
AR505_1067	methylthiol:corrinoid protein mtsB
AR505_1327	monomethylamine methyltransferase MtmB1
AR505_1328	monomethylamine methyltransferase MtmB2
AR505_1329	methyltransferase cognate corrinoid proteins MtmC1
AR505_1330	methyltransferase cognate corrinoid proteins MtmC2
AR505_1332	dimethylamine:corrinoid methyltransferase MtbB
AR505_1333	dimethylamine corrinoid protein MtbC
AR505_0772	trimethylamine:corrinoid methyltransferase MttB
AR505_0773	trimethylamine: corrinoid proteins MttC
AR505_1331	methylamine permease
AR505_1035	methylcobalamin:coenzyme M methyltransferase MtaA1
AR505_1063	methylcobalamin:coenzyme M methyltransferase MtaA2
AR505_0110	methyltransferase cognate corrinoid protein
AR505_1404	methylcobalamin:coenzyme M methyltransferase MtaA3
AR505_1575	methylcobalamin:coenzyme M methyltransferase MtaA4
AR505_1391	methyl-coenzyme M reductase C subunit McrC
AR505_1392	methyl-coenzyme M reductase component A2 AtwA
AR505_1396	methyl-coenzyme M reductase alpha subunit McrA
AR505_1397	methyl-coenzyme M reductase gamma subunit McrG
AR505_1398	methyl-coenzyme M reductase operon protein D McrD
AR505_1399	methyl-coenzyme M reductase beta subunit McrB
AR505_1622	F ₄₂₀ H ₂ dehydrogenase subunit N FpoN
AR505_1623	F ₄₂₀ H ₂ dehydrogenase subunit M FpoM
AR505_1624	F ₄₂₀ H ₂ dehydrogenase subunit L FpoL
AR505_1625	F ₄₂₀ H ₂ dehydrogenase subunit K FpoK
AR505_1626	hypothetical transmembrane protein
AR505_1627	NADH:ubiquinone oxidoreductase J FpoJ
AR505_1628	NADH:quinone oxidoreductase I FpoI
AR505_1629	NADH dehydrogenase subunit H FpoH
AR505_1630	NADH dehydrogenase subunit D FpoD
AR505_1631	NADH dehydrogenase subunit C FpoC
AR505_1632	NADH dehydrogenase subunit B FpoB
AR505_1633	NADH dehydrogenase subunit A FpoA
AR505_1634	NADP oxidoreductase coenzyme F ₄₂₀ dependent
AR505_0362	methanogenesis marker protein 13
AR505_0724	methanogenesis marker protein 16
AR505_0786	methanogenesis marker protein 2
AR505_1203	methanogenesis marker protein 8

AR505_1385	methanogenesis marker protein 7
AR505_1386	methanogenesis marker protein 17
AR505_1387	methanogenesis marker protein 15
AR505_1388	methanogenesis marker protein 5
AR505_1389	methanogenesis marker protein 6
AR505_1390	methanogenesis marker protein 3
AR505_1405	methanogenesis marker protein 1
AR505_1417	methanogenesis marker protein 4
AR505_1637	methanogenesis marker protein 11

LIPID METABOLISM

Biosynthesis general

AR505_0892	geranylgeranyl reductase family protein
AR505_0928	acyl carrier protein phosphodiesterase AcpD
AR505_1433	geranylgeranyl reductase
AR505_1618	geranylgeranyl reductase
AR505_1646	geranylgeranyl reductase family protein

Lipid backbone

AR505_0626	NAD(P)-dependent dehydrogenase	glycerol-1-phosphate
------------	--------------------------------	----------------------

Phospholipid biosynthesis

AR505_0918	CDP-alcohol phosphatidyltransferase
AR505_0933	cardiolipin synthase
AR505_1147	phospholipase D/transphosphatidylase PID
AR505_1433	digeranylgeranylglycerophospholipid reductase DGGGPR
AR505_1587	digeranylgeranylglyceryl phosphate synthase DGGGPS
AR505_1588	geranylgeranylglyceryl phosphate synthase GGGPS
AR505_1616	CDP-diglyceride synthetase CdsA
AR505_1783	CDP-diacylglycerol—glycerol-3-phosphate 3-phosphatidyltransferase

Mevalonate pathway

AR505_0004	acetyl-CoA acetyltransferase
AR505_0601	hydroxymethylglutaryl-CoA synthase
AR505_0602	acetyl-CoA acetyltransferase
AR505_0768	hydroxymethylglutaryl-CoA reductase (NADPH) HmgA
AR505_1431	mevalonate kinase Mvk

Elongation of isoprenoid side chains

AR505_0191	isopentenyl diphosphate delta-isomerase Fni
AR505_0192	isopentenyl phosphate kinase Ippk
AR505_1587	prenyltransferase UbiA
AR505_0190	bifunctional short chain isoprenyl diphosphate synthase IdsA/GGPS
AR505_1619	octaprenyl-diphosphate synthase IspB

MOBILE ELEMENTS

CRISPR-associated genes

AR505_1089	CRISPR-associated endonuclease Cas3-HD
AR505_1090	CRISPR type I-E/ECOLI-associated protein CasA/Cse1
AR505_1091	CRISPR type I-E/ECOLI-associated protein CasB/Cse2 complex
AR505_1092	CRISPR-associated protein Cas7/Cse4/CasC
AR505_1093	CRISPR-associated protein Cas5/CasD
AR505_1094	CRISPR-associated protein Cas6/Cse3/CasE
AR505_1095	CRISPR-associated endonuclease Cas1

Toxin/antitoxin

AR505_0857	prevent-host-death family protein
AR505_0858	addiction module toxin, RelE/StbE family

AR505_0980	toxin-antitoxin system, toxin component, HipA family
AR505_1466	addiction module antitoxin RelB/DinJ
AR505_1468	addiction module antitoxin RelB/DinJ
AR505_1566	death-on-curing family protein hypothetical protein

Transposase

AR505_0010	transposase
AR505_0106	transposase
AR505_0107	transposase
AR505_0147	transposase IS4 family
AR505_0151	transposase IS4 family
AR505_0213	transposase IS116/IS110/IS902 family
AR505_0215	transposase IS605 OrfB family
AR505_0276	transposase IS605 OrfB family
AR505_0290	transposase IS605 OrfB family
AR505_0371	transposase IS605 OrfB family
AR505_0372	transposase
AR505_0440	transposase IS4 family
AR505_0498	transposase IS605 OrfB family
AR505_0516	transposase IS605 OrfB family
AR505_0523	transposase IS605 OrfB family
AR505_0525	transposase
AR505_0528	transposase
AR505_0574	transposase
AR505_0580	transposase IS605 OrfB family
AR505_0639	transposase IS605 OrfB family
AR505_0677	transposase IS605 OrfB family
AR505_0708	transposase
AR505_0784	transposase IS4 family
AR505_0860	transposase IS605 OrfB family
AR505_0903	transposase IS605 OrfB family
AR505_0913	transposase IS605 OrfB family
AR505_1219	transposase IS605 OrfB family
AR505_1239	transposase
AR505_1356	transposase IS4 family
AR505_1423	transposase
AR505_1458	transposase IS4 family protein
AR505_1562	transposase
AR505_1563	transposase
AR505_1574	transposase
AR505_1692	transposase IS605 OrfB family
AR505_1703	transposase
AR505_1714	transposase IS4 family
AR505_1765	transposase IS605 OrfB family
AR505_1775	transposase IS605 OrfB family
AR505_1777	transposase IS605 OrfB family

Integrase

AR505_0313	phage integrase
AR505_0669	integrase catalytic subunit
AR505_0931	phage integrase
AR505_1543	phage integrase
AR505_1640	phage integrase
AR505_1697	phage integrase family protein
AR505_1772	group II intron maturase
AR505_1518	prophage Lp3 helicase
AR505_1570	phage integrase

NITROGEN METABOLISM

Potential Fixation

AR505_0186	nitroreductase family protein
AR505_0207	nitrilase/cyanide hydratase and apolipoprotein <i>N</i> -acyltransferase
AR505_0359	nitrogenase iron protein NifH
AR505_0591	nitroreductase family protein
AR505_0822	nitroreductase family protein
AR505_1268	dinitrogenase iron-molybdenum cofactor biosynthesis protein
AR505_1288	oxidoreductase/nitrogenase component 1
AR505_1289	nitrogenase
AR505_1502	oxidoreductase/nitrogenase component 1

Other

AR505_0956	hydroxylamine reductase Hcp
AR505_1059	FeS cluster assembly scaffold protein NifU
AR505_1060	cysteine desulfurase NifS
AR505_1447	nitrogenase cofactor biosynthesis protein NifB
AR505_1501	nitrogenase iron protein NifH

Regulation

AR505_0206	nitrogen regulatory protein P-II
AR505_0402	nitrogen regulatory protein P-II

Transport

AR505_0205	ammonium transporter Amt
------------	--------------------------

NUCLEIC ACID METABOLISM

DNA-binding proteins

AR505_0051	histone acetyltransferase ELP3 family
AR505_0603	DNA-binding protein
AR505_0732	NAD-dependent deacetylase SIR2 family
AR505_0777	DNA-binding protein
AR505_1236	archaeal histone
AR505_1617	DNA/RNA-binding protein
AR505_1668	OB fold nucleic acid binding domain-containing protein

Helicase

AR505_0025	ATP-dependent DNA helicase
AR505_0039	ATP-dependent DNA helicase
AR505_0583	helicase SNF2 family
AR505_0613	helicase, superfamily II
AR505_0805	ATP-dependent DNA helicase
AR505_0814	DNA repair helicase Rad3
AR505_1115	DEAD/DEAH box helicase domain-containing protein
AR505_1117	ATP-dependent RNA helicase
AR505_1132	ATP-dependent DNA helicase UvrD/REP family
AR505_1251	DNA helicase
AR505_1267	helicase
AR505_1278	DEAD/DEAH box helicase domain-containing protein
AR505_1321	ATP-dependent RNA helicase
AR505_1337	DEAD/DEAH box helicase domain-containing protein
AR505_1369	ATP-dependent DNA helicase
AR505_1500	DNA helicase
AR505_1531	ATP-dependent DNA helicase
AR505_1662	DEAD/DEAH box helicase domain-containing protein

Recombination and repair

AR505_0027	8-oxoguanine DNA-glycosylase Ogg
AR505_0028	endonuclease IV
AR505_0117	ssDNA exonuclease RecJ
AR505_0125	replication-associated recombination protein A
AR505_0178	endonuclease IV
AR505_0187	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase
AR505_0189	DNA repair and recombination protein RadB
AR505_0329	DNA mismatch endonuclease Vsr
AR505_0391	formamidopyrimidine-DNA glycosylase MutM
AR505_0420	ribonuclease H
AR505_0448	6- <i>O</i> -methylguanine DNA methyltransferase Ogt
AR505_0693	endoribonuclease L-PSP
AR505_0798	ssDNA exonuclease RecJ
AR505_1055	site-specific recombinase
AR505_1056	site-specific recombinase
AR505_1069	DNA repair photolyase
AR505_1084	exodeoxyribonuclease VII small subunit XseB
AR505_1085	exodeoxyribonuclease VII large subunit XseA
AR505_1139	exonuclease
AR505_1154	archaeal Holliday junction resolvase Hjc

AR505_1298	GTP:adenosylcobinamide-phosphate guanylyltransferase CobU endonuclease III Nth
AR505_1305	DNA alkylation repair enzyme
AR505_1309	ssDNA exonuclease RecJ
AR505_1402	excinuclease ABC A subunit UvrA
AR505_1578	DNA repair and recombination protein RadA
AR505_1585	uracil-DNA glycosylase Ung
AR505_1614	resolvase domain-containing protein
AR505_1729	

Regulation	
AR505_0907	peptidase U62 modulator of DNA gyrase
AR505_0908	peptidase U62 modulator of DNA gyrase

Restriction and modification	
AR505_0327	DNA-cytosine methyltransferase Dcm
AR505_0339	DNA-cytosine methyltransferase Dcm
AR505_0340	DNA-cytosine methyltransferase Dcm
AR505_0662	GTPase subunit of restriction endonuclease
AR505_0663	McrBC 5-methylcytosine restriction system component
AR505_0958	viral recombinase YgaJ family

PROTEIN FATE

Protein degradation	
AR505_0013	peptidase M48 family (4 TMHs)
AR505_0115	universal archaeal protein Kae1
AR505_0122	metal-dependent protease
AR505_0144	peptidase M24 family
AR505_0164	hypothetical protein
AR505_0188	Kae1-associated kinase Bud32
AR505_0264	peptidase M50 family (6 TMHs)
AR505_0270	peptidase M16 family
AR505_0449	aminoacyl-histidine dipeptidase PepD
AR505_0615	ATP-dependent protease S16 family
AR505_0688	amidase
AR505_0702	cysteine proteinase
AR505_0785	peptidase M50 family (6 TMHs)
AR505_0919	proline-specific peptidases
AR505_0967	proteasome endopeptidase complex
AR505_1001	peptidase U32 family
AR505_1143	ATP-dependent protease
AR505_1318	peptidase M18 family
AR505_1443	methionine aminopeptidase Map
AR505_1674	proteasome-activating nucleotidase

Protein folding	
AR505_0007	prefoldin alpha subunit PfdA
AR505_0092	thermosome subunit
AR505_0093	molecular chaperone GrpE
AR505_0094	chaperone protein DnaK
AR505_0095	chaperone protein DnaJ
AR505_0286	heat shock protein Hsp90
AR505_0836	peptidyl-prolyl cis-trans isomerase
AR505_1062	thermosome subunit
AR505_1228	chaperone protein DnaK
AR505_1232	chaperone protein DnaK
AR505_1248	ATP-dependent chaperone protein ClpB
AR505_1482	proteasome alpha subunit PsmA
AR505_1490	prefoldin beta subunit PfdB

Protein secretion	
AR505_0006	signal recognition particle receptor FtsY
AR505_0241	preprotein translocase subunit SecY
AR505_0667	signal peptidase I
AR505_0758	signal recognition particle SRP54 protein
AR505_0962	Type II/IV secretion system protein E
AR505_0986	signal peptidase I
AR505_1473	signal recognition particle SRP19 protein
AR505_1612	signal peptidase I
AR505_1828	signal peptidase I

AR505_1799	protein translocase subunit Sss1
------------	----------------------------------

PROTEIN SYNTHESIS

Other	
AR505_0131	translation-associated GTPase
AR505_1444	Sua5/YciO/YrdC/YwIC family translation factor
AR505_1683	tRNA methyltransferase subunit

Ribosomal proteins	
AR505_0008	ribosomal protein LX
AR505_0057	ribosomal protein L30e Rpl30e
AR505_0077	ribosomal protein S17e Rps17e
AR505_0118	ribosomal protein S15P Rps15p
AR505_0129	ribosomal protein L15e Rpl15e
AR505_0135	ribosomal protein L21e Rpl21e
AR505_0179	ribosomal protein L18e Rpl18e
AR505_0180	ribosomal protein L13P Rpl13p
AR505_0181	ribosomal protein S9P Rps9p
AR505_0218	ribosomal protein L3P Rpl3p
AR505_0219	ribosomal protein L4P Rpl4p
AR505_0220	ribosomal protein L23P Rpl23p
AR505_0221	ribosomal protein L2P Rpl2p
AR505_0222	ribosomal protein S19P Rps19p
AR505_0223	ribosomal protein L22P Rpl22p
AR505_0224	ribosomal protein S3P Rps3p
AR505_0225	ribosomal protein L29P Rpl29p
AR505_0228	ribosomal protein S17P Rps17p
AR505_0229	ribosomal protein L14e Rpl14e
AR505_0230	ribosomal protein L24P Rpl24p
AR505_0231	ribosomal protein S4e Rps4e
AR505_0232	ribosomal protein L5P Rpl5p
AR505_0233	ribosomal protein S8P Rps8p
AR505_0234	ribosomal protein L6P Rpl6p
AR505_0235	ribosomal protein L32e Rpl32e
AR505_0236	ribosomal protein L19e Rpl19e
AR505_0237	ribosomal protein L18P Rpl18p
AR505_0238	ribosomal protein S5P Rps5p
AR505_0239	ribosomal protein L30P Rpl30p
AR505_0240	ribosomal protein L15P Rpl15p
AR505_0277	ribosomal protein S3Ae Rps3ae
AR505_0283	ribosomal protein L37e Rpl37e
AR505_0468	ribosomal protein L40e Rpl40e
AR505_0776	ribosomal protein S19e Rps19e
AR505_0778	ribosomal protein L39e Rpl39e
AR505_0779	ribosomal protein L31e Rpl31e
AR505_1370	ribosomal protein S27e Rps27e
AR505_1371	ribosomal protein S24e Rps24e
AR505_1421	ribosomal protein L10e Rpl10e
AR505_1440	ribosomal protein S11P Rps11p
AR505_1441	ribosomal protein S4P Rps4p
AR505_1442	ribosomal protein S13P Rps13p
AR505_1453	ribosomal protein S10P Rps10p
AR505_1456	ribosomal protein S7P Rps7p
AR505_1457	ribosomal protein S12P Rps12p
AR505_1472	ribosomal protein S8e Rps8e
AR505_1483	Ribosome maturation protein SBDS
AR505_1487	ribosomal protein L37Ae Rpl37ae
AR505_1514	ribosomal protein L44e Rpl44e
AR505_1515	ribosomal protein S27e Rps27e
AR505_1671	ribosomal protein S2P Rps2p
AR505_1753	ribosomal protein S6e Rps6e
AR505_1757	ribosomal protein L24e Rpl24e
AR505_1758	ribosomal protein S28e Rps28e
AR505_1759	ribosomal protein L7Ae Rpl7ae
AR505_1794	ribosomal protein L12P Rpl12p
AR505_1795	acidic ribosomal protein P0 RplPO
AR505_1796	ribosomal protein L1P Rpl1p
AR505_1797	ribosomal protein L11P Rpl11p
AR505_1798	ribosomal protein L24 family

RNA processing

AR505_0827	wyosine biosynthesis protein TYW1
AR505_1601	RNA 3'-phosphate cyclase RtcA
AR505_0020	NMD3 family protein
AR505_0038	ribosomal RNA large subunit methyltransferase J RrmJ
AR505_0065	tRNA pseudouridine synthase A TruA
AR505_0120	fibrillarlin
AR505_0132	dimethyladenosine transferase KsgA
AR505_0142	archaease
AR505_0227	ribonuclease P subunit P29
AR505_0243	tRNA pseudouridine synthase B TruB
AR505_0438	archaeosine tRNA-ribosyltransferase TgtA
AR505_0464	ribonuclease Z Rnz
AR505_0637	archaeosine tRNA-ribosyltransferase TgtA
AR505_0809	tRNA-dihydrouridine synthase DusA
AR505_1021	2'-5' RNA ligase
AR505_1146	ribosomal-protein-alanine acetyltransferase RimI
AR505_1166	N ² ,N ² -dimethylguanosine tRNA methyltransferase Trm1
AR505_1233	pseudouridylate synthase
AR505_1274	tRNA pseudouridine synthase D TruD
AR505_1336	YbaK/EbsC family protein
AR505_1358	exosome subunit
AR505_1406	RNA-splicing ligase RtcB
AR505_1414	7-cyano-7-deazaguanosine biosynthesis protein QueE
AR505_1415	queuosine biosynthesis protein QueC
AR505_1416	6-pyruvoyl tetrahydropterin synthase QueD
AR505_1424	ribonuclease P subunit RPR2
AR505_1460	MiaB-like tRNA modifying enzyme
AR505_1484	exosome complex RNA-binding protein Rrp4
AR505_1485	exosome complex exonuclease Rrp41
AR505_1486	exosome complex RNA-binding protein Rrp42
AR505_1583	tRNA nucleotidyltransferase Cca
AR505_1586	N ² ,N ² -dimethylguanosine tRNA methyltransferase Trm
AR505_1638	RNA 2'-phosphotransferase Tpt1/KptA
AR505_1657	ribosomal protein L11 methyltransferase PrmA
AR505_1658	exosome complex RNA-binding protein Csl4
AR505_1791	RNA methyltransferase TrmH family
AR505_1808	tRNA intron endonuclease EndA
Translation factors	
AR505_0139	translation initiation factor aIF-1A
AR505_0226	translation initiation factor aSUI1
AR505_0252	peptide chain release factor aRF1
AR505_0506	cell division protein pelota PelA
AR505_0642	peptidyl-tRNA hydrolase
AR505_0780	translation initiation factor aIF-6
AR505_1011	elongation factor Tu domain 2 protein
AR505_1284	diphthine synthase DphB
AR505_1420	diphthine synthase DphB
AR505_1454	translation elongation factor aEF-1 alpha
AR505_1455	translation elongation factor aEF-2
AR505_1459	translation initiation factor aIF-2 alpha subunit
AR505_1516	translation initiation factor aIF-2 alpha subunit
AR505_1603	translation initiation factor aIF-2 beta subunit
AR505_1606	translation initiation factor aIF-5A
AR505_1752	translation initiation factor aIF-2 gamma subunit
AR505_1755	translation initiation factor aIF-2
AR505_1774	translation elongation factor aEF-1 beta
tRNA aminoacylation	
AR505_0068	glutamyl-tRNA ^{Gln} amidotransferase subunit D GatD
AR505_0069	glutamyl-tRNA ^{Gln} amidotransferase subunit E GatE
AR505_0198	alanyl-tRNA synthetase AlaS
AR505_0200	aspartate--tRNA synthetase AspS
AR505_0201	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit B GatB
AR505_0202	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit A GatA
AR505_0203	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit C GatC
AR505_0247	tryptophanyl-tRNA synthetase TrpS
AR505_0248	phenylalanyl-tRNA synthetase alpha subunit PheS

AR505_0253	arginine-tRNA synthetase ArgS
AR505_0387	lysyl-tRNA synthetase LysS
AR505_0394	histidyl-tRNA synthetase HisS
AR505_0397	threonyl-tRNA synthetase ThrS
AR505_0455	isoleucyl-tRNA synthetase IleS
AR505_0709	methionyl-tRNA synthetase MetG
AR505_0710	methionyl-tRNA synthetase beta subunit MetG
AR505_0767	phenylalanyl-tRNA synthetase subunit beta PheT
AR505_0972	leucyl-tRNA synthetase LeuS
AR505_1121	glutamyl-tRNA synthetase GltX
AR505_1150	aspartyl-tRNA synthetase AspS
AR505_1191	cysteinyl-tRNA synthetase CysS
AR505_1325	pyrrolysine-tRNA ligase PylS
AR505_1339	valyl-tRNA synthetase ValS
AR505_1341	glycyl-tRNA synthetase GlyS
AR505_1426	seryl-tRNA synthetase SerS
AR505_1448	alanyl-tRNA synthetase AlaS
AR505_1494	tyrosyl-tRNA synthetase TyrS
AR505_1684	prolyl-tRNA synthetase ProS

PURINES AND PYRIMIDINES

Purine biosynthesis	
AR505_0037	phosphoribosylformylglycinamide cyclo-ligase PurM
AR505_0066	phosphoribosylamine--glycine ligase PurD
AR505_0084	adenine phosphoribosyltransferase Apt
AR505_0141	phosphoribosylglycinamide formyltransferase PurN
AR505_0257	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-monophosphate synthetase-like protein
AR505_0284	amidophosphoribosyltransferase PurF
AR505_0301	adenine phosphoribosyltransferase Apt
AR505_0622	phosphoribosylaminoimidazole-succinocarboxamide synthase PurC
AR505_0705	AMP phosphorylase
AR505_0742	adenylosuccinate lyase PurB
AR505_1071	exopolyphosphatase Ppx
AR505_1496	adenine phosphoribosyltransferase Apt
AR505_1595	phosphoribosylaminoimidazole carboxylase PurE
AR505_1656	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase PurH
AR505_1667	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-monophosphate-formate ligase PurP
AR505_1680	phosphoribosylformylglycinamide synthase I PurQ
AR505_1681	phosphoribosylformylglycinamide synthase II PurL
AR505_1682	phosphoribosylformylglycinamide synthase PurS
AR505_1804	phosphoribosylaminoimidazole carboxylase PurE
Purine interconversion	
AR505_0262	adenylate kinase Adk
AR505_1168	adenylosuccinate synthase PurA
AR505_1784	adenylate kinase Adk
Pyrimidine biosynthesis	
AR505_0060	orotidine 5'-phosphate decarboxylase PyrF
AR505_0281	dihydroorotase PyrC
AR505_0436	aspartate carbamoyltransferase regulatory subunit PyrI
AR505_0437	aspartate carbamoyltransferase PyrB
AR505_0500	carbamoyl-phosphate synthase large subunit CarB
AR505_0501	carbamoyl-phosphate synthase small subunit CarA
AR505_0503	carbamoyl-phosphate synthase large subunit CarB
AR505_0504	carbamoyl-phosphate synthase small subunit CarA
AR505_1029	dihydroorotate dehydrogenase PyrD
AR505_1030	dihydroorotate dehydrogenase electron transfer subunit PyrK
AR505_1581	cytosine deaminase
AR505_1615	orotate phosphoribosyltransferase PyrE
Pyrimidine interconversion	

AR505_1827	CMP/dCMP deaminase	CMP/dCMP deaminase
AR505_0076	thymidylate synthase	ThyX
AR505_0251	uridylate kinase	PyrH
AR505_1102	thymidylate kinase	Tmk
AR505_1287	deoxycytidine triphosphate deaminase	Dcd
AR505_1346	thioredoxin-disulfide reductase	TrxB
AR505_1690	thymidylate kinase	Tmk
Interconversion		
AR505_0706	GMP synthase subunit A	GuaA
AR505_1165	NTPase	
AR505_1247	anaerobic ribonucleoside-triphosphate reductase	NrdD
AR505_1743	5'-nucleotidase	SurE
AR505_1756	nucleoside diphosphate kinase	Ndk
AR505_1802	GMP synthase subunit A	GuaA
AR505_1803	GMP synthase subunit B	GuaAb
AR505_1827	CMP/dCMP deaminase	
Salvage		
AR505_1636	undecaprenyl pyrophosphate synthetase	UppS
AR505_1344	cytosine deaminase	
AR505_1382	N-methylhydantoinase	A/acetone carboxylase beta subunit
AR505_1641	thymidine phosphorylase	
Salvage and carbon fixation		
AR505_1642	ribulose biphosphate carboxylase	RbcL
AR505_1643	ribose-1,5-bisphosphate isomerase	E2b2
Transport		
AR505_0995	xanthine/uracil permease family protein	

REGULATION

Protein interaction		
AR505_0138	serine/threonine protein kinase	RIO1 family
AR505_0204	TPR repeat-containing protein	
AR505_0259	phosphate uptake regulator	PhoU
AR505_0260	phosphate uptake regulator	PhoU
AR505_0275	TPR repeat-containing protein	
AR505_0366	TPR repeat-containing protein	
AR505_0367	TPR repeat-containing protein	
AR505_0368	TPR repeat-containing protein	
AR505_0370	TPR repeat-containing protein	
AR505_0373	TPR repeat-containing protein	
AR505_0419	Sell repeat-containing protein	
AR505_0536	TPR repeat-containing protein	
AR505_0557	TPR repeat-containing protein	
AR505_0641	TPR repeat-containing protein	
AR505_0793	TPR repeat-containing protein	
AR505_0795	TPR repeat-containing protein	
AR505_0824	HPr kinase	
AR505_0898	TPR repeat-containing protein	
AR505_0899	TPR repeat-containing protein	
AR505_0917	TPR repeat-containing protein	
AR505_1020	TPR repeat-containing protein	
AR505_1048	TPR repeat-containing protein	
AR505_1145	TPR repeat-containing protein	
AR505_1212	TPR repeat-containing protein	
AR505_1213	TPR repeat-containing protein	
AR505_1214	TPR repeat-containing protein	
AR505_1216	TPR repeat-containing protein	
AR505_1225	TPR repeat-containing protein	
AR505_1273	TPR repeat-containing protein	
AR505_1334	TPR repeat-containing protein	
AR505_1351	TPR repeat-containing protein	
AR505_1463	TPR repeat-containing protein	
Signal transduction		
AR505_0425	signal transduction protein with CBS domains	

AR505_0609	low molecular weight phosphotyrosine protein phosphatase
AR505_0624	protein-tyrosine phosphatase
AR505_0788	signal transduction histidine kinase
AR505_1169	signal transduction histidine kinase
AR505_1170	signal transduction histidine kinase
Transcriptional regulator	
AR505_0043	transcriptional regulator ArsR family
AR505_0049	XRE family transcriptional regulator
AR505_0162	transcriptional regulator AsnC family
AR505_0199	transcriptional regulator AsnC family
AR505_0272	transcriptional regulator LysR family
AR505_0383	nickel responsive transcriptional regulator NikR
AR505_0457	transcriptional regulator LysR family
AR505_0462	transcriptional regulator ArsR family
AR505_0465	HTH/CBS domain-containing protein
AR505_0532	HTH domain-containing protein
AR505_0599	transcriptional regulator
AR505_0600	HTH domain-containing protein
AR505_0718	TfoX N-terminal domain protein
AR505_0734	transcriptional regulator HxIR family
AR505_0774	transcriptional regulator MarR family
AR505_0790	transcriptional regulator LytR family
AR505_0791	transcriptional regulator LytS family
AR505_0797	transcriptional regulator HxIR family
AR505_0801	HTH domain-containing protein
AR505_0831	transcriptional regulator MarR family
AR505_0843	transcriptional regulator
AR505_0859	transcriptional regulator TetR family
AR505_0955	transcriptional regulator HxIR family
AR505_0979	HTH domain-containing protein
AR505_0982	transcriptional regulator ArsR family
AR505_1012	transcriptional regulator XRE family
AR505_1099	transcriptional regulator MarR family
AR505_1176	transcriptional regulator TetR family
AR505_1179	metal dependent transcriptional regulator
AR505_1226	transcriptional regulator ArsR family
AR505_1237	transcriptional regulator HxIR family
AR505_1302	nickel-responsive transcriptional regulator NikR
AR505_1314	HTH domain-containing protein
AR505_1673	HTH domain-containing protein
AR505_1679	transcriptional regulator MarR family
AR505_1809	transcriptional regulator ArsR family
AR505_1811	transcriptional regulator
Other	
AR505_0645	carbon starvation protein CstA
AR505_0984	sugar fermentation stimulation protein SfsA

TRANSCRIPTION	
RNA polymerase	
AR505_0053	DNA-directed RNA polymerase subunit H RpoH
AR505_0054	DNA-directed RNA polymerase subunit B RpoB
AR505_0055	DNA-directed RNA polymerase subunit A' RpoA1
AR505_0056	DNA-directed RNA polymerase subunit A'' RpoA2
AR505_0182	DNA-directed RNA polymerase subunit N RpoN
AR505_0922	DNA-directed RNA polymerase subunit K RpoK
AR505_1373	DNA-directed RNA polymerase subunit E RpoE
AR505_1374	DNA-directed RNA polymerase RpoE
AR505_1439	DNA-directed RNA polymerase subunit D RpoD
AR505_1488	DNA-directed RNA polymerase subunit P RpoP
Translation factors	
AR505_1807	transcription initiation factor TFIIB Tfb2
AR505_0810	transcription initiation factor TFIIB Tfb
AR505_1651	transcription factor S Tfs
Other	
AR505_1605	C/D box methylation guide ribonucleoprotein complex aNOP56 subunit
AR505_1601	RNA 3'-phosphate cyclase RtcA

AR505_0598	polyphosphate:AMP phosphotransferase
AR505_0578	ribonuclease III Rnc
AR505_0137	RNA-binding protein
AR505_1408	RNA-binding protein
AR505_1411	RNA-binding protein

TRANSPORTERS

Amino acids

AR505_0830	amino acid/peptide transporter
AR505_0944	amino acid carrier protein AgcS
AR505_1242	amino acid/peptide transporter

Cations

AR505_0507	transporter Na ⁺ /H ⁺ antiporter family
AR505_0258	divalent cation transporter mgtE family
AR505_0369	sodium bile acid symporter family
AR505_0385	transporter Na ⁺ /H ⁺ antiporter family
AR505_0696	transporter CDF family
AR505_0812	Na ⁺ /Pi-cotransporter
AR505_0835	transporter Na ⁺ /H ⁺ antiporter family
AR505_1074	potassium uptake protein TrkA family
AR505_1075	potassium uptake protein TrkH family
AR505_1133	cation-transporting P-type ATPase heavy metal-translocating P-type ATPase
AR505_1510	copper ion binding protein
AR505_1511	copper translocating P-type ATPase
AR505_1222	ferrous iron transport protein B FeoB
AR505_1223	ferrous iron transport protein A FeoA
AR505_1506	iron chelate uptake ABC transporter permease
AR505_1507	iron chelate uptake ABC transporter permease inner membrane subunit
AR505_0620	sodium:solute symporter
AR505_1100	K ⁺ -dependent Na ⁺ /Ca ⁺ exchanger
AR505_0287	sodium/proline symporter PutP
AR505_1227	heavy metal translocating P-type ATPase
AR505_1271	heavy metal translocating P-type ATPase

Other

AR505_0030	ABC transporter permease protein
AR505_0031	ABC transporter ATP-binding protein
AR505_0111	ABC transporter ATP-binding protein
AR505_0112	ABC transporter substrate-binding protein
AR505_0113	ABC transporter permease protein
AR505_0127	permease
AR505_0163	mechanosensitive ion channel protein
AR505_0193	drug resistance MFS transporter
AR505_0285	Na ⁺ -dependent transporter SNF family
AR505_0296	MatE efflux family protein
AR505_0303	ABC transporter solute binding protein
AR505_0304	ABC transporter ATP binding protein
AR505_0305	ABC transporter permease protein
AR505_0308	ABC transporter ATP-binding protein
AR505_0309	ABC transporter permease protein
AR505_0310	ABC transporter solute-binding protein
AR505_0311	transporter DMT family
AR505_0364	MFS transporter
AR505_0408	ABC transporter permease protein
AR505_0409	ABC transporter permease protein
AR505_0410	ABC transporter ATP-binding protein
AR505_0411	ABC transporter permease protein
AR505_0412	ABC transporter ATP-binding protein
AR505_0417	ABC transporter ATP-binding protein
AR505_0418	ABC transporter permease protein
AR505_0422	ABC transporter ATP-binding protein
AR505_0423	ABC transporter permease protein
AR505_0456	transporter DMT family
AR505_0476	ABC transporter solute-binding protein
AR505_0477	ABC transporter permease protein
AR505_0478	ABC transporter ATP-binding protein
AR505_0517	ABC transporter ATP-binding protein
AR505_0520	ABC transporter ATP-binding protein
AR505_0521	ABC transporter permease protein

AR505_0526	transporter RND family
AR505_0605	ABC transporter permease protein
AR505_0606	ABC transporter ATP-binding protein
AR505_0701	ABC transporter ATP-binding protein
AR505_0703	MATE efflux family protein
AR505_0712	ABC transporter ATP-binding protein
AR505_0713	ABC transporter permease protein
AR505_0714	ABC transporter permease protein
AR505_0715	ABC transporter solute-binding protein
AR505_0737	Na ⁺ dependent transporter SBF family
AR505_0739	MFS transporter
AR505_0746	mechanosensitive ion channel protein
AR505_0806	MFS transporter
AR505_0815	Na ⁺ dependent transporter SBF family
AR505_0905	EamA-like transporter family
AR505_0911	MFS transporter
AR505_0941	MFS transporter
AR505_0957	HPP family protein
AR505_1014	ABC transporter ATP-binding protein
AR505_1015	ABC transporter permease protein
AR505_1034	MatE efflux family protein
AR505_1052	MFS transporter
AR505_1065	MFS transporter
AR505_1138	transporter SDF family
AR505_1195	ABC transporter substrate-binding protein
AR505_1197	ABC transporter permease protein
AR505_1198	ABC transporter ATP-binding protein
AR505_1246	Na ⁺ -driven multidrug efflux pump
AR505_1272	transporter MIP family
AR505_1291	ABC transporter ATP-binding protein
AR505_1292	ABC transporter permease protein
AR505_1293	ABC transporter substrate-binding protein
AR505_1310	small multidrug resistance protein
AR505_1311	small multidrug resistance protein
AR505_1378	small multidrug resistance protein
AR505_1379	small multidrug resistance protein
AR505_1462	MFS transporter
AR505_1491	ABC transporter ATP-binding protein
AR505_1492	ABC transporter permease protein
AR505_1498	MFS transporter
AR505_1504	ABC transporter permease protein
AR505_1505	ABC transporter ATP-binding protein
AR505_1508	ABC transporter ATP-binding protein
AR505_1523	ABC transporter substrate-binding protein
AR505_1525	ABC transporter permease protein
AR505_1526	ABC transporter ATP-binding protein
AR505_1548	ABC transporter substrate-binding protein
AR505_1550	ABC transporter permease protein
AR505_1551	ABC transporter ATP-binding protein
AR505_1576	MFS transporter
AR505_1686	sulfate permease SulP
AR505_1705	ABC transporter ATP-binding protein
AR505_1706	ABC transporter permease protein
AR505_1708	ABC transporter substrate-binding protein
AR505_1076	drug resistance transporter Bcr/CflA subfamily
AR505_1081	small multidrug resistance protein
AR505_1082	small multidrug resistance protein
AR505_1101	ABC transporter ATP-binding protein

UNKNOWN FUNCTION

Enzyme

AR505_0011	hydrolase, TatD family
AR505_0099	methyltransferase
AR505_0254	acetyltransferase
AR505_0426	ATPase (AAA+ superfamily)
AR505_0447	oxidoreductase DSBA family
AR505_0459	DNase TatD family
AR505_0505	ATPase (AAA+ superfamily)
AR505_0522	ATPase (AAA+ superfamily)
AR505_0530	ATPase (AAA+ superfamily)
AR505_0537	SAM-dependent methyltransferase
AR505_0587	ATPase (AAA+ superfamily)

AR505_0717	ATPase (AAA+ superfamily)
AR505_0781	Zn-dependent hydrolase
AR505_0863	ATPase
AR505_0893	ATPase
AR505_0895	ATPase
AR505_0900	ATPase
AR505_0904	GNAT family acetyltransferases
AR505_0943	GNAT family acetyltransferase
AR505_0963	hydroase HD superfamily
AR505_0970	oxidoreductase
AR505_0973	SAM-dependent methyltransferase
AR505_0981	SAM-dependent methyltransferases
AR505_0983	ATPase
AR505_0996	acetyltransferase
AR505_1000	short-chain dehydrogenase/reductase SDR
AR505_1008	SAM-dependent methyltransferases
AR505_1079	ATPase
AR505_1194	SAM-dependent methyltransferase
AR505_1196	SAM-dependent methyltransferase
AR505_1244	GNAT family acetyltransferases
AR505_1285	SAM-dependent methyltransferase
AR505_1367	archaeal ATPase
AR505_1381	haloacid dehalogenase-like hydrolase
AR505_1403	phosphoesterase
AR505_1422	haloacid dehalogenase-like hydrolase
AR505_1427	haloacid dehalogenase-like hydrolase
AR505_1471	phosphodiesterase
AR505_1474	carbohydrate kinase YjeF family
AR505_1475	phosphoesterase
AR505_1493	phosphoesterase DHHA1
AR505_1557	Atpase
AR505_1558	nucleotidyltransferase
AR505_1593	ATPase
AR505_1613	haloacid dehalogenase-like hydrolase
AR505_1695	Metal-dependent hydrolases beta-lactamase family
AR505_1738	ATPase
AR505_1744	GNAT family acetyltransferases
AR505_1781	Fe-S oxidoreductase
AR505_1814	sugar phosphate isomerase/epimerase
AR505_0685	peptidyl-prolyl cis-trans isomerase FKBP-type
AR505_1028	peptidyl-prolyl cis-trans isomerase
AR505_1235	peptidyl-prolyl cis-trans isomerase
AR505_0070	methyltransferase
AR505_0307	SAM-dependent methyltransferase
AR505_0844	GNAT family acetyltransferase
AR505_1218	haloacid dehalogenase-like hydrolase
AR505_1437	GTPase
AR505_1653	RNA-metabolising metallo-beta-lactamase
AR505_1676	GTPase
Other	
AR505_1352	alpha/beta hydrolase fold protein
AR505_0968	universal archaeal KH-domain/beta-lactamase-domain protein
AR505_1691	TOPRIM domain-containing protein
AR505_0012	beta-lactamase domain-containing protein
AR505_0071	metallo-beta-lactamase domain-containing protein
AR505_0098	pyridoxamine 5'-phosphate oxidase-related protein
AR505_0119	NUDIX domain-containing protein
AR505_0261	crcB protein CrcB
AR505_0298	Cob/MinD domain containing protein
AR505_0546	amidohydrolase family protein
AR505_0636	pap2 family protein
AR505_0699	PHP domain-containing protein
AR505_0711	php domain-containing protein
AR505_0721	CAAX amino terminal protease family
AR505_0722	von Willebrand factor type A domain protein
AR505_0733	macro domain protein
AR505_0890	SMC domain-containing protein
AR505_0891	SMC domain-containing protein
AR505_0924	pyridoxamine 5'-phosphate oxidase family protein
AR505_0926	NfeD family protein
AR505_0935	PHP domain-containing protein
AR505_1204	PP-loop domain-containing protein
AR505_1234	Pirin family protein

AR505_1257	NYN domain-containing protein
AR505_1340	CBS domain-containing protein
AR505_1342	CBS domain-containing protein
AR505_1407	Metal-dependent phosphohydrolase HD superfamily
AR505_1499	thioesterase family protein
AR505_1544	virulence-associated E family protein
AR505_1582	hydrolase beta-lactamase family
AR505_1621	radical SAM domain protein
AR505_1675	radical SAM domain-containing proteinB
AR505_1696	CBS domain-containing protein
AR505_1813	CAAX amino terminal protease family protein
AR505_0064	translin family DNA-binding protein
AR505_1177	MMPL domain-containing protein
AR505_1445	metallo-beta-lactamase domain protein
AR505_0059	radical SAM domain protein
AR505_0074	MORN repeat-containing protein
AR505_0075	TraB family protein
AR505_0165	radical SAM domain-containing protein
AR505_0195	alpha-NAC homolog
AR505_0208	sterol binding protein
AR505_0216	TIGR01210 family protein
AR505_0332	MORN repeat-containing protein
AR505_0393	small GTP-binding protein
AR505_1019	Raf kinase inhibitor-like protein
AR505_1023	ATP/GTP-binding protein
AR505_1178	radical SAM domain containing protein
AR505_1645	Met-10+ like-protein

VITAMINS AND COFACTORS

Cobalamin

AR505_0747	pyridoxamine 5'-phosphate oxidase PPOX
AR505_0680	3-oxoadipate enol-lactonase PcaD
AR505_0299	cobalamin biosynthesis protein CbiX
AR505_0360	cobalamin biosynthesis protein CbiX
AR505_0363	cobyricin acid a,c-diamide synthase CbiA
AR505_0378	cobalt-precorrin-5 (C1)-methyltransferase CbiD
AR505_0379	cobalt-precorrin 5A hydrolase CbiG
AR505_0380	precorrin-6X reductase CbiJ
AR505_0381	cobyricin acid a,c-diamide synthase CbiA
AR505_0398	cobaltochelataase CobN
AR505_0404	magnesium chelatase ChlD
AR505_0405	magnesium chelatase ChII
AR505_0406	cobaltochelataase CobN
AR505_0413	precorrin-2 C20-methyltransferase CbiL
AR505_0414	precorrin-4 C11-methyltransferase CbiF
AR505_0415	precorrin-3B C17-methyltransferase CbiH
AR505_0416	precorrin-8X methylmutase CbiC
AR505_0444	cobyricin acid a,c-diamide adenosyltransferase CbaA
AR505_0473	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase CobT
AR505_0597	anaerobic cobalt chelatase CbiK
AR505_0716	cobalamin (vitamin B12) biosynthesis protein CbiX
AR505_0769	cobaltochelataase subunit
AR505_0770	cobaltochelataase subunit
AR505_0771	cobaltochelataase subunit
AR505_0837	cobalt ABC transporter ATP-binding protein CbiO
AR505_0838	cobalt ABC transporter ATP-binding protein CbiO
AR505_0839	cobalt ABC transporter, permease protein CbiQ
AR505_0840	cobalt transport protein CbiN
AR505_0841	cobalt transport protein CbiM
AR505_0947	cobalamin biosynthesis protein CobW
AR505_1040	uroporphyrinogen III synthase HemD
AR505_1041	uroporphyrin-III C-methyltransferase CobA
AR505_1042	porphobilinogen deaminase HemC
AR505_1043	glutamate-1-semialdehyde aminomutase HemL
AR505_1044	porphobilinogen synthase HemB
AR505_1045	glutamyl-tRNA reductase HemA
AR505_1046	siroheme synthase CysG
AR505_1136	cobyric acid synthase CbiP
AR505_1137	cobyric acid synthase CbiP
AR505_1295	adenosylcobinamide-phosphosphate synthase CbiB

AR505_1296	adenosylcobinamide amidohydrolase CbiZ
AR505_1297	adenosylcobalamin synthase CobS
AR505_1377	uroporphyrinogen decarboxylase
AR505_1503	cobalamin biosynthesis protein CbiX
AR505_1771	L-threonine kinase PduX
Coenzyme F430	
AR505_1211	coenzyme F ₃₉₀ synthetase FtsA
Tetrahydrofolate	
AR505_1639	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase FolD
Metal-binding pterin	
AR505_0832	molybdate ABC transporter ATP-binding protein ModC
AR505_1435	molybdenum cofactor biosynthesis protein A MoaA1
AR505_1263	molybdenum cofactor biosynthesis protein A MoaA1
Nicotinate	
AR505_0121	ATP-NAD kinase
AR505_0143	L-aspartate dehydrogenase
AR505_0377	NAD synthetase NadE
AR505_0421	aspartate 1-decarboxylase PanD
AR505_0471	quinolinate phosphoribosyltransferase (decarboxylating) NadC
AR505_0616	nicotinamide-nucleotide adenyltransferase
AR505_1155	quinolinate synthetase A protein NadA
AR505_1654	quinolinate phosphoribosyltransferase (decarboxylating) NadC
Others	
AR505_1027	cysteine desulfurase SufS subfamily SufS
AR505_0169	dihydropteroate synthase FolP
AR505_0729	bifunctional protein FolC
AR505_1304	bifunctional protein FolC
AR505_0015	arsenate reductase
AR505_1206	NIF3 family protein
AR505_1316	1,4-dihydroxy-2-naphthoate octaprenyltransferase MenA
AR505_0938	FeS assembly ATPase SufC
AR505_0939	FeS assembly protein SufBD
AR505_1279	iron-sulfur cluster assembly protein
AR505_1447	nitrogenase cofactor biosynthesis protein NifB
AR505_1268	dinitrogenase iron-molybdenum cofactor biosynthesis protein
AR505_1413	dinitrogenase iron-molybdenum cofactor biosynthesis protein
Pantothenate	
AR505_1689	bifunctional phosphopantothenate-cysteine ligase/phosphopantothenoylcysteine decarboxylase CoaBC
AR505_0680	3-oxoadipate enol-lactonase PcaD
Riboflavin	
AR505_1294	threonine-phosphate decarboxylase CobD
AR505_1180	3,4-dihydroxy-2-butanone-4-phosphate synthase RibB
AR505_1182	riboflavin synthase RibC
AR505_1183	6,7-dimethyl-8-ribityllumazine synthase RibH
AR505_1243	nucleotide pyrophosphatase MazG
AR505_1602	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase RibD
Thiamine	
AR505_0032	thiamine biosynthesis protein ThiC1
AR505_0100	thiamine monophosphate synthase ThiE
AR505_0101	tyrosine lyase ThiH
AR505_0102	thiazole synthase ThiG
AR505_0103	thiamine biosynthesis protein ThiF
AR505_0104	ThiS sulfur-carrier protein

AR505_0128	thiazole biosynthesis/tRNA modification protein ThiI
AR505_0166	thiamine-monophosphate kinase ThiL
AR505_0173	thiazole biosynthesis adenyltransferase ThiF
AR505_0458	thiazole biosynthesis adenyltransferase ThiF
AR505_0618	thiazole biosynthesis adenyltransferase ThiF
AR505_0643	thiamine monophosphate synthase ThiE
AR505_0644	hydroxyethylthiazole kinase ThiM
AR505_0650	4-amino-2-methyl-5-hydroxymethylpyrimidine phosphate kinase ThiD
AR505_0726	ApbE family protein
AR505_0765	phosphomethylpyrimidine kinase ThiD
AR505_1060	cysteine desulfurase NifS
AR505_1660	thiamine biosynthesis ATP pyrophosphatase ThiI
Ubiquinone	
AR505_0114	methylase involved in ubiquinone/menaquinone biosynthesis
AR505_0312	ubiquinone/menaquinone biosynthesis methyltransferase UbiE
AR505_0969	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
AR505_1172	3-octaprenyl-4-hydroxybenzoate decarboxylase UbiD
AR505_1317	ubiquinone/menaquinone biosynthesis methyltransferase

Table A.4.1 Percentage codon usage in Methanomassiliicoccales genomes

Amino acid [#]	Codon	ISO4-H5	ISO4-G1	ISO4-G11	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10	Mpt1
Ser (S)	UCA	0.5 [7.1]	0.5 [8.6]	0.3 [5.2]	0.3 [4.0]	0.3 [4.9]	0.7 [9.8]	0.4 [5.2]	0.3 [4.3]	2.1 [28.2]	0.3 [5.2]	1 [15.1]
	UCC	2.8 [42.8]	2.5 [39.9]	3.4 [51.0]	3.4 [54.3]	2 [32.9]	2.7 [39.2]	2.8 [39.5]	3.1 [48.4]	0.9 [11.9]	2.3 [36.8]	1.5 [22.7]
	UCG	1.0 [15.5]	1.4 [21.6]	1.2 [17.5]	1.0 [15]	1.8 [30.2]	1.1 [15.6]	1.7 [23.7]	1.2 [18.3]	0.5 [6.5]	1.4 [22.7]	1.4 [21.6]
	UCU	0.5 [8.5]	0.4 [5.8]	0.3 [4.9]	0.3 [4.7]	0.2 [4]	0.6 [9.2]	0.4 [5.7]	0.4 [6.2]	2.0 [26.5]	0.3 [5.2]	0.8 [12.5]
	AGC	1.3 [19.4]	1.2 [19.8]	1.1 [16.9]	1.2 [18.8]	1.6 [25.8]	1.5 [22.4]	1.7 [23.5]	1.1 [17.3]	1.2 [15.8]	1.7 [27.3]	1.4 [20.6]
	AGU	0.4 [6.7]	0.3 [4.4]	0.3 [4.4]	0.2 [3.1]	0.1 [2.3]	0.3 [3.8]	0.2 [2.3]	0.4 [5.5]	0.8 [11.0]	0.2 [2.7]	0.5 [7.5]
Phe (F)	UUC	3.6 [92.3]	3.6 [95.3]	3.7 [95.1]	3.7 [95.9]	3.2 [93.8]	3.5 [93.5]	3.5 [96.4]	3.5 [93.8]	1.7 [45.1]	3.3 [91.7]	3.1 [80.0]
	UUU	0.3 [7.7]	0.2 [4.7]	0.2 [4.9]	0.2 [4.1]	0.2 [6.2]	0.2 [6.5]	0.1 [3.6]	0.2 [6.2]	2.0 [54.9]	0.3 [8.3]	0.8 [20.0]
Thr (T)	ACA	0.6 [10.4]	0.9 [16.5]	0.5 [9.3]	0.4 [7.0]	0.2 [4.4]	0.9 [17.8]	0.4 [8.4]	0.6 [10.7]	2.2 [41.2]	0.3 [5.8]	1.8 [31.4]
	ACC	3.8 [66.2]	2.8 [51.0]	3.6 [64.9]	3.9 [73.3]	3 [60.7]	2.2 [42.4]	3.2 [60.4]	3.0 [58.7]	0.9 [16.5]	3.2 [64.5]	1.8 [30.6]
	ACG	0.7 [12.4]	1.4 [25.8]	1.1 [19.8]	0.8 [14]	1.5 [29.8]	1.5 [30]	1.2 [23.7]	1.3 [24.5]	0.6 [10.3]	1.1 [22.0]	1.6 [27.1]
	ACU	0.6 [10.9]	0.4 [6.7]	0.3 [6.0]	0.3 [5.7]	0.2 [5]	0.5 [9.8]	0.4 [7.6]	0.3 [6.0]	1.7 [32.0]	0.4 [7.6]	0.6 [19.8]
Asn (N)	AAC	3.0 [76.9]	3.1 [84.0]	2.9 [82.9]	3.0 [88.1]	2.3 [84.5]	2.2 [66.8]	2.5 [82.8]	2.7 [79.3]	1.8 [38.8]	2.4 [81.4]	2.7 [65.2]
	AAU	0.9 [23.1]	0.6 [16.0]	0.6 [17.7]	0.4 [11.9]	0.4 [15.5]	1.1 [33.2]	0.5 [17.2]	0.7 [20.7]	2.8 [61.2]	0.5 [18.6]	1.5 [34.8]
Lys (K)	AAA	1.7 [29.3]	0.9 [15.8]	1.2 [23.3]	0.9 [15.3]	0.3 [7.5]	1.4 [25.4]	1 [19.4]	1.5 [25.3]	4.3 [67.4]	0.6 [13.4]	3.3 [48.7]
	AAG	4.2 [70.7]	5.0 [84.2]	4.0 [76.7]	4.8 [84.7]	3.7 [92.5]	4.2 [74.6]	4 [80.6]	4.4 [74.7]	2.1 [32.6]	4.3 [86.6]	3.5 [51.3]
Glu (E)	GAA	2.3 [34.1]	1.5 [22.9]	1.7 [25.9]	1.2 [17.5]	1 [14.7]	2 [28]	1.3 [21]	1.9 [28.7]	4.7 [69.1]	1.3 [19.0]	3.1 [47.6]
	GAG	4.4 [65.9]	5.2 [77.1]	4.9 [74.1]	5.5 [82.5]	6 [85.3]	5 [72]	5.1 [79]	4.8 [71.3]	2.1 [30.9]	5.5 [81.0]	3.4 [52.4]
Tyr (Y)	UAC	2.6 [70.4]	2.8 [76.9]	2.8 [77.5]	2.8 [82.2]	2 [73.7]	2 [64.6]	2.7 [77.3]	2.3 [65.7]	1.4 [38.4]	2.2 [73.7]	1.7 [52.7]
	UAU	1.1 [29.6]	0.8 [23.1]	0.8 [22.5]	0.6 [17.8]	0.7 [26.3]	1.1 [35.4]	0.8 [22.7]	1.2 [34.3]	2.3 [61.6]	0.8 [26.3]	1.6 [47.3]
Val (V)	GUA	1.0 [13.1]	0.7 [9.2]	0.6 [8.3]	0.5 [6.6]	0.4 [5.4]	1 [12.9]	0.4 [5.9]	1.0 [13.2]	2.3 [32.7]	0.6 [7.5]	1.4 [19.4]
	GUC	3.5 [47.5]	4.2 [55.1]	4.3 [55.2]	4.7 [59.8]	3.4 [41.1]	2.8 [36.7]	4.2 [56.9]	4.0 [51.0]	1.3 [19.0]	3.1 [38.4]	2.5 [33.6]
	GUG	2.1 [28.4]	2.2 [28]	2.3 [29.3]	2.1 [25.8]	3.9 [48.3]	2.8 [36.6]	2.3 [30.9]	2.4 [30.3]	1.2 [17.6]	3.9 [47.8]	2.1 [28.6]
	GUU	0.8 [11]	0.6 [7.7]	0.6 [7.2]	0.6 [7.8]	0.4 [5.2]	1 [13.8]	0.5 [6.4]	0.4 [5.6]	2.2 [30.7]	0.5 [6.3]	1.4 [18.4]
Gln (Q)	CAA	0.3 [10.9]	0.2 [7.9]	0.2 [9.9]	0.1 [5.5]	0.2 [9.9]	0.3 [13.3]	0.1 [6.1]	0.2 [11.1]	0.7 [30.4]	0.3 [11.8]	0.6 [28.8]
	CAG	2.1 [89.1]	2.2 [92.1]	1.9 [90.1]	2.2 [94.5]	2.3 [90.1]	1.6 [86.7]	2 [93.9]	1.9 [88.9]	1.6 [69.6]	2.2 [88.2]	1.5 [71.2]
Met (M)	AUG	3.2 [100.0]	3.6 [100.0]	3.3 [100.0]	3.3 [100.0]	3.2 [100]	3.6 [100]	3.2 [100]	3.5 [100.0]	2.8 [100.0]	3.1 [100.0]	3.3 [100.0]
Cys (C)	UGC	1.2 [74.5]	1.3 [81.6]	1.3 [79.8]	1.4 [87.2]	1.1 [89]	1.2 [83.9]	1.6 [94]	1.3 [75.2]	0.9 [55.6]	1.1 [90.5]	1.0 [69.6]
	UGU	0.4 [25.5]	0.3 [18.4]	0.3 [20.2]	0.2 [12.8]	0.1 [11]	0.2 [16.1]	0.1 [6]	0.4 [24.8]	0.7 [44.4]	0.1 [9.5]	0.4 [30.4]
Leu (L)	CUA	0.2 [2.7]	0.2 [2.9]	0.2 [2.4]	0.2 [2.3]	0.4 [3.7]	0.2 [2.5]	0.1 [1.4]	0.2 [2.2]	0.6 [7.2]	0.3 [3.1]	0.3 [3.3]
	CUC	3.5 [42.5]	3.1 [38.5]	4.3 [54.0]	4.0 [50.5]	2.5 [25.7]	2.2 [26.8]	3.5 [43.9]	3.2 [40.1]	1.1 [13.2]	2.6 [27.3]	1.7 [21.9]
	CUG	2.8 [34.4]	3.5 [42.2]	2.4 [29.4]	2.7 [34.8]	5.5 [56.9]	3.7 [44.2]	3.4 [43.7]	2.9 [37.0]	2.3 [26.8]	5.1 [54.1]	2.4 [31]
	CUU	1.0 [11.6]	0.7 [8.7]	0.6 [6.9]	0.7 [8.8]	0.6 [6.4]	1.3 [15.5]	0.6 [7.1]	0.9 [11.3]	2.0 [22.8]	0.7 [7.3]	1.8 [22.6]
	UUA	0.2 [2.7]	0.1 [1.5]	0.1 [1.7]	0.1 [0.8]	0.1 [1]	0.2 [2.1]	0.1 [0.7]	0.1 [1.6]	1.5 [17.1]	0.1 [1.4]	0.5 [5.9]
	UUG	0.5 [6.1]	0.5 [6.2]	0.4 [5.5]	0.2 [2.8]	0.6 [6.4]	0.7 [8.9]	0.2 [3.2]	0.6 [7.9]	1.1 [12.9]	0.6 [6.8]	1.2 [15.3]
	UUA	0.2 [2.7]	0.1 [1.5]	0.1 [1.7]	0.1 [0.8]	0.1 [1]	0.2 [2.1]	0.1 [0.7]	0.1 [1.6]	1.5 [17.1]	0.1 [1.4]	0.5 [5.9]
Ala (A)	GCA	2.0 [25.7]	1.7 [22.9]	1.1 [13.6]	1.5 [17.5]	0.6 [6.1]	1.7 [20.5]	1 [11]	1.5 [19.1]	3.1 [42.0]	0.6 [6.7]	2.4 [31.3]
	GCC	3.5 [44]	3.1 [40.4]	4.4 [53.5]	4.1 [48.7]	5.3 [57.6]	3.3 [41.1]	4.9 [51.4]	4.1 [50.6]	1.3 [17.5]	4.8 [52.4]	2.0 [25.9]
	GCG	1.5 [18.6]	2.2 [28.4]	2.0 [24.1]	2.3 [27.1]	2.8 [30]	2.2 [26.6]	2.9 [30]	2.0 [24.8]	0.7 [9.1]	3.0 [33.1]	2.4 [30.2]
	GCU	0.9 [11.8]	0.6 [8.3]	0.7 [8.8]	0.6 [6.8]	0.6 [6.2]	1 [11.9]	0.7 [7.6]	0.4 [5.5]	2.3 [31.3]	0.7 [7.8]	1.0 [12.6]
O (Pyl)	UAG	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]	0.0 [100.0]
Trp (W)	UGG	1.0 [100.0]	0.9 [100.0]	1.0 [100.0]	0.9 [100.0]	1.1 [100]	0.9 [100]	1 [100]	0.9 [100.0]	0.9 [100.0]	1.1 [100.0]	0.9 [100.0]
Pro (P)	CCA	0.2 [5.3]	0.3 [6.5]	0.2 [3.9]	0.2 [4.0]	0.3 [7.5]	0.2 [5.4]	0.2 [3.7]	0.2 [4.5]	1.2 [32.8]	0.3 [6.2]	0.4 [10.5]
	CCC	2.2 [56.6]	1.8 [47.7]	2.5 [62.7]	2.5 [61.6]	1.9 [41.3]	1.6 [40.4]	1.7 [41.7]	1.8 [46.9]	0.5 [13.2]	2.0 [45.4]	1.0 [27.4]
	CCG	0.8 [20.1]	1.3 [32.9]	1.0 [23.7]	1.0 [25.9]	1.9 [41.1]	1.4 [35.6]	1.7 [41.5]	1.3 [33.2]	0.8 [21.4]	1.7 [38.5]	1.7 [45.5]

	CCU	0.7 [18.0]	0.5 [12.8]	0.4 [9.6]	0.3 [8.5]	0.5 [10.1]	0.7 [18.6]	0.5 [13]	0.6 [15.4]	1.2 [32.5]	0.4 [9.9]	0.6 [16.6]
His (H)	CAC	1.1 [67.4]	1.2 [70.6]	1.2 [72.3]	1.3 [80.1]	1.2 [62.5]	1 [60.2]	1 [63.8]	1.0 [60.8]	0.6 [38.2]	1.3 [71.1]	0.9 [58.8]
	CAU	0.6 [32.6]	0.5 [29.4]	0.5 [27.7]	0.3 [19.9]	0.7 [37.5]	0.6 [39.8]	0.6 [36.2]	0.6 [39.2]	1.0 [61.8]	0.5 [28.9]	0.6 [41.2]
Asp (D)	GAC	4.0 [61.6]	4.6 [67.4]	4.7 [68.1]	5.1 [76.0]	4.6 [77.5]	3.6 [55.9]	4.7 [70.8]	4.9 [70.6]	2.0 [33.0]	4.5 [75.9]	3.1 [50.8]
	GAU	2.5 [38.4]	2.2 [32.6]	2.2 [31.4]	1.6 [24.0]	1.3 [22.5]	2.8 [44.1]	1.9 [29.2]	2.0 [29.4]	4.1 [67.0]	1.4 [24.1]	3.0 [49.2]
Arg (R)	CGA	0.0 [0.3]	0.0 [0.3]	0.0 [0.2]	0.0 [0.2]	0.5 [6.6]	0.1 [2.1]	0.1 [1.4]	0.0 [0.5]	0.2 [4.3]	0.2 [3.7]	0.1 [2.6]
	CGC	1.2 [23.3]	0.9 [18.6]	1.7 [32.4]	1.5 [28.0]	2.3 [32.3]	0.9 [15.2]	1.9 [31.5]	1.0 [19.2]	0.5 [12.6]	1.8 [29.4]	0.6 [12.5]
	CGG	0.2 [3.3]	0.1 [1.5]	0.2 [2.9]	0.1 [2.0]	1.7 [24.3]	0.4 [7.1]	0.5 [7.7]	0.2 [4.0]	0.2 [4.9]	1.4 [22.8]	0.2 [4.8]
	CGU	0.7 [14.6]	0.5 [9.6]	0.7 [13.6]	0.4 [8.3]	0.4 [5.8]	0.4 [6.2]	0.3 [4.7]	0.7 [12.1]	0.5 [13.5]	0.2 [3.8]	0.3 [7.4]
	AGA	0.7 [14.8]	0.7 [13.6]	0.5 [9.7]	0.5 [9.0]	0.4 [5.1]	1.4 [23.1]	0.5 [23.1]	0.9 [16.4]	1.8 [45.2]	0.4 [6.5]	1.6 [34.6]
	AGG	2.2 [43.6]	2.7 [56.4]	2.2 [41.4]	2.8 [52.6]	1.8 [25.8]	2.7 [46.4]	0.5 [7.9]	2.6 [47.9]	0.8 [19.5]	2.1 [33.8]	1.7 [38]
Ile (I)	AUA	1.0 [14.3]	1.5 [19.7]	1.3 [18.4]	0.8 [11.3]	1 [17.2]	3.7 [53.1]	2.8 [46.8]	2.3 [34.5]	2.5 [31.4]	1.3 [22.2]	3.2 [41.8]
	AUC	5.0 [73.3]	5.4 [73.8]	5.0 [74.7]	5.6 [82.1]	4.4 [77]	2.8 [40.3]	4.7 [75.5]	4.0 [60.2]	2.6 [32.0]	4.3 [70.4]	3.5 [45.3]
	AUU	0.8 [12.4]	0.5 [6.5]	0.5 [6.9]	0.4 [6.6]	0.3 [5.8]	0.5 [6.6]	0.3 [5.2]	0.3 [5.3]	2.9 [36.7]	0.4 [7.4]	1.0 [13.0]
Gly (G)	GGA	3.2 [41.2]	2.8 [37.3]	1.9 [23.9]	2.7 [34.6]	1.3 [15.9]	2 [24.4]	1.5 [18.4]	2.5 [30.9]	3.2 [44.4]	1.1 [13.0]	2.6 [32.4]
	GGC	1.9 [25.2]	2.0 [26.2]	2.5 [31]	2.3 [28.8]	4.2 [51.4]	2.9 [35.6]	3.5 [42.1]	1.9 [23.3]	1.6 [22.1]	4.0 [47.8]	2.5 [30.9]
	GGG	0.9 [12.0]	1.4 [18.1]	1.9 [23.2]	1.9 [23.5]	2 [24.7]	2.1 [26]	2.8 [33.4]	2.3 [28.2]	0.7 [9.5]	2.7 [32.5]	1.6 [19.9]
	GGU	1.7 [21.6]	1.4 [18.3]	1.7 [21.8]	1.0 [13.1]	0.7 [8]	1.1 [14]	0.5 [6.2]	1.4 [17.6]	1.7 [24.0]	0.5 [6.7]	1.4 [16.8]
Stop codons*												
<i>ochre</i>	UAA	13.4	14.1	11.3	8.8	13.3	18	10.9	14.1	45.2	17.5	33.1
<i>amber</i>	UAG	1.4 (2.7)	1.6 (3.2)	1.0 (2.4)	0.5 (2.5)	11.1 (16.2)	6.6 (10.1)	2.1 (5.1)	1.6 (2.8)	5.0 (5.3)	11.0 (11.3)	1.8 (2.3)
<i>opal</i>	UGA	84.1	84.4	86.3	89.1	70.4	72	83.9	84.3	49.7	71.5	65
Translation initiator												
M	AUG	93.6	93.5	89.7	84.5	76.4	85	81.2	83.7	84.4	75.8	85.5
L	GUG	1.7	4.0	7.1	11.2	6.8	5	5	5.2	8.0	9.2	9.7
V	UUG	4.7	2.5	3.2	4.2	11.9	6.6	12	11.1	7.5	15.0	4.7
I	ATT	0	0	0	0	0.7	0.1	0.8	0	0	0	0

number indicates percentage of codon in genome, number in square bracket indicates percentage of codon used for each amino acid.

*the number in brackets indicates total in-frame UAG, without considering its use as a STOP codon or as a Pyl codon.

Table A.4.2 CRISPR associated genes in *Mbb.* spp.

gene	ISO4-H5	ISO4-G1	ISO4-G11	BRN A1	RumE n M1	RumE n M2	1R26	Mx12 01	Mx1	B10	MpT1	Reference*
<i>cas1</i>	-	-	-	-	-	-	-	+	+	+	+	SERP2463
<i>cas2</i>	-	-	-	-	-	-	-	-	-	-	-	SERP2462
<i>cas3'</i>	+	+	+	+	+	+	+	-	+	-	+	APE1232
<i>cas3''</i>	-	-	-	-	-	-	-	-	-	-	-	APE1231
<i>cas4</i>	-	-	-	-	-	-	+	-	-	-	-	APE1239
<i>cas5</i>	-	-	-	-	-	-	-	-	-	-	-	APE1234
<i>cas6</i>	+	-	-	-	-	-	-	-	-	-	-	PF1131
<i>cas6e</i>	-	-	-	-	-	-	-	-	-	-	-	<i>ygcH</i>
<i>cas6f</i>	-	-	-	-	-	-	-	-	-	-	-	<i>y1727</i>
<i>cas7</i>	+	-	-	-	-	-	-	-	-	-	-	<i>ygcJ</i>
<i>cas8a1</i>	-	-	-	-	-	-	-	-	-	-	-	LA3191
<i>cas8a2</i>	-	-	-	-	-	-	-	-	-	-	-	MJ0385
<i>cas8b</i>	-	-	-	-	-	-	-	-	-	-	-	MTH1090
<i>cas8c</i>	-	-	-	-	-	-	-	-	-	+	-	BH0338
<i>cas9</i>	-	-	-	-	-	-	-	-	-	-	-	Spy1046
<i>cas10/c</i>	-	-	-	-	-	-	-	-	-	-	-	MTH326
<i>sm1</i>	-	-	-	-	-	-	-	-	-	-	-	MTH326
<i>cas10d</i>	-	-	-	-	-	-	-	-	-	-	-	Slr7011
<i>csy1</i>	-	-	-	-	-	-	-	-	-	-	-	Y1724
<i>csy2</i>	-	-	-	-	-	-	-	-	-	-	-	Y1725
<i>csy3</i>	-	-	-	-	-	-	-	-	-	-	-	Y1726
<i>cse1</i>	+	-	-	-	-	-	-	-	-	-	-	<i>ygcL</i>
<i>cse2</i>	-	-	-	-	-	-	-	-	-	-	-	<i>ygcK</i>
<i>csc1</i>	-	-	-	-	-	-	-	-	-	-	-	alr1563
<i>csc2</i>	-	-	-	-	-	-	-	-	-	-	-	slr7012
<i>csa5</i>	-	-	-	-	-	-	-	-	-	-	-	MJ0380
<i>csn2</i>	-	-	-	-	-	-	-	-	-	-	-	SPy1049
<i>csm2</i>	-	-	-	-	-	-	-	-	-	-	-	MTH1081
<i>csm3</i>	-	-	-	-	-	-	-	-	-	-	-	MTH1080
<i>csm4</i>	-	-	-	-	-	-	-	-	-	-	-	MTH1079
<i>csm5</i>	-	-	-	-	-	-	-	-	-	-	-	MTH1078
<i>csm6</i>	-	-	-	-	-	-	-	-	-	-	-	APE2256
<i>cmr1</i>	-	-	-	-	-	-	-	-	-	-	-	PF1130
<i>cmr3</i>	-	-	-	-	-	-	-	-	-	-	-	PF1128
<i>cmr4</i>	-	-	-	-	-	-	-	-	-	-	-	PF1126
<i>cmr5</i>	-	-	-	-	-	-	-	-	-	-	-	MTH324
<i>cmr6</i>	-	-	-	-	-	-	-	-	-	-	-	PF1124
<i>csb1</i>	-	-	-	-	-	-	-	-	-	-	-	Balac_1306
<i>csb2</i>	-	-	-	-	-	-	-	-	-	-	-	Balac_1305
<i>csb3</i>	-	-	-	-	-	-	-	-	-	-	-	Balac_1303
<i>csx17</i>	-	-	-	-	-	-	-	-	-	-	-	Btus_2683
<i>csx14</i>	-	-	-	-	-	-	-	-	-	-	-	GSU0052
<i>csx10</i>	-	-	-	-	-	-	-	-	-	-	-	Caur_2274
<i>csx16</i>	-	-	-	-	-	-	-	-	-	-	-	VVA1548
<i>csaX</i>	-	-	-	-	-	-	-	-	-	-	-	SSO1438
<i>csx3</i>	-	-	-	-	-	-	-	-	-	-	-	AF1864
<i>csx1</i>	-	-	-	-	-	-	-	-	-	-	-	MJ1666
<i>csx15</i>	-	-	-	-	-	-	-	-	-	-	-	TTE2665
<i>csf1</i>	-	-	-	-	-	-	-	-	-	-	-	AFE_1038
<i>csf2</i>	-	-	-	-	-	-	-	-	-	-	-	AFE_1039
<i>csf3</i>	-	-	-	-	-	-	-	-	-	-	-	AFE_1040
<i>csf4</i>	-	-	-	-	-	-	-	-	-	-	-	AFE_1037

Prediction cutoff: E-04. +Represents the gene is predicted in the particular genome. *Reference protein is displayed in either locus tag or gene name within the NCBI protein database

Table A.4.3 Predicted pyrrolysine usage in the ISO4-G11 genome

Locus tag	Predicted gene product	Distance (codons)*	Class [#]	Merge with
ISO4G11_0002	trimethylamine:corrinoid methyltransferase	164	1	ISO4G11_0003
ISO4G11_0009	monomethylamine:corrinoid methyltransferase MttB	259	1	ISO4G11_0010
ISO4G11_0011	monomethylamine:corrinoid methyltransferase MtmB	257	1	ISO4G11_0012
ISO4G11_0065	adenosylcobinamide amidohydrolase	77	1	ISO4G11_0066
ISO4G11_0237	serine hydroxymethyltransferase	350	1	ISO4G11_0238
ISO4G11_0250	hypothetical protein	3	3	-
ISO4G11_0274	FMN reductase	44	3	-
ISO4G11_0371	adhesin-like protein	332	1	ISO4G11_0372
ISO4G11_0437	DNA helicase	374	1	ISO4G11_0438
ISO4G11_0457	hypothetical protein	24, 18	3	-
ISO4G11_0513	uncharacterized protein	13	1	-
ISO4G11_0515	ATPase family	174	1	-
ISO4G11_0551	dimethylamine:corrinoid methyltransferase MtbB	115	1	ISO4G11_0552
ISO4G11_0579	uncharacterized protein	147	3	-
ISO4G11_0596	transcriptional regulator	149	1	ISO4G11_0597
ISO4G11_0645	phage-type endonuclease	81	1	ISO4G11_0646
ISO4G11_0683	hypothetical protein	1	3	-
ISO4G11_0686	hypothetical protein	8	2	-
ISO4G11_0719	hypothetical protein	28	1	-
ISO4G11_0741	hypothetical protein	224	1	ISO4G11_0740
ISO4G11_0750	type III restriction enzyme	695	1	ISO4G11_0751
ISO4G11_0768	protein tyrosine phosphatase	7	2	-
ISO4G11_0770	modE molybdate transport repressor domain	134	1	ISO4G11_0771
ISO4G11_0858	adenosylhomocysteinase	42	1	-
ISO4G11_0862	dephospho-CoA kinase	10	2	-
ISO4G11_0872	mobile mystery protein	3	2	-
ISO4G11_1175	Transposase	230	1	ISO4G11_1176
ISO4G11_1233	hypothetical protein	218	1	ISO4G11_1232
ISO4G11_1353	TPR-repeat lipoprotein	26	2	-
ISO4G11_1446	hypothetical protein	276	3	-
ISO4G11_1514	dimethylamine:corrinoid methyltransferase MtbB	112	1	ISO4G11_1513
ISO4G11_1647	hypothetical protein	93	3	-
ISO4G11_1701	hypothetical protein	253	3	-
ISO4G11_1730	hypothetical protein	4	3	-

*Distance between amber codon to the next opal or ochre stop codon. [#] (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales

Table A.4.4 Predicted pyrrolysine usage in the ISO4-G1 genome

Locus_tag	Predicted gene product	Distance (codons)*	Class [#]	Merge with
ISO4G1_0043	nucleotide kinase	18	2	-
ISO4G1_0180	phosphomannomutase/phosphoglucomutase	54	1	ISO4G1_0181
ISO4G1_0211	type IV leader peptidase family protein	140	1	ISO4G1_0212
ISO4G1_0245	amidohydrolase	298	1	ISO4G1_0246
ISO4G1_0292	radical SAM enzyme TIGR01210 family	86	1	ISO4G1_0293
ISO4G1_0371	hypothetical protein	20	3	-
ISO4G1_0394	hypothetical protein	122	3	-
ISO4G1_0470	trimethylamine:corrinoide methyltransferase MttB	161	1	ISO4G1_0471
ISO4G1_0477	dimethylamine:corrinoide methyltransferase MtbB	103	1	ISO4G1_0478
ISO4G1_0490	hypothetical protein	318, 269	2	-
ISO4G1_0554	type 11 methyltransferase	276	1	ISO4G1_0555
ISO4G1_0572	aconitate hydratase 1 AcnA	285	1	ISO4G1_0573
ISO4G1_0606	hypothetical protein	30, 7	2	-
ISO4G1_0654	monomethylamine:corrinoide methyltransferase MtmB	259	1	ISO4G1_0655
ISO4G1_0687	hypothetical protein	99	2	-
ISO4G1_0698	hypothetical protein	404	3	-
ISO4G1_0710	ATP-dependent DNA helicase	297, 222	1	ISO4G1_0711, ISO4G1_0712
ISO4G1_0713	hypothetical protein	6	3	-
ISO4G1_0714	hypothetical protein	135	3	-
ISO4G1_0767	hypothetical protein	199	3	-
ISO4G1_0792	ATP-dependent DNA helicase	552	1	ISO4G1_0793
ISO4G1_0800	sugar fermentation stimulation protein A	62	1	-
ISO4G1_0803	VTC domain-containing protein	65	1	ISO4G1_0804
ISO4G1_0806	hypothetical protein	83	3	-
ISO4G1_0851	hypothetical protein	178	3	-
ISO4G1_0871	type II secretion system protein	299	1	ISO4G1_0872
ISO4G1_0938	dimethylamine:corrinoide methyltransferase MtbB	112	1	ISO4G1_0939
ISO4G1_0946	trimethylamine:corrinoide methyltransferase MttB	160	1	ISO4G1_0947
ISO4G1_0968	hypothetical protein	369, 312, 305, 100, 98	3	-
ISO4G1_00984	non-ribosomal peptide synthetase	4141, 1774	1	ISO4G1_0985, ISO4G1_0986
ISO4G1_1003	X-prolyl dipeptidylaminopeptidase	69	1	-
ISO4G1_1018	ATP-dependent DNA ligase	542	1	ISO4G1_1019
ISO4G1_1063	nitrogenase component 1 type oxidoreductase	11	1	-
ISO4G1_1090	Na/Pi-cotransporter II-related protein	160	1	ISO4G1_1089
ISO4G1_1122	archaeosine tRNA-ribosyltransferase	25	2	-
ISO4G1_1230	trimethylamine:corrinoide methyltransferase MttB	164	1	ISO4G1_1231
ISO4G1_1234	dimethylamine:corrinoide methyltransferase MtbB	113	1	ISO4G1_1235
ISO4G1_1238	monomethylamine:corrinoide methyltransferase MtmB	279	1	ISO4G1_1239
ISO4G1_1296	tripartite tricarboxylate transporter TctA family	5	2	-
ISO4G1_1349	iron ABC transporter ATP-binding protein	8	1	-
ISO4G1_1444	trimethylamine:corrinoide methyltransferase MttB	162	1	ISO4G1_1445
ISO4G1_1478	nitrogenase iron protein NifH	171	1	ISO4G1_1477
ISO4G1_1480	glycosyl transferase GT8 family	207, 101	1	ISO4G1_1481, ISO4G1_1482

*Distance between amber codon to the next opal or ochre stop codon. [#] (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales

Table A.4.5 Predicted pyrrolysine usage in the BRNA1 genome

Locus_tag	Predicted gene product	Distance (codons)*	Class [#]	Merge with
TALC_00050	putative nucleotide kinase (CMP and AMP kinases -like protein)	50	2	-
TALC_00054	eukaryotic-type DNA primase, large subunit	91	1	-
TALC_00068	glycosyltransferases involved in cell wall biogenesis	190	1	TALC_00067
TALC_00088	hypothetical protein	4	3	-
TALC_00154	hypothetical protein	169	2	TALC_00155
TALC_00163	hypothetical protein	12	2	-
TALC_00237	BC-type spermidine/putrescine transport systems, ATPase component	69	1	TALC_00238
TALC_00301	dimethylamine:corrinoid methyltransferase MtbB	111	1	-
TALC_00305	trimethylamine:corrinoid methyltransferase MttB	171	1	-
TALC_00366	hypothetical protein	20	2	-
TALC_00418	dinitrogenase iron-molybdenum cofactor	352	1	TALC_00417
TALC_00490	Acetyltransferase (GNAT) family	47	1	TALC_00491
TALC_00532	NaMN:DMB phosphoribosyltransferase	142	1	TALC_00531
TALC_00554	carbamoylphosphate synthase small subunit	218	1	TALC_00555
TALC_00591	hypothetical protein	365	1	TALC_00592
TALC_00657	hypothetical protein	164	1	TALC_00655
TALC_00720	phenylacetate-CoA ligase	392	1	TALC_00719
TALC_00726	putative phosphatase	181	1	TALC_00727
TALC_00896	ABC-type cobalamin/Fe ³⁺ -siderophores transport systems, ATPase	39	1	-
TALC_00943	phosphoglycerate mutase	140	1	TALC_00944
TALC_01010	hypothetical protein	469	2	TALC_01011
TALC_01032	uncharacterized protein	23	1	-
TALC_01093	monomethylamine:corrinoid methyltransferase MtmB	257	1	-
TALC_01094	monomethylamine:corrinoid methyltransferase MtmB	259	1	-
TALC_01102	trimethylamine:corrinoid methyltransferase MttB	168	1	-
TALC_01103	dimethylamine:corrinoid methyltransferase MtbB	112	1	-
TALC_01170	hypothetical protein	66	2	-
TALC_01197	cobalamin biosynthesis protein CobN-related Mg-chelatase	281	1	TALC_01196
TALC_01236	putative amidohydrolase	55	1	TALC_01237
TALC_01357	Na ⁺ /proline symporter	141	1	TALC_01358
TALC_01508	L-asparaginase/archaeal Glu-tRNA ^{Gln} amidotransferase subunit D	128	1	TALC_01507
TALC_01548	8-oxoguanine DNA glycosylase, N-terminal domain protein	99	1	TALC_01549

*Distance between amber codon to the next opal or ochre stop codon. [#] (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales

Table A.4.6 Predicted pyrrollysine usage in the MpT1 genome

Locus_tag	Predicted gene product	Distance (codons)*	Class [#]	Merge with
Mpt1_c01150	integrase core domain protein	3	2	-
Mpt1_c02990	hypothetical protein	59	1	-
Mpt1_c03550	hypothetical protein	14	3	-
Mpt1_c03980	putative nickel-responsive regulator	21	2	-
Mpt1_c04300	hypothetical protein	7	3	-
Mpt1_c04430	integrase core domain protein	3	2	-
Mpt1_c05280	hypothetical protein	62	2	-
Mpt1_c05350	hypothetical protein	34, 1	3	-
Mpt1_c05360	hypothetical protein	36, 31	3	-
Mpt1_c05730	monomethylamine:corrinoid methyltransferase MtmB	258	1	-
Mpt1_c05760	monomethylamine:corrinoid methyltransferase MtmB	259	1	-
Mpt1_c07680	integrase core domain protein	3	2	-
Mpt1_c08050	sirohdrochlorin cobaltochelata	154	1	Mpt1_c08040
Mpt1_c08460	hypothetical protein	16	2	-
Mpt1_c08720	hypothetical protein	127	2	-
Mpt1_c09890	hypothetical protein	31	3	-
Mpt1_c10480	hypothetical protein	14	2	-
Mpt1_c11820	archaea bacterial proteins of unknown function	11	2	-
Mpt1_c11860	dephospho-CoA kinase	10	2	-
Mpt1_c11940	cell division protein FtsZ 1	7	2	-
Mpt1_c12980	hypothetical protein	32	3	-
Mpt1_c13190	hypothetical protein	134	3	-
Mpt1_c13990	3' ribonuclease Y	45	2	-
Mpt1_c14260	hypothetical protein	12	3	-
Mpt1_c14440	3' bifunctional enzyme Fae/Hps	2	2	-

*Distance between amber codon to the next opal or ochre stop codon. [#] (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrollysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales

Table A.4.7 Predicted pyrrollysine usage in the RumEn M1 genome

Locus_tag	Predicted gene product	Distance (codons)*	Class [#]	Merge with
AOA80_00040	geranylgeranylglyceryl phosphate synthase	45	2	-
AOA80_00095	4Fe-4S ferredoxin	16, 32, 69, 80, 159	2	-
AOA80_00125	hypothetical protein	73, 82	2	-
AOA80_00170	ATPase	32	2	-
AOA80_00200	hypothetical protein	4	2	-
AOA80_00225	hypothetical protein	8	2	-
AOA80_00235	hypothetical protein	99	2	-
AOA80_00240	UDP-glucose 4-epimerase	17	2	-
AOA80_00265	hypothetical protein	365	2	-
AOA80_00280	hypothetical protein	6	2	-
AOA80_00335	aspartate carbamoyltransferase	151	2	-
AOA80_00450	hypothetical protein	31	2	-
AOA80_00530	arginyl-tRNA synthetase	161	2	-
AOA80_00615	reductase	29	2	-
AOA80_00700	hypothetical protein	182	2	-
AOA80_00750	hypothetical protein	27	2	-
AOA80_00785	transferase	5	2	-
AOA80_00805	hypothetical protein	11	2	-
AOA80_00820	hypothetical protein	9, 31	2	-
AOA80_00860	hypothetical protein	13, 25	2	-
AOA80_00865	hypothetical protein	26	2	-
AOA80_00935	UDP-N-acetylglucosamine 2-epimerase	3	2	-
AOA80_00955	hypothetical protein	7, 26	2	-
AOA80_00965	hypothetical protein	7	3	-
AOA80_01005	hypothetical protein	30	2	-
AOA80_01030	hypothetical protein	4	2	-
AOA80_01040	hypothetical protein	22	2	-
AOA80_01070	hypothetical protein	118, 396	2	-
AOA80_01075	hypothetical protein	6	2	-
AOA80_01255	hypothetical protein	81	2	-
AOA80_01320	hypothetical protein	11	3	-
AOA80_01330	hydrogenase assembly protein HypC	100	2	-
AOA80_01335	hypothetical protein	60	3	-
AOA80_01345	hypothetical protein	71	2	-
AOA80_01390	hypothetical protein	1	2	-
AOA80_01445	hypothetical protein	296	2	-
AOA80_01470	hypothetical protein	2, 16	2	-
AOA80_01515	hypothetical protein	271	2	-
AOA80_01560	hypothetical protein	24	2	-
AOA80_01590	CopG family transcriptional regulator	16	2	-
AOA80_01610	cell division protein FtsZ	32	2	-
AOA80_01615	cell division protein FtsZ	17, 58	2	-
AOA80_01670	hypothetical protein	38, 77, 88, 99, 107, 146, 165	2	-
AOA80_01690	hypothetical protein	7	2	-
AOA80_01705	hypothetical protein	13	2	-
AOA80_01710	hypothetical protein	6	2	-
AOA80_01720	hypothetical protein	3	2	-
AOA80_01755	riboflavin deaminase	70	2	-
AOA80_01765	hypothetical protein	28	2	-
AOA80_01790	hypothetical protein	46	2	-
AOA80_01830	hypothetical protein	8	2	-
AOA80_01915	hypothetical protein	12	2	-
AOA80_01925	hypothetical protein	30	3	-
AOA80_01970	hypothetical protein	38	2	-
AOA80_02040	hypothetical protein	34	2	-
AOA80_02130	hypothetical protein	167	3	-
AOA80_02165	hypothetical protein	2	2	-
AOA80_02190	hypothetical protein	79, 238	2	-
AOA80_02285	hypothetical protein	47, 83	2	-
AOA80_02290	hypothetical protein	77	2	-
AOA80_02325	hypothetical protein	13, 42	2	-
AOA80_02370	methylthiol--CoM methyltransferase	8	2	-
AOA80_02395	hypothetical protein	57	2	-
AOA80_02480	RNA-associated protein	5	2	-
AOA80_02540	radical SAM protein	109, 15	2	-
AOA80_02545	hypothetical protein	15	2	-
AOA80_02580	DEAD/DEAH box helicase	37	2	-
AOA80_02595	hypothetical protein	6, 28, 57	2	-

AOA80_02615	hypothetical protein	108, 115	3	-
AOA80_02620	hypothetical protein	66, 88, 359,	3	-
AOA80_02705	hypothetical protein	31	2	-
AOA80_02725	nucleic acid-binding protein	48	2	-
AOA80_02805	glutamine amidotransferase	31	2	-
AOA80_02825	hypothetical protein	273	2	-
AOA80_02860	hypothetical protein	28	2	-
AOA80_02925	hypothetical protein	129	2	-
AOA80_02950	hypothetical protein	60	3	-
AOA80_03095	hypothetical protein	186	2	-
AOA80_03125	ABC transporter ATP-binding protein	479	2	-
AOA80_03220	hypothetical protein	7	2	-
AOA80_03250	hypothetical protein	10, 33	2	-
AOA80_03330	hypothetical protein	33, 68	2	-
AOA80_03360	hypothetical protein	51	3	-
AOA80_03380	hypothetical protein	33, 155,	2	-
		159, 612		
AOA80_03480	hypothetical protein	36	2	-
AOA80_03545	hypothetical protein	47, 56, 128	2	-
AOA80_03575	hypothetical protein	8	2	-
AOA80_03600	hypothetical protein	2	2	-
AOA80_03775	ATPase	25	2	-
AOA80_03820	hypothetical protein	80, 89, 240	2	-
AOA80_03845	glycosyl transferase family 2	8	2	-
AOA80_03915	hypothetical protein	130	2	-
AOA80_03960	hypothetical protein	4, 281	2	-
AOA80_03970	hypothetical protein	2, 59, 71,	2	-
		76, 80		
AOA80_03975	aspartate aminotransferase	7, 10, 26,	2	-
		77		
AOA80_04090	hypothetical protein	27, 141	3	-
AOA80_04145	hypothetical protein	66, 162	2	-
AOA80_04210	RNA-binding protein	34	2	-
AOA80_04235	hypothetical protein	16, 23, 251,	2	-
		335, 350		
AOA80_04240	hypothetical protein	84, 99	2	-
AOA80_04245	hypothetical protein	3	2	-
AOA80_04330	hypothetical protein	61, 84, 125,	2	-
		142, 143,		
		287		
AOA80_04335	hypothetical protein	146, 230,	2	-
		657		
AOA80_04370	hypothetical protein	17	2	-
AOA80_04385	hypothetical protein	19	3	-
AOA80_04460	hypothetical protein	3	3	-
AOA80_04520	hypothetical protein	20	2	-
AOA80_04570	hypothetical protein	17, 51	2	-
AOA80_04645	hypothetical protein	10, 15, 20,	3	-
		36, 108		
AOA80_04705	hypothetical protein	32	2	-
AOA80_04720	hypothetical protein	6	2	-
AOA80_04765	hypothetical protein	15	3	-
AOA80_04790	hypothetical protein	26	3	-
AOA80_04825	hypothetical protein	28, 119,	2	-
		127, 170		
AOA80_04835	hypothetical protein	50	2	-
AOA80_04880	hypothetical protein	2	2	-
AOA80_04890	hypothetical protein	6	2	-
AOA80_04905	hypothetical protein	0 (end of contig)	3	-
AOA80_04920	hypothetical protein	57	3	-
AOA80_05005	hypothetical protein	19, 29, 41,	2	-
		44		
AOA80_05050	hypothetical protein	43	2	-
AOA80_05055	hypothetical protein	265	2	-
AOA80_05060	hypothetical protein	81, 260,	2	-
		331, 337		
AOA80_05080	phosphoribosylaminoimidazole-succinocarboxamide synthase	6	2	-
AOA80_05090	hypothetical protein	41	3	-
AOA80_05110	hypothetical protein	16	2	-
AOA80_05200	hypothetical protein	25	2	-
AOA80_05220	hypothetical protein	13	2	-
AOA80_05260	hypothetical protein	66, 73	2	-
AOA80_05290	hypothetical protein	4, 81	2	-

AOA80_05300	hypothetical protein	22	2	-
AOA80_05315	hypothetical protein	9	2	-
AOA80_05330	hypothetical protein	15	2	-
AOA80_05360	hypothetical protein	24	2	-
AOA80_05380	hypothetical protein	14, 38, 69	2	-
AOA80_05410	hypothetical protein	50	3	-
AOA80_05490	hypothetical protein	152, 157	2	-
AOA80_05510	hypothetical protein	2	2	-
AOA80_05535	hypothetical protein	15, 39, 56, 65, 67, 71	3	-
AOA80_05545	hypothetical protein	13	2	-
AOA80_05570	hypothetical protein	17	2	-
AOA80_05575	GTPase	8	2	-
AOA80_05580	hypothetical protein	19	2	-
AOA80_05595	hypothetical protein	32, 130	2	-
AOA80_05630	hypothetical protein	21	2	-
AOA80_05670	hypothetical protein	17	2	-
AOA80_05695	hypothetical protein	32, 55, 545	2	-
AOA80_05700	hypothetical protein	3	2	-
AOA80_05705	translation initiation factor IF-2 subunit gamma	17	2	-
AOA80_05740	hypothetical protein	68	2	-
AOA80_05755	hypothetical protein	105, 176, 316, 494, 676, 773	2	-
AOA80_05900	hypothetical protein	13	2	-
AOA80_05920	hypothetical protein	6	2	-
AOA80_05925	hypothetical protein	66	2	-
AOA80_05945	hypothetical protein	54, 159, 334	2	-
AOA80_05965	ATPase	11	2	-
AOA80_05975	hypothetical protein	3, 14	2	-
AOA80_06020	nitrate ABC transporter ATP-binding protein	124	2	-
AOA80_06025	XRE family transcriptional regulator	121	2	-
AOA80_06095	mRNA 3'-end processing factor	2	2	-
AOA80_06170	carbon monoxide dehydrogenase	1	2	-
AOA80_06205	nitroreductase	27	2	-
AOA80_06260	aspartate aminotransferase	164, 168	2	-
AOA80_06395	hypothetical protein	25	2	-
AOA80_06495	50S ribosomal protein L31	3	2	-
AOA80_06520	aromatic acid decarboxylase	43	2	-
AOA80_06585	glyoxalase	17	2	-
AOA80_06600	hypothetical protein	78	2	-
AOA80_06665	hypothetical protein	109	2	-
AOA80_06795	hypothetical protein	34	2	-
AOA80_06800	glutamate synthase	14, 59	2	-
AOA80_06810	hypothetical protein	37	2	-
AOA80_06830	hypothetical protein	4	3	-
AOA80_06885	hypothetical protein	41, 99	3	-
AOA80_06890	hypothetical protein	86, 126, 185	3	-
AOA80_06920	DNA-directed RNA polymerase subunit E	64	2	-
AOA80_06995	hypothetical protein	9, 22	2	-
AOA80_07025	hypothetical protein	74	2	-
AOA80_07045	hypothetical protein	102	2	-
AOA80_07085	hypothetical protein	138	3	-
(contig end no start codon)				
AOA80_07150	hypothetical protein	23	2	-
AOA80_07185	hypothetical protein	113	2	-
AOA80_07210	hypothetical protein	10, 533	2	-
AOA80_07225	ketoisovalerate oxidoreductase	194	2	-
AOA80_07240	hypothetical protein	54	2	-
AOA80_07265	hypothetical protein	6	2	-
AOA80_07310	hypothetical protein	112	2	-
AOA80_07330	hypothetical protein	30, 52	3	-
AOA80_07355	hypothetical protein	94, 118	2	-
AOA80_07360	hypothetical protein	45	2	-
AOA80_07375	hypothetical protein	28	2	-
AOA80_07405	hypothetical protein	226	2	-
AOA80_07515	hypothetical protein	8	3	-
AOA80_07530	hypothetical protein	75	2	-
AOA80_07540	hypothetical protein	21	2	-
AOA80_07545	hypothetical protein	31	3	-
AOA80_07575	tryptophan synthase subunit beta	7	2	-

AOA80_07680	hypothetical protein (wrongly annotated monomethylamine:corrinoid methyltransferase)	257	1	AOA80_07675
AOA80_07710	Seryl-tRNA synthetase	46	2	-
AOA80_07720	hypothetical protein (wrongly annotated monomethylamine:corrinoid methyltransferase)	257	1	AOA80_07725
AOA80_07740	hypothetical protein	135	2	-
AOA80_07745	hypothetical protein	31	2	-
AOA80_07795	hypothetical protein	296	2	-
AOA80_07855	hypothetical protein	19	2	-
AOA80_07870	hypothetical protein	3	2	-
AOA80_07965	arylsulfatase	14	2	-
AOA80_07970	hypothetical protein	39	2	-
AOA80_07990	hypothetical protein	1	2	-
AOA80_08050	diphthine synthase	22, 144,	2	-
		196, 211		
AOA80_08055	hypothetical protein	115, 121,	2	-
		228, 606		
AOA80_08085	hypothetical protein	20	3	-
AOA80_08105	hypothetical protein	29	2	-
AOA80_08155	hypothetical protein	267, 355	2	-
AOA80_08255	hypothetical protein	58	2	-
AOA80_08275	hypothetical protein	44, 47, 60	2	-
AOA80_08315	NAD-dependent dehydratase	103, 109,	2	-
		435		
AOA80_08375	hypothetical protein	282	2	-
AOA80_08415	hypothetical protein	17, 35	2	-
AOA80_08475	hypothetical protein	11	2	-
AOA80_08520	hypothetical protein	2	2	-
AOA80_08540	hypothetical protein	37, 84, 100	2	-
AOA80_08585	phosphatidylglycerophosphate synthase	6	2	-
AOA80_08590	hypothetical protein	17	2	-
AOA80_08760	cytidylate kinase	134	2	-
AOA80_08765	H/ACA RNA-protein complex component Cbf5p	3	2	-
AOA80_08790	hypothetical protein	243, 260	2	-
AOA80_08810	hypothetical protein	12	2	-
AOA80_08825	hypothetical protein	6, 8	2	-
AOA80_08845	hypothetical protein	55	2	-
AOA80_08870	tRNA pseudouridine synthase	23	2	-
AOA80_08910	hypothetical protein	12	2	-
AOA80_08935	hypothetical protein	40	2	-
AOA80_08945	hypothetical protein	2, 5	3	-
AOA80_09005	hypothetical protein	7	2	-
AOA80_09020	hypothetical protein	14, 93, 105,	2	-
		124, 160		
AOA80_09050	hypothetical protein	49, 73, 129,	2	-
		174, 179		
AOA80_09055	hypothetical protein	58	2	-
AOA80_09065	hypothetical protein	1, 45	2	-
AOA80_09075	hypothetical protein	292	2	-
AOA80_09080	hypothetical protein	84	2	-
AOA80_09110	hypothetical protein	17	2	-
AOA80_09155	hypothetical protein	31, 34, 68	3	-
AOA80_09190	hypothetical protein	10	2	-
AOA80_09220	hypothetical protein	99, 127,	2	-
		241, 434,		
		453, 559,		
		598		
AOA80_09225	hypothetical protein	452, 551,	2	-
		579, 693,		
		886, 905,		
		1011, 1050		
AOA80_09250	hypothetical protein	34	2	-
AOA80_09375	site-specific recombinase	194	2	-
AOA80_09405	hypothetical protein	42, 55	2	-
AOA80_09425	XRE family transcriptional regulator	9, 59	2	-
AOA80_09430	hypothetical protein	9, 77, 235	2	-
AOA80_09470	hypothetical protein	261	2	-
AOA80_09520	cob(I)yrinic acid a,c-diamide adenosyltransferase	49	2	-
AOA80_09540	thioredoxin	45, 121	2	-
AOA80_09545	hypothetical protein	58, 119	2	-
AOA80_09635	ABC transporter ATP-binding protein	361	2	-
AOA80_09645	hypothetical protein	16	2	-
AOA80_09665	hypothetical protein	7, 141	2	-
AOA80_09685	hypothetical protein	14	3	-
AOA80_09735	hypothetical protein	8	3	-

AOA80_09760	hypothetical protein	62	2	-
AOA80_09815	hypothetical protein	89, 124, 287, 332, 344, 413	2	-
AOA80_09820	glucose-1-phosphate thymidyltransferase	12, 31, 84, 143	2	-
AOA80_09850	polyphosphate kinase	82	2	-
AOA80_09960	hypothetical protein	4	2	-
AOA80_09990	hypothetical protein	163	2	-
AOA80_10060	hypothetical protein	21	3	-
AOA80_10120	hypothetical protein	2, 78	3	-
AOA80_10260	hypothetical protein	57	2	-
AOA80_10265	hypothetical protein	24, 105	2	-
AOA80_10320	hypothetical protein	11	2	-
AOA80_10345	hypothetical protein	374	3	-
AOA80_10445	ATP-dependent helicase	47, 195, 219	2	-
AOA80_10450	acetylpyruvase	8, 25, 214, 235, 275, 337, 449, 496, 513	2	-
AOA80_10540	hypothetical protein	19, 398	2	-
AOA80_10560	phosphomethylpyrimidine synthase	20, 29	2	-
AOA80_10625	hypothetical protein	278	3	-
AOA80_10710	hypothetical protein	138	2	-
AOA80_10745	hypothetical protein	22	3	-
AOA80_10775	hypothetical protein	23, 24, 34	3	-
AOA80_10780	hypothetical protein	48, 150	2	-
AOA80_10825	hypothetical protein	81, 108	2	-
AOA80_10850	hypothetical protein	86, 117, 122	2	-
AOA80_10870	hypothetical protein	1	3	-
AOA80_10935	hypothetical protein	32	2	-
AOA80_10980	transcriptional regulator	48	2	-
AOA80_11025	hypothetical protein	127, 215	3	-
AOA80_11030	hypothetical protein	88	2	-
AOA80_11185	hypothetical protein	12, 16, 27	2	-
AOA80_11270	ATP-dependent protease	10, 320	2	-
AOA80_11275	hypothetical protein	36	2	-
AOA80_11410	hypothetical protein	40	2	-
AOA80_11420	hypothetical protein	3	2	-
AOA80_11475	hypothetical protein	61	2	-
AOA80_11485	hypothetical protein	9	2	-
AOA80_11535	hypothetical protein	7	3	-

*Distance between amber codon to the next opal or ochre stop codon. # (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales

Table A.4.8 Predicted pyrrollysine usage in the RumEn M2 genome

Locus_tag	Predicted gene product	Distance (codons)*	Class [#]	-
AOA81_00085	YgiQ family radical SAM protein	39	2	-
AOA81_00090	hypothetical protein	1, 11, 14	2	-
AOA81_00120	hypothetical protein	31, 168	3	-
AOA81_00125	hypothetical protein	38	2	-
AOA81_00250	hypothetical protein	19	2	-
AOA81_00255	hypothetical protein	48, 120, 192	2	-
AOA81_00290	hypothetical protein	7	2	-
AOA81_00295	hypothetical protein	79	2	-
AOA81_00375	hypothetical protein	6	3	-
AOA81_00490	hypothetical protein	7	3	-
AOA81_00525	hypothetical protein	8	2	-
AOA81_00535	hypothetical protein	17	2	-
AOA81_00590	hypothetical protein	9	2	-
AOA81_00645	glutamate 5-kinase	22	2	-
AOA81_00660	hypothetical protein	34	2	-
AOA81_00720	hypothetical protein	1	3	-
AOA81_00810	dihydropteroate synthase DHPS	19	2	-
AOA81_00900	hypothetical protein	10, 13, 53	2	-
AOA81_00940	excinuclease ABC subunit C	29	2	-
AOA81_01005	hypothetical protein	88	3	-
AOA81_01210	seryl-tRNA synthetase	44, 136	2	-
AOA81_01275	GTP-binding protein	5, 14	2	-
AOA81_01310	hypothetical protein	7, 24, 51	3	-
AOA81_01500	hypothetical protein	12	2	-
AOA81_01515	hypothetical protein	19, 64, 101, 104	2	-
AOA81_01530	acetolactate synthase	313	3	-
AOA81_01550	hypothetical protein	29	2	-
AOA81_01555	hypothetical protein	12	2	-
AOA81_01560	hypothetical protein	1	3	-
AOA81_01565	hypothetical protein	80	2	-
AOA81_01620	twitching motility protein PilT	109, 356	2	-
AOA81_01625	hypothetical protein	33	2	-
AOA81_01660	transcriptional regulator	14	2	-
AOA81_01680	hypothetical protein	9, 12, 28	2	-
AOA81_01720	hypothetical protein	55	2	-
AOA81_01860	hypothetical protein	41	2	-
AOA81_02180	3-phosphoglycerate kinase	17	2	-
AOA81_02325	ATP-dependent helicase	45, 150	2	-
AOA81_02345	hypothetical protein	2	2	-
AOA81_02470	metal-dependent hydrolase	6	2	-
AOA81_02495	signal recognition particle-docking protein FtsY	4, 22	2	-
AOA81_02560	ATP synthase subunit F	93	2	-
AOA81_02755	hypothetical protein	10	2	-
AOA81_02915	hypothetical protein	2	2	-
AOA81_02995	ATP-dependent DNA ligase	2	2	-
AOA81_03120	hypothetical protein	126	2	-
AOA81_03250	ABC transporter ATP-binding protein	20	2	-
AOA81_03305	endonuclease IV	2	2	-
AOA81_03495	orotidine 5'-phosphate decarboxylase	12, 1178	2	-
AOA81_03525	hypothetical protein	23	2	-
AOA81_03555	modification methylase HemK	121	2	-
AOA81_03565	hypothetical protein	85, 153	2	-
AOA81_03690	hypothetical protein	17, 96, 142, 172	3	-
AOA81_03715	molecular chaperone DnaJ	58	2	-
AOA81_03740	hypothetical protein	92, 154, 176, 220	2	-
AOA81_03750	hypothetical protein	6	2	-
AOA81_03910	geranylgeranyl pyrophosphate synthase	43	2	-
AOA81_03940	hypothetical protein	7	2	-
AOA81_03970	hypothetical protein	17	2	-
AOA81_03975	GTP cyclohydrolase	66, 83, 86	2	-
AOA81_04165	hypothetical protein	24	2	-
AOA81_04185	hypothetical protein	13, 78, 92, 115	2	-
AOA81_04205	arginyl-tRNA synthetase	167	2	-
AOA81_04305	hypothetical protein	28, 102	3	-
AOA81_04350	hypothetical protein	1	3	-
AOA81_04390	hypothetical protein	21	2	-

AOA81_04395	hypothetical protein	52	2	-
AOA81_04425	homoserine dehydrogenase	524	2	-
AOA81_04435	hypothetical protein	6	2	-
AOA81_04525	hypothetical protein	6	2	-
AOA81_04575	hypothetical protein	8	3	-
AOA81_04595	tRNA-modifying protein	15	2	-
AOA81_04625	hypothetical protein	4	3	-
AOA81_04695	hypothetical protein	16, 76, 238	2	-
AOA81_04755	hypothetical protein	12	3	-
AOA81_04910	hypothetical protein	23	2	-
AOA81_04920	hypothetical protein	31, 97	3	-
AOA81_04950	hypothetical protein	14	3	-
AOA81_04985	fructose 1,6-bisphosphatase	222	2	-
AOA81_05000	quinolinate synthetase	4	2	-
AOA81_05070	hypothetical protein	15	3	-
AOA81_05145	ATPase	50	2	-
AOA81_05165	hypothetical protein	211	2	-
AOA81_05220	hypothetical protein	8	2	-
AOA81_05460	hydroxyethylthiazole kinase	48, 64, 94	2	-
AOA81_05560	ubiquinone biosynthesis methyltransferase UbiE	14	2	-
AOA81_05570	hypothetical protein	102, 131	2	-
AOA81_05600	hypothetical protein	20, 23	2	-
AOA81_05605	hypothetical protein	93	2	-
AOA81_05625	topoisomerase I	7	2	-
AOA81_05665	hypothetical protein	27	2	-
AOA81_05710	hypothetical protein	21	3	-
AOA81_05810	hypothetical protein	614	1	-
AOA81_05840	tRNA (pseudouridine-N ₁)-methyltransferase	27	2	-
AOA81_05860	hypothetical protein	7	2	-
AOA81_05880	3-hydroxy-3-methylglutaryl-CoA reductase	64, 100, 164, 216, 245	2	-
AOA81_05965	hypothetical protein	18	2	-
AOA81_06015	hypothetical protein	126	2	-
AOA81_06100	hypothetical protein	43	2	-
AOA81_06310	hypothetical protein	6, 20	3	-
AOA81_06320	hypothetical protein	45	2	-
AOA81_06425	hypothetical protein	7	2	-
AOA81_06445	hypothetical protein	16	2	-
AOA81_06635	hypothetical protein	69	3	-
AOA81_06660	hypothetical protein	23, 279	3	-
AOA81_06705	hypothetical protein	9, 32	2	-
AOA81_06715	hypothetical protein	7	2	-
AOA81_06830	hypothetical protein	3	2	-
AOA81_06845	threonine synthase	163	2	-
AOA81_06925	hypothetical protein	13	2	-
AOA81_06935	hypothetical protein	7	2	-
AOA81_06950	hypothetical protein	6	3	-
AOA81_06990	hypothetical protein	2	2	-

*Distance between amber codon to the next opal or ochre stop codon. # (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other *Methanomassiliicoccales*

Table A.4.9 Predicted pyrrollysine usage in 1R26

Locus_tag	Predicted gene product	Distance (codons)*	Class	Merge with
AUQ37_00065	hypothetical protein	34	3	-
AUQ37_00335	hypothetical protein	77	2	-
AUQ37_00520 [#]	hypothetical protein	58, 111, 177	3	-
AUQ37_04330	dimethylamine methyltransferase	112	1	AUQ37_04335
AUQ37_04480 [#]	hypothetical protein	58, 106, 217, 287	3	-
AUQ37_04495	hypothetical protein	50	2	-
AUQ37_04535	hypothetical protein	98	3	-
AUQ37_04740	hypothetical protein	31	3	-
AUQ37_04745	hypothetical protein	54	2	-
AUQ37_04935	hypothetical protein	94	3	-
AUQ37_05005	hypothetical protein	7	3	-
AUQ37_05015	hypothetical protein	43	2	-
AUQ37_05040	hypothetical protein	19	2	-
AUQ37_05140	hypothetical protein	8	2	-
AUQ37_05225	hypothetical protein	132	2	-
AUQ37_05365	hypothetical protein	276	2	-
AUQ37_05400	hypothetical protein	11, 83	3	-
AUQ37_05455	ArsR family transcriptional regulator	23, 40	2	-
AUQ37_05460	hypothetical protein	87	2	-
AUQ37_05815	hypothetical protein	170	1	AUQ37_05810
AUQ37_05940	hypothetical protein	63	2	-
AUQ37_05965	dimethylamine methyltransferase	112	1	AUQ37_05970
AUQ37_05980	Trimethylamine methyltransferase	0*	1	AUQ37_05975 (pseudo)
AUQ37_06000	hypothetical protein – wrong annotation, monomethylamine methyltransferase	259	1	AUQ37_06005
AUQ37_06010	hypothetical protein – wrong annotation, monomethylamine methyltransferase	257	1	AUQ37_06015
AUQ37_06190	hypothetical protein	21	3	-
AUQ37_06225	hypothetical protein	62, 80	3	-
AUQ37_06455	hypothetical protein	1	2	-
AUQ37_06480	hypothetical protein	385	1	AUQ37_06485
AUQ37_06510	hypothetical protein	55	2	-
AUQ37_06525	hypothetical protein	0	2	-
AUQ37_06545	hypothetical protein	199	1	AUQ37_06540
AUQ37_06620	hypothetical protein	81, 190	3	-
AUQ37_06625	hypothetical protein	108	3	-
AUQ37_06870	hypothetical protein	2	2	-
AUQ37_07100	hypothetical protein	28	2	-
AUQ37_01045	hypothetical protein	156, 187	3	-
AUQ37_01125	hypothetical protein	55	1	-
AUQ37_07200	hypothetical protein	1	2	-
AUQ37_07335	hypothetical protein	38	3	-
AUQ37_07630	hypothetical protein	30, 57	3	-
AUQ37_07805	hypothetical protein	40	3	-
AUQ37_07950	hypothetical protein	227	2	-
AUQ37_08100	hypothetical protein	221	1	-
AUQ37_08175	AMP kinase	30	2	-
AUQ37_08385	hypothetical protein	23	2	-
AUQ37_01425	hypothetical protein	54, 109	2	-
AUQ37_01585	hypothetical protein	1, 37	2	-
AUQ37_08580	hypothetical protein	24	3	-
AUQ37_08765	hypothetical protein	33	2	-
AUQ37_01855	hypothetical protein	4, 149	2	-
AUQ37_02030	hypothetical protein	3, 28, 133	3	-
AUQ37_02055	ribosome biogenesis protein	42	2	-
AUQ37_02245	hypothetical protein	174	2	-
AUQ37_02300	hypothetical protein	19	3	-
AUQ37_02400	hypothetical protein	44, 71	3	-
AUQ37_02460	hypothetical protein	871	2	-
AUQ37_02465	hypothetical protein	9, 33, 63	2	-
AUQ37_02495	hypothetical protein	164	1	AUQ37_02500
AUQ37_02845	hypothetical protein	72	3	-
AUQ37_03025	hypothetical protein	43, 87	3	-
AUQ37_03075	hypothetical protein	31	2	-
AUQ37_03390	hypothetical protein	8, 14	2	-
AUQ37_03520	hypothetical protein	40	2	-
AUQ37_03530	hypothetical protein	23	2	-
AUQ37_03870	hypothetical protein	1	3	-

AUQ37_03880	hypothetical protein	13	2	-
AUQ37_03985	hypothetical protein	2	3	-
AUQ37_03990	hypothetical protein	18, 54	3	-
AUQ37_04025	hypothetical protein	210	2	-
AUQ37_04140	hypothetical protein	729	2	-
AUQ37_04145	hypothetical protein	12	2	-
AUQ37_04180	hypothetical protein	45	2	-
AUQ37_04220	hypothetical protein	96	3	-
AUQ37_04265	hypothetical protein	291	3	-

*Distance between amber codon to the next opal or ochre stop codon. # (Class 1) genes which have amber codon read-through and subsequent incorporation of pyrrolysine; (Class 2) genes that utilised the amber codon as a stop codon; (Class 3) genes with uncertain amber codon usage due to lack of homologous genes. Genes in bold indicate homologous genes with in-frame amber codon exist in other Methanomassiliicoccales. AUQ37_05980 was merged with the pseudogene in 5'.

Table A.4.10 Domains of predicted secretome in the Methanomassiliicoccales

Pfam/TIGRfam	ISO4-H5	ISO4-G1	ISO4-G11	BRNA1	RumEn M1	RumEn M2	1R26	Mx1201	Mx1	B10	MpT1
Repeat domains (containing PF13306, Leucine rich repeats (6 copies), PF13754, Bacterial Ig-like domain (group 3), PF09479, Listeria-Bacteroides repeat domain, PF05345, Putative Ig domain, PF02368, Bacterial Ig-like domain (group 2), TIGR02167: bacterial surface protein 26-residue repeat)	16	5	20	9	4	4	10	4	23	10	7
Lipo-box containing protein											
TIGR03075: PQQ- dependent dehydrogenase, methanol/ethanol family	1	-	-	-	-	-	-	-	-	-	-
PF03306: Alpha- acetolactate decarboxylase	1	-	-	-	-	-	-	-	-	-	-
PF01048: Phosphorylase superfamily	1	-	1	-	-	-	-	-	-	-	-
PF04519: Polymer- forming cytoskeletal	-	1	-	-	-	-	-	-	-	-	-
PF02129: X-Pro dipeptidyl-peptidase (S15 family)	-	1	-	-	-	-	-	-	-	-	-
PF12682: Flavodoxin: This is a family of flavodoxins	-	-	1	-	-	-	-	-	-	-	-
PF13360: PQQ-like domain	-	-	1	-	-	-	-	-	-	-	-
PF13229: Right handed beta helix region	-	-	1	-	-	-	-	-	-	-	-
PF06508, Queuosine biosynthesis protein QueC	-	-	-	-	-	-	1	1	-	-	-
PF01981, Peptidyl-tRNA hydrolase PTH2	-	-	-	-	-	-	-	-	1	-	-
PF01040: UbiA prenyltransferase family	-	-	-	-	1	-	1	-	-	-	-
PF16927: N-terminal 7TM region of histidine kinase	-	-	-	-	1	-	-	-	-	-	-
PF00091: Tubulin/FtsZ family, GTPase domain	-	-	-	-	1	-	-	-	-	-	-
PF01058: NADH ubiquinone oxidoreductase, 20 Kd subunit	-	-	-	-	2	-	-	-	-	-	-

PF07992: Pyridine nucleotide-disulphide oxidoreductase	-	-	-	-	1	-	-	-	-	-	-
PF12697: Alpha/beta hydrolase family	-	-	-	-	1	-	-	-	-	-	-
PF01855: Pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-bdg	-	-	-	-	1	-	-	-	-	-	-
PF06197: Protein of unknown function (DUF998)	-	-	-	-	-	1	-	-	-	-	-
PF07690: Major Facilitator Superfamily	-	-	-	-	-	-	1	-	-	-	-
PF01226: Formate/nitrite transporter	-	-	-	-	-	-	1	-	-	-	-
PF01497: Periplasmic binding protein	-	-	-	-	-	-	1	-	-	-	-
PF00801: PKD domain	-	-	-	-	-	-	1	-	-	-	-
PF00561: alpha/beta hydrolase fold	-	-	-	-	-	-	1	-	-	-	-
Integral membrane protein (3 or more TMH)											
PF00924: Mechanosensitive ion channel	1	1	1	1	1	1	-	-	-	1	1
PF01032: FecCD transport family	2	1	1	1	1	-	1	1	-	-	-
PF07690: Major Facilitator Superfamily	1	2	-	-	-	-	1	2	1	2	-
PF00909: Ammonium Transporter Family	-	1	1	-	-	-	-	-	1	1	-
PF06961: Protein of unknown function	1	-	-	1	-	-	-	-	-	-	-
PF01940: Integral membrane protein DUF92	1	-	-	-	-	-	-	-	-	-	-
PF00892: EamA-like transporter family	1	-	1	-	-	-	-	-	-	-	-
PF00950: ABC 3 transport family	1	1	1	-	-	-	1	-	-	-	-
PF02554: Carbon starvation protein CstA	1	-	1	-	-	-	-	-	-	-	-
PF00999: Sodium/hydrogen exchanger family	1	-	1	-	-	-	-	-	-	1	-
PF01554: MatE: The MatE domain	1	-	-	-	-	-	-	-	-	-	-
PF00893: Small Multidrug Resistance protein	-	1	1	-	1	-	-	1	-	-	-
PF06197: Protein of unknown function (DUF998)	-	1	-	1	1	-	-	-	-	1	-
TIGR01525: heavy metal translocating P-type ATPase	-	1	-	-	-	-	-	-	-	-	-
PF01970: Tripartite tricarboxylate transporter TctA family	-	1	-	-	-	-	-	-	-	-	-
TIGR01511 (Role:96): (Role:145): copper-translocating P-type ATPase	-	1	-	-	-	-	-	-	-	-	-
PF01497: Periplasmic binding protein	-	-	1	-	1	-	-	-	-	-	-
PF01040: UbiA prenyltransferase family	-	-	1	-	-	-	-	-	-	-	-
PF13593: SBF-like CPA transporter family	-	-	1	-	-	-	-	-	-	-	-
PF01595, Domain of unknown function DUF21	-	-	-	1	-	-	-	1	1	-	1
PF00474, Sodium:solute symporter family	-	-	-	1	-	-	-	-	-	-	-
PF02659, Putative manganese efflux pump	-	-	1	1	-	-	1	1	-	1	-

PF01758, Sodium Bile acid symporter family	-	-	-	1	-	1	1	-	-	1	1
PF02386: Cation transport protein	-	-	-	-	1	-	-	-	-	-	-
PF03176, MMPL family	-	-	-	1	-	-	-	-	-	-	-
PF00083, Sugar (and other) transporter	-	-	-	1	-	-	-	-	-	-	-
PF09594: Protein of unknown function (DUF2029)	-	-	-	-	-	1	-	-	-	-	-
PF03186: CobD/Cbib protein	-	-	-	-	1	1	-	-	-	-	-
PF00361: Proton-conducting membrane transporter	-	-	-	-	1	-	-	-	-	-	-
PF13620, Carboxypeptidase regulatory-like domain	-	-	-	-	-	-	-	-	-	-	1
PF01864, Putative integral membrane protein DUF46	-	-	-	-	1	-	-	-	-	-	1
PF13360: PQQ-like domain	-	-	-	-	-	-	-	1	1	-	1
PF01956, Integral membrane protein DUF106	-	-	-	-	-	-	-	1	-	-	-
PF13515, Fusaric acid resistance protein-like	-	-	-	-	-	-	-	1	-	-	-
PF01957, NfeD-like C-terminal, partner-binding	-	-	-	-	-	-	-	-	1	-	-
PF03706, Lysylphosphatidylglycerol synthase TM region	-	-	-	-	-	-	-	-	1	-	-
PF12698, ABC-2 family transporter protein	-	-	-	-	-	-	-	-	1	-	-
PF09858, Predicted membrane protein (DUF2085)	-	-	-	-	-	-	-	-	-	1	-
PF01545, Cation efflux family	-	-	-	-	-	-	-	-	-	2	-
PF01384, Phosphate transporter family	-	-	-	-	-	-	-	-	-	1	-
PF01569, PAP2 superfamily	-	-	-	-	-	-	-	-	-	1	-
PF00482, Type II secretion system (T2SS), protein F	-	-	-	-	-	-	-	-	-	1	-
PF01699, Sodium/calcium exchanger protein	-	-	-	-	1	-	-	-	-	1	-
PF00662, NADH-Ubiquinone oxidoreductase (complex I), chain 5 N-terminus	-	-	-	-	-	-	-	-	-	1	-
PF00146: NADH dehydrogenase	-	-	-	-	1	-	-	-	-	-	-
PF06847: Archaeal Peptidase A24 C-terminus Type II	-	-	-	-	1	-	-	-	-	-	-
PF02517: CAAX protease self-immunity	-	-	-	-	1	-	-	-	-	-	-
PF00702: haloacid dehalogenase-like hydrolase	-	-	-	-	-	-	1	-	-	-	-
PF13630: SdpI/YhfL protein family	-	-	-	-	-	-	1	-	-	-	-

[illegible]

[illegible]

PF00254, FKBP-type peptidyl-prolyl cis-trans isomerase	-	-	-	-	-	-	-	-	-	1	-
PF01841, Transglutaminase-like superfamily	-	-	-	-	1	-	-	-	-	2	-
PF11611, Domain of unknown function (DUF4352)	-	-	-	-	-	-	-	-	-	1	-
PF14478, Domain of unknown function (DUF4430)	-	-	-	-	-	-	-	-	-	1	-
PF01297, Zinc-uptake complex component A periplasmic	-	-	-	-	-	-	-	-	-	2	-
PF13531, Bacterial extracellular solute- binding protein	-	-	-	-	-	-	-	-	-	1	-
PF13229, Right handed beta helix region	-	-	-	-	-	-	-	-	-	1	-
Secreted											
PF00070: Pyridine nucleotide-disulphide oxidoreductase	1	1	1	1	-	-	-	-	1	1	-
TIGR01766 (Role:154): transposase, IS605 OrfB family	1	-	-	-	-	-	-	-	-	-	-
PF00155: Aminotransferase class I and II	1	-	-	-	-	-	-	-	-	-	-
PF06508, Queuosine biosynthesis protein QueC	1	-	-	1	-	1	1	-	-	-	1
PF05935: Arylsulfotransferase (ASST)	1	-	-	-	-	-	-	-	-	-	-
PF03749: Sugar fermentation stimulation protein	1	-	-	-	-	-	-	-	-	-	-
PF00312: Ribosomal protein S15	1	-	-	-	-	-	-	-	-	-	-
PF00297: Ribosomal protein L3	1	-	-	-	-	-	-	-	1	-	1
PF08069: Ribosomal S13/S15 N-terminal domain	-	-	-	-	-	1	-	-	-	-	-
PF00297: Ribosomal protein L3	-	-	-	-	1	-	-	-	-	-	-
PF01656: CobQ/CobB/MinD/ParA nucleotide binding domain	-	-	-	-	-	1	-	-	-	-	-
PF01862: Pyruvoyl- dependent arginine decarboxylase (PvlArgDC)	-	-	-	-	-	1	-	-	-	-	-
PF13091: PLD-like domain	-	-	-	-	1	1	-	-	-	-	-
PF00112: Peptidase_C1	-	-	-	-	1	-	-	-	-	-	-
PF12849: PBP superfamily domain	-	-	-	-	1	-	-	-	-	-	-
PF02525: Flavodoxin-like fold	-	1	-	-	-	-	-	-	-	-	-
PF00764: Arginosuccinate synthase	-	1	-	-	-	-	-	-	-	-	-
PF01035: 6-O- methylguanine DNA methyltransferase, DNA binding domai	-	1	-	-	-	-	-	-	-	-	-
PF02153: Prephenate dehydrogenase	-	-	1	1	-	-	1	1	-	-	-
PF00148: Nitrogenase component 1 type Oxidoreductase	-	-	-	-	-	-	1	-	-	-	-

PF01841:											
Transglutaminase-like superfamily	-	-	1	-	1	-	-	-	-	-	-
PF13229, Right handed beta helix region	-	-	-	-	1	-	-	-	-	-	-
PF05048: Periplasmic copper-binding protein (NosD)	-	-	-	-	1	-	-	-	-	-	-
PF00275, EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)	-	-	-	-	-	-	-	-	-	-	1
PF08757, CotH protein	-	-	-	-	-	-	-	1	-	-	-
PF00254, FKBP-type peptidyl-prolyl cis-trans isomerase	-	-	-	-	-	-	-	1	-	-	-
PF12838, 4Fe-4S dicluster domain	-	-	-	-	-	-	-	-	1	-	-
PF01613, Flavin reductase like domain	-	-	-	-	-	-	-	-	1	1	-
PF12682, Flavodoxin	-	-	-	-	-	-	-	-	1	-	-
PF08445, FR47-like protein	-	-	-	-	-	-	-	-	1	-	-
PF00801, PKD domain	-	-	-	-	-	-	-	-	-	2	-
PF00753, Metallo-beta-lactamase superfamily	-	-	-	-	-	-	-	-	-	1	-
PF02113: D-Ala-D-Ala carboxypeptidase 3 (S13) family	-	-	-	-	1	-	-	-	-	-	-
PF02558: Ketopantoate reductase PanE/ApbA	-	-	-	-	1	-	-	-	-	-	-
PF01593: Flavin containing amine oxidoreductase	-	-	-	-	1	-	-	-	-	-	-
PF01855: Pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-bdg	-	-	-	-	1	-	-	-	-	-	-
PF00037: 4Fe-4S binding domain	-	-	-	-	1	-	-	-	-	-	-
PF08448: PAS fold	-	-	-	-	1	-	-	-	-	-	-
PF01981, Peptidyl-tRNA hydrolase PTH2	-	-	-	-	1	-	-	-	-	1	-
PF14276: Domain of unknown function (DUF4363)	-	-	-	-	1	-	-	-	-	-	-
PF02469: Fasciclin domain	-	-	-	-	1	-	-	-	-	-	-
PF01497, Periplasmic binding protein	-	-	-	-	-	-	-	-	-	3	-
PF08241, Methyltransferase domain	-	-	-	-	-	-	-	-	-	1	-
PF01041, DegT/DnrJ/EryC1/StrS aminotransferase family	-	-	-	-	-	-	-	-	-	1	-

Prediction cutoff: E-05. Pfam conserved between rumen members of Methanomassiliicoccales are highlighted, Pfam of interest are underlined. ** Including PF13306: Leucine rich repeats (6 copies), PF13754: Bacterial Ig-like domain (group 3), PF09479: Listeria-Bacteroides repeat domain, PF05345: Putative Ig domain, PF02368: Bacterial Ig-like domain (group 2), TIGR02167: bacterial surface protein 26-residue repeat.

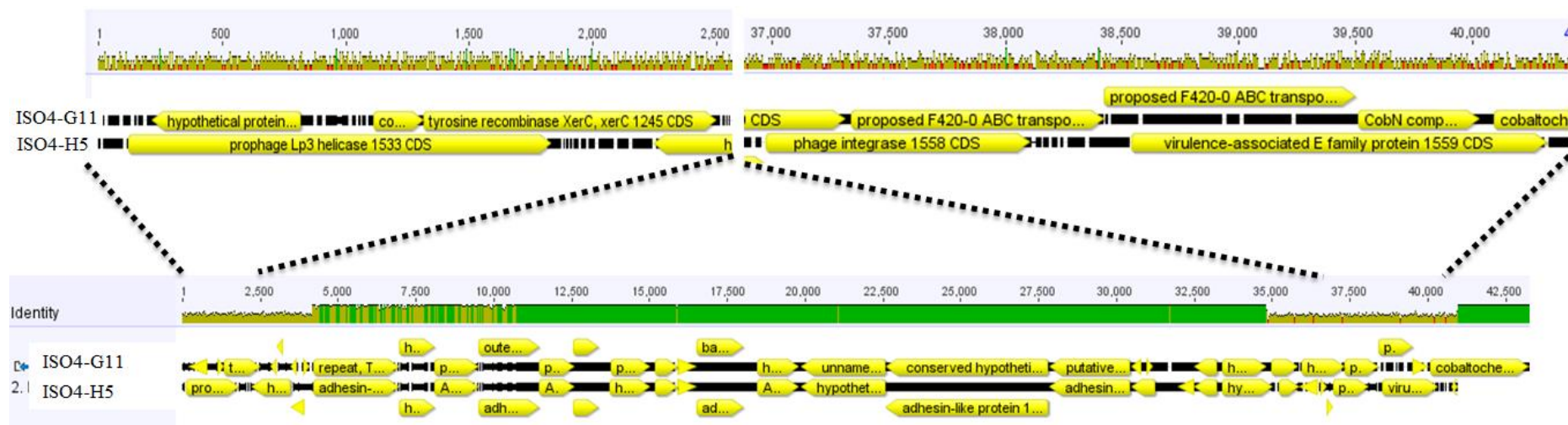


Figure A.4.1 Nucleotide alignment of horizontal transferred region between ISO4-H5 and ISO4-G11. Green area indicates 100% nucleotide identity, olive color indicates 50% nucleotide identity, red color indicates gap in sequence. Yellow block arrow indicates predicted coding sequence. Numbers indicates bases of queried sequence, not base number in genome sequence. Alignment was carried out by Geneious 6.1.5 (Kearse *et al.* 2012).

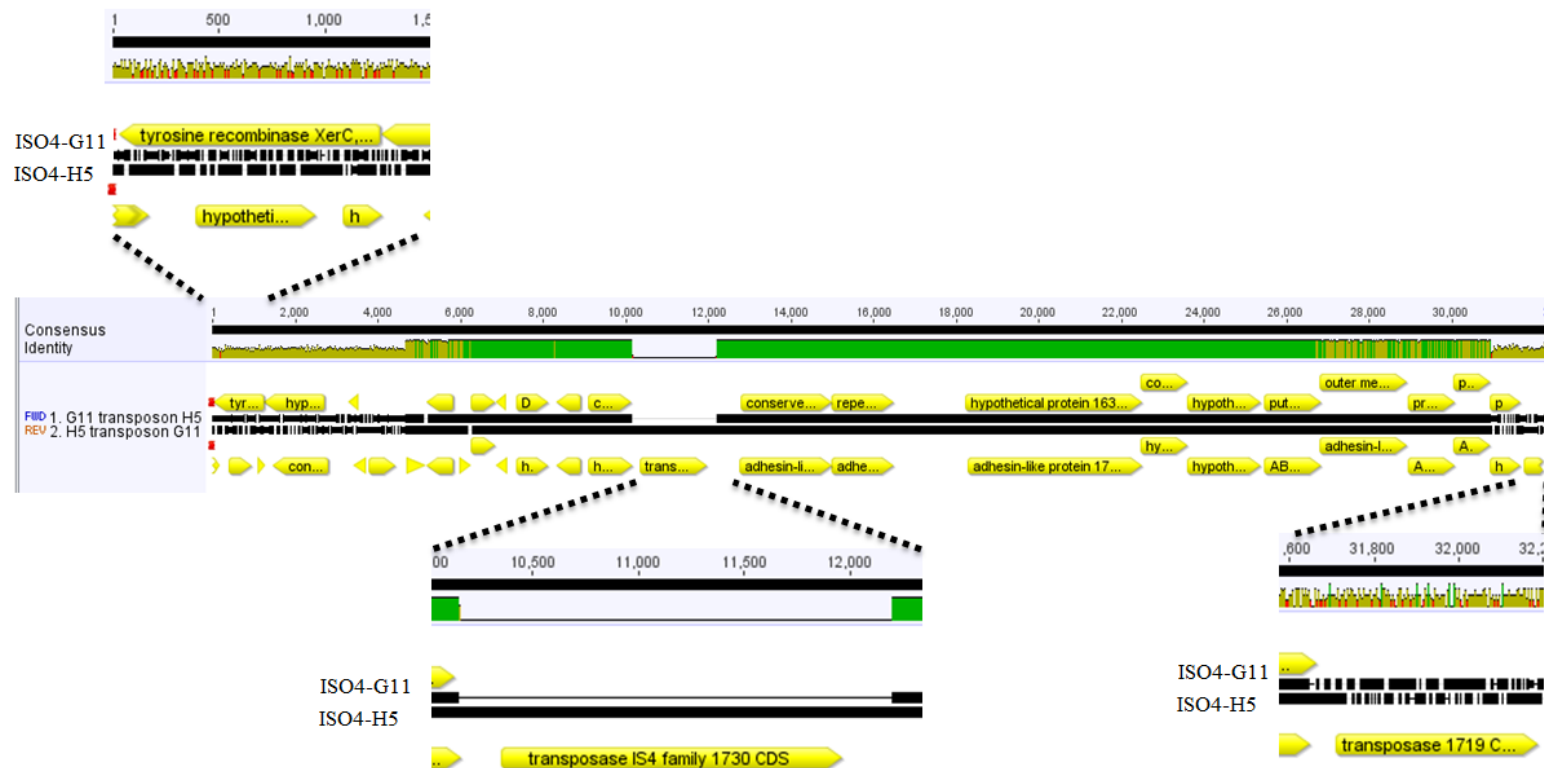


Figure A.4.2 Nucleotide alignment of horizontal transferred region between ISO4-H5 and ISO4-G11. Green area indicates 100% nucleotide identity, olive color indicates 50% nucleotide identity, red color indicates gap in sequence. Yellow block arrow indicates predicted coding sequence. Yellow block arrow indicates predicted coding sequence. Numbers indicates bases of queried sequence, not base number in genome sequence. Alignment carried out in Geneious 6.1.5 (Kearse *et al.* 2012).

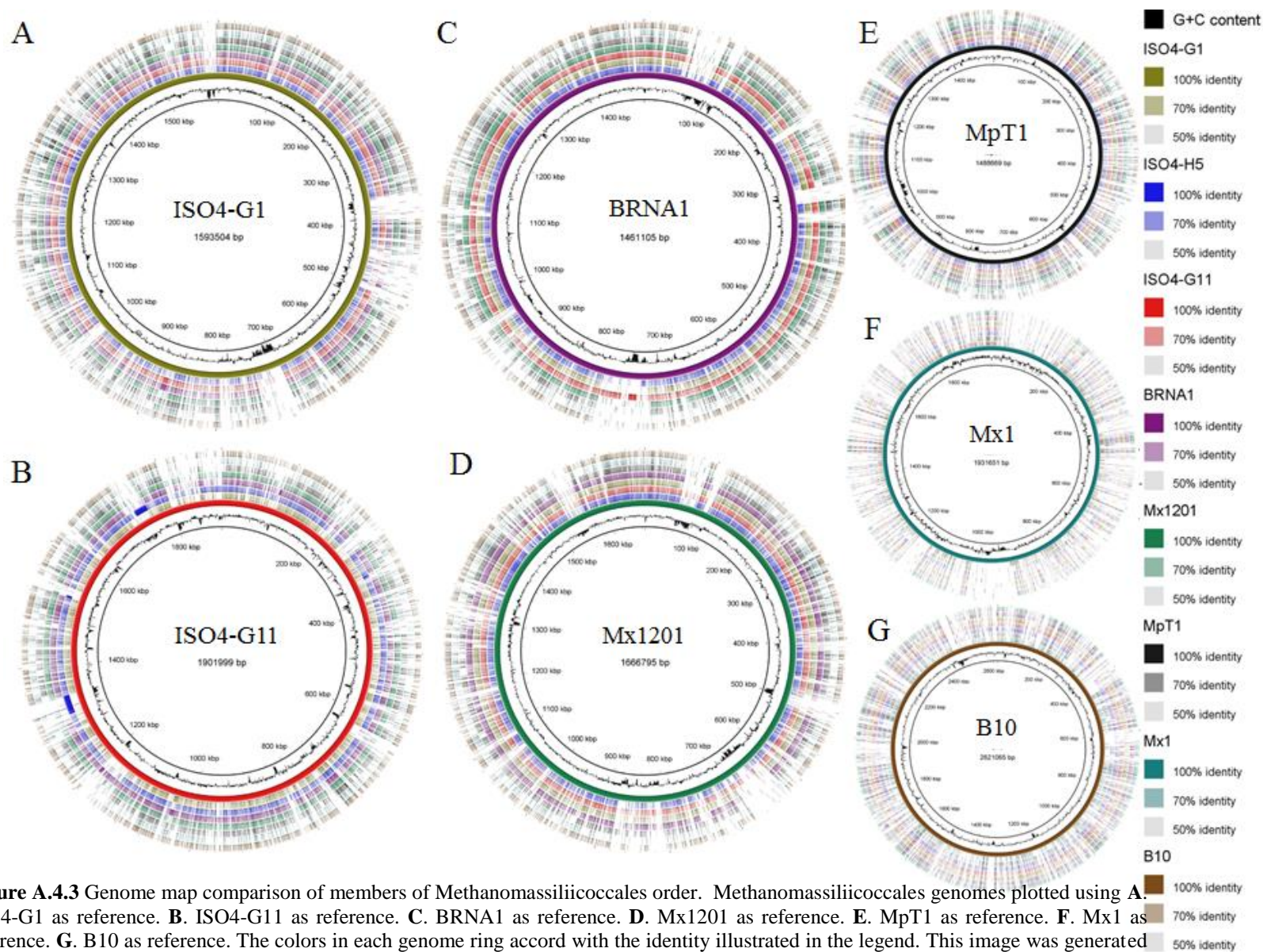


Figure A.4.3 Genome map comparison of members of Methanomassiliicoccales order. Methanomassiliicoccales genomes plotted using **A.** ISO4-G1 as reference. **B.** ISO4-G11 as reference. **C.** BRNA1 as reference. **D.** Mx1201 as reference. **E.** MpT1 as reference. **F.** Mx1 as reference. **G.** B10 as reference. The colors in each genome ring accord with the identity illustrated in the legend. This image was generated with Blast Ring Image Generator (Alikhan *et al.* 2011).

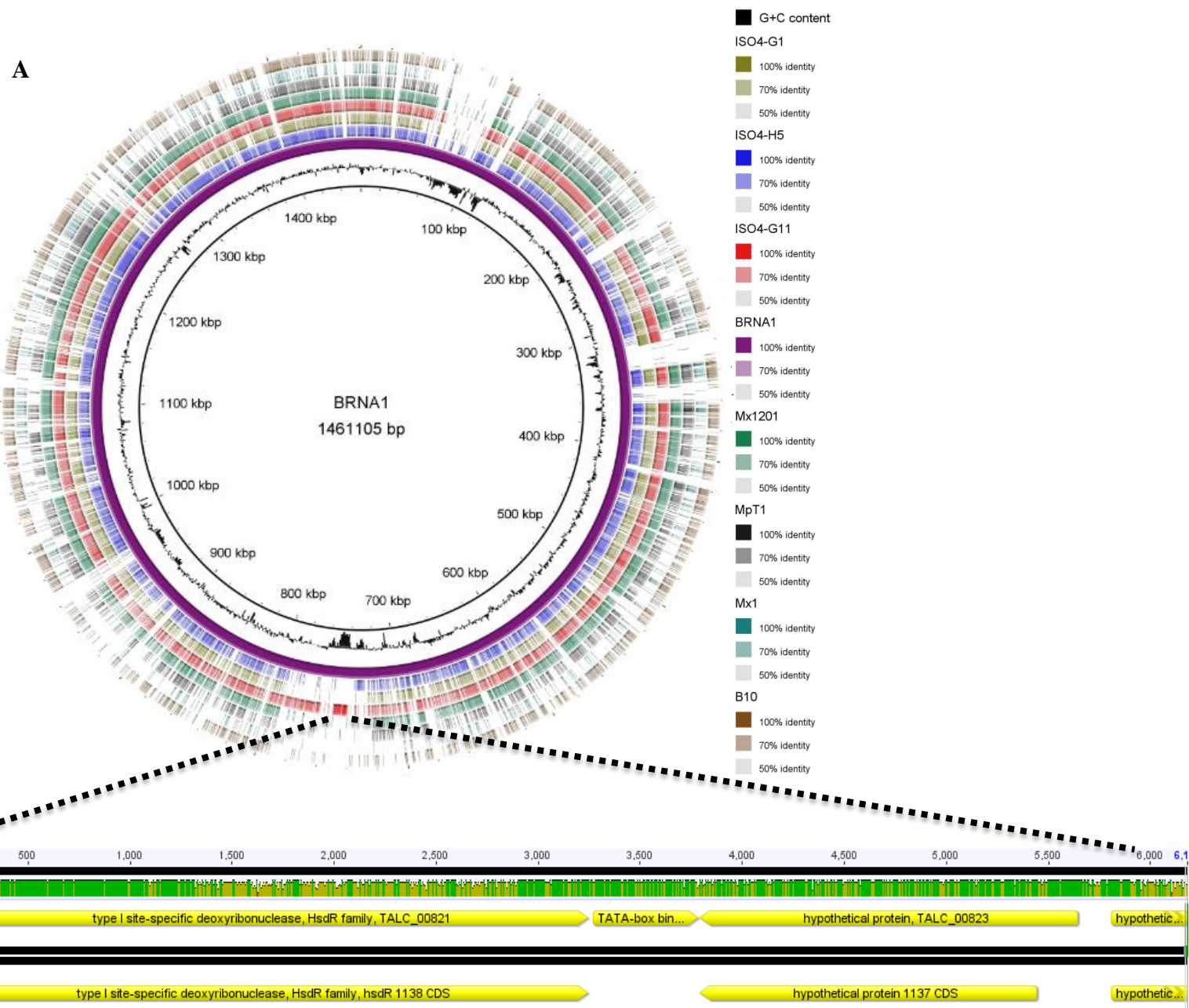


Figure A.4.4 Genome map comparison of members of Methanomassiliicoccales order. **A.** Methanomassiliicoccales genomes plotted using BRNA1 as reference. The colors in each genome ring accord with the identity illustrated in the legend. This image was generated with Blast Ring Image Generator (Alikhan *et al.* 2011). **B.** High nucleotide similarity region aligned between BRNA1 and ISO4-G11

Table A.4.11 Core genome of ISO4-H5 by functional category

Locus_tag	Predicted gene product	COG category
AR505_0001	Orc1/Cdc6 family replication initiation protein	[L]
AR505_0004	acetyl-CoA C-acetyltransferase	[I]
AR505_0006*	signal recognition particle receptor FtsY	[U]
AR505_0013*	ribosomal protein LX	[O]
AR505_0014*	DNA primase small subunit PriA	[G]
AR505_0022*	fumarate hydratase FumA	[C]
AR505_0023*	fumarate hydratase FumB	[C]
AR505_0032	thiamine biosynthesis protein ThiC1	[H]
AR505_0034	DNA gyrase A subunit GyrA	[L]
AR505_0036	hypothetical protein	[S]
AR505_0037*	phosphoribosylformylglycinamide cyclo-ligase PurM	[F]
AR505_0038*	ribosomal RNA large subunit methyltransferase J RrmJ	[J]
AR505_0039*	ATP-dependent DNA helicase	[R]
AR505_0040	CoB--CoM heterodisulfide reductase subunit D HdrD	[C]
AR505_0041	hypothetical protein	[S]
AR505_0043*	transcriptional regulator ArsR family	[S]
AR505_0044	tRNA 2'-O-methylase (pseudo)	[S]
AR505_0047*	thioredoxin TrxA	[O]
AR505_0048	thioredoxin-disulfide reductase TrxB1	[O]
AR505_0049*	XRE family transcriptional regulator	[K]
AR505_0050*	hypothetical protein	[K]
AR505_0051	histone acetyltransferase ELP3 family	[K]
AR505_0052	AAA family ATPase CDC48 subfamily	[O]
AR505_0053*	DNA-directed RNA polymerase subunit H RpoH	[K]
AR505_0054	DNA-directed RNA polymerase subunit B RpoB	[K]
AR505_0055	DNA-directed RNA polymerase subunit A' RpoA1	[K]
AR505_0056	DNA-directed RNA polymerase subunit A" RpoA2	[K]
AR505_0057*	ribosomal protein L30e Rpl30e	[J]
AR505_0058*	transcription elongation factor NusA-like protein	[K]
AR505_0059	radical SAM domain protein	[R]
AR505_0060*	orotidine 5'-phosphate decarboxylase PyrF	[F]
AR505_0066	phosphoribosylamine—glycine ligase PurD	[F]
AR505_0067	hydrogenase accessory protein HypB	[O]
AR505_0068*	glutamyl-tRNA(Gln) amidotransferase subunit D GatD	[J]
AR505_0069	glutamyl-tRNA(Gln) amidotransferase subunit E GatE	[J]
AR505_0076	thymidylate synthase ThyX	[F]
AR505_0077*	ribosomal protein S17e Rps17e	[J]
AR505_0080	hydrogenase expression/formation protein HypE	[O]
AR505_0092	thermosome subunit	[O]
AR505_0094	chaperone protein DnaK	[O]
AR505_0108*	glutamate-5-semialdehyde dehydrogenase ProA	[E]
AR505_0115*	universal archaeal protein Kae1	[O]
AR505_0118*	ribosomal protein S15P Rps15p	[J]
AR505_0120*	fibrillarlin	[J]
AR505_0124*	hypothetical protein	Not in COGs

AR505_0129*	ribosomal protein L15e Rpl15e	[J]
AR505_0130	DNA polymerase family B PolB	[L]
AR505_0131	translation-associated GTPase	[J]
AR505_0132*	dimethyladenosine transferase KsgA	[J]
AR505_0133*	conserved hypothetical protein	[J]
AR505_0135*	ribosomal protein L21e Rpl21e	[J]
AR505_0136	hypothetical protein	[J]
AR505_0137	RNA-binding protein	[R]
AR505_0138	serine/threonine protein kinase RIO1 family	[T]
AR505_0139*	translation initiation factor aIF-1A	[J]
AR505_0143*	L-aspartate dehydrogenase	[R]
AR505_0150	2,3-dihydroxy-isovalerate:NADP ⁺ oxidoreductase IlvC	[E]
AR505_0154*	glyceraldehyde-3-phosphate dehydrogenase Gap	[G]
AR505_0155*	phosphoglycerate kinase Pggk	[G]
AR505_0157	LL-diaminopimelate aminotransferase DapC	[E]
AR505_0158*	diaminopimelate epimerase DapF	[E]
AR505_0159	diaminopimelate decarboxylase LysA	[E]
AR505_0161	dihydrodipicolinate synthase DapA	[E]
AR505_0162*	transcriptional regulator AsnC family	[E]
AR505_0167*	conserved hypothetical protein	[S]
AR505_0177	6-phospho 3-hexuloisomerase hxlB	[M]
AR505_0178	endonuclease IV	[L]
AR505_0179*	ribosomal protein L18e Rpl18e	[J]
AR505_0180*	ribosomal protein L13P Rpl13p	[J]
AR505_0181*	ribosomal protein S9P Rps9p	[J]
AR505_0182*	DNA-directed RNA polymerase subunit N RpoN	[K]
AR505_0187*	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	[F]
AR505_0188*	Kae1-associated kinase Bud32	[T]
AR505_0191*	isopentenyl diphosphate delta-isomerase Fni	[C]
AR505_0194*	hydrogenase assembly chaperone HypC/HupF	[O]
AR505_0195*	alpha-NAC homolog	[K]
AR505_0200*	aspartate--tRNA synthetase AspS1	[J]
AR505_0202	Asp-tRNAAsn/Glu-tRNA Gln amidotransferase subunit A GatA	[J]
AR505_0203*	Asp-tRNAAsn/Glu-tRNA Gln amidotransferase subunit C GatC	[J]
AR505_0210*	GTP cyclohydrolase RibA	[S]
AR505_0212	CoA-disulfide reductase Cdr	[R]
AR505_0216*	TIGR01210 family protein	[R]
AR505_0218*	ribosomal protein L3P Rpl3p	[J]
AR505_0219*	ribosomal protein L4P Rpl4p	[J]
AR505_0220*	ribosomal protein L23P Rpl23p	[J]
AR505_0221	ribosomal protein L2P Rpl2p	[J]
AR505_0222	ribosomal protein S19P Rps19p	[J]
AR505_0223	ribosomal protein L22P Rpl22p	[J]
AR505_0224	ribosomal protein S3P Rps3p	[J]
AR505_0225*	ribosomal protein L29P Rpl29p	[J]
AR505_0226*	translation initiation factor aSUII	[J]
AR505_0228*	ribosomal protein S17P Rps17p	[J]
AR505_0229*	ribosomal protein L14e Rpl14e	[J]
AR505_0230*	ribosomal protein L24P Rpl24p	[J]
AR505_0232*	ribosomal protein L5P Rpl5p	[J]
AR505_0233*	ribosomal protein S8P Rps8p	[J]
AR505_0234*	ribosomal protein L6P Rpl6p	[J]
AR505_0235*	ribosomal protein L32e Rpl32e	[J]
AR505_0236*	ribosomal protein L19e Rpl19e	[J]
AR505_0237*	ribosomal protein L18P Rpl18p	[J]
AR505_0238*	ribosomal protein S5P Rps5p	[J]
AR505_0239*	ribosomal protein L30P Rpl30p	[J]

AR505_0240	ribosomal protein L15P Rpl15p	[J]
AR505_0241	preprotein translocase subunit SecY	[U]
AR505_0243*	tRNA pseudouridine synthase B TruB	[J]
AR505_0247	tryptophanyl-tRNA synthetase TrpS	[J]
AR505_0248	phenylalanyl-tRNA synthetase alpha subunit PheS	[J]
AR505_0251	uridylate kinase PyrH	[F]
AR505_0252*	peptide chain release factor aRF1	[J]
AR505_0253*	arginine-tRNA synthetase ArgS	[J]
AR505_0255*	hypothetical transmembrane protein	Not in COGs
AR505_0257*	5-formaminoimidazole-4-carboxamide-1-β-D-ribofuranosyl 5'-monophosphate synthetase-like protein	[R]
AR505_0262	adenylate kinase Adk	[F]
AR505_0263*	FAD linked oxidase domain-containing protein	[C]
AR505_0265	phosphoadenosine phosphosulfate reductase	[J]
AR505_0268*	pyruvoyl-dependent arginine decarboxylase PdaD	[S]
AR505_0273*	CoB--CoM heterodisulfide reductase subunit C HdrC	[C]
AR505_0274	CoB--CoM heterodisulfide reductase subunit B HdrB	[C]
AR505_0277*	ribosomal protein S3Ae Rps3ae	[J]
AR505_0283	ribosomal protein L37e Rpl37e	[J]
AR505_0284	amidophosphoribosyltransferase PurF	[F]
AR505_0291	hypothetical protein	[S]
AR505_0292	hypothetical protein	[T]
AR505_0293*	homoserine dehydrogenase MetL	[E]
AR505_0377	NAD synthetase NadE	[H]
AR505_0378	Cobalt-precorrin-5 (C ₁)-methyltransferase CbiD	[H]
AR505_0380	precorrin-6x reductase CbiJ	[H]
AR505_0386*	hypothetical protein	[U]
AR505_0387	lysyl-tRNA synthetase LysS	[J]
AR505_0388*	DNA topoisomerase VI subunit A	[L]
AR505_0389	DNA topoisomerase VI subunit B	[L]
AR505_0393	small GTP-binding protein	[R]
AR505_0394	histidyl-tRNA synthetase HisS	[J]
AR505_0405	magnesium chelatase ChlI	[H]
AR505_0412	ABC transporter ATP-binding protein	[V]
AR505_0413	precorrin-2 C20-methyltransferase CbiL	[H]
AR505_0414	precorrin-4 C11-methyltransferase CbiF	[H]
AR505_0415	precorrin-3B C17-methyltransferase CbiH	[H]
AR505_0416	precorrin-8X methylmutase CbiC	[H]
AR505_0418	ABC transporter permease protein	[V]
AR505_0421	aspartate 1-decarboxylase PanD	[H]
AR505_0425*	signal transduction protein with CBS domains	[K]
AR505_0427	phosphoenolpyruvate synthase PpsA1	[G]
AR505_0429	pyruvate ferredoxin oxidoreductase γ subunit PorC	[C]
AR505_0430*	pyruvate ferredoxin oxidoreductase Δ subunit PorD	[C]
AR505_0431	pyruvate ferredoxin oxidoreductase α subunit PorA	[C]
AR505_0432	pyruvate ferredoxin oxidoreductase β subunit PorB	[C]
AR505_0436*	aspartate carbamoyltransferase regulatory subunit PyrI	[F]

AR505_0437	aspartate carbamoyltransferase PyrB	[F]
AR505_0453*	hypothetical protein	[S]
AR505_0455	isoleucyl-tRNA synthetase IleS	[J]
AR505_0460	flap endonuclease Fen	[L]
AR505_0461	ribulose-phosphate 3-epimerase Rpe	[G]
AR505_0468	ribosomal protein L40e Rpl40e	[J]
AR505_0470	phosphopyruvate hydratase Eno	[G]
AR505_0475*	hydrogenase maturation factor HypF	[O]
AR505_0481*	methylthioadenosine phosphorylase MtnP	[F]
AR505_0485*	PHP domain-containing protein	[R]
AR505_0486*	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase HisE	[E]
AR505_0487	imidazoleglycerol-phosphate synthase cyclase subunit HisF	[E]
AR505_0488*	imidazoleglycerol-phosphate dehydratase HisB	[E]
AR505_0491	aspartate-semialdehyde dehydrogenase Asd	[E]
AR505_0494*	ATP phosphoribosyltransferase HisG	[E]
AR505_0495*	histidinol-phosphate aminotransferase HisC	[E]
AR505_0496*	imidazole glycerol phosphate synthase glutamine amidotransferase subunit HisH	[E]
AR505_0503*	carbamoyl-phosphate synthase large subunit CarB2	[F]
AR505_0531*	isopropylmalate/isohomocitrate dehydrogenases LeuB	[C]
AR505_0592*	aconitate hydratase 1 AcnA	[C]
AR505_0600*	HTH domain-containing protein	[K]
AR505_0601	hydroxymethylglutaryl-CoA synthase	[I]
AR505_0602	acetyl-CoA acetyltransferase	[I]
AR505_0603*	DNA-binding protein	[R]
AR505_0610*	homoserine kinase ThrB	[E]
AR505_0611*	threonine synthase ThrC	[E]
AR505_0615	ATP-dependent protease S16 family	[O]
AR505_0617	competence/damage-inducible protein CinA	[R]
AR505_0626*	NAD(P)-dependent glycerol-1-phosphate dehydrogenase	[C]
AR505_0637*	archaeosine tRNA-ribosyltransferase TgtA	[J]
AR505_0642*	peptidyl-tRNA hydrolase	[S]
AR505_0643*	thiamine monophosphate synthase ThiE2	[H]
AR505_0671	argininosuccinate lyase ArgH	[E]
AR505_0672*	argininosuccinate synthase ArgG	[E]
AR505_0673*	N-acetyl-gamma-glutamyl-phosphate reductase ArgC	[E]
AR505_0674	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein ArgJ	[E]
AR505_0676*	acetylornithine aminotransferase ArgD	[E]
AR505_0694	homoserine O-succinyltransferase MetA	[E]
AR505_0701	ABC transporter ATP-binding protein	[R]
AR505_0709*	methionyl-tRNA synthetase MetG1	[J]
AR505_0740	TATA-box-binding protein Tbp	[K]
AR505_0742	adenylosuccinate lyase PurB	[F]
AR505_0752	nitrate/sulfonate/bicarbonate ABC transporter ATPase NtrD	[P]
AR505_0757*	phosphoserine phosphatase SerB	[S]
AR505_0758	signal recognition particle SRP54 protein	[U]

AR505_0759*	hypothetical protein	[S]
AR505_0767*	phenylalanyl-tRNA synthetase subunit β PheT	[I]
AR505_0768*	hydroxymethylglutaryl-CoA reductase (NADPH) HmgA	[H]
AR505_0776	ribosomal protein S19e Rps19e	[J]
AR505_0777*	DNA-binding protein	[R]
AR505_0778*	ribosomal protein L39e Rpl39e	[J]
AR505_0779*	ribosomal protein L31e Rpl31e	[J]
AR505_0783*	hypothetical protein	[R]
AR505_0786	methanogenesis marker protein 2	[R]
AR505_0799	<i>O</i> -acetylserine sulfhydrylase	[E]
AR505_0810*	transcription initiation factor TFIIIB Tfb	[K]
AR505_0824*	HPr kinase	[C]
AR505_0826	hypothetical transmembrane protein	[S]
AR505_0827*	wyosine biosynthesis protein TYW1	[C]
AR505_0922*	DNA-directed RNA polymerase subunit K RpoK	[K]
AR505_0927*	SPFH domain / Band 7 family protein	[O]
AR505_0932	fructose-bisphosphate aldolase Fba	[G]
AR505_0947	cobalamin biosynthesis protein CobW	[R]
AR505_0967	Proteasome endopeptidase complex	[O]
AR505_0968	universal archaeal KH-domain/ β -lactamase-domain protein	[R]
AR505_0969	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	[H]
AR505_0972	leucyl-tRNA synthetase LeuS	[J]
AR505_0998	indolepyruvate ferredoxin oxidoreductase beta subunit IorB	[C]
AR505_0999*	indolepyruvate ferredoxin oxidoreductase α subunit IorA	[C]
AR505_1009*	phenylacetate-CoA ligase PaaF1	[H]
AR505_1014*	ABC transporter ATP-binding protein	[V]
AR505_1027*	cysteine desulfurase SufS subfamily SufS	[E]
AR505_1029	dihydroorotate dehydrogenase PyrD	[F]
AR505_1055*	site-specific recombinase	[L]
AR505_1073*	histidinol dehydrogenase HisD	[E]
AR505_1120*	aspartokinase beta subunit	[Unclassified]
AR505_1121	glutamyl-tRNA synthetase GltX	[J]
AR505_1142*	DNA primase DnaG	[L]
AR505_1143	ATP-dependent protease	[O]
AR505_1148	triose-phosphate isomerase TpiA	[G]
AR505_1149*	fructose 1,6-bisphosphatase Fbp	[G]
AR505_1150	aspartyl-tRNA synthetase AspS2	[J]
AR505_1151	tryptophan synthase beta subunit TrpB	[R]
AR505_1165*	NTPase	[F]
AR505_1166*	N ² ,N ² -dimethylguanosine tRNA methyltransferase Trm1	[J]
AR505_1168	adenylosuccinate synthase PurA	[F]
AR505_1172*	3-octaprenyl-4-hydroxybenzoate decarboxylyase UbiD	[H]
AR505_1180*	3,4-dihydroxy-2-butanone-4-phosphate synthase RibB	[H]
AR505_1181*	FAD synthase	[M]
AR505_1182*	riboflavin synthase RibC	[H]
AR505_1183*	6,7-dimethyl-8-ribityllumazine synthase RibH	[H]
AR505_1191	cysteinyI-tRNA synthetase CysS	[J]
AR505_1199*	alanine aminotransferase	[E]
AR505_1203*	methanogenesis marker protein 8	[S]
AR505_1204*	PP-loop domain-containing protein	[D]
AR505_1209	replication factor C small subunit	[L]
AR505_1217	formate-tetrahydrofolate ligase	[F]

AR505_1222	ferrous iron transport protein B FeoB	[P]
AR505_1233	pseudouridylyl synthase	[J]
AR505_1235	peptidyl-prolyl cis-trans isomerase	[O]
AR505_1274	tRNA pseudouridine synthase D TruD	[S]
AR505_1277*	ATP-dependent DNA ligase DnlI	[L]
AR505_1279*	iron-sulfur cluster assembly protein	[S]
AR505_1284	diphthine synthase DphB	[J]
AR505_1287*	deoxycytidine triphosphate deaminase Dcd	[F]
AR505_1299	DNA topoisomerase I TopA	[L]
AR505_1303	asparagine synthase (glutamine-hydrolyzing) AsnB	[E]
AR505_1305*	endonuclease III Nth	[L]
AR505_1307	hydrogenase expression/formation protein HypD	[O]
AR505_1318	peptidase M18 family	[E]
AR505_1320*	Methyltransferase corrinoid activation protein	[R]
AR505_1321	ATP-dependent RNA helicase	[K]
AR505_1324	pyrrolysine biosynthesis radical SAM protein PylB	[H]
AR505_1325	pyrrolysine--tRNA ligase PylS	[J]
AR505_1328	monomethylamine methyltransferase MtmB	[Unclassified]
AR505_1329	methyltransferase cognate corrinoid proteins	[R]
AR505_1339*	valyl-tRNA synthetase ValS	[J]
AR505_1341*	glycyl-tRNA synthetase GlyS	[J]
AR505_1349	hypothetical protein	[Unclassified]
AR505_1357	gliding motility-associated protein GldE	[R]
AR505_1370*	ribosomal protein S27e Rps27e	[J]
AR505_1373	DNA-directed RNA polymerase subunit E RpoE	[J]
AR505_1374	DNA-directed RNA polymerase RpoE	[K]
AR505_1375*	deoxyhypusine synthase Dys	[O]
AR505_1385*	methanogenesis marker protein 7	[R]
AR505_1387*	methanogenesis marker protein 15	[I]
AR505_1388*	methanogenesis marker protein 5	[S]
AR505_1389*	methanogenesis marker protein 6	[S]
AR505_1391*	methyl-coenzyme M reductase C subunit McrC	[H]
AR505_1392	methyl-coenzyme M reductase component A2 AtwA	[R]
AR505_1396	methyl-coenzyme M reductase α subunit McrA	[H]
AR505_1397	methyl-coenzyme M reductase γ subunit McrG	[H]
AR505_1398*	methyl-coenzyme M reductase operon protein D McrD	[H]
AR505_1399	methyl-coenzyme M reductase β subunit McrB	[H]
AR505_1401*	ornithine carbamoyltransferase ArgF	[E]
AR505_1406	RNA-splicing ligase RtcB	[S]
AR505_1408*	RNA-binding protein	[J]
AR505_1412	cell division ATPase MinD	[D]
AR505_1413	dinitrogenase iron-molybdenum cofactor biosynthesis protein	[S]
AR505_1414	7-cyano-7-deazaguanosine biosynthesis protein QueE	[R]
AR505_1415*	queuosine biosynthesis protein QueC	[H]
AR505_1416	6-pyruvoyl tetrahydropterin synthase QueD	[R]
AR505_1421	ribosomal protein L10e Rpl10e	[J]
AR505_1426*	seryl-tRNA synthetase SerS	[J]
AR505_1431	mevalonate kinase Mvk	[I]
AR505_1433	geranylgeranyl reductase	[C]

AR505_1434*	Ferredoxin	[C]
AR505_1435	molybdenum cofactor biosynthesis protein A MoaA	[R]
AR505_1437	GTPase	[R]
AR505_1438	DNA polymerase II large subunit DP2 PolD2	[L]
AR505_1439*	DNA-directed RNA polymerase subunit D RpoD	[K]
AR505_1440*	ribosomal protein S11P Rps11p	[J]
AR505_1441*	ribosomal protein S4P Rps4p	[J]
AR505_1442*	ribosomal protein S13P Rps13p	[J]
AR505_1447	nitrogenase cofactor biosynthesis protein NifB	[R]
AR505_1448	alanyl-tRNA synthetase AlaS	[J]
AR505_1449	chorismate synthase AroC	[E]
AR505_1453*	ribosomal protein S10P Rps10p	[J]
AR505_1454	translation elongation factor aEF-1 α	[J]
AR505_1455	translation elongation factor aEF-2	[J]
AR505_1456*	ribosomal protein S7P Rps7p	[J]
AR505_1457*	ribosomal protein S12P Rps12p	[J]
AR505_1459*	translation initiation factor aIF-2 α subunit	[J]
AR505_1472*	ribosomal protein S8e Rps8e	[J]
AR505_1475*	phosphoesterase	[R]
AR505_1476*	methyl-viologen-reducing hydrogenase α subunit MvhA	[C]
AR505_1477*	methyl-viologen-reducing hydrogenase γ subunit MvhG	[C]
AR505_1478*	methyl-viologen-reducing hydrogenase Δ subunit	[C]
AR505_1479	CoB--CoM heterodisulfide reductase subunit A HdrA	[C]
AR505_1482*	proteasome alpha subunit PsmA	[O]
AR505_1483	Ribosome maturation protein SBDS	[J]
AR505_1484	exosome complex RNA-binding protein Rrp4	[J]
AR505_1485*	exosome complex exonuclease Rrp41	[J]
AR505_1486	exosome complex RNA-binding protein Rrp42	[J]
AR505_1487*	ribosomal protein L37Ae	[J]
AR505_1488*	DNA-directed RNA polymerase subunit P RpoP	[K]
AR505_1490*	prefoldin beta subunit PfdB	[O]
AR505_1493*	phosphoesterase DHHA1	[R]
AR505_1494	tyrosyl-tRNA synthetase TyrS	[J]
AR505_1512*	4Fe-4S-binding-domain containing ABC transporter ATP-binding protein	[R]
AR505_1513*	ribose 5-phosphate isomerase A RpiA	[G]
AR505_1514*	ribosomal protein L44e Rpl44e	[J]
AR505_1515*	ribosomal protein S27e Rps27e	[J]
AR505_1516	translation initiation factor aIF-2 α subunit	[J]
AR505_1581	Cytosine deaminase	[F]
AR505_1585*	DNA repair and recombination protein RadA	[L]
AR505_1587	prenyltransferase UbiA	[H]
AR505_1588	geranylgeranylglycerol phosphate synthase GGGPS	[R]
AR505_1589*	hypothetical protein	[Unclassified]
AR505_1602*	Bifunctional diaminohydroxy-phosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase RibD	[H]
AR505_1603	translation initiation factor aIF-2 β subunit	[J]

AR505_1605	C/D box methylation guide ribonucleoprotein complex aNOP56 subunit	[J]
AR505_1606	translation initiation factor aIF-5A	[J]
AR505_1608*	phosphoglucomutase	[G]
AR505_1614*	uracil-DNA glycosylase Ung	[L]
AR505_1615	orotate phosphoribosyltransferase PyrE	[F]
AR505_1616*	hypothetical transmembrane protein	[I]
AR505_1617*	DNA/RNA-binding protein	[R]
AR505_1623*	F ₄₂₀ H ₂ dehydrogenase subunit M FpoM	[C]
AR505_1625*	F ₄₂₀ H ₂ dehydrogenase subunit K FpoK	[C]
AR505_1628*	F ₄₂₀ H ₂ dehydrogenase subunit I FpoI	[C]
AR505_1630*	F ₄₂₀ H ₂ dehydrogenase subunit D FpoD	[C]
AR505_1632*	F ₄₂₀ H ₂ dehydrogenase subunit B FpoB	[C]
AR505_1635*	Fe-S oxidoreductase	[C]
AR505_1636*	undecaprenyl pyrophosphate synthetase UppS	[I]
AR505_1637*	methanogenesis marker protein 11	[R]
AR505_1638	RNA 2'-phosphotransferase Tpt1/KptA	[J]
AR505_1639	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase FolD	[H]
AR505_1641	AMP phosphorylase DeoA	[F]
AR505_1642*	ribulose biphosphate carboxylase RbcL	[G]
AR505_1643*	ribose-1,5-bisphosphate isomerase E2b2	[J]
AR505_1647*	transaldolase	[G]
AR505_1648*	transketolase subunit B	[G]
AR505_1649*	transketolase subunit A	[G]
AR505_1650*	proliferating cell nuclear antigen PcnA	[L]
AR505_1655	hypothetical protein	[S]
AR505_1656	bifunctional phosphoribosylamino imidazolecarboxamide formyltransferase/IMP cyclohydrolase PurH	[F]
AR505_1658	exosome complex RNA-binding protein Csl4	[J]
AR505_1660	thiamine biosynthesis ATP pyrophosphatase ThiI	[H]
AR505_1661*	hypothetical protein	[Unclassified]
AR505_1663	hypothetical protein	[Unclassified]
AR505_1664*	phosphoglycerate dehydrogenase SerA	[E]
AR505_1665	Phosphoserine aminotransferase	[E]
AR505_1666	aspartate aminotransferase	[E]
AR505_1667	5-formaminoimidazole-4-carboxamide-1- β -D- ribofuranosyl 5'-monophosphate-formate ligase PurP	[R]
AR505_1671	ribosomal protein S2P Rps2p	[J]
AR505_1676*	GTPase	[R]
AR505_1679*	riboflavin kinase	[K]
AR505_1680*	phosphoribosylformylglycinamide synthase I PurQ	[F]
AR505_1681	phosphoribosylformylglycinamide synthase II PurL	[F]
AR505_1682*	phosphoribosylformylglycinamide synthase PurS	[F]
AR505_1683*	tRNA methyltransferase subunit	[J]
AR505_1684*	prolyl-tRNA synthetase ProS	[J]
AR505_1685*	ribose-phosphate diphosphokinase Prs	[F]

AR505_1687	hypothetical protein Ta0304	[S]
AR505_1695*	Metal-dependent hydrolases β-lactamase family	[H]
AR505_1751*	hypothetical protein	Not in COGs
AR505_1752*	translation initiation factor aIF-2 γ subunit	[R]
AR505_1753*	ribosomal protein S6e Rps6e	[J]
AR505_1755	translation initiation factor aIF-2	[J]
AR505_1756*	nucleoside diphosphate kinase Ndk	[J]
AR505_1757	ribosomal protein L24e Rpl24e	[J]
AR505_1758*	ribosomal protein S28e Rps28e	[J]
AR505_1759*	ribosomal protein L7Ae Rpl7ae	[J]
AR505_1780	malate dehydrogenase Mdh	[C]
AR505_1781	Fe-S oxidoreductase	[C]
AR505_1783*	CDP-diacylglycerol-serine O-phosphatidyltransferase PssA	[I]
AR505_1788	adenosylhomocysteinase AhcY2	[H]
AR505_1789*	hypothetical protein	[S]
AR505_1791	RNA methyltransferase TrmH family	[J]
AR505_1794*	ribosomal protein L12P Rpl12p	[J]
AR505_1795*	acidic ribosomal protein P0 RplPO	[J]
AR505_1796*	ribosomal protein L1P Rpl1p	[J]
AR505_1797*	ribosomal protein L11P Rpl11p	[J]
AR505_1799*	protein translocase subunit Sss1	[U]
AR505_1800	hypothetical protein	[Unclassified]
AR505_1801*	hypothetical protein	[S]
AR505_1802	GMP synthase subunit A GuaA	[F]
AR505_1803	GMP synthase subunit B GuaAb	[F]
AR505_1804*	phosphoribosylaminoimidazole carboxylase PurE	[F]
AR505_1811*	transcriptional regulator	[K]
AR505_1818*	A ₁ A ₀ -type ATP synthase subunit D	[C]
AR505_1819*	A ₁ A ₀ -type ATP synthase subunit B	[C]
AR505_1820*	A ₁ A ₀ -type ATP synthase subunit A	[C]
AR505_1821*	A ₁ A ₀ -type ATP synthase subunit F	[C]
AR505_1824*	A ₁ A ₀ -type ATP synthase subunit K	[C]
AR505_1827*	CMP/dCMP deaminase	[U]

#only one gene from each gene family is represented.
*represents gene families found conserved across the incomplete genomes

Table A.4.12 Gene families unique to ISO4-H5

Locus_tag	Predicted gene product	COG category
AR505_0002	hypothetical transmembrane protein	Not in COGs
AR505_0005	adhesin-like protein	[S]
AR505_0023	hypothetical transmembrane protein	Not in COGs
AR505_0061	adhesin-like protein	[R]
AR505_0062	hypothetical protein	Not in COGs
AR505_0063	hypothetical protein	Not in COGs
AR505_0083	hypothetical protein	Not in COGs
AR505_0088	hypothetical transmembrane protein	Not in COGs
AR505_0090	hypothetical protein	Not in COGs
AR505_0098	pyridoxamine 5'-phosphate oxidase-related protein	[R]

AR505_0106	transposase	[L]
AR505_0107	transposase	[L]
AR505_0110	methyltransferase cognate corrinoïd protein	[R]
AR505_0114	methylase involved in ubiquinone/ menaquinone biosynthesis	[R]
AR505_0116	hypothetical protein	Not in COGs
AR505_0123	phosphoglucosamine mutase GlmM	[G]
AR505_0148	hypothetical protein	Not in COGs
AR505_0156	hypothetical protein	Not in COGs
AR505_0164	peptidase A24B	[O]
AR505_0170	hypothetical transmembrane protein	[M]
AR505_0171	hypothetical transmembrane protein	Not in COGs
AR505_0174	hypothetical protein	Not in COGs
AR505_0175	hypothetical protein	[O]
AR505_0176	hypothetical protein	Not in COGs
AR505_0183	hypothetical protein	Not in COGs
AR505_0185	hypothetical transmembrane protein	Not in COGs
AR505_0186	nitroreductase family protein	[C]
AR505_0207	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	[R]
AR505_0213	transposase IS116/IS110/IS902 family	[L]
AR505_0214	hypothetical protein	Not in COGs
AR505_0256	hypothetical transmembrane protein	Not in COGs
AR505_0275	TPR repeat-containing protein	[R]
AR505_0279	hypothetical protein	Not in COGs
AR505_0285	Na ⁺ -dependent transporter SNF family	[R]
AR505_0288	hypothetical transmembrane protein	Not in COGs
AR505_0288	NADPH-dependent FMN reductase	[R]
AR505_0296	MatE efflux family protein	[V]
AR505_0297	hypothetical protein	Not in COGs
AR505_0298	Cob/MinD domain containing protein	[D]
AR505_0299	cobalamin biosynthesis protein CbiX	[S]
AR505_0300	hypothetical protein	Not in COGs
AR505_0301	adenine phosphoribosyltransferase Apt	[F]
AR505_0302	hypothetical transmembrane protein	Not in COGs
AR505_0303	ABC transporter solute binding protein	[P]
AR505_0306	hypothetical protein	[P]
AR505_0307	SAM-dependent methyltransferase	[P]
AR505_0310	ABC transporter solute-binding protein	Not in COGs
AR505_0312	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	[R]
AR505_0313	phage integrase	[L]
AR505_0315	hypothetical protein	Not in COGs
AR505_0316	hypothetical protein	Not in COGs
AR505_0318	hypothetical protein	Not in COGs
AR505_0319	hypothetical protein	Not in COGs
AR505_0324	hypothetical protein	Not in COGs
AR505_0325	hypothetical protein	Not in COGs
AR505_0326	hypothetical protein	Not in COGs
AR505_0327	DNA-cytosine methyltransferase Dcm	[L]
AR505_0328	hypothetical protein	[Unclassified]
AR505_0329	DNA mismatch endonuclease Vsr	[L]
AR505_0330	conserved hypothetical protein	[S]
AR505_0331	hypothetical protein	Not in COGs
AR505_0332	MORN repeat-containing protein	[S]

AR505_0333	hypothetical protein	Not in COGs
AR505_0334	hypothetical protein	Not in COGs
AR505_0335	hypothetical protein	Not in COGs
AR505_0336	conserved hypothetical protein	Not in COGs
AR505_0337	hypothetical protein	Not in COGs
AR505_0338	hypothetical protein	Not in COGs
AR505_0339	DNA-cytosine methyltransferase Dcm	[L]
AR505_0340	DNA-cytosine methyltransferase Dcm	[L]
AR505_0341	hypothetical protein	Not in COGs
AR505_0342	hypothetical protein	Not in COGs
AR505_0343	hypothetical protein	Not in COGs
AR505_0344	hypothetical protein	Not in COGs
AR505_0345	hypothetical protein	Not in COGs
AR505_0346	hypothetical protein	Not in COGs
AR505_0347	hypothetical transmembrane protein	Not in COGs
AR505_0348	hypothetical transmembrane protein	Not in COGs
AR505_0349	hypothetical transmembrane protein	Not in COGs
AR505_0350	hypothetical transmembrane protein	Not in COGs
AR505_0351	hypothetical transmembrane protein	Not in COGs
AR505_0352	hypothetical transmembrane protein	[R]
AR505_0355	adhesin-like protein	Not in COGs
AR505_0356	hypothetical protein	Not in COGs
AR505_0357	hypothetical protein	Not in COGs
AR505_0358	hypothetical protein	Not in COGs
AR505_0365	hypothetical transmembrane protein	Not in COGs
AR505_0366	TPR repeat-containing protein	[R]
AR505_0370	TPR repeat-containing protein	[R]
AR505_0374	DNA polymerase III PolC	[L]
AR505_0376	<i>N</i> -carbamoyl-D-amino acid amidohydrolase AguB	[R]
AR505_0384	hypothetical protein	Not in COGs
AR505_0390	hypothetical transmembrane protein	Not in COGs
AR505_0392	hypothetical transmembrane protein	[S]
AR505_0395	hypothetical protein	[G]
AR505_0396	hypothetical protein	Not in COGs
AR505_0399	hypothetical protein	[J]
AR505_0400	hypothetical protein	[H]
AR505_0407	adhesin-like protein	Not in COGs
AR505_0419	Sell repeat-containing protein	[R]
AR505_0424	hypothetical transmembrane protein	Not in COGs
AR505_0426	ATPase (AAA+ superfamily)	[R]
AR505_0428	HTH domain-containing protein	[K]
AR505_0439	hypothetical transmembrane protein	Not in COGs
AR505_0440	transposase IS4 family	[L]
AR505_0441	hypothetical transmembrane protein	[S]
AR505_0442	hypothetical protein	Not in COGs
AR505_0443	universal stress protein UspA	[T]
AR505_0445	cell division control protein Cdc48	[O]
AR505_0446	flavodoxin	[C]
AR505_0448	6- <i>O</i> -methylguanine DNA methyltransferase Ogt	[L]
AR505_0449	aminoacyl-histidine dipeptidase PepD	[E]
AR505_0450	hypothetical protein	Not in COGs
AR505_0456	transporter DMT family	[E]
AR505_0457	transcriptional regulator LysR family	[K]
AR505_0459	DNase TatD family	[L]
AR505_0462	transcriptional regulator ArsR family	[K]

AR505_0469	hypothetical protein	Not in COGs
AR505_0476	ABC transporter solute-binding protein	[P]
AR505_0480	hypothetical transmembrane protein	Not in COGs
AR505_0492	transcription regulator	[Q]
AR505_0493	HipA-like protein	[Unclassified]
AR505_0502	hypothetical protein	Not in COGs
AR505_0514	hypothetical protein	[E]
AR505_0519	hypothetical transmembrane protein	Not in COGs
AR505_0522	ATPase (AAA+ superfamily)	[R]
AR505_0523	transposase IS605 OrfB family	[L]
AR505_0527	Fic family protein	[S]
AR505_0529	hypothetical protein	Not in COGs
AR505_0533	hypothetical protein	[R]
AR505_0534	hypothetical protein	[Unclassified]
AR505_0535	hypothetical protein	Not in COGs
AR505_0537	SAM-dependent methyltransferase	[R]
AR505_0538	hypothetical transmembrane protein	[S]
AR505_0539	polysaccharide biosynthesis protein	[R]
AR505_0544	phosphoglycolate/pyridoxal phosphate phosphatase family	[G]
AR505_0545	4-hydroxy-2-oxovalerate aldolase DmpG	[E]
AR505_0550	glycosyl transferase GT2 family	[R]
AR505_0553	dTDP-glucose 4,6-dehydratase RfbB	[M]
AR505_0554	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC	[M]
AR505_0555	polysaccharide/polyol phosphate ABC transporter permease protein	[M]
AR505_0556	polysaccharide/polyol phosphate ABC transporter ATP-binding protein	[M]
AR505_0557	TPR repeat-containing protein	[M]
AR505_0558	LPS biosynthesis protein LICD family	[M]
AR505_0559	glycosyl transferase GT8 family	[M]
AR505_0561	glycosyl transferase GT2 family	[M]
AR505_0562	hypothetical protein	[Unclassified]
AR505_0563	hypothetical protein	[S]
AR505_0564	hypothetical protein	Not in COGs
AR505_0565	hypothetical protein	Not in COGs
AR505_0566	hypothetical protein	[G]
AR505_0567	hypothetical protein	[Unclassified]
AR505_0568	hypothetical protein	[Unclassified]
AR505_0570	hypothetical protein	Not in COGs
AR505_0571	hypothetical protein	Not in COGs
AR505_0572	hypothetical transmembrane protein	Not in COGs
AR505_0573	hypothetical protein	Not in COGs
AR505_0574	transposase	[L]
AR505_0575	hypothetical transmembrane protein	[Unclassified]
AR505_0578	ribonuclease III Rnc	[T]
AR505_0581	hypothetical protein	Not in COGs
AR505_0582	hypothetical protein	Not in COGs
AR505_0583	helicase SNF2 family	[L]
AR505_0584	hypothetical protein	[S]
AR505_0585	hypothetical protein	Not in COGs
AR505_0586	hypothetical protein	Not in COGs
AR505_0587	ATPase (AAA+ superfamily)	[R]
AR505_0588	hypothetical protein	[Unclassified]
AR505_0589	hypothetical transmembrane protein	Not in COGs
AR505_0590	hypothetical transmembrane protein	Not in COGs
AR505_0591	nitroreductase family protein	[C]
AR505_0593	hypothetical transmembrane protein	Not in COGs
AR505_0594	adhesin-like protein	Not in COGs

AR505_0599	transcriptional regulator	[K]
AR505_0604	phosphoglycolate phosphatase	[R]
AR505_0605	ABC transporter permease protein	[V]
AR505_0606	ABC transporter ATP-binding protein	[V]
AR505_0607	hypothetical transmembrane protein	[R]
AR505_0612	Fic family protein	Not in COGs
AR505_0614	adhesin-like protein	[H]
AR505_0621	hypothetical transmembrane protein	Not in COGs
AR505_0623	hypothetical protein	Not in COGs
AR505_0624	protein-tyrosine phosphatase	[T]
AR505_0627	NADPH-dependent FMN reductase	[R]
AR505_0628	hypothetical protein	Not in COGs
AR505_0636	pap2 family protein	[I]
AR505_0646	adhesin-like protein	Not in COGs
AR505_0647	hypothetical protein	Not in COGs
AR505_0648	hypothetical protein	Not in COGs
AR505_0649	hypothetical protein	Not in COGs
AR505_0654	adhesin-like protein	Not in COGs
AR505_0656	hypothetical transmembrane protein	Not in COGs
AR505_0657	adhesin-like protein	Not in COGs
AR505_0658	adhesin-like protein	Not in COGs
AR505_0665	hypothetical protein	Not in COGs
AR505_0666	adhesin-like protein	[Unclassified]
AR505_0670	adhesin-like protein	Not in COGs
AR505_0677	transposase IS605 OrfB family	[L]
AR505_0682	hypothetical transmembrane protein	Not in COGs
AR505_0683	hypothetical transmembrane protein	[D]
AR505_0684	hypothetical protein	Not in COGs
AR505_0686	hypothetical protein	Not in COGs
AR505_0687	hypothetical protein	[L]
AR505_0702	cysteine proteinase	[O]
AR505_0704	adhesin-like protein	[S]
AR505_0714	ABC transporter permease protein	[P]
AR505_0715	ABC transporter solute-binding protein	[P]
AR505_0716	cobalamin (vitamin B12) biosynthesis protein CbiX	[S]
AR505_0722	von Willebrand factor type A domain protein	[Unclassified]
AR505_0723	hypothetical transmembrane protein	Not in COGs
AR505_0727	hypothetical protein	Not in COGs
AR505_0729	bifunctional protein FolC	[H]
AR505_0730	hypothetical transmembrane protein	[R]
AR505_0731	hypothetical transmembrane protein	Not in COGs
AR505_0739	MFS transporter	[G]
AR505_0741	hypothetical protein	[S]
AR505_0743	hypothetical transmembrane protein	Not in COGs
AR505_0744	adhesin-like protein	Not in COGs
AR505_0745	hypothetical protein	Not in COGs
AR505_0746	mechanosensitive ion channel protein	[M]
AR505_0754	nitrate/sulfonate/bicarbonate ABC transporter substrate-binding protein	[P]
AR505_0775	NADPH-dependent FMN reductase	[R]
AR505_0782	hypothetical transmembrane protein	[S]
AR505_0787	hypothetical protein	Not in COGs
AR505_0788	signal transduction histidine kinase	[T]
AR505_0789	hypothetical protein	Not in COGs

AR505_0790	transcriptional regulator LytR family	[T]
AR505_0791	transcriptional regulator LytS family	[T]
AR505_0792	hypothetical protein	Not in COGs
AR505_0793	TPR repeat-containing protein	[R]
AR505_0794	hypothetical protein	Not in COGs
AR505_0795	TPR repeat-containing protein	[R]
AR505_0796	isochorismatase hydrolase	[Q]
AR505_0797	transcriptional regulator HxlR family	Not in COGs
AR505_0798	ssDNA exonuclease RecJ	[L]
AR505_0803	hypothetical protein	Not in COGs
AR505_0804	hypothetical protein	Not in COGs
AR505_0805	ATP-dependent DNA helicase	[L]
AR505_0807	adhesin-like protein	[R]
AR505_0808	hypothetical protein	Not in COGs
AR505_0811	hypothetical protein	Not in COGs
AR505_0813	hypothetical protein	[L]
AR505_0816	hypothetical transmembrane protein	[R]
AR505_0817	hypothetical protein	[S]
AR505_0818	hypothetical protein	Not in COGs
AR505_0820	hypothetical protein	Not in COGs
AR505_0821	hypothetical protein	Not in COGs
AR505_0823	hypothetical transmembrane protein	Not in COGs
AR505_0829	hypothetical transmembrane protein	[Unclassified]
AR505_0833	hypothetical protein	Not in COGs
AR505_0843	transcriptional regulator	[K]
AR505_0844	GNAT family acetyltransferase	Not in COGs
AR505_0846	hypothetical protein	Not in COGs
AR505_0848	hypothetical protein	Not in COGs
AR505_0849	hypothetical protein	[R]
AR505_0850	hypothetical protein	Not in COGs
AR505_0851	adhesin-like protein	[R]
AR505_0852	hypothetical protein	Not in COGs
AR505_0853	hypothetical protein	Not in COGs
AR505_0854	cell division control protein Cdc48	[O]
AR505_0855	hypothetical protein	Not in COGs
AR505_0856	hypothetical transmembrane protein	Not in COGs
AR505_0858	addiction module toxin, RelE/StbE family	[R]
AR505_0859	transcriptional regulator TetR family	[K]
AR505_0861	hypothetical protein	Not in COGs
AR505_0862	hypothetical protein	Not in COGs
AR505_0863	ATPase	[R]
AR505_0864	hypothetical protein	Not in COGs
AR505_0865	hypothetical protein	Not in COGs
AR505_0866	hypothetical protein	Not in COGs
AR505_0867	hypothetical protein	Not in COGs
AR505_0868	hypothetical protein	Not in COGs
AR505_0869	hypothetical protein	Not in COGs
AR505_0871	hypothetical protein	Not in COGs
AR505_0872	hypothetical protein	[Unclassified]
AR505_0873	hypothetical protein	[Unclassified]
AR505_0874	adhesin-like protein	[R]
AR505_0876	hypothetical protein	[Unclassified]
AR505_0877	hypothetical protein	Not in COGs
AR505_0878	hypothetical protein	Not in COGs
AR505_0879	hypothetical protein	Not in COGs
AR505_0880	hypothetical protein	Not in COGs
AR505_0882	hypothetical protein	Not in COGs
AR505_0883	hypothetical protein	Not in COGs
AR505_0884	sulfurtransferase DndC	[H]
AR505_0885	DNA sulfur modification protein DndD	[L]
AR505_0886	type III restriction endonuclease	[L]
AR505_0887	hypothetical protein	Not in COGs
AR505_0888	hypothetical protein	[J]
AR505_0889	hypothetical protein	Not in COGs

AR505_0890	SMC domain-containing protein	[R]
AR505_0891	SMC domain-containing protein	[R]
AR505_0892	geranylgeranyl reductase family protein	[C]
AR505_0894	hypothetical protein	[O]
AR505_0895	ATPase	[R]
AR505_0896	hypothetical protein	Not in COGs
AR505_0900	ATPase	[R]
AR505_0904	GNAT family acetyltransferases	[R]
AR505_0905	EamA-like transporter family	[R]
AR505_0906	hypothetical protein	Not in COGs
AR505_0909	hypothetical transmembrane protein	[R]
AR505_0910	hypothetical protein	Not in COGs
AR505_0912	hypothetical transmembrane protein	Not in COGs
AR505_0914	hypothetical protein	Not in COGs
AR505_0915	NADPH-dependent FMN reductase	[R]
AR505_0916	hypothetical protein	Not in COGs
AR505_0917	TPR repeat-containing protein	[R]
AR505_0918	CDP-alcohol phosphatidyltransferase	[I]
AR505_0919	proline-specific peptidases	[R]
AR505_0923	hypothetical transmembrane protein	Not in COGs
AR505_0925	hypothetical protein	Not in COGs
AR505_0928	acyl carrier protein	
	phosphodiesterase AcpD	[I]
AR505_0929	hypothetical protein	Not in COGs
AR505_0931	phage integrase	[L]
AR505_0934	hypothetical transmembrane protein	Not in COGs
AR505_0936	hypothetical protein	Not in COGs
AR505_0940	hypothetical transmembrane protein	Not in COGs
AR505_0945	hypothetical protein	Not in COGs
AR505_0946	hypothetical protein	Not in COGs
AR505_0948	hypothetical protein	Not in COGs
AR505_0954	hypothetical protein	[Unclassified]
AR505_0959	hypothetical protein	Not in COGs
AR505_0961	hypothetical protein	Not in COGs
AR505_0965	hypothetical protein	[Unclassified]
AR505_0971	hypothetical protein	Not in COGs
AR505_0973	SAM-dependent methyltransferase	[R]
AR505_0974	hypothetical protein	Not in COGs
AR505_0977	hypothetical protein	Not in COGs
AR505_0979	HTH domain-containing protein	[K]
AR505_0985	adhesin-like protein	Not in COGs
AR505_0986	signal peptidase I	Not in COGs
AR505_0987	hypothetical protein	Not in COGs
AR505_0988	hypothetical transmembrane protein	Not in COGs
AR505_0989	hypothetical transmembrane protein	Not in COGs
AR505_0990	hypothetical transmembrane protein	Not in COGs
AR505_0991	adhesin-like protein	Not in COGs
AR505_0992	adhesin-like protein	[Unclassified]
AR505_0993	hypothetical transmembrane protein	Not in COGs
AR505_0994	hypothetical protein	[R]
AR505_1002	conserved hypothetical	Not in COGs
AR505_1003	conserved hypothetical	Not in COGs
AR505_1004	hypothetical protein	[S]
AR505_1006	hypothetical transmembrane protein	Not in COGs
AR505_1013	hypothetical transmembrane protein	[Unclassified]
AR505_1015	ABC transporter permease protein	[R]
AR505_1016	hypothetical protein	[R]
AR505_1020	TPR repeat-containing protein	[R]
AR505_1022	hypothetical protein	Not in COGs

AR505_1024	hypothetical transmembrane protein	Not in COGs
AR505_1025	hypothetical transmembrane protein	Not in COGs
AR505_1026	hypothetical transmembrane protein	Not in COGs
AR505_1032	adhesin-like protein	[Unclassified]
AR505_1033	adhesin-like protein	[N]
AR505_1034	MatE efflux family protein	[V]
AR505_1035	methylcobalamin:coenzyme M methyltransferase MtaA	[H]
AR505_1038	hypothetical protein	[Unclassified]
AR505_1040	uroporphyrinogen III synthase HemD	[H]
AR505_1049	hypothetical transmembrane protein	Not in COGs
AR505_1050	hypothetical protein	Not in COGs
AR505_1051	hypothetical protein	Not in COGs
AR505_1054	hypothetical protein	Not in COGs
AR505_1061	hypothetical protein	Not in COGs
AR505_1075	potassium uptake protein TrkH family	[P]
AR505_1076	drug resistance transporter Bcr/CflA subfamily	[P]
AR505_1078	hypothetical protein	Not in COGs
AR505_1087	hypothetical protein	Not in COGs
AR505_1089	CRISPR-associated endonuclease Cas3-HD	[R]
AR505_1090	CRISPR type I-E/E .coli-associated protein CasA/Cse1	[Unclassified]
AR505_1091	CRISPR type I-E/E .coli-associated protein CasB/Cse2 complex	[Unclassified]
AR505_1092	CRISPR-associated protein Cas7/Cse4/CasC	[Unclassified]
AR505_1093	CRISPR-associated protein Cas5/CasD	[Unclassified]
AR505_1094	CRISPR-associated protein Cas6/Cse3/CasE	[Unclassified]
AR505_1095	CRISPR-associated endonuclease Cas1	[L]
AR505_1096	hypothetical protein	Not in COGs
AR505_1097	hypothetical protein	Not in COGs
AR505_1098	hypothetical protein	Not in COGs
AR505_1099	transcriptional regulator MarR family	[K]
AR505_1103	hypothetical protein	[I]
AR505_1107	hypothetical protein	Not in COGs
AR505_1109	hypothetical transmembrane protein	Not in COGs
AR505_1110	hypothetical transmembrane protein	Not in COGs
AR505_1112	hypothetical protein	Not in COGs
AR505_1113	hypothetical protein	Not in COGs
AR505_1116	hypothetical protein	Not in COGs
AR505_1124	hypothetical protein	Not in COGs
AR505_1125	hypothetical protein	Not in COGs
AR505_1129	hypothetical protein	Not in COGs
AR505_1130	hypothetical protein	Not in COGs
AR505_1131	hypothetical protein	Not in COGs
AR505_1132	ATP-dependent DNA helicase UvrD/REP family	[L]
AR505_1138	transporter SDF family	[E]
AR505_1140	hypothetical transmembrane protein	[S]
AR505_1141	hypothetical protein	Not in COGs
AR505_1144	hypothetical protein	Not in COGs
AR505_1147	phospholipase D/transphosphatidylase PID	[I]
AR505_1151	tryptophan synthase beta subunit TrpB	[R]
AR505_1156	hypothetical transmembrane protein	[R]
AR505_1162	phosphoribosylanthranilate isomerase TrpF	[E]

AR505_1167	hypothetical protein	Not in COGs
AR505_1169	signal transduction histidine kinase	[T]
AR505_1170	signal transduction histidine kinase	[T]
AR505_1171	hypothetical protein	Not in COGs
AR505_1173	adhesin-like protein	Not in COGs
AR505_1174	hypothetical protein	[L]
AR505_1176	transcriptional regulator TetR family	[K]
AR505_1185	hydrogenase nickel insertion protein HypA	[J]
AR505_1186	hypothetical transmembrane protein	Not in COGs
AR505_1187	conserved hypothetical	Not in COGs
AR505_1188	hypothetical transmembrane protein	[Unclassified]
AR505_1190	hypothetical protein	Not in COGs
AR505_1194	SAM-dependent methyltransferase	[R]
AR505_1195	ABC transporter substrate-binding protein	[P]
AR505_1196	SAM-dependent methyltransferase	[R]
AR505_1200	hypothetical transmembrane protein	Not in COGs
AR505_1201	hypothetical protein	Not in COGs
AR505_1202	hypothetical protein	Not in COGs
AR505_1207	hypothetical transmembrane protein	Not in COGs
AR505_1208	hypothetical transmembrane protein	Not in COGs
AR505_1213	TPR repeat-containing protein	[R]
AR505_1215	hypothetical protein	[R]
AR505_1224	hypothetical protein	Not in COGs
AR505_1220	hypothetical transmembrane protein	Not in COGs
AR505_1221	hypothetical transmembrane protein	Not in COGs
AR505_1229	transcriptional regulator	[Unclassified]
AR505_1230	hypothetical protein	[Unclassified]
AR505_1231	hypothetical protein	[O]
AR505_1239	transposase	[L]
AR505_1240	cell wall/surface repeat-containing protein	Not in COGs
AR505_1241	hypothetical protein	Not in COGs
AR505_1244	GNAT family acetyltransferases	[R]
AR505_1246	Na ⁺ -driven multidrug efflux pump	Not in COGs
AR505_1247	anaerobic ribonucleoside-triphosphate reductase NrdD	[O]
AR505_1250	hypothetical protein	Not in COGs
AR505_1251	DNA helicase	[L]
AR505_1252	hypothetical protein	Not in COGs
AR505_1253	hypothetical protein	[K]
AR505_1254	hypothetical protein	Not in COGs
AR505_1255	hypothetical protein	[Unclassified]
AR505_1256	hypothetical protein	Not in COGs
AR505_1258	hypothetical protein	Not in COGs
AR505_1266	hypothetical protein	[R]
AR505_1267	helicase	[L]
AR505_1269	hypothetical transmembrane protein	[Unclassified]
AR505_1270	hypothetical protein	Not in COGs
AR505_1276	hypothetical protein	[Unclassified]
AR505_1283	hypothetical transmembrane protein	[S]
AR505_1286	hypothetical protein	Not in COGs
AR505_1290	adhesin-like protein	Not in COGs
AR505_1292	ABC transporter permease protein	[P]
AR505_1293	ABC transporter substrate-binding protein	[P]
AR505_1297	adenosylcobalamin synthase CobS	[H]

AR505_1300	hypothetical protein	Not in COGs
AR505_1301	hypothetical protein	[Unclassified]
AR505_1309	DNA alkylation repair enzyme	[L]
AR505_1319	hypothetical protein	Not in COGs
AR505_1326	hypothetical protein	Not in COGs
AR505_1330	methyltransferase cognate	
	corrinoid proteins	[R]
AR505_1334	TPR repeat-containing protein	[R]
AR505_1343	universal stress protein UspA	[T]
AR505_1345	hypothetical protein	Not in COGs
AR505_1347	hypothetical transmembrane protein	Not in COGs
AR505_1350	hypothetical transmembrane protein	Not in COGs
AR505_1352	alpha/beta hydrolase fold protein	[I]
AR505_1354	hypothetical transmembrane protein	[Unclassified]
AR505_1356	transposase IS4 family	[Unclassified]
AR505_1359	hypothetical transmembrane protein	Not in COGs
AR505_1360	hypothetical protein	Not in COGs
AR505_1361	hypothetical protein	Not in COGs
AR505_1362	hypothetical protein	Not in COGs
AR505_1364	hypothetical protein	[L]
AR505_1365	hypothetical protein	[L]
AR505_1366	hypothetical protein	Not in COGs
AR505_1367	archaeal ATPase	[R]
AR505_1376	isopropylmalate/isohomocitrate dehydrogenase	[E]
AR505_1380	hypothetical protein	Not in COGs
AR505_1418	hypothetical transmembrane protein	[R]
AR505_1419	hypothetical transmembrane protein	Not in COGs
AR505_1422	haloacid dehalogenase-like hydrolase	[R]
AR505_1428	hypothetical transmembrane protein	Not in COGs
AR505_1436	hypothetical protein	Not in COGs
AR505_1451	hypothetical transmembrane protein	Not in COGs
AR505_1463	TPR repeat-containing protein	[R]
AR505_1466	addiction module antitoxin RelB/DinJ	[L]
AR505_1467	hypothetical protein	[K]
AR505_1480	hypothetical transmembrane protein	Not in COGs
AR505_1495	Fic family protein	[S]
AR505_1503	cobalamin biosynthesis protein CbiX	[S]
AR505_1506	iron chelate uptake ABC transporter permease	[P]
AR505_1507	iron chelate uptake ABC transporter permease inner membrane subunit	[P]
AR505_1509	adhesin-like protein	[N]
AR505_1528	hypothetical protein	Not in COGs
AR505_1533	hypothetical transmembrane protein	[R]
AR505_1535	hypothetical protein	Not in COGs
AR505_1536	hypothetical transmembrane protein	[Unclassified]
AR505_1539	hypothetical transmembrane protein	Not in COGs
AR505_1541	hypothetical protein	Not in COGs
AR505_1545	hypothetical protein	Not in COGs
AR505_1557	Atpase	[R]
AR505_1558	nucleotidyltransferase	[R]
AR505_1559	adhesin-like protein	[R]
AR505_1560	adhesin-like protein	Not in COGs
AR505_1561	adhesin-like protein	Not in COGs
AR505_1563	transposase	[L]
AR505_1564	ClpP class periplasmic serine protease	[O]
AR505_1565	hypothetical protein	Not in COGs

AR505_1566	death-on-curing family protein	[R]
AR505_1567	hypothetical protein	Not in COGs
AR505_1568	hypothetical protein	Not in COGs
AR505_1569	hypothetical protein	Not in COGs
AR505_1570	phage integrase	[L]
AR505_1571	hypothetical protein	Not in COGs
AR505_1572	hypothetical protein	Not in COGs
AR505_1573	hypothetical protein	[L]
AR505_1580	hypothetical protein	Not in COGs
AR505_1592	hypothetical protein	Not in COGs
AR505_1593	ATPase	[K]
AR505_1600	hypothetical protein	Not in COGs
AR505_1612	signal peptidase I	[Unclassified]
AR505_1652	hypothetical transmembrane protein	[R]
AR505_1659	hypothetical protein	Not in COGs
AR505_1672	hypothetical protein	[S]
AR505_1677	hypothetical transmembrane protein	[S]
AR505_1678	hypothetical transmembrane protein	Not in COGs
AR505_1686	sulfate permease SulP	[P]
AR505_1694	hypothetical protein	[S]
AR505_1697	phage integrase family protein	[L]
AR505_1698	hypothetical protein	[Unclassified]
AR505_1699	hypothetical protein	Not in COGs
AR505_1700	hypothetical protein	Not in COGs
AR505_1701	hypothetical protein	Not in COGs
AR505_1702	hypothetical protein	Not in COGs
AR505_1704	hypothetical protein	[Unclassified]
AR505_1711	hypothetical transmembrane protein	[R]
AR505_1218	haloacid dehalogenase-like hydrolase	[R]
AR505_1713	hypothetical transmembrane protein	[Unclassified]
AR505_1720	hypothetical protein	Not in COGs
AR505_1722	hypothetical protein	[O]
AR505_1724	hypothetical protein	Not in COGs
AR505_1728	hypothetical protein	Not in COGs
AR505_1730	hypothetical protein	Not in COGs
AR505_1731	hypothetical protein	Not in COGs
AR505_1734	hypothetical protein	Not in COGs
AR505_1735	hypothetical protein	[L]
AR505_1736	hypothetical protein	[O]
AR505_1737	hypothetical protein	Not in COGs
AR505_1738	ATPase	[O]
AR505_1739	hypothetical transmembrane protein	Not in COGs
AR505_1741	adhesin-like protein	Not in COGs
AR505_1742	hypothetical protein	Not in COGs
AR505_1744	GNAT family acetyltransferases	[R]
AR505_1747	hypothetical transmembrane protein	Not in COGs
AR505_1749	hypothetical transmembrane protein	[Unclassified]
AR505_1750	hypothetical transmembrane protein	Not in COGs
AR505_1760	hypothetical transmembrane protein	Not in COGs
AR505_1761	adhesin-like protein	Not in COGs
AR505_1762	hypothetical transmembrane protein	[S]
AR505_1776	retron-type reverse transcriptase	[L]
AR505_1777	transposase IS605 OrfB family	[L]
AR505_1778	glycosyl transferase GT2 family	[M]
AR505_1779	hypothetical transmembrane protein	Not in COGs
AR505_1790	hypothetical protein	Not in COGs
AR505_1792	cell division protein FtsZ	[D]
AR505_1793	hypothetical protein	[K]
AR505_1813	CAAX amino terminal protease family protein	Not in COGs

#only one gene from each gene family is represented.
 *represents gene families found conserved across the incomplete genomes

Table A.4.13 Gene families unique to ISO4-G1

Locus tag	Predicted gene product	COG category
ISO4G1_0002	signal peptidase I	[U]
ISO4G1_0017	CAAX amino terminal protease family protein	Not in COGs
ISO4G1_0018	hypothetical protein	[X]
ISO4G1_0021	transcriptional regulator	[K]
ISO4G1_0022	hypothetical protein	[S]
ISO4G1_0038	cell division GTPase	[D]
ISO4G1_0048	hypothetical protein	[Unclassified]
ISO4G1_0049	hypothetical protein	[Unclassified]
ISO4G1_0052	prefoldin alpha subunit PfdA	[O]
ISO4G1_0056	metallo- β -lactamase domain-containing protein	[R]
ISO4G1_0067	hypothetical protein	[R]
ISO4G1_0077	geranylgeranyl pyrophosphate synthase	[H]
ISO4G1_0079	NADPH-dependent FMN reductase	[R]
ISO4G1_0086	hypothetical protein	[K]
ISO4G1_0088	hypothetical protein	Not in COGs
ISO4G1_0089	cell surface protein	Not in COGs
ISO4G1_0090	hypothetical protein	Not in COGs
ISO4G1_0091	divergent AAA domain-containing protein	[K]
ISO4G1_0100	hypothetical protein	Not in COGs
ISO4G1_0107	hypothetical protein	Not in COGs
ISO4G1_0108	hypothetical protein	Not in COGs
ISO4G1_0112	hypothetical protein	[S]
ISO4G1_0115	AMP-binding enzyme	[I]
ISO4G1_0116	GDSL-like lipase	[E]
ISO4G1_0133	hypothetical protein	[X]
ISO4G1_0139	geranylgeranyl reductase family protein	[C]
ISO4G1_0142	ribonuclease III Rnc	[K]
ISO4G1_0147	GNAT family acetyltransferase	[K]
ISO4G1_0161	F ₄₂₀ dehydrogenase subunit J FpoJ	Not in COGs
ISO4G1_0166	geranylgeranyl pyrophosphate synthase	[H]
ISO4G1_0169	hypothetical protein	Not in COGs
ISO4G1_0170	transposase	Not in COGs
ISO4G1_0178	hypothetical protein	[X]
ISO4G1_0179	cell surface protein	Not in COGs
ISO4G1_0180	phosphomannomutase/phosphoglucosyltransferase	[G]
ISO4G1_0187	ArsR family transcriptional regulator	[R]
ISO4G1_0190	aldehyde dehydrogenase family protein	[C]
ISO4G1_0191	hypothetical protein	[C]
ISO4G1_0192	hypothetical protein	[C]
ISO4G1_0193	hypothetical protein	[C]
ISO4G1_0195	hypothetical protein	Not in COGs
ISO4G1_0196	hypothetical protein	Not in COGs
ISO4G1_0198	ABC transporter ATP-binding protein	[R]
ISO4G1_0210	mechanosensitive ion channel protein	[M]
ISO4G1_0211	hypothetical protein	[N]
ISO4G1_0219	hypothetical protein	[S]
ISO4G1_0220	hypothetical protein	Not in COGs
ISO4G1_0221	hypothetical protein	Not in COGs

ISO4G1_0241	hypothetical protein	Not in COGs
ISO4G1_0242	hypothetical protein	Not in COGs
ISO4G1_0243	hypothetical protein	[X]
ISO4G1_0247	transporter monovalent cation:	
ISO4G1_0251	proton antiporter-2 family	[P]
ISO4G1_0252	methytransferase cognate	
ISO4G1_0253	corrinoid protein	[R]
ISO4G1_0254	SPFH domain-band 7 family	
ISO4G1_0255	protein	[S]
ISO4G1_0256	hypothetical protein	[Unclassified]
ISO4G1_0258	hypothetical protein	Not in COGs
ISO4G1_0262	hypothetical protein	Not in COGs
ISO4G1_0266	hypothetical protein	Not in COGs
ISO4G1_0275	hypothetical protein	Not in COGs
ISO4G1_0276	nitroreductase family protein	[C]
ISO4G1_0281	hypothetical protein	[S]
ISO4G1_0285	hypothetical protein	Not in COGs
ISO4G1_0323	hypothetical protein	Not in COGs
ISO4G1_0324	hypothetical protein	Not in COGs
ISO4G1_0328	hypothetical protein	Not in COGs
ISO4G1_0334	hypothetical protein	Not in COGs
ISO4G1_0336	hypothetical protein	Not in COGs
ISO4G1_0338	adenosylcobinamide	
ISO4G1_0339	amidohydrolase CbiZ	[S]
ISO4G1_0342	adenosylcobinamide	
ISO4G1_0344	amidohydrolase CbiZ	[S]
ISO4G1_0345	HAD-superfamily hydrolase	[R]
ISO4G1_0347	hypothetical protein	Not in COGs
ISO4G1_0354	hypothetical protein	Not in COGs
ISO4G1_0356	hypothetical protein	Not in COGs
ISO4G1_0361	MATE efflux family protein	[V]
ISO4G1_0362	iron-containing alcohol	
ISO4G1_0369	dehydrogenase	[C]
ISO4G1_0371	hypothetical protein	[R]
ISO4G1_0372	hypothetical protein	Not in COGs
ISO4G1_0377	ZIP zinc transporter family	
ISO4G1_0385	protein	[P]
ISO4G1_0387	allosteric regulator of homoserine	
ISO4G1_0388	dehydrogenase	[E]
ISO4G1_0390	hypothetical protein	Not in COGs
ISO4G1_0392	hypothetical protein	Not in COGs
ISO4G1_0395	integrase family protein	[L]
ISO4G1_0396	hypothetical protein	Not in COGs
ISO4G1_0397	hypothetical protein	Not in COGs
ISO4G1_0398	hypothetical protein	Not in COGs
ISO4G1_0399	hypothetical protein	Not in COGs
ISO4G1_0400	hypothetical protein	[Unclassified]
ISO4G1_0402	hypothetical protein	[X]
ISO4G1_0403	hypothetical protein	Not in COGs
ISO4G1_0404	hypothetical protein	Not in COGs
ISO4G1_0405	hypothetical protein	Not in COGs
ISO4G1_0406	hypothetical protein	Not in COGs
ISO4G1_0407	hypothetical protein	Not in COGs
ISO4G1_0408	hypothetical protein	Not in COGs
ISO4G1_0409	hypothetical protein	Not in COGs
ISO4G1_0410	hypothetical protein	Not in COGs
ISO4G1_0411	hypothetical protein	[C]
ISO4G1_0412	hypothetical protein	Not in COGs
ISO4G1_0413	hypothetical protein	Not in COGs
ISO4G1_0414	hypothetical protein	Not in COGs
ISO4G1_0416	hypothetical protein	Not in COGs
ISO4G1_0417	hypothetical protein	Not in COGs
ISO4G1_0418	hypothetical protein	Not in COGs
ISO4G1_0419	hypothetical protein	Not in COGs

ISO4G1_0420	TIGR02543 family repeat-	
ISO4G1_0421	containing cell surface protein	[S]
ISO4G1_0423	TIGR02543 family repeat-	
ISO4G1_0424	containing cell surface protein	Not in COGs
ISO4G1_0425	hypothetical protein	Not in COGs
ISO4G1_0426	hypothetical protein	Not in COGs
ISO4G1_0427	cell surface protein	[R]
ISO4G1_0428	hypothetical protein	Not in COGs
ISO4G1_0429	hypothetical protein	Not in COGs
ISO4G1_0432	hypothetical protein	Not in COGs
ISO4G1_0435	MFS transporter	[G]
ISO4G1_0436	hypothetical protein	[S]
ISO4G1_0444	hypothetical protein	[L]
ISO4G1_0445	alpha/beta fold family hydrolase	[R]
ISO4G1_0456	transcriptional regulator	[X]
ISO4G1_0458	flavodoxin	Not in COGs
ISO4G1_0459	hypothetical protein	Not in COGs
ISO4G1_0460	XRE family transcriptional	
ISO4G1_0466	regulator	[Unclassified]
ISO4G1_0469	hypothetical protein	[X]
ISO4G1_0473	hypothetical protein	[U]
ISO4G1_0476	EamA-like transporter family	
ISO4G1_0479	protein	[G]
ISO4G1_0480	hypothetical protein	[X]
ISO4G1_0482	hypothetical protein	Not in COGs
ISO4G1_0484	ATPase AAA+ superfamily	[S]
ISO4G1_0489	TIGR02543 family repeat-	
ISO4G1_0490	containing cell surface protein	Not in COGs
ISO4G1_0491	archaeal ATPase	[R]
ISO4G1_0492	hypothetical protein	Not in COGs
ISO4G1_0493	signal peptidase I	[U]
ISO4G1_0494	hypothetical protein	Not in COGs
ISO4G1_0495	hypothetical protein	Not in COGs
ISO4G1_0496	hypothetical protein	Not in COGs
ISO4G1_0497	hypothetical protein	Not in COGs
ISO4G1_0498	ATPase	[R]
ISO4G1_0499	hypothetical protein	Not in COGs
ISO4G1_0501	hypothetical protein	Not in COGs
ISO4G1_0510	hypothetical protein	[X]
ISO4G1_0512	hypothetical protein	[Unclassified]
ISO4G1_0513	hypothetical protein	Not in COGs
ISO4G1_0514	hypothetical protein	Not in COGs
ISO4G1_0515	hypothetical protein	Not in COGs
ISO4G1_0516	hypothetical protein	[Unclassified]
ISO4G1_0517	hypothetical protein	[X]
ISO4G1_0518	cell surface protein	[C]
ISO4G1_0524	hypothetical protein	Not in COGs
ISO4G1_0527	electron transfer flavoprotein	
ISO4G1_0532	domain-containing protein	[C]
ISO4G1_0533	hypothetical protein	Not in COGs
ISO4G1_0537	hypothetical protein	[L]
ISO4G1_0539	hypothetical protein	Not in COGs
ISO4G1_0542	nitroreductase family protein	[C]
ISO4G1_0543	geranylgeranyl reductase family	
ISO4G1_0544	protein	[C]
ISO4G1_0551	hypothetical protein	Not in COGs
ISO4G1_0553	hypothetical protein	[R]
ISO4G1_0555	pyridoxamine 5'-phosphate oxidase-	
ISO4G1_0558	like FMN-binding protein	[R]
ISO4G1_0563	PAS domain-containing protein	[T]
ISO4G1_0564	GNAT family acetyltransferase	[J]
ISO4G1_0566	hypothetical protein	[X]
ISO4G1_0568	hypothetical protein	[X]
	SAM-dependent	
	methyltransferase	[Q]
	iron ABC transporter substrate-	
	binding protein	[P]
	DEAD/DEAH box helicase	[L]
	MATE efflux family protein	[V]
	divergent AAA domain-containing	
	protein	[K]
	MMPL family transporter	[R]

ISO4G1_0570	hypothetical protein	[S]
ISO4G1_0587	bifunctional protein FolC	[H]
ISO4G1_0588	alpha-L-glutamate ligase RimK family	[H]
ISO4G1_0589	alpha-L-glutamate ligase RimK family	[H]
ISO4G1_0595	response regulator domain-containing protein	[T]
ISO4G1_0597	xylose isomerase-like TIM barrel domain-containing protein	[Unclassified]
ISO4G1_0604	hydrolase TatD family	[H]
ISO4G1_0606	hypothetical protein	Not in COGs
ISO4G1_0611	hypothetical protein	Not in COGs
ISO4G1_0612	hypothetical protein	Not in COGs
ISO4G1_0635	hypothetical protein	Not in COGs
ISO4G1_0638	cell surface protein	[X]
ISO4G1_0639	HAD-superfamily hydrolase	[R]
ISO4G1_0642	ABC transporter ATP-binding/permease protein	[V]
ISO4G1_0644	SAM-dependent methyltransferase	[Q]
ISO4G1_0645	iron ABC transporter ATP-binding protein	[P]
ISO4G1_0646	iron ABC transporter permease protein	[P]
ISO4G1_0647	iron ABC transporter substrate-binding protein	[Q]
ISO4G1_0649	SAM-dependent methyltransferase	[Q]
ISO4G1_0651	hypothetical protein	Not in COGs
ISO4G1_0652	hypothetical protein	Not in COGs
ISO4G1_0656	addiction module antitoxin, RelB/DinJ family	[L]
ISO4G1_0660	pyrrolysine biosynthesis protein PylD	[X]
ISO4G1_0662	small multidrug resistance protein	[P]
ISO4G1_0663	small multidrug resistance protein	[P]
ISO4G1_0670	ThiF family protein	[H]
ISO4G1_0672	hypothetical protein	[S]
ISO4G1_0674	NADPH-dependent FMN reductase	[R]
ISO4G1_0675	hypothetical protein	Not in COGs
ISO4G1_0676	cobaltochelatase CobN	[H]
ISO4G1_0679	hypothetical protein	[P]
ISO4G1_0680	<i>O</i> -methyltransferase	[Q]
ISO4G1_0683	hypothetical protein	Not in COGs
ISO4G1_0687	hypothetical protein	Not in COGs
ISO4G1_0692	ATP-dependent DNA helicase	[L]
ISO4G1_0694	hypothetical protein	Not in COGs
ISO4G1_0695	ATP-dependent DNA helicase	[L]
ISO4G1_0696	hypothetical protein	Not in COGs
ISO4G1_0697	hypothetical protein	Not in COGs
ISO4G1_0698	hypothetical protein	Not in COGs
ISO4G1_0699	hypothetical protein	Not in COGs
ISO4G1_0700	type III restriction system endonuclease	[X]
ISO4G1_0701	type III restriction system methylase	[X]
ISO4G1_0702	type III restriction system methylase	[X]
ISO4G1_0703	RloB-like protein	[X]
ISO4G1_0704	ATPase AAA	[R]
ISO4G1_0705	RloA-like protein	[R]
ISO4G1_0706	Sel1 domain-containing protein	[R]
ISO4G1_0707	Sel1 domain-containing protein	[R]
ISO4G1_0708	hypothetical protein	Not in COGs
ISO4G1_0709	PD-(D/E)XK nuclease superfamily protein	Not in COGs
ISO4G1_0710	ATP-dependent DNA helicase	[L]
ISO4G1_0713	hypothetical protein	Not in COGs
ISO4G1_0714	hypothetical protein	Not in COGs
ISO4G1_0715	hypothetical protein	Not in COGs

ISO4G1_0716	SAM-dependent methyltransferase	[Q]
ISO4G1_0717	reverse transcriptase	[L]
ISO4G1_0718	hypothetical protein	Not in COGs
ISO4G1_0719	hypothetical protein	Not in COGs
ISO4G1_0720	Sel1 domain-containing protein	[R]
ISO4G1_0722	hypothetical protein	Not in COGs
ISO4G1_0724	hypothetical protein	[Unclassified]
ISO4G1_0726	hypothetical protein	Not in COGs
ISO4G1_0727	DNA double-strand break repair protein Mre11	[L]
ISO4G1_0728	ATPase AAA	[S]
ISO4G1_0731	cell surface protein	Not in COGs
ISO4G1_0732	ribosomal-protein-alanine acetyltransferase RimI	[R]
ISO4G1_0733	phospholipase-like protein	[I]
ISO4G1_0736	ArsR family transcriptional regulator	[M]
ISO4G1_0740	MATE efflux family protein	[V]
ISO4G1_0741	hypothetical protein	[C]
ISO4G1_0744	hypothetical protein	Not in COGs
ISO4G1_0745	NADPH-dependent FMN reductase	[R]
ISO4G1_0746	transcriptional regulator	[K]
ISO4G1_0747	sodium bile acid symporter family protein	[R]
ISO4G1_0749	TPR repeat-containing protein	[O]
ISO4G1_0752	hypothetical protein	[R]
ISO4G1_0755	cobaltochelatase CobN	[H]
ISO4G1_0760	hypothetical protein	Not in COGs
ISO4G1_0763	Sel1 domain-containing protein	[R]
ISO4G1_0764	hypothetical protein	Not in COGs
ISO4G1_0765	HAD-superfamily hydrolase	[R]
ISO4G1_0766	hypothetical protein	Not in COGs
ISO4G1_0767	hypothetical protein	Not in COGs
ISO4G1_0768	hypothetical protein	Not in COGs
ISO4G1_0769	short-chain dehydrogenase/reductase	[R]
ISO4G1_0772	hypothetical protein	Not in COGs
ISO4G1_0774	hypothetical protein	Not in COGs
ISO4G1_0775	hypothetical protein	Not in COGs
ISO4G1_0778	MarR family transcriptional regulator	[K]
ISO4G1_0782	potassium transport protein TrkA	[P]
ISO4G1_0783	potassium transport protein TrkH	[P]
ISO4G1_0784	hypothetical protein	Not in COGs
ISO4G1_0785	ATPase AAA	[R]
ISO4G1_0786	hypothetical protein	[Unclassified]
ISO4G1_0789	thioesterase family protein	[Q]
ISO4G1_0790	hypothetical protein	[S]
ISO4G1_0791	PD-(D/E)XK nuclease superfamily protein	Not in COGs
ISO4G1_0792	ATP-dependent DNA helicase	[L]
ISO4G1_0797	CDP-alcohol phosphatidyltransferase family protein	[I]
ISO4G1_0802	hypothetical protein	[Unclassified]
ISO4G1_0805	hypothetical protein	[X]
ISO4G1_0806	hypothetical protein	Not in COGs
ISO4G1_0808	flavodoxin	[C]
ISO4G1_0812	hypothetical protein	Not in COGs
ISO4G1_0814	hypothetical protein	[K]
ISO4G1_0817	cell surface protein	[X]
ISO4G1_0819	CorA-like Mg ²⁺ transporter protein	[P]
ISO4G1_0820	peptidase M50 family	[M]
ISO4G1_0822	hypothetical protein	[S]
ISO4G1_0829	hypothetical protein	Not in COGs
ISO4G1_0830	hypothetical protein	Not in COGs
ISO4G1_0831	hypothetical protein	[Unclassified]
ISO4G1_0834	CopG family transcriptonal regulator	[X]
ISO4G1_0835	cell division protein FtsZ	[C]
ISO4G1_0838	GNAT family acetyltransferase	[K]
ISO4G1_0840	carbamoyl-phosphate synthase small subunit CarA	[E]

ISO4G1_0842	hypothetical protein	Not in COGs
ISO4G1_0847	hypothetical protein	Not in COGs
ISO4G1_0848	SAM-dependent methyltransferase	[Q]
ISO4G1_0849	hypothetical protein	[Unclassified]
ISO4G1_0851	hypothetical protein	[L]
ISO4G1_0852	hypothetical protein	Not in COGs
ISO4G1_0855	metallo- β -lactamase domain-containing protein	[X]
ISO4G1_0866	hypothetical protein	Not in COGs
ISO4G1_0867	hypothetical protein	Not in COGs
ISO4G1_0870	hypothetical protein	Not in COGs
ISO4G1_0872	type II secretion system protein	[X]
ISO4G1_0874	methyltransferase family protein	[Q]
ISO4G1_0876	cell division protein Fic	[S]
ISO4G1_0878	hypothetical protein	Not in COGs
ISO4G1_0879	trypsin-like peptidase domain-containing protein	[O]
ISO4G1_0880	carbon-nitrogen hydrolase	[R]
ISO4G1_0881	hypothetical protein	[K]
ISO4G1_0883	hypothetical protein	Not in COGs
ISO4G1_0885	hypothetical protein	Not in COGs
ISO4G1_0888	iron ABC transporter substrate-binding protein	[P]
ISO4G1_0889	nitrogenase iron protein NifH	[P]
ISO4G1_0890	hypothetical protein	Not in COGs
ISO4G1_0892	hypothetical protein	[G]
ISO4G1_0894	cobaltochelatase subunit	[H]
ISO4G1_0898	FAD/FMN-containing dehydrogenase	[C]
ISO4G1_0903	ABC transporter ATP-binding/permease protein	[V]
ISO4G1_0904	ABC transporter ATP-binding/permease protein	[V]
ISO4G1_0905	hypothetical protein	Not in COGs
ISO4G1_0908	universal stress protein	[T]
ISO4G1_0909	hypothetical protein	[S]
ISO4G1_0910	hypothetical protein	[S]
ISO4G1_0912	hypothetical protein	Not in COGs
ISO4G1_0914	MFS transporter	[G]
ISO4G1_0915	hypothetical protein	Not in COGs
ISO4G1_0916	hypothetical protein	[Unclassified]
ISO4G1_0918	hypothetical protein	[Unclassified]
ISO4G1_0921	hypothetical protein	[N]
ISO4G1_0924	hypothetical protein	Not in COGs
ISO4G1_0925	4Fe-4S binding domain-containing protein	[C]
ISO4G1_0926	metallo- β -lactamase family protein/flavodoxin	[C]
ISO4G1_0927	hypothetical protein	Not in COGs
ISO4G1_0929	hypothetical protein	[L]
ISO4G1_0935	iron dependent repressor	[K]
ISO4G1_0937	MarR family transcriptional regulator	[K]
ISO4G1_0940	hypothetical protein	[S]
ISO4G1_0942	hypothetical protein	[E]
ISO4G1_0943	hypothetical protein	Not in COGs
ISO4G1_0944	TauE family protein	[X]
ISO4G1_0945	trimethylamine:corrinoid methyltransferase MttB	[H]
ISO4G1_0948	MFS transporter	[G]
ISO4G1_0949	hypothetical protein	Not in COGs
ISO4G1_0951	cell surface protein	[R]
ISO4G1_0959	inositol monophosphatase	[G]
ISO4G1_0965	iron transporter FeoA	[P]
ISO4G1_0968	hypothetical protein	Not in COGs
ISO4G1_0969	iron transporter FeoA	[P]
ISO4G1_0972	hypothetical protein	Not in COGs
ISO4G1_0974	Sel1 domain-containing protein	[R]
ISO4G1_0976	hypothetical protein	[Unclassified]
ISO4G1_0978	molecular chaperone GrpE	[O]
ISO4G1_0980	nitrogenase-related protein	[C]
ISO4G1_0981	nitrogenase iron protein NifH	[P]
ISO4G1_0982	universal stress protein	[T]

ISO4G1_0983	4'-phosphopantetheinyl transferase	[H]
ISO4G1_0984	non-ribosomal peptide synthetase	[Q]
ISO4G1_0991	nitrate/sulfonate/bicarbonate ABC transporter substrate-binding protein	[P]
ISO4G1_0993	hypothetical protein	Not in COGs
ISO4G1_0998	cobalamin 5'-phosphate synthase CobS	[H]
ISO4G1_1001	hypothetical protein	Not in COGs
ISO4G1_1003	X-Pro dipeptidyl-peptidase	[X]
ISO4G1_1012	isopropylmalate/isohomocitrate dehydrogenase	[C]
ISO4G1_1014	hypothetical protein	Not in COGs
ISO4G1_1015	cation diffusion facilitator family transporter	[P]
ISO4G1_1023	hypothetical protein	Not in COGs
ISO4G1_1024	4Fe-4S binding domain-containing protein	[C]
ISO4G1_1027	hypothetical protein	[Unclassified]
ISO4G1_1033	LD-carboxypeptidase S66 family	[V]
ISO4G1_1035	hypothetical protein	[X]
ISO4G1_1036	hypothetical protein	[X]
ISO4G1_1039	isochorismatase family protein	[Q]
ISO4G1_1040	hypothetical protein	[S]
ISO4G1_1043	hypothetical protein	Not in COGs
ISO4G1_1046	MFS transporter	[G]
ISO4G1_1048	hypothetical protein	Not in COGs
ISO4G1_1059	hypothetical protein	Not in COGs
ISO4G1_1063	nitrogenase component 1 type oxidoreductase	[C]
ISO4G1_1064	nitrogenase component 1 type oxidoreductase	[C]
ISO4G1_1065	iron ABC transporter ATP-binding protein	[P]
ISO4G1_1066	iron ABC transporter permease protein	[P]
ISO4G1_1067	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1068	TPR repeat-containing protein	[M]
ISO4G1_1072	hypothetical protein	Not in COGs
ISO4G1_1073	hypothetical protein	Not in COGs
ISO4G1_1074	hypothetical protein	Not in COGs
ISO4G1_1075	2'-5' RNA ligase	[J]
ISO4G1_1076	protein-tyrosine phosphatase	[T]
ISO4G1_1083	TPR repeat-containing protein	[R]
ISO4G1_1085	hypothetical protein	[I]
ISO4G1_1095	cobaltochelatase CobN	[H]
ISO4G1_1096	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1100	hypothetical protein	Not in COGs
ISO4G1_1112	nitroreductase family protein	[C]
ISO4G1_1113	FKBP-type peptidyl-prolyl cis-trans isomerase	[O]
ISO4G1_1117	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1118	MarR family transcriptional regulator	[K]
ISO4G1_1119	hypothetical protein	[X]
ISO4G1_1123	archaeosine tRNA-ribosyltransferase	[O]
ISO4G1_1125	hypothetical protein	[X]
ISO4G1_1130	Sel1 domain-containing protein	[R]
ISO4G1_1131	hypothetical protein	Not in COGs
ISO4G1_1139	transglutaminase domain-containing protein	[E]
ISO4G1_1140	DNA alkylation repair enzyme	[X]
ISO4G1_1142	GNAT family acetyltransferase	[K]
ISO4G1_1153	hypothetical protein	[S]
ISO4G1_1154	transposase	Not in COGs
ISO4G1_1155	MATE efflux family protein	[V]
ISO4G1_1156	Na ⁺ /H ⁺ antiporter NhaC family	[C]
ISO4G1_1165	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1174	nitrogenase-related protein	[C]

ISO4G1_1177	hypothetical protein	[M]
ISO4G1_1179	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1182	4Fe-4S binding domain-containing protein	[X]
ISO4G1_1183	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1193	isochorismatase family protein	[Q]
ISO4G1_1194	hypothetical protein	Not in COGs
ISO4G1_1197	5'-nucleotidase	Not in COGs
ISO4G1_1200	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1201	hypothetical protein	Not in COGs
ISO4G1_1205	hypothetical protein	Not in COGs
ISO4G1_1207	4Fe-4S dicluster domain-containing protein	[C]
ISO4G1_1212	cell surface protein	[S]
ISO4G1_1220	hypothetical protein	Not in COGs
ISO4G1_1221	hypothetical protein	Not in COGs
ISO4G1_1223	cobaltochelatase subunit	[H]
ISO4G1_1226	hypothetical protein	Not in COGs
ISO4G1_1227	hypothetical protein	[X]
ISO4G1_1232	hypothetical protein	[X]
ISO4G1_1233	transposase	[L]
ISO4G1_1242	metallo- β -lactamase domain-containing protein	[R]
ISO4G1_1243	hypothetical protein	Not in COGs
ISO4G1_1244	hypothetical protein	[X]
ISO4G1_1256	cobalamin biosynthesis protein CbiX	[S]
ISO4G1_1257	hypothetical protein	Not in COGs
ISO4G1_1264	hypothetical protein	Not in COGs
ISO4G1_1267	flavodoxin	[Unclassified]
ISO4G1_1272	transglutaminase domain-containing protein	[E]
ISO4G1_1277	hypothetical protein	Not in COGs
ISO4G1_1282	hypothetical protein	[J]
ISO4G1_1293	ABC transporter permease protein	[C]
ISO4G1_1307	PAC2 family protein	[R]
ISO4G1_1308	ATPase	[R]
ISO4G1_1310	flavin oxidoreductase	[R]
ISO4G1_1311	hypothetical protein	[X]
ISO4G1_1312	HxlR family transcriptional regulator	[K]
ISO4G1_1313	metallophosphoesterase	[R]
ISO4G1_1314	hypothetical protein	Not in COGs
ISO4G1_1316	hypothetical protein	Not in COGs
ISO4G1_1320	adenine phosphoribosyltransferase	[F]
ISO4G1_1321	hypothetical protein	[S]
ISO4G1_1323	PAP2 superfamily protein	[Unclassified]
ISO4G1_1326	cell surface protein	[X]
ISO4G1_1331	hypothetical protein	Not in COGs
ISO4G1_1333	hypothetical protein	Not in COGs
ISO4G1_1336	hypothetical protein	[S]
ISO4G1_1337	hypothetical protein	[X]
ISO4G1_1348	MORN repeat-containing protein	[S]
ISO4G1_1352	SAM-dependent methyltransferase	[Q]
ISO4G1_1359	hypothetical protein	[S]
ISO4G1_1361	hypothetical protein	Not in COGs
ISO4G1_1363	phosphoglucosamine mutase GlmM	[G]
ISO4G1_1371	ribosomal protein L6P Rpl6p	Not in COGs
ISO4G1_1372	hypothetical protein	Not in COGs
ISO4G1_1377	Fic family protein	[D]
ISO4G1_1379	phenazine biosynthesis-like protein	[R]
ISO4G1_1380	hypothetical protein	[X]
ISO4G1_1389	HPP family protein	[T]
ISO4G1_1390	hypothetical protein	Not in COGs
ISO4G1_1392	TetR family transcriptional regulator	[K]

ISO4G1_1393	heavy metal translocating P-type ATPase	[P]
ISO4G1_1396	chorismate mutase/prephenate dehydrogenase	[J]
ISO4G1_1400	shikimate kinase	[E]
ISO4G1_1404	hypothetical protein	[R]
ISO4G1_1407	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1409	hypothetical protein	Not in COGs
ISO4G1_1411	heavy-metal-associated domain-containing protein	[P]
ISO4G1_1412	ArsR family transcriptional regulator	[K]
ISO4G1_1413	NADPH-dependent FMN reductase	[R]
ISO4G1_1415	hypothetical protein	Not in COGs
ISO4G1_1418	TraB family protein	[S]
ISO4G1_1419	hypothetical protein	Not in COGs
ISO4G1_1423	heavy metal-associated domain-containing protein	[P]
ISO4G1_1426	EamA-like transporter family protein	[G]
ISO4G1_1427	EamA-like transporter family protein	[G]
ISO4G1_1434	hypothetical protein	Not in COGs
ISO4G1_1435	oligosaccharyl transferase	[R]
ISO4G1_1448	MarR family transcriptional regulator	[K]
ISO4G1_1453	GHMP family kinase	[R]
ISO4G1_1458	hypothetical protein	[S]
ISO4G1_1461	EamA-like transporter family protein	[G]
ISO4G1_1466	hypothetical protein	[X]
ISO4G1_1468	hypothetical protein	Not in COGs
ISO4G1_1469	hypothetical protein	Not in COGs
ISO4G1_1471	hypothetical protein	Not in COGs
ISO4G1_1475	iron ABC transporter substrate-binding protein	[P]
ISO4G1_1476	nitrogenase component 1 type oxidoreductase	[C]
ISO4G1_1478	nitrogenase iron protein NifH	[P]
ISO4G1_1482	glycosyl transferase GT8 family	[M]
ISO4G1_1483	hypothetical protein	Not in COGs
ISO4G1_1485	hypothetical protein	Not in COGs
ISO4G1_1495	hypothetical protein	Not in COGs
ISO4G1_1504	bifunctional phosphoglucose/phosphomannose isomerase	[M]
ISO4G1_1505	bifunctional phosphoglucose/phosphomannose isomerase	[M]
ISO4G1_1507	hypothetical protein	[S]
ISO4G1_1508	hypothetical protein	[S]
ISO4G1_1510	hypothetical protein	Not in COGs
ISO4G1_1511	hypothetical protein	Not in COGs
ISO4G1_1512	Sell domain-containing protein	[R]
ISO4G1_1519	cobaltochelatase CobN	[H]
ISO4G1_1521	hypothetical protein	[P]
ISO4G1_1522	hypothetical protein	Not in COGs
ISO4G1_1526	hypothetical protein	[S]
ISO4G1_1528	restriction endonuclease	[S]
ISO4G1_1529	helicase	[K]
ISO4G1_1530	PD-(D/E)XK nuclease superfamily protein	[Unclassified]
ISO4G1_1531	type I restriction-modification system M subunit HsdM	[V]
ISO4G1_1533	type I restriction-modification system S subunit HsdS	[V]
ISO4G1_1534	type I restriction-modification system S subunit HsdS	[V]
ISO4G1_1535	hypothetical protein	[R]
ISO4G1_1536	hypothetical protein	Not in COGs
ISO4G1_1537	signal peptidase I	[U]
ISO4G1_1538	hypothetical protein	Not in COGs
ISO4G1_1539	HIRAN domain-containing protein	[X]
ISO4G1_1541	hypothetical protein	Not in COGs

ISO4G1_1544	acetyl-CoA acetyltransferase	Not in COGs

*only one gene from each gene family is represented.

Table A.4.14 Gene families unique to ISO4-G11

Locus_tag	Predicted gene product	COG category
ISO4G11_0013	TetR family transcriptional regulator	[K]
ISO4G11_0021	porphobilinogen deaminase	[H]
ISO4G11_0024	DNA-formamidopyrimidine glycosylase	[L]
ISO4G11_0025	hypothetical protein	Not in COGs
ISO4G11_0031	hypothetical protein	Not in COGs
ISO4G11_0033	zinc/iron permease	[P]
ISO4G11_0041	radical SAM protein	[R]
ISO4G11_0045	isochorismatase family protein amidases nicotinamidase-like protein	[Q]
ISO4G11_0051	UDP- <i>N</i> -acetylmuramoylalanine-D-glutamate ligase	[M]
ISO4G11_0057	hypothetical protein	[X]
ISO4G11_0058	Sell domain protein repeat-containing protein	[R]
ISO4G11_0059	nitroreductase	[C]
ISO4G11_0064	cobalamin synthase	[H]
ISO4G11_0074	AMP-binding enzyme	[I]
ISO4G11_0075	hypothetical protein	Not in COGs
ISO4G11_0076	hypothetical protein	Not in COGs
ISO4G11_0078	hypothetical protein	Not in COGs
ISO4G11_0082	hypothetical protein	Not in COGs
ISO4G11_0084	hypothetical protein	Not in COGs
ISO4G11_0085	sirohdrochlorin cobaltochelataze	[S]
ISO4G11_0088	hypothetical protein	Not in COGs
ISO4G11_0089	TetR family transcriptional regulator	[K]
ISO4G11_0090	FMN reductase	[R]
ISO4G11_0091	hypothetical protein	Not in COGs
ISO4G11_0092	hypothetical protein	Not in COGs
ISO4G11_0095	hypothetical protein	[X]
ISO4G11_0098	transposase	Not in COGs
ISO4G11_0104	hypothetical protein	Not in COGs
ISO4G11_0110	hypothetical protein	[N]
ISO4G11_0111	hypothetical protein	[R]
ISO4G11_0114	hypothetical protein	Not in COGs
ISO4G11_0116	pyruvate-formate lyase-activating enzyme	[O]
ISO4G11_0118	hypothetical protein	Not in COGs
ISO4G11_0126	hypothetical protein	Not in COGs
ISO4G11_0129	segregation and condensation protein A	[S]
ISO4G11_0131	hypothetical protein	Not in COGs
ISO4G11_0165	geranylgeranyl reductase family	[C]
ISO4G11_0171	hypothetical protein	[X]
ISO4G11_0187	transporter	[G]
ISO4G11_0200	hypothetical protein	[Unclassified]
ISO4G11_0206	cytosine deaminase	[F]
ISO4G11_0207	hypothetical protein	Not in COGs
ISO4G11_0208	hypothetical protein	Not in COGs
ISO4G11_0209	hypothetical protein	[S]
ISO4G11_0210	hypothetical protein	Not in COGs
ISO4G11_0213	periplasmic binding protein	[P]
ISO4G11_0217	cobaltochelataze subunit CobN	[H]
ISO4G11_0223	cell filamentation protein Fic	[S]
ISO4G11_0229	hypothetical protein	Not in COGs
ISO4G11_0235	ATPase	[R]
ISO4G11_0238	hypothetical protein	Not in COGs
ISO4G11_0239	hypothetical protein	Not in COGs

ISO4G11_0240	transposase	[L]
ISO4G11_0241	hypothetical protein	Not in COGs
ISO4G11_0242	hypothetical protein	Not in COGs
ISO4G11_0243	ribonuclease III	[K]
ISO4G11_0244	hypothetical protein	[X]
ISO4G11_0246	hypothetical protein	Not in COGs
ISO4G11_0248	hypothetical protein	Not in COGs
ISO4G11_0250	hypothetical protein	Not in COGs
ISO4G11_0251	hypothetical protein	Not in COGs
ISO4G11_0252	hypothetical protein	Not in COGs
ISO4G11_0253	hypothetical protein	Not in COGs
ISO4G11_0254	hypothetical protein	Not in COGs
ISO4G11_0256	hypothetical protein	[X]
ISO4G11_0260	toxin of toxin-antitoxin (TA) system	[S]
ISO4G11_0261	antitoxin PHD	[D]
ISO4G11_0262	toxin HipA	[R]
ISO4G11_0263	DNA-binding protein	[K]
ISO4G11_0264	hypothetical protein	Not in COGs
ISO4G11_0265	chromosome segregation protein SMC	[R]
ISO4G11_0266	hypothetical protein	Not in COGs
ISO4G11_0267	hypothetical protein	Not in COGs
ISO4G11_0269	hypothetical protein	Not in COGs
ISO4G11_0271	hypothetical protein	Not in COGs
ISO4G11_0275	hypothetical protein	[R]
ISO4G11_0279	cell filamentation protein Fic	[S]
ISO4G11_0284	hypothetical protein	[R]
ISO4G11_0288	hypothetical protein	[R]
ISO4G11_0289	hypothetical protein	Not in COGs
ISO4G11_0291	periplasmic binding protein	[P]
ISO4G11_0295	cobaltochelataze, CobN subunit	[H]
ISO4G11_0297	transposase	[L]
ISO4G11_0298	hypothetical protein	Not in COGs
ISO4G11_0299	hypothetical protein	[R]
ISO4G11_0300	Na ⁺ -dependent transporter	Not in COGs
ISO4G11_0302	hypothetical protein	Not in COGs
ISO4G11_0306	TPR repeat protein, SEL1 subfamily	[R]
ISO4G11_0310	ATPase	[R]
ISO4G11_0311	hypothetical protein	Not in COGs
ISO4G11_0316	hypothetical protein	Not in COGs
ISO4G11_0317	hypothetical protein	Not in COGs
ISO4G11_0318	multidrug transporter MatE	[V]
ISO4G11_0319	geranylgeranyl reductase	[C]
ISO4G11_0325	hypothetical protein	[X]
ISO4G11_0344	electron transfer flavoprotein	[C]
ISO4G11_0349	hypothetical protein	Not in COGs
ISO4G11_0352	cell wall/surface repeat protein	Not in COGs
ISO4G11_0354	hypothetical protein	[X]
ISO4G11_0355	hypothetical protein	[R]
ISO4G11_0361	periplasmic binding protein	[P]
ISO4G11_0365	hypothetical protein	Not in COGs
ISO4G11_0370	hypothetical protein	Not in COGs
ISO4G11_0371	hypothetical protein	[S]
ISO4G11_0373	hypothetical protein	Not in COGs
ISO4G11_0379	hypothetical protein	Not in COGs
ISO4G11_0380	hypothetical protein	Not in COGs
ISO4G11_0382	hypothetical protein	Not in COGs
ISO4G11_0383	hypothetical protein	Not in COGs
ISO4G11_0385	hypothetical protein	[R]
ISO4G11_0386	TPR repeat protein, SEL1 subfamily	[R]
ISO4G11_0390	hypothetical protein	Not in COGs
ISO4G11_0395	hypothetical protein	Not in COGs
ISO4G11_0403	hypothetical protein	[Unclassified]
ISO4G11_0405	transcriptional regulator	[K]
ISO4G11_0406	transporter	[G]
ISO4G11_0407	carbon starvation protein CstA	[T]
ISO4G11_0409	cell wall-binding protein	[S]
ISO4G11_0410	hypothetical protein	Not in COGs
ISO4G11_0413	TetR family transcriptional regulator	[K]
ISO4G11_0416	hypothetical protein	Not in COGs
ISO4G11_0418	hypothetical protein	Not in COGs

ISO4G11_0420	hypothetical protein	Not in COGs
ISO4G11_0424	Adhesin-like protein	[S]
ISO4G11_0432	phosphoglycolate phosphatase	[R]
ISO4G11_0436	hypothetical protein	Not in COGs
ISO4G11_0437	DNA helicase	[L]
ISO4G11_0440	hypothetical transmembrane protein	Not in COGs
ISO4G11_0442	group II intron reverse transcriptase/maturase	[L]
ISO4G11_0457	hypothetical protein	Not in COGs
ISO4G11_0462	ACP phosphodiesterase	[I]
ISO4G11_0465	Na ⁺ /H ⁺ antiporter	[P]
ISO4G11_0469	multidrug transporter	Not in COGs
ISO4G11_0471	trimethylamine corrinoid protein 2	[R]
ISO4G11_0476	hypothetical protein	[Unclassified]
ISO4G11_0477	Trk system potassium uptake protein TrkA	[P]
ISO4G11_0478	Trk-type K ⁺ transport systems, membrane component	[P]
ISO4G11_0479	hypothetical protein	Not in COGs
ISO4G11_0480	hypothetical protein	Not in COGs
ISO4G11_0488	hypothetical protein	[R]
ISO4G11_0489	methyltransferase domain protein	[Q]
ISO4G11_0490	hypothetical protein	[Unclassified]
ISO4G11_0492	hypothetical protein	Not in COGs
ISO4G11_0493	hypothetical protein	Not in COGs
ISO4G11_0494	hypothetical protein	Not in COGs
ISO4G11_0495	hypothetical protein	Not in COGs
ISO4G11_0496	hypothetical protein	[S]
ISO4G11_0498	hypothetical protein	Not in COGs
ISO4G11_0501	ATPase AAA	[R]
ISO4G11_0506	regulatory protein TetR	[K]
ISO4G11_0507	hypothetical protein	Not in COGs
ISO4G11_0508	hypothetical protein	[X]
ISO4G11_0513	hypothetical protein	Not in COGs
ISO4G11_0514	hypothetical protein	[X]
ISO4G11_0515	ATPase AAA	[V]
ISO4G11_0529	ubiquinone/menaquinone biosynthesis methylase	[Q]
ISO4G11_0531	hypothetical protein	Not in COGs
ISO4G11_0532	oxidoreductase/nitrogenase component 1	[C]
ISO4G11_0533	peptide ABC transporter ATP-binding protein	[E]
ISO4G11_0534	peptide ABC transporter ATP-binding protein	[E]
ISO4G11_0535	peptide ABC transporter permease	[E]
ISO4G11_0536	peptide ABC transporter permease	[E]
ISO4G11_0537	peptide ABC transporter substrate-binding protein	[E]
ISO4G11_0539	hypothetical protein	Not in COGs
ISO4G11_0541	pyridoxamine 5'-phosphate oxidase	[R]
ISO4G11_0545	hypothetical protein	[T]
ISO4G11_0557	hypothetical protein	Not in COGs
ISO4G11_0559	hypothetical transmembrane protein	Not in COGs
ISO4G11_0560	adhesin-like protein	[M]
ISO4G11_0563	hypothetical protein	[S]
ISO4G11_0578	hypothetical protein	Not in COGs
ISO4G11_0579	hypothetical protein	[R]
ISO4G11_0580	nucleoside-diphosphate-sugar epimerases	[M]
ISO4G11_0583	dTDP-4-dehydrorhamnose 3,5-epimerase	[M]
ISO4G11_0585	glycosyltransferase group 2 family protein	[R]
ISO4G11_0590	ADP-L-glycero-D-manno-heptose-6-epimerase	[M]
ISO4G11_0591	RfaE, domain I	[M]
ISO4G11_0592	hypothetical protein	[M]
ISO4G11_0593	DNA helicase	[L]

ISO4G11_0596	TetR family transcriptional regulator	[K]
ISO4G11_0613	phospholipase D/transphosphatidylase	[I]
ISO4G11_0624	hypothetical protein	[S]
ISO4G11_0626	ATPase	[R]
ISO4G11_0632	hypothetical transmembrane protein	Not in COGs
ISO4G11_0633	hypothetical transmembrane protein	Not in COGs
ISO4G11_0638	hypothetical transmembrane protein	Not in COGs
ISO4G11_0643	periplasmic binding protein	[P]
ISO4G11_0644	hypothetical protein	Not in COGs
ISO4G11_0649	hypothetical protein	Not in COGs
ISO4G11_0655	hypothetical protein	[X]
ISO4G11_0656	hypothetical protein	Not in COGs
ISO4G11_0657	hypothetical protein	[X]
ISO4G11_0658	hypothetical protein	Not in COGs
ISO4G11_0659	hypothetical protein	Not in COGs
ISO4G11_0660	hypothetical protein	Not in COGs
ISO4G11_0661	hypothetical protein	Not in COGs
ISO4G11_0680	hypothetical protein	Not in COGs
ISO4G11_0681	hypothetical protein	Not in COGs
ISO4G11_0682	hypothetical protein	Not in COGs
ISO4G11_0683	hypothetical protein	Not in COGs
ISO4G11_0684	hypothetical protein	[X]
ISO4G11_0687	chromosome segregation protein SMC	[R]
ISO4G11_0688	hypothetical protein	Not in COGs
ISO4G11_0689	hypothetical protein	Not in COGs
ISO4G11_0695	phosphoglucosamine mutase	[G]
ISO4G11_0705	cobaltochelatase subunit CobN	[H]
ISO4G11_0709	nitrogenase molybdenum-iron protein	[C]
ISO4G11_0710	hypothetical protein	Not in COGs
ISO4G11_0714	hypothetical protein	Not in COGs
ISO4G11_0719	hypothetical protein	Not in COGs
ISO4G11_0720	hypothetical protein	Not in COGs
ISO4G11_0721	hypothetical protein	[Unclassified]
ISO4G11_0722	hypothetical protein	[R]
ISO4G11_0724	hypothetical protein	Not in COGs
ISO4G11_0727	ATPase	[R]
ISO4G11_0732	hypothetical protein	Not in COGs
ISO4G11_0733	hypothetical protein	Not in COGs
ISO4G11_0736	hypothetical transmembrane protein	Not in COGs
ISO4G11_0741	conserved hypothetical	Not in COGs
ISO4G11_0742	hypothetical protein	Not in COGs
ISO4G11_0743	hypothetical protein	Not in COGs
ISO4G11_0745	hypothetical protein	[X]
ISO4G11_0747	hypothetical protein	[S]
ISO4G11_0748	packaged DNA stabilization protein gp26	[M]
ISO4G11_0749	hypothetical transmembrane protein	Not in COGs
ISO4G11_0750	type III restriction protein res subunit	[L]
ISO4G11_0752	hypothetical protein	Not in COGs
ISO4G11_0767	TetR family transcriptional regulator	[K]
ISO4G11_0768	protein tyrosine phosphatase	[T]
ISO4G11_0776	hypothetical protein	Not in COGs
ISO4G11_0785	hypothetical protein	Not in COGs
ISO4G11_0789	hypothetical transmembrane protein	Not in COGs
ISO4G11_0798	hypothetical transmembrane protein	[X]
ISO4G11_0811	hypothetical protein	Not in COGs
ISO4G11_0812	hypothetical protein	[L]
ISO4G11_0826	carbonic anhydrase	[P]
ISO4G11_0830	CAAX amino terminal protease family	Not in COGs
ISO4G11_0835	hypothetical protein	Not in COGs
ISO4G11_0837	DNA-methyltransferase (Dcm)	Not in COGs

ISO4G11_0839	H/ACA RNA-protein complex component Gar1	[J]
ISO4G11_0843	hypothetical protein	Not in COGs
ISO4G11_0851	hypothetical protein	Not in COGs
ISO4G11_0855	cell division GTPase	Not in COGs
ISO4G11_0867	CDP-glycerol:poly (glycerophosphate) glycerophosphotransferase	[M]
ISO4G11_0872	cell filamentation protein Fic	[S]
ISO4G11_0886	hypothetical transmembrane protein	Not in COGs
ISO4G11_0888	LPS biosynthesis protein	[M]
ISO4G11_0894	β -1,4-galactosyltransferase	[S]
ISO4G11_0896	hypothetical transmembrane protein	Not in COGs
ISO4G11_0897	hypothetical protein	[S]
ISO4G11_0902	guanylate kinase	Not in COGs
ISO4G11_0904	hypothetical protein	Not in COGs
ISO4G11_0907	hypothetical protein	Not in COGs
ISO4G11_0911	hypothetical transmembrane protein	Not in COGs
ISO4G11_0916	hypothetical protein	[R]
ISO4G11_0917	hypothetical protein	Not in COGs
ISO4G11_0922	hypothetical protein	Not in COGs
ISO4G11_0925	hypothetical protein	[S]
ISO4G11_0935	hypothetical protein	Not in COGs
ISO4G11_0943	hypothetical protein	Not in COGs
ISO4G11_0945	hypothetical protein	[S]
ISO4G11_0951	hypothetical protein	[S]
ISO4G11_0959	hypothetical protein	Not in COGs
ISO4G11_0961	hypothetical protein	[E]
ISO4G11_0965	ABC-2 type transporter	[R]
ISO4G11_0971	hypothetical transmembrane protein	Not in COGs
ISO4G11_0972	carbohydrate binding protein	[Unclassified]
ISO4G11_0973	nitroreductase	[C]
ISO4G11_0974	hypothetical protein	Not in COGs
ISO4G11_0975	hypothetical protein	Not in COGs
ISO4G11_0978	hypothetical protein	Not in COGs
ISO4G11_0981	GCN5 family acetyltransferase	[K]
ISO4G11_0983	hypothetical protein	Not in COGs
ISO4G11_0998	peptidyl-prolyl cis-trans isomerase	[O]
ISO4G11_1001	Listeria/Bacterioides repeat protein	Not in COGs
ISO4G11_1002	hypothetical protein	[R]
ISO4G11_1013	hypothetical protein	Not in COGs
ISO4G11_1025	hypothetical protein	Not in COGs
ISO4G11_1034	adhesin-like protein	[R]
ISO4G11_1035	hypothetical protein	[X]
ISO4G11_1045	hypothetical protein	Not in COGs
ISO4G11_1046	hypothetical protein	Not in COGs
ISO4G11_1048	hypothetical protein	Not in COGs
ISO4G11_1054	hypothetical protein	Not in COGs
ISO4G11_1061	hypothetical protein	Not in COGs
ISO4G11_1064	hypothetical protein	[R]
ISO4G11_1065	transglutaminase-like superfamily	[E]
ISO4G11_1074	flavodoxin	[E]
ISO4G11_1081	hypothetical transmembrane protein	Not in COGs
ISO4G11_1083	hypothetical transmembrane protein	Not in COGs
ISO4G11_1085	ATPase	[R]
ISO4G11_1086	hypothetical protein	Not in COGs
ISO4G11_1087	hypothetical protein	[U]
ISO4G11_1088	site-specific recombinase XerD	[L]
ISO4G11_1096	hypothetical protein	Not in COGs
ISO4G11_1097	hypothetical protein	Not in COGs
ISO4G11_1103	hypothetical protein	Not in COGs
ISO4G11_1116	hypothetical protein	Not in COGs
ISO4G11_1120	hypothetical protein	[Unclassified]
ISO4G11_1124	adhesin-like protein	Not in COGs
ISO4G11_1125	adhesin-like protein	Not in COGs
ISO4G11_1128	hypothetical protein	[X]

ISO4G11_1129	hypothetical protein	Not in COGs
ISO4G11_1131	hypothetical protein	Not in COGs
ISO4G11_1132	hypothetical protein	Not in COGs
ISO4G11_1133	hypothetical protein	Not in COGs
ISO4G11_1134	hypothetical protein	Not in COGs
ISO4G11_1139	hypothetical protein	[X]
ISO4G11_1140	hypothetical transmembrane protein	Not in COGs
ISO4G11_1142	MarR family transcriptional regulator	[K]
ISO4G11_1145	hypothetical protein	Not in COGs
ISO4G11_1146	hypothetical transmembrane protein	Not in COGs
ISO4G11_1154	molybdopterin biosynthesis MoeB protein	[H]
ISO4G11_1156	hypothetical protein	Not in COGs
ISO4G11_1157	hypothetical protein	Not in COGs
ISO4G11_1163	hypothetical protein	Not in COGs
ISO4G11_1164	hypothetical protein	Not in COGs
ISO4G11_1166	AAA ATPase	[K]
ISO4G11_1167	small-conductance mechanosensitive channel	[M]
ISO4G11_1174	hypothetical protein	Not in COGs
ISO4G11_1175	hypothetical protein	[L]
ISO4G11_1179	hypothetical protein	[X]
ISO4G11_1181	hypothetical protein	Not in COGs
ISO4G11_1185	hypothetical protein	[Unclassified]
ISO4G11_1188	hypothetical protein	Not in COGs
ISO4G11_1189	periplasmic binding protein	[P]
ISO4G11_1209	MATE efflux family protein	[V]
ISO4G11_1212	permease	[R]
ISO4G11_1216	hypothetical protein	Not in COGs
ISO4G11_1217	hypothetical protein	Not in COGs
ISO4G11_1219	site-specific recombinase, DNA invertase	[L]
ISO4G11_1220	hypothetical protein	Not in COGs
ISO4G11_1221	hypothetical protein	Not in COGs
ISO4G11_1222	hypothetical protein	Not in COGs
ISO4G11_1223	hypothetical protein	Not in COGs
ISO4G11_1226	acetyltransferase	[K]
ISO4G11_1228	periplasmic binding protein	[P]
ISO4G11_1231	hypothetical protein	Not in COGs
ISO4G11_1234	transposase	[L]
ISO4G11_1235	ATPase AAA	[O]
ISO4G11_1236	adhesin-like protein	[R]
ISO4G11_1237	hypothetical protein	Not in COGs
ISO4G11_1239	hypothetical protein	[S]
ISO4G11_1240	hypothetical protein	Not in COGs
ISO4G11_1241	hypothetical transmembrane protein	Not in COGs
ISO4G11_1242	hypothetical protein	[R]
ISO4G11_1246	hypothetical protein	Not in COGs
ISO4G11_1248	hypothetical protein	Not in COGs
ISO4G11_1249	hypothetical transmembrane protein	Not in COGs
ISO4G11_1262	hypothetical protein	Not in COGs
ISO4G11_1264	hypothetical protein	Not in COGs
ISO4G11_1265	hypothetical protein	Not in COGs
ISO4G11_1269	periplasmic binding protein	[P]
ISO4G11_1272	hypothetical protein	Not in COGs
ISO4G11_1287	transposase	[X]
ISO4G11_1289	hypothetical transmembrane protein	Not in COGs
ISO4G11_1298	hypothetical transmembrane protein	Not in COGs
ISO4G11_1310	hypothetical protein	Not in COGs
ISO4G11_1311	ABC-type Fe ³⁺ -siderophore transport system, permease component	[P]
ISO4G11_1312	vitamin B12 ABC transporter, permease component BtuC	[P]
ISO4G11_1314	periplasmic binding protein	[P]
ISO4G11_1319	hypothetical protein	[E]
ISO4G11_1321	acetyltransferase	[K]
ISO4G11_1331	nitrilase	[R]

ISO4G11_1351	hypothetical transmembrane protein	[S]
ISO4G11_1353	hypothetical protein	[R]
ISO4G11_1354	hypothetical protein	Not in COGs
ISO4G11_1355	Tfp pilus assembly protein PilF	[R]
ISO4G11_1364	hypothetical transmembrane protein	Not in COGs
ISO4G11_1369	Sell domain protein repeat-containing protein	[R]
ISO4G11_1372	molecular chaperone	[O]
ISO4G11_1373	hypothetical protein	[Unclassified]
ISO4G11_1374	hypothetical protein	Not in COGs
ISO4G11_1375	hypothetical protein	[O]
ISO4G11_1376	molecular chaperone DnaK	[O]
ISO4G11_1382	adhesin-like protein	[S]
ISO4G11_1383	hypothetical protein	Not in COGs
ISO4G11_1384	hypothetical protein	[X]
ISO4G11_1385	site-specific recombinase XerD	[L]
ISO4G11_1387	Fic family protein	[D]
ISO4G11_1389	ABC transporter related protein	[P]
ISO4G11_1391	periplasmic binding protein	[P]
ISO4G11_1398	CobN component of cobalt chelatase involved in B12 biosynthesis	[H]
ISO4G11_1399	hypothetical transmembrane protein	[P]
ISO4G11_1414	4-oxalocrotonate tautomerase	[R]
ISO4G11_1423	helicase	[L]
ISO4G11_1436	hypothetical protein	Not in COGs
ISO4G11_1437	hypothetical protein	Not in COGs
ISO4G11_1438	glycosyl transferase family	[M]
ISO4G11_1439	glycosyltransferase WbsX family protein	[M]
ISO4G11_1440	ADP-heptose:LPS heptosyltransferase	[M]
ISO4G11_1443	hypothetical protein	Not in COGs
ISO4G11_1444	hypothetical protein	[Q]
ISO4G11_1445	hypothetical protein	Not in COGs
ISO4G11_1446	hypothetical protein	Not in COGs
ISO4G11_1447	hypothetical protein	Not in COGs
ISO4G11_1453	cell filamentation protein Fic	[D]
ISO4G11_1454	hypothetical protein	Not in COGs
ISO4G11_1455	hypothetical protein	Not in COGs
ISO4G11_1458	exonuclease SbcC	[L]
ISO4G11_1459	exonuclease SbcD	[L]
ISO4G11_1470	ABC transporter substrate-binding protein	[P]
ISO4G11_1480	alcohol dehydrogenase, class IV	[C]
ISO4G11_1488	nicotinate phosphoribosyltransferase	[H]
ISO4G11_1492	transcriptional regulator	[T]
ISO4G11_1494	hypothetical transmembrane protein	[S]
ISO4G11_1495	hypothetical transmembrane protein	[Unclassified]
ISO4G11_1504	Mg-dependent DNase	[L]
ISO4G11_1509	hypothetical protein	[R]
ISO4G11_1518	hypothetical protein	Not in COGs
ISO4G11_1522	hypothetical protein	[Unclassified]
ISO4G11_1523	hypothetical protein	[X]
ISO4G11_1524	hypothetical protein	Not in COGs
ISO4G11_1539	amino acid transporter	[E]
ISO4G11_1540	hypothetical protein	[X]

ISO4G11_1541	TetR family transcriptional regulator	[K]
ISO4G11_1542	adhesin-like protein	[R]
ISO4G11_1543	hypothetical protein	Not in COGs
ISO4G11_1545	IclR family transcriptional regulator	[K]
ISO4G11_1552	hypothetical protein	[X]
ISO4G11_1559	ATPase	Not in COGs
ISO4G11_1602	metal-binding protein	[S]
ISO4G11_1609	adhesin-like protein	[R]
ISO4G11_1623	hypothetical transmembrane protein	Not in COGs
ISO4G11_1628	site-specific recombinase XerD	[L]
ISO4G11_1630	hypothetical protein	Not in COGs
ISO4G11_1637	hypothetical protein	Not in COGs
ISO4G11_1639	hypothetical protein	Not in COGs
ISO4G11_1646	hypothetical protein	[X]
ISO4G11_1647	hypothetical protein	Not in COGs
ISO4G11_1654	isocitrate/isopropylmalate dehydrogenase	[C]
ISO4G11_1659	ATPase (AAA+ superfamily)	[R]
ISO4G11_1662	Rrf2 family transcriptional regulator	[K]
ISO4G11_1666	hypothetical transmembrane protein	[X]
ISO4G11_1667	hypothetical protein	[X]
ISO4G11_1681	hypothetical transmembrane protein	[S]
ISO4G11_1695	hypothetical protein	Not in COGs
ISO4G11_1697	hypothetical protein	Not in COGs
ISO4G11_1698	hypothetical protein	[J]
ISO4G11_1700	hypothetical protein	Not in COGs
ISO4G11_1701	hypothetical protein	Not in COGs
ISO4G11_1702	hypothetical protein	Not in COGs
ISO4G11_1703	hypothetical transmembrane protein	Not in COGs
ISO4G11_1707	hypothetical protein	Not in COGs
ISO4G11_1709	nitrogenase	[C]
ISO4G11_1710	hypothetical protein	Not in COGs
ISO4G11_1711	type 11 methyltransferase	[Q]
ISO4G11_1712	periplasmic binding protein	[P]
ISO4G11_1715	hypothetical protein	Not in COGs
ISO4G11_1717	ATPase	[R]
ISO4G11_1719	adhesin-like protein	[U]
ISO4G11_1720	hypothetical protein	[S]
ISO4G11_1723	hypothetical protein	Not in COGs
ISO4G11_1724	hypothetical protein	[Unclassified]
ISO4G11_1726	hypothetical protein	Not in COGs
ISO4G11_1727	hypothetical protein	Not in COGs
ISO4G11_1729	hypothetical protein	[S]
ISO4G11_1730	hypothetical protein	Not in COGs
ISO4G11_1731	hypothetical protein	Not in COGs
ISO4G11_1732	hypothetical protein	Not in COGs
ISO4G11_1734	hypothetical protein	[Unclassified]
ISO4G11_1736	hypothetical protein	Not in COGs
ISO4G11_1749	hypothetical protein	Not in COGs
ISO4G11_1750	hypothetical protein	[X]
ISO4G11_1754	hypothetical protein	Not in COGs

*only one gene from each gene family is represented.

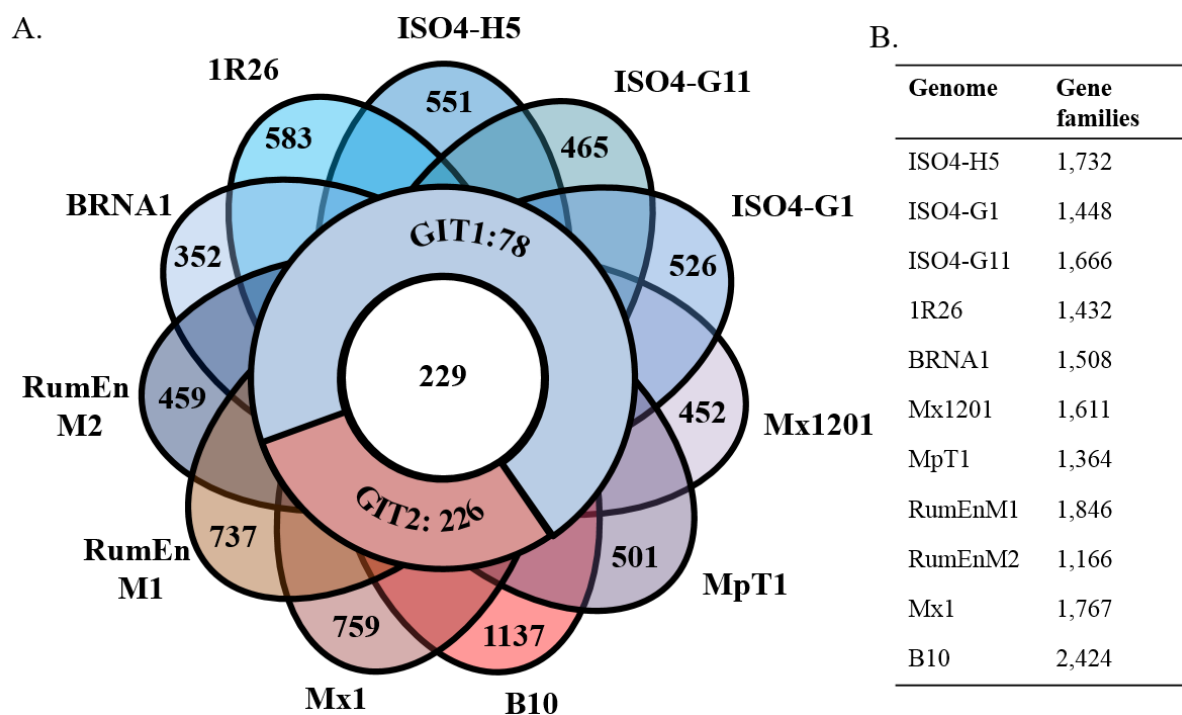


Figure A.4.5 Conserved and novel gene families among the 11 Methanomassiliicoccales genomes analysed. **A.** Venn diagram indicating the number of conserved gene families between completed genomes based on BLASTp analysis, using a 50% identity and 50% coverage cutoff. Regions that do not overlap with other genomes depict the number of unique gene families under the same criteria. **B.** Table listing the total number of gene families in each of the Methanomassiliicoccales genomes.

Table A.4.11 Genes involved in methanogenesis and energy generation in Methanomassiliicoccales

[illegible]

Methyltransferase corrinoid activation protein												
										WP_019178502.1		
ramA	AR505_1320	ISO4G1_0653	ISO4G11_0018	TALC_01088	AOA80_07690 (pseudo)	AOA81_01050	AUQ37_06035	MMALV_11240	MMINT_08890	WP_019176361.1	Mpt1_c05140 Mpt1_c05740	
			ISO4G11_0448					AUQ37_06040 (interrupted)	MMALV_09430	MMINT_05880		WP_019176312.1
		ISO4G1_1056							MMALV_13490	MMINT_15750		WP_019176767.1
										WP_026068898.1		
Methylamine transporter												
mtmP												
mtbP	AR505_1242							MMALV_05040				
		ISO4G1_1219	ISO4G11_0753	TALC_01005			AUQ37_04890		MMINT_08970			
mttP	AR505_1331							MMALV_11390				
	AR505_0749	ISO4G1_1228		TALC_01100			AUQ37_05990	MMALV_11340	MMINT_08990			
Methyl-compound corrinoid pteins												
mtaC1	AR505_0950	ISO4G1_1058	ISO4G11_0444		AOA80_00415		AUQ37_01185	MMALV_09460	MMINT_02810	WP_019176359.1	Mpt1_c05100	
mtaC2	AR505_0952		ISO4G11_0653		AOA80_03335				MMINT_03150	WP_019177725.1		
mtaC3					AOA80_00085				MMINT_05930	WP_019178087.1		
mtmC1	AR505_1329	ISO4G1_1237	ISO4G11_0008	TALC_01095			AUQ37_05995	MMALV_11310	MMINT_08940	WP_019176307.1	Mpt1_c05770	
mtmC2								MMALV_04350	MMINT_08880	WP_019176313.1		
mtmC3										WP_019178555.1		
mtmC4										WP_019178518.1		
mtbC	AR505_1333	ISO4G1_0742	ISO4G11_0550	TALC_00300			AUQ37_04325	MMALV_11380	MMINT_09030	WP_019178525.1		
mtbC2		ISO4G1_1236	ISO4G11_1514	TALC_01104			AUQ37_05960					
mttC	AR505_0773	ISO4G1_1229	ISO4G11_0001	TALC_01101			AUQ37_05985 (pseudo)	MMALV_11350	MMINT_09000	WP_019178521.1		
mtsB1	AR505_1067		ISO4G11_0447		AOA80_02370		AUQ37_08035	MMALV_13480		WP_019177198.1		
mtsB2										WP_019177442.1		
mtxC1	AR505_1330	ISO4G1_0251						MMALV_04220	MMINT_15770	WP_019176763.1		
mtxC2									MMINT_04600	WP_019178649.1		
mtxC3										WP_019177907.1		
Methylcobalamin: and methylthiol: coenzyme M methyltransferases												
mta/mt bA1	AR505_1035	ISO4G1_0538	ISO4G11_0086	TALC_00463	AOA80_07810	AOA81_01055	AUQ37_01300	MMALV_05210	MMINT_07210	WP_019176765.1		
mta/mt bA2	AR505_1063	ISO4G1_0617	ISO4G11_0224		AOA80_08780		AUQ37_02825 + AUQ37_02830	MMALV_09620	MMINT_15760	WP_019177502.1	Mpt1_c01960	
mta/mt bA3	AR505_1404	ISO4G1_1013	ISO4G11_1691		AOA80_03175			MMALV_13470				
mta/mt bA4	AR505_1575											
mtsA1	AR505_1066		ISO4G11_0446		AOA80_02375		AUQ37_08040			WP_019177199.1		
mtsA2								MMALV_11470		WP_019177441.1		
Methanogenesis Marker proteins												

[illegible]

<i>corA</i>	AR505_1041	-	-	TALC_01211	AOA80_08495	-	AUQ37_03770	MMALV_12560	MMINT_17270	WP_019176692.1	Mpt1_c07030
Heterodisulfide reductase											
<i>hdrA</i>	AR505_1479	ISO4G1_1281	ISO4G11_1403	TALC_00332	AOA80_02455	AOA81_00385	AUQ37_03270	MMALV_03030	MMINT_04810	WP_019177460.1	Mpt1_c10580
<i>hdrB1</i>	AR505_0274	ISO4G1_0352	ISO4G11_0773	TALC_01276	AOA80_00670	AOA81_04325	AUQ37_05955	MMALV_13660	MMINT_03230	WP_019177711.1	Mpt1_c08830
<i>hdrB2</i>	AR505_0679	-	ISO4G11_0083	TALC_01035	-	-	-	MMALV_07360	MMINT_05370	WP_019176125.1	-
<i>hdrC1</i>	AR505_0273	ISO4G1_0351	ISO4G11_0772	TALC_01277	AOA80_00665	AOA81_04320	AUQ37_05950	MMALV_13670	MMINT_03240	WP_019177712.1	Mpt1_c08840
<i>hdrC2</i>	-	-	-	-	-	-	-	-	-	WP_019176126.1	Mpt1_c02960
<i>hdrD1</i>	AR505_0040	ISO4G1_0085	ISO4G11_1012	TALC_01537	AOA80_10440	AOA81_02315	AUQ37_07515	MMALV_16610	MMINT_01020	WP_019178460.1	Mpt1_c00310
<i>hdrD2</i>	AR505_0168	ISO4G1_0217	ISO4G11_1159	TALC_01391	AOA80_05385	AOA81_02260	-	MMALV_14890	MMINT_02470	WP_019177852.1	Mpt1_c10580
<i>hdrD3</i>	-	-	-	-	-	-	-	-	-	WP_019177557.1	-
Methyl viologen hydrogenase											
<i>mvhD1</i>	AR505_1478	ISO4G1_1280	ISO4G11_1402	TALC_00333	AOA80_02450	AOA81_00390	AUQ37_03265	MMALV_03040	MMINT_04820	WP_019177459	Mpt1_c10570
<i>mvhD2</i>	-	-	-	-	AOA80_05200	-	-	-	MMINT_05200	WP_019176201.1	-
<i>mvhD3</i>	-	-	-	-	-	-	-	-	-	WP_019176130.1	-
<i>mvhG</i>	AR505_1477	ISO4G1_1279	ISO4G11_1401	TALC_00334	AOA80_02445	AOA81_00395	AUQ37_03260	MMALV_03050	MMINT_04830	WP_019177458.1	Mpt1_c10560
<i>mvhA</i>	AR505_1476	ISO4G1_1278	ISO4G11_1400	TALC_00335	AOA80_02440	AOA81_00400	AUQ37_03255	MMALV_03060	MMINT_04840	WP_019177457.1	Mpt1_c10550
Fpo-like complex											
<i>fpoA</i>	AR505_1633	ISO4G1_0154	ISO4G11_0152	TALC_00209	AOA80_02800	AOA81_00760	AUQ37_00795	MMALV_01955	MMINT_01985	WP_019176183.1	Mpt1_c12660
<i>fpoB</i>	AR505_1632	ISO4G1_0155	ISO4G11_0151	TALC_00210	AOA80_02795	AOA81_00755	AUQ37_00800	MMALV_01960	MMINT_02000	WP_019176182.1	Mpt1_c12650
<i>fpoC</i>	AR505_1631	ISO4G1_0156	ISO4G11_0150	TALC_00211	AOA80_02790	AOA81_00750	AUQ37_00805	MMALV_01970	MMINT_02010	WP_019176181.1	Mpt1_c12640
<i>fpoD</i>	AR505_1630	ISO4G1_0157	ISO4G11_0149	TALC_00212	AOA80_02785	AOA81_00745	AUQ37_00810	MMALV_01980	MMINT_02020	WP_019176180.1	Mpt1_c12630
<i>fpoH</i>	AR505_1629	ISO4G1_0158	ISO4G11_0148	TALC_00213	AOA80_02780	AOA81_00740 (pseudo)	AUQ37_00815 (pseudo)	MMALV_01990	MMINT_02030	WP_019176179.1	Mpt1_c12620
<i>fpoI</i>	AR505_1628	ISO4G1_0159	ISO4G11_0147	TALC_00214	AOA80_02775	AOA81_00735	AUQ37_00820	MMALV_02000	MMINT_02040	WP_019176178.1	Mpt1_c12610
<i>fpoJ</i>	AR505_1627	ISO4G1_0160	ISO4G11_0146	TALC_00215	AOA80_02770	AOA81_00730	AUQ37_00825	MMALV_02010	MMINT_02050	WP_019176177.1	Mpt1_c12600
Hypothetical protein	AR505_1626	ISO4G1_0161	ISO4G11_0145	TALC_00216	AOA80_02765	AOA81_00725	AUQ37_00830	MMALV_02020	MMINT_02060	WP_019176176.1	Mpt1_c12590
<i>fpoK</i>	AR505_1625	ISO4G1_0162	ISO4G11_0144	TALC_00217	AOA80_02760	AOA81_00720	AUQ37_00835	MMALV_02030	MMINT_02070	WP_019176175.1	Mpt1_c12580
<i>fpoL</i>	AR505_1624	ISO4G1_0163	ISO4G11_0143	TALC_00218	AOA80_02755	AOA81_00715	AUQ37_00840	MMALV_02040	MMINT_02080	WP_019176174.1	Mpt1_c12570
<i>fpoM</i>	AR505_1623	ISO4G1_0164	ISO4G11_0142	TALC_00219	AOA80_02750	AOA81_00710	AUQ37_00845	MMALV_02050	MMINT_02090	WP_019176173.1	Mpt1_c12560
<i>fpoN</i>	AR505_1622	ISO4G1_0165	ISO4G11_0141	TALC_00220	AOA80_02745	AOA81_00705	AUQ37_00850	MMALV_02060	MMINT_02100	WP_019176172.1	Mpt1_c12550
<i>fpoFO</i>	-	-	-	-	-	-	-	-	-	-	-
Energy conserving hydrogenase											
<i>echA1</i>	-	-	-	-	AOA80_10430	-	-	-	MMINT_01030	WP_019178471.1	
<i>echA2</i>	-	-	-	-	-	-	-	-	MMINT_17050	WP_019176386.1	
<i>echB1</i>	-	-	-	-	AOA80_11085	-	-	-	MMINT_01040	WP_019178472.1	
<i>echB2</i>	-	-	-	-	-	-	-	-	MMINT_17040	WP_019176385.1	
<i>echC1</i>	-	-	-	-	AOA80_11080	-	-	-	MMINT_01050	WP_019178473.1	
<i>echC2</i>	-	-	-	-	-	-	-	-	MMINT_17030	WP_019176384.1	
<i>echD1</i>	-	-	-	-	AOA80_11075	-	-	-	MMINT_01060	WP_019178474.1	
<i>echD2</i>	-	-	-	-	-	-	-	-	MMINT_17020	WP_019176383.1	
<i>echE1</i>	-	-	-	-	AOA80_11070	-	-	-	MMINT_01070	WP_019178475.1	
<i>echE2</i>	-	-	-	-	-	-	-	-	MMINT_17010	WP_019176382.1	
<i>echF1</i>	-	-	-	-	AOA80_11065 (pseudo)	-	-	-	MMINT_01080	WP_019178476.1	
<i>echF2</i>	-	-	-	-	-	-	-	-	MMINT_17000	-	
Hyf-like hydrogenase											

[illegible]

<i>ahaH</i>	AR505_1826	ISO4G1_0004	ISO4G11_0815	TALC_00004	AOA80_00805	AOA81_02535	AUQ37_01965	MMALV_00050	MMINT_00050	WP_019178382.1	Mpt1_c12340
<i>ahaI</i>	AR505_1825	ISO4G1_0005	ISO4G11_0816	TALC_00005	AOA80_00810	AOA81_02540	AUQ37_01960 (pseudo)	MMALV_00060	MMINT_00060	WP_019178381.1	Mpt1_c12330
<i>ahaK</i>	AR505_1824	ISO4G1_0006	ISO4G11_0817	TALC_00006	AOA80_00815	AOA81_02545	AUQ37_01955	MMALV_00070	MMINT_00070	WP_019178380.1	Mpt1_c12320
<i>ahaE</i>	AR505_1823	ISO4G1_0007	ISO4G11_0818	TALC_00007	AOA80_00820	AOA81_02550	AUQ37_01950	MMALV_00080	MMINT_00080	WP_019178379.1	Mpt1_c12310
<i>ahaC</i>	AR505_1822	ISO4G1_0008	ISO4G11_0819	TALC_00008	AOA80_00825	AOA81_02555	AUQ37_01945	MMALV_00090	MMINT_00090	WP_019178378.1	Mpt1_c12300
<i>ahaF</i>	AR505_1821	ISO4G1_0009	ISO4G11_0820	TALC_00009	AOA80_00830	AOA81_02560	AUQ37_01940	MMALV_00100	MMINT_00100	WP_019178377.1	Mpt1_c12290
<i>ahaA</i>	AR505_1820	ISO4G1_0010	ISO4G11_0821	TALC_00010	AOA80_00835	AOA81_02565 (pseudo)	AUQ37_01935	MMALV_00110	MMINT_00110	WP_019178376.1	Mpt1_c12280
<i>ahaB</i>	AR505_1819	ISO4G1_0011	ISO4G11_0822	TALC_00011	AOA80_00840	AOA81_02570	AUQ37_01930	MMALV_00120	MMINT_00120	WP_019178375.1	Mpt1_c12270
<i>ahaD</i>	AR505_1818	ISO4G1_0012	ISO4G11_0823	TALC_00012	AOA80_00845	AOA81_02575	AUQ37_01925	MMALV_00130	MMINT_00130	WP_019178374.1	Mpt1_c12260

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes.+indicates functional protein is translated from two genes merged by amber codon read-through. Methyl:coenzyme M reductase subunit X (*mrtX*), methanol:corrinoid methyltransferase (*mtaB*), monomethylamine:corrinoid methyltransferase (*mtmB*), dimethylamine:corrinoid methyltransferase (*mtbB*), trimethylamine:corrinoid methyltransferase (*mttB*), methylamine methyltransferase corrinoid activation protein (*ramA*), monomethylamine permease (*mtmP*), dimethylamine permease (*mtbP*), trimethylamine permease (*mttP*), methanol corrinoid protein (*mtaC*), monomethylamine corrinoid protein (*mtmC*), dimethylamine corrinoid protein (*mtbC*), trimethylamine corrinoid protein (*mttC*), methylthiol corrinoid protein (*mtsB*), corrinoid protein with unknown substrate (*mtxC*), methyl:coenzyme M methyltransferase (*mtaA*), bifunctional methylthiol:corrinoid methyltransferase (*mtsA*), methanogenesis marker protein (*mmp1-17*), (2*R*)-phospho-3-sulfolactate synthase (*comA*), 2-phosphosulfolactate phosphohydrolase (*comB*), (2*R*)-3-sulfolactate dehydrogenase (*comC*), sulfopyruvate decarboxylase (*comDE*), uroporphyrinogen-III C-methyltransferase (*corA*), heterodisulfide reductase (*hdr*), methylviologen hydrogenase (*mvh*), F₄₂₀H₂ dehydrogenase-like complex subunit (*fpoA-O*), energy-conserving hydrogenase (*echA-F*), Hyf-like hydrogenase (*hyf*), A₁A₀ ATP synthase subunits are present (*ahaA-K*).

Table A.4.12 Genes involved in central carbon metabolism in Methanomassiliicoccales

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Gluconeogenesis											
<i>pgm</i>	AR505_1608	ISO4G1_1503	ISO4G11_0127	TALC_00241	AOA80_09650	AOA81_01905	AUQ37_00975 (pseudo)	MMALV_02250	MMINT_16490	WP_019178100.1	Mpt1_c11280
<i>pgi</i>	AR505_0560	ISO4G1_1504	ISO4G11_0584	TALC_00585	AOA80_10780	AOA81_01605 (pseudo),	AUQ37_06535 (pseudo)	MMALV_01010	MMINT_07950	WP_019177252.1	-
	AR505_1769	ISO4G1_1505				AOA81_05095	MMALV_05310				
<i>tpiA</i>	AR505_1148	ISO4G1_0734	ISO4G11_0602	TALC_00680	AOA80_09265	AOA81_04980	AUQ37_01925 (pseudo)	MMALV_09930	MMINT_11880	WP_026068833.1	Mpt1_c07300
<i>fbp</i>	AR505_1149	ISO4G1_0735	ISO4G11_0603	TALC_00681	AOA80_09260	AOA81_04985	AUQ37_07155	MMALV_09940	MMINT_11890	WP_026068834.1	Mpt1_c07310
<i>pfkB</i>	-	-	-	-	-	-	-	-	-	WP_019176285.1	-
<i>fba</i>	AR505_0932	ISO4G1_1397	ISO4G11_1452	TALC_00560, TALC_00670	AOA80_11330	AOA81_06970	AUQ37_06665 (pseudo)	MMALV_05100	MMINT_14400	WP_019176284.1	Mpt1_c09850
	AR505_0508		ISO4H11_0601	AOA80_10200	MMALV_05100		MMINT_14400	WP_019176284.1	Mpt1_c10430		
<i>gap2</i>	AR505_0154	ISO4G1_0260	ISO4G11_1178	TALC_01406	AOA80_06285 AOA80_06265	AOA81_02175	AUQ37_09135	MMALV_15110	MMINT_02260	WP_019177881.1	Mpt1_c00900
<i>pgk</i>	AR505_0155	ISO4G1_0261	ISO4G11_1177	TALC_01405	AOA80_11340	AOA81_02180	AUQ37_09140	MMALV_15100	MMINT_02310	WP_019177877.1	Mpt1_c00890
<i>gpmA</i>	AR505_0942	ISO4G1_0737	ISO4G11_0453	TALC_00943	AOA80_11335	-	AUQ37_01310	MMALV_09640			
<i>apgM</i>	AR505_0474	ISO4G1_0995	ISO4G11_1484	TALC_00533	AOA80_07955	AOA81_03110	AUQ37_07750	MMALV_04820	MMINT_12550	WP_019176885.1	Mpt1_c02310
						AOA81_05970					
<i>eno</i>	AR505_0470	ISO4G1_0594	ISO4G11_1491	TALC_00528	AOA80_10720	AOA81_05650	AUQ37_07770 (pseudo)	MMALV_04790	MMINT_08060	WP_026068854.1	Mpt1_c03940
	AR505_0472	ISO4G1_0443	ISO4G11_0575	TALC_01169	AOA80_11320	AOA81_02890 (pseudo)	AUQ37_00215	MMALV_12140	MMINT_13110	WP_019177575.1	Mpt1_c07690
<i>ppsA</i>	AR505_1104	ISO4G1_0509									
<i>porA</i>	AR505_0431	ISO4G1_0440	ISO4G11_0518	TALC_01166	AOA80_06560	AOA81_02905	AUQ37_00235	MMALV_12090	MMINT_03660	WP_019177572.1	Mpt1_c07640
					AOA80_05885						
					AOA80_01355 (pseudo)						
					AOA80_05880						
<i>porB</i>	AR505_0432	ISO4G1_0439	ISO4G11_0519	TALC_01165	AOA80_01350	AOA81_02910 (pseudo)	AUQ37_00240 (pseudo)	MMALV_12080	MMINT_03670	WP_019177571.1	Mpt1_c07630
<i>porC</i>	AR505_0429	ISO4G1_0442	ISO4G11_0516	TALC_01168	AOA80_06555	AOA81_02895	AUQ37_00225	MMALV_12110	MMINT_03640	WP_026068932.1	Mpt1_c07660
					AOA80_06570 (pseudo)						

<i>porD</i>	AR505_0430	ISO4G1_0441	ISO4G11_0517	TALC_01167	AOA80_01360 , AOA80_06565 AOA80_00190 AOA80_04255	AOA81_02900	AUQ37_00230	MMALV_12100	MMINT_03650	WP_019177573.1	Mpt1_c07650
<i>acs/acdA</i>	AR505_1282	ISO4G1_1025	ISO4G11_0077	TALC_01130	AOA81_03020	AOA81_03020	AUQ37_00410	MMALV_11710	MMINT_06050	WP_019176444.1	Mpt1_c02450
<i>ppcA</i>	-	-	-	-	-	-	-	-	MMINT_00470	WP_019176213.1	
Incomplete TCA cycle											
<i>gluA</i>	AR505_0499		ISO4G11_0693								
	, AR505_0678	ISO4G1_0688	, ISO4G11_1468	-	AOA80_05790	-	-	-	MMINT_18640	WP_019178659.1	-
<i>acnA</i>	AR505_0592	ISO4G1_0573	ISO4G11_0272	TALC_00589	-	AOA81_06915	AUQ37_04625	MMALV_05560	MMINT_07370	-	Mpt1_c02920
<i>ldh</i> (NAD ⁺)	AR505_1376	ISO4G1_1012	ISO4G11_1654	TALC_00501	AOA80_06985	AOA81_04485	AUQ37_08765	MMALV_04330	-	WP_019176816.1	Mpt1_c03670
<i>ldh</i> (NADP ⁺)	AR505_0531	ISO4G1_0567	ISO4G11_0277	TALC_00573	-	AOA81_03260	AUQ37_00567	-	MMINT_05170	WP_026068719.1	Mpt1_c02660 , Mpt1_c03670
<i>korA</i>	-	ISO4G1_0862	ISO4G11_0987	TALC_00345	AOA80_07230	AOA81_05180	-	-	MMINT_08420	WP_019176337.1	-
<i>korB</i>	-	ISO4G1_0863	ISO4G11_0986	TALC_00344	AOA80_07225	AOA81_05175	-	-	MMINT_08430	WP_019176336.1	-
<i>korG</i>	-	ISO4G1_0864	ISO4G11_0985	TALC_00343	-	AOA81_05170 (pseudo)	-	-	MMINT_08440	-	-
<i>korD</i>	-	ISO4G1_0861	-	TALC_00346	AOA80_07235	AOA81_05185	-	-	MMINT_08410	WP_019176338.1	-
<i>sucC</i>	-	-	-	-	-	-	-	-	-	WP_019177398.1	-
<i>sucD</i>	-	-	-	-	-	-	-	-	-	WP_019177399.1	-
<i>sdhA</i>	-	-	-	-	-	-	-	-	-	-	-
<i>sdhB</i>	-	-	-	-	-	-	-	-	-	-	-
<i>sdhC</i>	-	-	-	-	-	-	-	-	-	-	-
<i>sdhD</i>	-	-	-	-	-	-	-	-	-	-	-
<i>tfrA</i>	-	-	-	-	-	-	-	-	-	WP_019176936.1	-
<i>tfrB</i>	-	-	-	-	-	-	-	-	-	WP_019178460.1	-
<i>nfrA</i>	-	-	-	-	-	-	-	-	-	-	-
<i>nfrB</i>	-	-	-	-	-	-	-	-	-	-	-
<i>fumA</i>	AR505_0022	ISO4G1_0065	ISO4G11_0790	TALC_01553	AOA80_10615	AOA81_02405	AUQ37_02080 (pseudo)	MMALV_16760	MMINT_19270	WP_019178423.1	Mpt1_c14310
<i>fumB</i>	AR505_0023	ISO4G1_0066	ISO4G11_0791	TALC_01554	AOA80_10610	AOA81_02400	AUQ37_02085 (pseudo)	MMALV_16770	MMINT_19280	WP_019178422.1	Mpt1_c14320
<i>maeI</i>	AR505_1780	ISO4G1_0047	ISO4G11_0866	TALC_00057		AOA81_02790	AUQ37_08155	MMALV_00650	MMINT_19680	WP_019178295.1	Mpt1_c11760
<i>purA</i>	AR505_1168	ISO4G1_0684	ISO4G11_0612	TALC_00689	AOA80_09160 (pseudo)	AOA81_05040 (pseudo)	AUQ37_07105 (pseudo)	MMALV_10030	MMINT_12990	WP_019177117.1	Mpt1_c06950
<i>purB</i>	AR505_0742	ISO4G1_0911	ISO4G11_1050	TALC_00921	AOA80_11375 (pseudo)	AOA81_05825	AUQ37_01480	MMALV_07730	MMINT_10940	WP_019177003.1	Mpt1_c04990
<i>serC</i>	AR505_1665	ISO4G1_0121	ISO4G11_1530	TALC_00176	AOA80_03930	AOA81_01820	AUQ37_00625 (pseudo)	MMALV_01640	MMINT_01870	WP_026069026.1	Mpt1_c13090
Pentose phosphate pathway											
<i>tktA N'</i>	AR505_1649	ISO4G1_0136	ISO4G11_0168	TALC_00193	AOA80_06125	AOA81_03775	AUQ37_00715	MMALV_01800	MMINT_17780	WP_019176117.1	Mpt1_c12820
<i>tktA C'</i>	AR505_1648	ISO4G1_0137	ISO4G11_0167	TALC_00194	AOA80_06130	AOA81_03780	AUQ37_00720	MMALV_01810	MMINT_17770	WP_019176116.1	Mpt1_c12810
<i>rpe</i>	AR505_0461	ISO4G1_0602	ISO4G11_1502	TALC_00519	AOA80_06835	AOA81_05705	AUQ37_08010 (pseudo)	MMALV_04660	MMINT_07420	WP_019176846.1	Mpt1_c03860

<i>rpiA</i>	AR505_1513	ISO4G1_1303	ISO4G11_0890	TALC_00307	AOA80_00160	AOA81_03850	AUQ37_06850	MMALV_00820	MMINT_05570	WP_019176373.1	Mpt1_c10780
<i>prs</i>	AR505_1685	ISO4G1_1451	ISO4G11_1427	TALC_00147	AOA80_05650	AOA81_01710	AUQ37_02260	MMALV_02800	MMINT_18540	WP_019178734.1	Mpt1_c13340
Reductive acetyl-CoA pathway											
<i>fdhAB</i>	-	-	-	-	-	-	-	-	-	-	-
<i>fhs</i>	AR505_1217	ISO4G1_0964	ISO4G11_1362	TALC_00725	AOA80_02845 (pseudo)	AOA81_06540	AUQ37_05415 (pseudo)	MMALV_10510	MMINT_00330	WP_019176194.1	Mpt1_c06480
<i>folD</i>	AR505_1639	ISO4G1_0148	ISO4G11_0158	TALC_00203	AOA80_02840 (pseudo)	AOA81_00790	AUQ37_00765	MMALV_01900	MMINT_16400	WP_019176192.1	Mpt1_c12720
<i>metV</i>	-	-	-	-	AOA80_04305 (pseudo)	-	-	-	MMINT_00380	WP_019176202.1	-
<i>metF</i>	-	-	-	-	AOA80_04300	AOA81_00805	-	-	MMINT_00390	WP_019176203.1	-
Methylene tetrahydro folate reductase (ferredoxin)	-	-	-	-	-	-	-	-	-	-	-
<i>acsE</i>	-	-	-	-	AOA80_04280	AOA81_00810	-	-	MMINT_00400	WP_019176206.1	-
<i>acsA</i>	-	-	-	-	AOA80_10155 (pseudo)	AOA81_00590	-	-	MMINT_19140	WP_019176239.1	-
<i>acsB</i>	-	-	-	-	AOA80_09460	AOA81_06000	-	-	-	-	Mpt1_c02980
<i>cdhA</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cdhB</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cdhC</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cdhD</i>	-	-	-	-	AOA80_10150 (pseudo)	AOA81_00595	-	-	MMINT_19130	WP_019176238.1	-
<i>cdhE</i>	-	-	-	-	AOA80_10145 (pseudo)	AOA81_00600	-	-	MMINT_19120	WP_019176237.1	-
Other enzymes of interest											
<i>adh</i>	AR505_0483	ISO4G1_0362	ISO4G11_1480	TALC_00541	-	-	AUQ37_07725	MMALV_04880	-	-	-
<i>ldhA</i>	-	-	-	TALC_01217	AOA80_03925	AOA81_01825	AUQ37_02340	MMALV_05640	-	-	-
<i>ald</i>	AR505_1599	ISO4G1_0190	ISO4G11_0117	TALC_00254	AOA80_03010	AOA81_04480	-	-	-	-	-
<i>deoA</i>	AR505_1641	ISO4G1_0145	ISO4G11_0103	TALC_00201	AOA80_01145	AOA81_00815 (pseudo)	AUQ37_00755 (pseudo)	MMALV_01880	MMINT_17690	WP_019176103.1	Mpt1_c12740
	AR505_0705	ISO4G1_0953	ISO4G11_0160								
<i>rbcL</i>	AR505_1642	ISO4G1_0144	ISO4G11_0161	TALC_00200	AOA80_01150 (pseudo)	AOA81_00820	AUQ37_00750	MMALV_01870	MMINT_17700	WP_019176104.1	Mpt1_c12750
<i>e2b2</i>	AR505_1643	ISO4G1_0143	ISO4G11_0162	TALC_00199	AOA80_01155	AOA81_00825	AUQ37_00745 (pseudo)	MMALV_01860	MMINT_17710	WP_019176105.1	Mpt1_c12760

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Phosphoglucumutase (*pgm*), phosphoglucose isomerase (*pgi*), triose-phosphate isomerase (*TpiA*), fructose-1,6-bisphosphatase (*fbp*), phosphofructokinase (*pfkB*), fructose-bisphosphate aldolase (*fba*), glyceraldehyde-3-phosphate dehydrogenase (*gap2*), phosphoglycerate kinase (*pgk*), phosphoglycerate mutase (*apgM*), phosphopyruvate hydratase (*eno*), phosphoenolpyruvate synthase (*ppsA*), pyruvate:ferredoxin oxidoreductase (*porABCD*), acetyl CoA synthetase (*acs/acdA*), phosphoenolpyruvate carboxylase (*ppcA*), aconitate hydratase (*acnA*), isocitrate dehydrogenase (*idh*), 2-oxoglutarate synthase (*korABDG*), succinyl-CoA synthetase (*sucCD*), succinate:quinone oxidoreductase (*sdhABCD*), thiol:fumarate reductase (*tfrAB*), NADPH-FMN oxidoreductase (*nfrAB*), fumarate hydratase (*fumAB*),

NAD-dependent malic enzyme (*maeI*), adenylosuccinate synthetase (*purA*), adenylosuccinate lyase (*purB*), phosphoserine aminotransferase/aspartate aminotransferase (*serC/aat*), transketolase (*tktA*), ribulose-phosphate 3-epimerase (*rpe*), ribose-5-phosphate isomerase (*rpiA*), ribose-phosphate diphosphokinase (*prs*), NADP-dependent formate dehydrogenase (*fdhAB*), formate-tetrahydrofolate ligase (*fhs*), NADP-dependent methylene tetrahydrofolate dehydrogenase (*folD*), 5,10-methylenetetrahydrofolate reductase (*metVF*), methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase (*acsE*), carbon monoxide dehydrogenase (*cdhABCDE*), acetyl-CoA decarbonylase (*acsAE*), alcohol dehydrogenase (*adh*), lactate dehydrogenase (*ldhA*), aldehyde dehydrogenase (*ald*), AMP phosphorylase (*deoA*), ribose-1,5-bisphosphate isomerase (*e2b2*), ribulose 1,5-bisphosphate carboxylase (*rbcL*).

Table A.4.17 Genes involved in amino acid metabolism in Methanomassiliicoccales

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Glutamate											
<i>gdhA</i>	AR505_0145	ISO4G1_0129	ISO4G11_1197	TALC_01422	AOA80_04200 (pseudo)	-	AUQ37_02735	MMALV_06300	-	WP_026068644.1	-
Glutamine											
<i>glnA</i>	AR505_0091	ISO4G1_1386	ISO4G11_1073	TALC_01482	AOA80_00710	AOA81_00865	AUQ37_07285	MMALV_16060	MMINT_03850	WP_026068923.1	Mpt1_c00250
<i>amtB</i>	AR505_0205	ISO4G1_1253	ISO4G11_1600	TALC_00998	AOA80_01865	-	AUQ37_05600	MMALV_14360	MMINT_08960	WP_019178560.1	Mpt1_c05750
Arginine											
<i>argJ</i>	AR505_0674	ISO4G1_1106	ISO4G11_0428	TALC_00630	AOA80_03500 (pseudo)	AOA81_05420	AUQ37_02785	MMALV_06150	MMINT_07650	WP_019177288.1	Mpt1_c03210
<i>argB</i>	AR505_0675	ISO4G1_1105	ISO4G11_0429	TALC_00631	AOA80_03505	AOA81_05415 (pseudo)	AUQ37_02780	MMALV_06160	MMINT_07660	-	Mpt1_c03220
<i>argC</i>	AR505_0673	ISO4G1_1107	ISO4G11_0427	TALC_00629	AOA80_03495	AOA81_05425	AUQ37_02790	MMALV_06140	MMINT_07640	WP_019177289.1	Mpt1_c03200
<i>arg5,6</i>	-	-	-	-	-	-	-	-	-	-	-
<i>argD</i>	AR505_0676	ISO4G1_1104	ISO4G11_0430	TALC_00632	AOA80_03510	AOA81_05410	AUQ37_02775	MMALV_06170	MMINT_07670	WP_019177286.1	Mpt1_c03230
<i>argF</i>	AR505_1401	ISO4G1_0613	ISO4G11_1688	TALC_00466	AOA80_02905	AOA81_01080	AUQ37_02810	MMALV_03950	MMINT_15810	WP_019176758.1	Mpt1_c01930
<i>argG</i>	AR505_0672	ISO4G1_1108	ISO4G11_0423	TALC_00628	AOA80_03490	AOA81_05430	AUQ37_02795	MMALV_06120	MMINT_07630	WP_019177290.1	Mpt1_c03190
<i>argH</i>	AR505_0671	ISO4G1_1109	ISO4G11_0422	TALC_00627	AOA80_03485	AOA81_05435	AUQ37_02800 (pseudo)	MMALV_06110	MMINT_07620	WP_019177291.1	Mpt1_c03180
Proline											
<i>proA</i>	AR505_0108	ISO4G1_1376	ISO4G11_0919	TALC_01468	AOA80_06140	AOA81_00650	AUQ37_04015	MMALV_15640	MMINT_03600	WP_019177916.1	Mpt1_c10170
<i>proB</i>	AR505_0109	ISO4G1_1375	ISO4G11_0920	TALC_01467	AOA80_06145	AOA81_00645	AUQ37_04010	MMALV_15630	MMINT_03590	WP_019177915.1	Mpt1_c10160
<i>proC</i>	AR505_1634	ISO4G1_0153	ISO4G11_0153	TALC_00208	AOA80_02810	AOA81_00765	AUQ37_00790	MMALV_01950	MMINT_01980	WP_019176184.1	Mpt1_c12670
<i>putP</i>	AR505_0287	ISO4G1_0569	ISO4G11_1006	TALC_01357	AOA80_01965	AOA81_06055	AUQ37_06365	MMALV_13380	MMINT_01840	WP_019178133.1	Mpt1_c04660
Asparagine/ alanine											
				TALC_00175				MMALV_01630	MMINT_01710	WP_019178142.1	Mpt1_c01680
<i>ast</i>	AR505_1666	ISO4G1_0120	ISO4G11_1529	TALC_00438	AOA80_03280	AOA81_01815	AUQ37_02955	MMALV_03620	MMINT_07580	WP_019177332.1	Mpt1_c13100
<i>aat</i>	AR505_1199	ISO4G1_0877	ISO4G11_0227	TALC_00711	AOA80_10820	AOA81_05120	AUQ37_06995	MMALV_10320	MMINT_07890	WP_026068856.1	Mpt1_c06640
	AR505_0736	ISO4G1_0511	ISO4G11_1076	TALC_00744		AOA81_05605		MMALV_03160	MMINT_07720		Mpt1_c03990
<i>asnB</i>					-	AOA81_00025	AUQ37_00495			WP_019177232.1	
	AR505_1303	ISO4G1_0590	ISO4G11_1341	TALC_01117				MMALV_11530	MMINT_08200		Mpt1_c03330
Histidine											
<i>hisA</i>	AR505_0497	ISO4G1_0667	ISO4G11_1464	TALC_00552	AOA80_07885	AOA81_03155	AUQ37_07665	MMALV_05000	MMINT_14550	WP_026068714.1	Mpt1_c02390
<i>hisB</i>	AR505_0488	ISO4G1_1137	ISO4G11_1476	TALC_00545	AOA80_07890	AOA81_03145	AUQ37_07705	MMALV_04920	MMINT_14560	WP_019176491.1	Mpt1_c02380
								MMALV_04980			
<i>hisC</i>	AR505_0495	ISO4G1_0665	ISO4G11_1466	TALC_00550	AOA80_07875	AOA81_03165	AUQ37_07675		MMINT_14530	WP_019176494.1	Mpt1_c02410
								MMALV_00840			
<i>hisF</i>	AR505_0487	ISO4G1_1136	ISO4G11_1477	TALC_00544	AOA80_07895 (pseudo)	AOA81_03140	AUQ37_07710	MMALV_04910	MMINT_14570	WP_026068713.1	Mpt1_c02370
<i>hisG</i>	AR505_0494	ISO4G1_0664	ISO4G11_1467	TALC_00549	AOA80_07870	AOA81_03170	AUQ37_07685	MMALV_04970	MMINT_14520	WP_019176495.1	Mpt1_c02420
<i>hisH</i>	AR505_0496	ISO4G1_0666	ISO4G11_1465	TALC_00551	AOA80_07880	AOA81_03160	AUQ37_07670	MMALV_04990	MMINT_14540	WP_026068715.1	Mpt1_c02400
<i>hisI</i>	AR505_0486	ISO4G1_1135	ISO4G11_1478	TALC_00543	AOA80_07900	AOA81_03135	AUQ37_07715	MMALV_04900	MMINT_14580	WP_019176489.1	Mpt1_c02360
<i>hisJ</i>	-	-	ISO4G11_0196	-	-	-	-	-	-	-	-

<i>hisD</i>	AR505_1073	ISO4G1_0781	ISO4G11_1475	TALC_00752	AOA80_02095	AOA81_00230	AUQ37_05105 (pseudo)	MMALV_07480	MMINT_11150	WP_019176957.1	Mpt1_c02110
Serine											
<i>serA</i>	AR505_1664	ISO4G1_0122	ISO4G11_1531	TALC_00177	AOA80_03925	AOA81_01825 AOA81_03570	AUQ37_00630	MMALV_01650	MMINT_01880	-	Mpt1_c13080
<i>serB</i>	AR505_0073	ISO4G1_1420	ISO4G11_0706	TALC_01501	AOA80_11345	, AOA81_05830	AUQ37_01485	MMALV_16250	MMINT_01210	-	Mpt1_c13640
<i>serC</i>	AR505_1665	ISO4G1_0121	ISO4G11_1530	TALC_00176	AOA80_03930	AOA81_01820	AUQ37_00625 (pseudo)	MMALV_01640	MMINT_01870	WP_026069026.1	Mpt1_c13090
Cysteine											
<i>cysE</i>	AR505_1192	ISO4G1_0954	ISO4G11_0222	TALC_00713	AOA80_09095	AOA81_06490	AUQ37_06985	MMALV_10360	MMINT_08710	WP_026068840.1	Mpt1_c04500
<i>cysK</i>	AR505_0800	ISO4G1_0383	ISO4G11_0186	TALC_01462	AOA80_01530	AOA81_06485	AUQ37_08265	MMALV_06500	MMINT_11280	WP_019178685.1	Mpt1_c03020
<i>cysM</i>	AR505_0695	ISO4G1_1045	-	TALC_00651	AOA80_01540	-	-	-	-	WP_019177668.1	-
<i>cys4</i>	-	-	-	-	-	-	-	MMALV_09490	-	-	-
<i>cys3</i>	-	-	-	-	-	-	-	MMALV_09480	-	-	-
<i>sepS</i>	-	-	-	-	-	-	-	-	-	-	-
<i>pseS</i>	-	-	-	-	-	-	-	-	-	-	-
Glycine											
<i>glyA</i>	-	ISO4G1_0934	ISO4G11_0236	TALC_00697	AOA80_10770	AOA81_05090	-	MMALV_10170	MMINT_07960	WP_019177251.1	Mpt1_c07180
Chrorismate											
<i>aroA</i>	AR505_0512	ISO4G1_1401	ISO4G11_1448	TALC_00564	AOA80_03190	AOA81_06975	AUQ37_06645	MMALV_05140	MMINT_14440	WP_019176506.1	Mpt1_c09820
	AR505_0508	ISO4G1_1397	ISO4G11_1452								Mpt1_c09850
<i>fbA</i>	, AR505_0932	, ISO4G1_1494	, ISO4G11_0601	TALC_00560	AOA80_10200	AOA81_06970	AUQ37_06665 (pseudo)	MMALV_05100	MMINT_14400	WP_019176511.1	, Mpt1_c10430
<i>aroB</i>	AR505_0509	ISO4G1_1398	ISO4G11_1451	TALC_00561	AOA80_10205	AOA81_01375	AUQ37_06660	MMALV_05110	MMINT_14410	WP_019176509.1	Mpt1_c10440
<i>aroF</i>	AR505_1449	ISO4G1_1402	ISO4G11_0665	TALC_00394	AOA80_00970	AOA81_06965	AUQ37_03115 (pseudo)	MMALV_03310	MMINT_14450	WP_019176505.1	Mpt1_c09810
<i>aroE</i>	AR505_0510	ISO4G1_1399	ISO4G11_1450	TALC_00562	AOA80_02175	AOA81_06955	AUQ37_06655	MMALV_05120	MMINT_14420	-	Mpt1_c09840
<i>aroL</i>	-	-	-	-	-	-	-	-	-	-	-
<i>aroK</i>	AR505_0511	ISO4G1_1400	ISO4G11_1449	TALC_00563	AOA80_02170	AOA81_06960	AUQ37_06650	MMALV_05130	MMINT_14430	WP_019176507.1	Mpt1_c09830
Phenylalanine											
<i>pheA</i>	AR505_0515	ISO4G1_1403	ISO4G11_0281	TALC_00571	AOA80_03190	AOA81_01370	AUQ37_06640	MMALV_05150	MMINT_14600	WP_026068711.1	Mpt1_c07490
Tyrosine											
<i>tyrA</i>	AR505_1450	ISO4G1_1396	ISO4G11_0666	TALC_00393	AOA80_00975	AOA81_06980	AUQ37_03600	MMALV_03300	MMINT_14460	-	Mpt1_c10450
<i>aro8</i>	AR505_1429	ISO4G1_1204	ISO4G11_1173	TALC_00438			AUQ37_02955			-	Mpt1_c01680
Tryptophan											
<i>trpA</i>	AR505_1164	-	ISO4G11_1072	TALC_01440	-	-	AUQ37_08270	MMALV_09260	-	WP_019176707.1	Mpt1_c00530
<i>trpB</i>	AR505_1163	-	ISO4G11_1071	TALC_01439	AOA80_07575 (pseudo)	-	AUQ37_08265	MMALV_09270	MMINT_06500	WP_019176708.1	Mpt1_c00520
<i>trpC</i> (bifunc tional)	-	-	-	-	-	-	-	-	-	WP_019176709.1	-
<i>trpC</i>	AR505_1161	-	ISO4G11_1069	TALC_01437	-	-	AUQ37_08255	MMALV_09290	-	-	Mpt1_c00500
<i>trpF</i>	AR505_1162	-	ISO4G11_1070	TALC_01438	-	-	AUQ37_08260	MMALV_09280	-	-	Mpt1_c00510
	AR505_1160										
<i>trpD</i>	, AR505_0997	-	ISO4G11_1068	TALC_01436	AOA80_05365	-	AUQ37_08250	MMALV_09300	MMINT_02540	WP_019176712.1	Mpt1_c00490
<i>trpE</i>	AR505_1158	-	ISO4G11_1066	TALC_01434	-	-	AUQ37_08240	MMALV_09320	-	WP_026068755.1	Mpt1_c00470

<i>trpG</i>	AR505_1159	-	ISO4G11_1067	TALC_01435	-	-	AUQ37_08245	MMALV_09310	-	WP_019177873.1	Mpt1_c00480
Lysine											
<i>lysC</i>	AR505_0160	ISO4G1_0207	ISO4G11_1170	TALC_01399	AOA80_06245	AOA81_02200	AUQ37_07580 (pseudo)	MMALV_15030	MMINT_02370	WP_019177873.1	Mpt1_c00850
<i>metL</i>	AR505_0293	-	-	-	AOA80_01575 (pseudo)	AOA81_04425	AUQ37_06415	-	-	WP_019176487.1	
<i>asd</i>	AR505_0491	ISO4G1_0661	ISO4G11_1473	TALC_00548	AOA80_00980	AOA81_01390	AUQ37_07690 (pseudo)	MMALV_04960	MMINT_14470	WP_019176503.1	Mpt1_c02440
<i>dapA</i>	AR505_0161	ISO4G1_0208	ISO4G11_1169	TALC_01398	AOA80_06235	AOA81_02210	AUQ37_07570 (pseudo)	MMALV_15000	MMINT_02390	WP_019177871.1	Mpt1_c00830
<i>dapB</i>	AR505_0728	ISO4G1_0796	ISO4G11_0081	TALC_01007	AOA80_06240 (pseudo)	AOA81_04815	AUQ37_07575	MMALV_08600	MMINT_02380	WP_019177872.1	Mpt1_c00840
<i>dapL</i>	AR505_0157	ISO4G1_0204	ISO4G11_1173	TALC_01402	AOA80_06260	AOA81_02185 (pseudo)	AUQ37_07595	MMALV_15060	MMINT_02340	WP_019177876.1	Mpt1_c00880
<i>dapF</i>	AR505_0158	ISO4G1_0205	ISO4G11_1172	TALC_01401	AOA80_06255	AOA81_02190	AUQ37_07590	MMALV_15050	MMINT_02350	WP_019177875.1	Mpt1_c00870
<i>lysA</i>	AR505_0159	ISO4G1_0206	ISO4G11_1171	TALC_01400	AOA80_06250	AOA81_02195	AUQ37_07585	MMALV_15040	MMINT_02360	WP_019177874.1	Mpt1_c00860
Pyrrolysine											
<i>pylB</i>	AR505_1324	ISO4G1_0658	ISO4G11_0015	TALC_00497	AOA80_07705	-	AUQ37_08740	MMALV_04280	MMINT_08920	WP_019178530.1	Mpt1_c05690
<i>pylC</i>	AR505_1323	ISO4G1_0659	ISO4G11_0016	TALC_01090	AOA80_07700	-	AUQ37_06025 (pseudo)	MMALV_11270	MMINT_08910	WP_019176309.1 WP_019178531.1	Mpt1_c03070
<i>pylD</i>	AR505_1322	ISO4G1_0660	ISO4G11_0017	TALC_01089	AOA80_07695	-	AUQ37_06030	MMALV_11260	MMINT_08900	WP_026069110.1 WP_019178556.1	Mpt1_c05680
Methionine											
<i>metA</i>	AR505_0694	ISO4G1_0381	ISO4G11_0185	TALC_00650			AUQ37_02535	MMALV_06490	MMINT_11300	-	Mpt1_c03450
<i>metX</i>					AOA80_01535 (pseudo)	-	-	-	-	WP_026069128.1	-
<i>metZ</i>	-	-	-	-		-	-	-	-	-	-
<i>oah</i>	AR505_0738 , AR505_0799	ISO4G1_0382	ISO4G11_0049	TALC_00626 , TALC_01463	AOA80_01530	-	AUQ37_04355	MMALV_06100	MMINT_11290	WP_019178666.1	Mpt1_c03170
<i>metB</i>	-	-	-	-	AOA80_01430	-	-	MMALV_09480	-	WP_026069129.1 WP_019178065.1	-
<i>mdeA</i>	-	-	-	-	-	-	-	MMALV_09500	-	-	-
<i>metC</i>	-	-	-	-		-	-	-	-	WP_019178701.1	-
<i>metH</i>	-	-	-	-	AOA80_05425 , AOA80_05440	AOA81_01065	-	MMALV_04220	-	-	-
<i>metE</i>	-	-	-	-		-	-	-	-	-	-
<i>mmuM</i>	-	-	-	-	-	-	-	-	-	-	-
SAM cycle											
<i>metK</i>	AR505_0579 AR505_0327	-	-	-	AOA80_03765		-	-	MMINT_07810	WP_019177266.1	-
<i>dcm</i>	, AR505_0339	ISO4G1_0395	ISO4G11_1725	-	-	, AOA81_04845	AUQ37_04255	-	MMINT_10170	-	Mpt1_c08470

<i>ahcy</i>	AR505_0340 AR505_0547 AR505_1788	ISO4G1_0041	ISO4G11_0858	TALC_00076	AOA80_07050	AOA81_02745 (pseudo)	AUQ37_08195	MMALV_00570	MMINT_02630	WP_026069069.1	Mpt1_c11910
Threonine											
<i>thrB</i>	AR505_0610	ISO4G1_0580	ISO4G11_0957	TALC_00598	AOA80_11020	AOA81_06850	AUQ37_04275	MMALV_05660	MMINT_15310	WP_019176554.1	Mpt1_c02830
<i>thrC</i>	AR505_0611	ISO4G1_0581	ISO4G11_0958	TALC_00599	AOA80_11015	AOA81_06845	AUQ37_04270	MMALV_05670	MMINT_15300	WP_019176555.1	Mpt1_c02820
Branched chain leucine, valine, isoleucine											
	AR505_0152										
<i>ilvB</i>	AR505_0153	-	ISO4G11_1180	TALC_01407			AUQ37_01135	MMALV_15130	MMINT_12080		
			ISO4G11_1182	TALC_01409	AOA80_06290	AOA81_02165	AUQ37_09130	MMALV_15170	MMINT_02270	WP_026068987.1	Mpt1_c00920
<i>ilvN</i>	AR505_0542 AR505_1768	-	ISO4G11_0876	TALC_00065		AOA81_01530	AUQ37_08115	MMALV_00740	MMINT_12090	-	Mpt1_c11510
<i>ilvC</i>	AR505_0150	ISO4G1_1327	ISO4G11_1183	TALC_01411	AOA80_06300 (pseudo)	AOA81_02160 (pseudo)	AUQ37_01120	MMALV_15180	MMINT_02280	WP_019177885.1	Mpt1_c00940
<i>ilvD</i>	AR505_1462	-	ISO4G11_0667	TALC_00391	AOA80_02245	AOA81_07005	AUQ37_03125 (pseudo)	MMALV_03290	MMINT_14670	WP_019177408.1	Mpt1_c00760
<i>ilvE</i>	AR505_1767	ISO4G1_1502	ISO4G11_0877	TALC_00066	AOA80_05900	AOA81_01535	AUQ37_08110	MMALV_00750	MMINT_00560	WP_019176466.1	Mpt1_c11520
<i>leuA</i>	AR505_0631	ISO4G1_0375	ISO4G11_0979	TALC_00615	AOA80_09055	AOA81_04500	AUQ37_04460	MMALV_05860	MMINT_13330	WP_026068862.1 WP_019178159.1	Mpt1_c02690
<i>leuC</i>	AR505_0632	-	-	-	AOA80_04060	AOA81_05500	AUQ37_04625	MMALV_05870	MMINT_13340		Mpt1_c02680
										WP_019177309.1 WP_019178158.1	
<i>leuD</i>	AR505_0633	-	-	-	AOA80_04055	AOA81_05495	AUQ37_04450	MMALV_05880	MMINT_13350	WP_019177308.1	Mpt1_c02670
<i>leuB</i>	AR505_0634	ISO4G1_0567 ISO4G1_1012	ISO4G11_0277	TALC_00573 TALC_00501	AOA80_03430 AOA80_11525 (pseudo)	AOA81_03260 AOA81_05490	AUQ37_04445	MMALV_05890	MMINT_13360	WP_019177307.1	Mpt1_c02660 Mpt1_c03670
<i>cimA</i>	-	-	-	-	AOA80_03415	AOA81_03245	AUQ37_07620 AUQ37_06715	-	-	WP_026068862.1	Mpt1_c02550
<i>sbatI</i>	AR505_0285	ISO4G1_0485	ISO4G11_0755	-	-	-	-	-	-	-	-
Agmatine											
<i>speA</i>	AR505_0268	ISO4G1_0346	ISO4G11_0762	TALC_01282	AOA80_00635	AOA81_04280	AUQ37_05920	MMALV_13720	MMINT_03300	WP_019177718.1	Mpt1_c08900
Methionine salvage/spermidine biosynthesis											
<i>speD</i>	-	-	ISO4G11_0389	TALC_00987	AOA80_11220	AOA81_06205	AUQ37_02310	-	-	WP_026068816.1	Mpt1_c05830
<i>speE</i>	-	-	-	-							
				TALC_00237	AOA80_09640	AOA81_01895	AUQ37_00965	MMALV_02230		WP_019178102.1	-
<i>potA</i>	-	-	-						MMINT_10520		-
				TALC_00239	AOA80_09635	AOA81_01890	AUQ37_00960	MMALV_02220		WP_019178103.1	-
<i>potB</i>	-	-	-	TALC_00236	-	AOA81_01885	AUQ37_00955	MMALV_02210	MMINT_10530	-	-
<i>potC</i>	-	-	-	-	-	-	-	-	-	-	-
<i>potD</i>	-	-	-	-	-	-	-	-	-	-	-
Methionine salvage											
<i>mtmN</i>	AR505_1118	ISO4G1_1493	ISO4G11_0050	TALC_00995	-	-	-	-	-	-	-

<i>mtnK</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnA</i>	-	ISO4G1_0186	ISO4G11_0121	TALC_00247	AOA80_09670	AOA81_01930	-	MMALV_02310	-	-	Mpt1_c11230
<i>mtnB</i>	-	ISO4G1_0185	ISO4G11_0122	TALC_00246	AOA80_09665	AOA81_01925	AUQ37_07845	MMALV_02300	-	-	-
<i>mtnC</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnW</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnX</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnE</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnP</i>	AR505_0481	ISO4G1_1133	ISO4G11_1482	TALC_00535	AOA80_07930	AOA81_03125	AUQ37_07735	MMALV_04860	MMINT_14620	-	Mpt1_c02330
Aryl pyruvates salvage											
<i>iorA</i>	AR505_0999	ISO4G1_0837	ISO4G11_0640	TALC_00960	AOA80_06550	AOA81_06165	-	MMALV_09390	MMINT_12480	WP_019176899.1	Mpt1_c05230
<i>iorB</i>	AR505_0998	ISO4G1_0836	ISO4G11_0639	TALC_00961	AOA80_06545	AOA81_06160	-	MMALV_09380	MMINT_12490	WP_019176900.1	Mpt1_c05240
Amino acid permease											
<i>Amino acid permease</i>	AR505_0830	ISO4G1_0565	ISO4G11_1511	TALC_01421	-	-	AUQ37_07635	MMALV_06350	MMINT_03580	WP_049796369.1	-

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Glutamate dehydrogenase (*gdhA*), glutamine synthetase (*glnA*), ammonium transporter (*atmB*), ornithine acetyltransferase (*argJ*), acetylglutamate kinase (*argB*), *N*-acetylglutamylphosphate reductase (*argC*), acetylglutamate kinase/*N*-acetyl- γ -glutamyl-phosphate reductase (*arg5,6*), acetylornithine aminotransferase (*argD*), ornithine carbamoyltransferase (*argF*), argininosuccinate synthase (*argG*), argininosuccinase (*argH*), glutamate-5-semialdehyde dehydrogenase (*proA*), glutamate 5-kinase (*proB*), pyrroline-5-carboxylate reductase (*proC*), proline:Na⁺ symporter (*putP*), aspartate amino transferase (*ast*), alanine aminotransferase (*aat*), asparagine synthase (*asnB*), [*N*-(5-phosphoribosyl) formimino]-5-aminoimidazole-4-carboxamide ribonucleotide isomerase (*hisA*), IGP dehydratase (*hisB*), histidinol-phosphate aminotransferase (*hisC*), IGP synthase cycloligase subunit (*hisF*), ATP phosphoribosyl transferase (*hisG*), IGP synthase glutamine amidotransferase subunit (*hisH*), phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase (*hisI*), histidine-binding periplasmic protein precursor (*hisJ*), histidinal dehydrogenase (*hisD*), phosphoglycerate dehydrogenase (*serA*), phosphoserine phosphatase (*serB*), phosphoserine aminotransferase (*serC*), serine acetyltransferase (*cysE*), cysteine synthase subunit A (*cysK*), *O*-acetylserine sulfhydrylase (*cysM*), cystathionine β -synthase (*cys4*), cystathionine γ -lyase (*cys3*), *O*-phosphoseryl-tRNA ligase (*sepS*), Sep-tRNA:Cys-tRNA synthase (*pscS*), serine hydroxymethyltransferase (*glyA*), 3-phosphoshikimate-1-carboxyvinyltransferase (*aroA*), fructose 1,6-bisphosphate aldolase (*fba*), dehydroquinase synthase (*aroB*), chorismate synthase (*aroF/aroC*), shikimate dehydrogenase (*aroE*), shikimate kinase (*aroL/aroK*), prephenate dehydratase (*pheA*), prephenate dehydrogenase (*tyrA*), aromatic amino acid aminotransferase (*aro8*), tryptophan synthase (*trpAB*), indole-3-glycerol phosphate synthase (*trpC*), phosphoribosyl anthranilate isomerase (*trpF*), anthranilate phosphoribosyltransferase (*trpD*), anthranilate synthase (*trpEG*), aspartate kinase (*lysC*), bifunctional aspartate kianse/homoserine dehydrogenase (*metL*), dihydrodipicolinate synthase (*dapA*), 4-hydroxy-tetrahydrodipicolinate reductase (*dapB*), L,L-diaminopimelate aminotransferase (*dapL*), diaminopimelate epimerase (*dapF*), diaminopimelate decarboxylase (*lysA*), methylornithine synthase (*pylB*), (2*R*,3*R*)-3-methylornithyl-*N*⁶-lysine synthase (*pylC*), pyrrolysine synthase (*pylD*), homoserine *O*-succinyltransferase (*metA*), homoserine *O*-acetyltransferase (*metX*), *O*-succinyl-L-homoserine sulfhydrylase (*metZ*), *O*-acetylhomoserine aminocarboxypropyltransferase (*oah*), *O*-succinylhomoserine(thiol)-lyase/*O*-succinylhomoserine lyase (*metB*), methionine γ -lyase (*mdeA*), cystathionine β -lyase (*metC*), cobalamin-independent methionine synthase (*metE*), methionine synthase (*methH*), homocysteine *S*-methyltransferase (*mmuM*), *S*-adenosylmethionine synthetase (*metK*), DNA-cytosine methyltransferase (*dcm*), *S*-adenosyl-L-homocysteinase (*ahcY*), homoserine kinase (*thrB*), threonine synthase (*thrC*), acetolactate synthase large subunit (*ilvB*), acetolactate synthase small subunit (*ilvN*), 2,3-dihydroxy-isovalerate:NADP⁺ oxidoreductase (*ilvC*), dihydroxy-isovalerate dehydratase (*ilvD*), branched-chain amino acid aminotransferase (*ilvE*), 2-isopropylmalate synthase (*leuA*), isopropylmalate dehydratase (*leuCD*), 3-isopropylmalate dehydrogenase (*leuB*), *R*-citramalate synthase (*cimA*), branched-chain amino acid transporter (*sbat1*), arginine decarboxylase (*speA*), agmatinase (*speB*), adenosylmethionine decarboxylase (*speD*), spermidine synthase (*speE*), putrescine/spermidine ABC transporter (*potABCD*), 5'-methylthioadenosine/*S*-adenosylhomocysteine nucleosidease (*mtnN*), 5'-methylthioribose kinase (*mtnK*), 5'-methylthioribose 1-phosphate isomerase (*mtnA*), methylthioribulose-1-phosphate dehydratase (*mtnB*), acireductone synthase (*mtnC*), 2,3-diketo-5-methylthiopentyl-1-

phosphate enolase (*mtnW*), 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase (*mtnX*), 2-oxo-4-methylthiobutanoate-glutamine aminotransferase (*mtnE*), S-methyl-5'-thioadenosine phosphorylase (*mtnP*), indolepyruvate oxidoreductase (*iorAB*).

Table A.4.18 Genes involved in nucleotide biosynthesis in Methanomassiliicoccales

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Purine biosynthesis											
<i>purB</i>	AR505_0742	ISO4G1_0911	ISO4G11_1050	TALC_00921	AOA80_11375 (pseudo)	AOA81_05825	AUQ37_01480	MMALV_07730	MMINT_10940	WP_019177003.1	Mpt1_c04990
<i>purF</i>	AR505_0284	ISO4G1_0359	ISO4G11_0781	TALC_01266	AOA80_00720	AOA81_04370	AUQ37_06300 (pseudo)	MMALV_13560	MMINT_03370	WP_019177701.1	Mpt1_c08300
<i>purP</i>	AR505_0257	ISO4G1_0335	ISO4G11_1551	TALC_00174	AOA80_00545	AOA81_01810	AUQ37_05855	MMALV_01620	MMINT_02910	WP_019178145.1	Mpt1_c09180
domain											
protein	AR505_1667	ISO4G1_0119		TALC_01295	AOA81_04225	AOA81_04225	MMALV_13860	MMINT_01670	WP_019177740.1	Mpt1_c13110	
<i>ade2</i>	AR505_1804	ISO4G1_1515	ISO4G11_0841	TALC_00033	AOA80_05525	AOA81_02650	AUQ37_01825	MMALV_00360	MMINT_02590	WP_026069067.1	Mpt1_c12090
<i>purD</i>	AR505_0066	ISO4G1_1432	ISO4G11_1038	TALC_01510	AOA80_09550	AOA81_03530	AUQ37_04805 (pseudo)	MMALV_16330	MMINT_19510	WP_019178274.1	Mpt1_c13740
<i>purH</i>	AR505_1656	ISO4G1_0130	ISO4G11_0175	TALC_00185	AOA80_04270	AOA81_03735	AUQ37_00665 (pseudo)	MMALV_01730	MMINT_00450	WP_019176210.1	Mpt1_c12920
<i>purC</i>	AR505_0622	ISO4G1_0671	ISO4G11_0967	TALC_00471	AOA80_05080	AOA81_05535 (pseudo)	AUQ37_04510	MMALV_05760	MMINT_15090	WP_019176588.1	Mpt1_c11990
<i>purM</i>	AR505_0037	ISO4G1_0078	ISO4G11_1009	TALC_01540	AOA80_10465	AOA81_02340	AUQ37_02170	MMALV_16640	MMINT_19240	WP_026069089.1	Mpt1_c14130
<i>purQ</i>	AR505_1680	ISO4G1_0105	ISO4G11_0941	TALC_00152	AOA80_05685	AOA81_01740	AUQ37_02295	MMALV_01470	MMINT_18470	WP_019178718.1	Mpt1_c13280
<i>purL</i>	AR505_1681	ISO4G1_0104	ISO4G11_0940	TALC_00151	AOA80_05670 (pseudo)	AOA81_01735	AUQ37_02290	MMALV_01460	MMINT_18480	WP_019178719.1	Mpt1_c13290
<i>purS</i>	AR505_1682	ISO4G1_0103	ISO4G11_0939	TALC_00150	AOA80_05675	AOA81_01730	AUQ37_02285	MMALV_01450	MMINT_18490	WP_019178720.1	Mpt1_c13310
	AR505_0084	ISO4G1_1391									Mpt1_c13300
<i>apt</i>	AR505_0301	ISO4G1_1320	ISO4G11_0744	TALC_01490	-	AOA81_03635	AUQ37_07350	MMALV_16130	MMINT_04670	-	Mpt1_c00150
	AR505_1496						AUQ37_06900				
<i>purN</i>	AR505_0141	ISO4G1_1335	ISO4G11_1195	TALC_01418	AOA80_10665	AOA81_02135	AUQ37_01070	MMALV_15280	MMINT_03630	WP_019177929.1	Mpt1_c00990
NCAIR											
mutase											
(PurE)-	AR505_1595	ISO4G1_1354	ISO4G11_0112	TALC_00266	AOA80_09320 (pseudo)	AOA81_00205	AUQ37_06110	MMALV_02500	MMINT_10890	WP_026068828.1	Mpt1_c07930
related											
protein											
Purine interconversion											
<i>adk</i>	AR505_0262	ISO4G1_0337	ISO4G11_0754	TALC_01289	AOA80_00570	AOA81_04250	AUQ37_05780	MMALV_13800	MMINT_02950	WP_019177734.1	Mpt1_c09070
<i>purA</i>	AR505_1168	ISO4G1_0684	ISO4G11_0612	TALC_00689	AOA80_09160 (pseudo)	AOA81_05040 (pseudo)	AUQ37_07105 (pseudo)	MMALV_10030	MMINT_12290	WP_019177117.1	Mpt1_c06950
<i>add</i>											
<i>guaB</i>	AR505_1340	ISO4G1_0550	ISO4G11_0525	TALC_01078	AOA80_08965	AOA81_06755	AUQ37_06110	MMALV_10930	MMINT_10450	WP_026068845.1	Mpt1_c06190
Pyrimidine biosynthesis											
<i>pyrB</i>	AR505_0437	ISO4G1_1149	ISO4G11_1349	TALC_01157	AOA80_00335	AOA81_02935	AUQ37_00280 (pseudo)	MMALV_12010	MMINT_05510	WP_026068695.1	Mpt1_c07580
<i>pyrI</i>	AR505_0436	ISO4G1_1150	ISO4G11_1348	TALC_01158	AOA80_00330	AOA81_02930	AUQ37_00275	MMALV_12020	MMINT_05500	WP_019176408.1	Mpt1_c07590

<i>pyrC</i>	AR505_0281	ISO4G1_0357	ISO4G11_0778	TALC_01269	AOA80_00705	AOA81_04355	AUQ37_06285 (pseudo)	MMALV_13600	MMINT_03400	WP_026068955.1	Mpt1_c08340
<i>pyrD</i>	AR505_1029	ISO4G1_1070	ISO4G11_0378	TALC_01017	AOA80_09045	AOA81_06435	AUQ37_02360 (pseudo)	MMALV_07220	MMINT_08570	WP_019177150.1	Mpt1_c05890
<i>pyrK</i>	AR505_1030	ISO4G1_1069	ISO4G11_0377	TALC_01016	AOA80_09050	AOA81_06440	AUQ37_02365	MMALV_07210	MMINT_08580	WP_019177149.1	Mpt1_c05900
<i>pyrE</i>	AR505_1615	ISO4G1_0172	ISO4G11_0135	TALC_00226	AOA80_03860	AOA81_01845	AUQ37_00910 (pseudo)	MMALV_02120	MMINT_01930	WP_019178120.1	Mpt1_c12480
<i>pyrF</i>	AR505_0060 AR505_0500	ISO4G1_1436	ISO4G11_1033	TALC_01515	AOA80_07505	AOA81_03495	AUQ37_04830	MMALV_16380	MMINT_19560	WP_019178279.1	Mpt1_c13790
<i>carB</i>	AR505_0503 AR505_0501	ISO4G1_0839	ISO4G11_1462	TALC_00553	AOA80_11600	AOA81_03230	AUQ37_07660	MMALV_05010	MMINT_06210	WP_019176516.1	Mpt1_c02580
<i>carA</i>	AR505_0504	ISO4G1_0840	ISO4G11_1461	TALC_00554	AOA80_11590	AOA81_03235	AUQ37_07655	MMALV_05020	MMINT_06200	WP_019176517.1	Mpt1_c02570
Pyrimidine interconversion											
<i>pyrH</i>	AR505_0251 AR505_1102	ISO4G1_0330 ISO4G1_1455	ISO4G11_1557	TALC_01301	AOA80_00520	-	AUQ37_05825	MMALV_13920	MMINT_02860	WP_019177745.1	Mpt1_c09230
<i>tmk</i>	AR505_1690	ISO4G1_1086	ISO4G11_0928	TALC_00143	AOA80_05625	AOA81_01685	AUQ37_02245	MMALV_01370	MMINT_18610	WP_026069141.1	Mpt1_c13380
<i>thyX</i>	AR505_0076	ISO4G1_1417	ISO4G11_0708	TALC_01498	AOA80_07340	AOA81_03585 (pseudo)	-	MMALV_16220	MMINT_01230	WP_026069046.1	Mpt1_c00060
<i>trxA</i>	AR505_0047	ISO4G1_0096	ISO4G11_1019	TALC_01529	AOA80_03085	AOA81_03405	AUQ37_04905	MMALV_16520	MMINT_19530	WP_019178276.1	Mpt1_c14010
<i>trxB</i>	AR505_0048 AR505_1346	ISO4G1_0097 ISO4G1_0547	ISO4G11_0538 ISO4G11_1020	TALC_01069 TALC_01528	AOA80_09000 AOA80_03080	AOA81_06725 AOA81_03415 (pseudo)	AUQ37_04900 (pseudo)	MMALV_16510 MMALV_10860	MMINT_17530 MMINT_17540	WP_019178572.1 WP_019178573.1 WP_019177165.1	Mpt1_c14020
<i>dcd</i>	AR505_1287	ISO4G1_1032	ISO4G11_0071	TALC_01127	AOA80_08040	AOA81_03040	AUQ37_00445	MMALV_11680	MMINT_14300	WP_019176464.1	Mpt1_c02190
<i>cmk</i>	-	ISO4G1_0321	-	TALC_01309	AOA80_08760	AOA81_04145	-	MMALV_11680	MMINT_04580	WP_019177505.1	Mpt1_c09370
Others											
<i>guaA</i>	AR505_0706	ISO4G1_1061	ISO4G11_0198	TALC_01003	AOA80_05520	AOA81_02645	AUQ37_01810	-	MMINT_02570	-	-
<i>guaAa</i>	AR505_1803	ISO4G1_1514	ISO4G11_0842	TALC_00034	-	-	-	MMALV_00370	MMINT_02580	WP_019178350.1	Mpt1_c12080
<i>guaAb</i>	AR505_1802	ISO4G1_1513	ISO4G11_0844	TALC_00036	-	-	-	MMALV_00390	MMINT_02560	WP_019178347.1	Mpt1_c12060
<i>ndk</i>	AR505_1756	ISO4G1_1497	ISO4G11_0884	TALC_00115	AOA80_05850	AOA81_01595	AUQ37_03475	MMALV_01070	MMINT_19180	WP_026069122.1	Mpt1_c11420
<i>gmK</i>	-	-	-	-	-	-	-	-	-	-	-
<i>prsA</i>	AR505_1685	ISO4G1_1451	ISO4G11_0932	TALC_00147	AOA80_05650	AOA81_01710	AUQ37_02260	MMALV_01410	MMINT_18540	WP_019178734.1	Mpt1_c13340
<i>rdgB</i>	AR505_0187	ISO4G1_0263	ISO4G11_1618	TALC_01364	AOA80_00245	AOA81_03885	AUQ37_05555	MMALV_14540	MMINT_05400	WP_026068692.1	Mpt1_c00560
<i>udk</i>	-	-	-	-	-	-	-	-	-	-	-
<i>mtnN</i>	AR505_1118	ISO4G1_1493	ISO4G11_0050	TALC_00995	-	-	-	-	-	-	-
<i>nrdJ</i>	AR505_0964	ISO4G1_0875	ISO4G11_0491	TALC_00972	-	-	AUQ37_08310	MMALV_09160	MMINT_04250	-	Mpt1_c05370
<i>comEB</i>	AR505_1827	ISO4G1_0003	ISO4G11_0814	TALC_00003	AOA80_00800	AOA81_02530	AUQ37_01970	MMALV_00040	MMINT_00040	WP_019178383.1	Mpt1_c12350

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Bifunctional enzyme adenosuccinate lyase (*purB*), amidophosphoribosyl transferase (*purF*), 5-formaminoimidazole-4-carboxamide-1- β -D-ribofuranosyl 5'-monophosphate synthetase (*purP*), phosphoribosylaminoimidazole carboxylase (*ade2*), phosphoribosylamineglycine ligase (*purD*), bifunctional AICAR transformylase/IMP cyclohydrolase (*purH*), phosphoribosylaminoimidazole-succinocarboxamide synthase (*purC*), phosphoribosylformylglycinamide cyclo-ligase (*purM*), phosphoribosylformylglycinamide synthetase subunit Q (*purQ*), phosphoribosylformylglycinamide synthetase subunit L (*purL*),

phosphoribosylformylglycinamide synthetase subunit S (*purS*), adenine phosphoribosyltransferase (*apt*), phosphoribosylglycinamide formyltransferase (*purN*), *N*⁵-carboxyaminoimidazole ribonucleotide mutase (*purE*), adenylate kinase (*adk*), adenylosuccinate synthetase (*purA*), adenosine deaminase (*add*), IMP dehydrogenase (*guaB*), aspartate transcarbamylase (*pyrB*), aspartate transcarbamylase regulatory subunit (*pyrI*), dihydroorotase (*pyrC*), dihydroorotate dehydrogenase (*pyrD*), dihydroorotate dehydrogenase electron transfer subunit (*pyrK*), orotate phosphoribosyltransferase (*pyrE*), orotidine-5'-phosphate decarboxylase (*pyrF*), carbamoyl phosphate synthase (*carAB*), UMP kinase (*pyrH*), thymidylate kinase (*tmk*), flavin-dependent thymidylate synthase (*thyX*), thioredoxin (*trxA*), thioredoxin-disulfide reductase (*trxB*), CMP/dCMP deaminase (*dcd*), cytidylate kinase (*cmk*), GMP synthase (*guaA/guaAab*), broad substrate specificity nucleoside diphosphate kinase (*ndk*), guanylate kinase (*gmk*), ribose-phosphate diphosphokinase (*prsA*), dITP/XTP pyrophosphatase (*rdgB*), uridine kinase/cytidine kinase (*udk*), MTA/SAH nucleosidase (*mtnN*), ribonucleoside-diphosphate reductase (*nrdJ*), dCMP deaminase (*comEB*).

Table A.4.19 Genes involved in cell replication in Methanomassiliicoccales

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Chromosome replication											
Replicative DNA helicase Mcm	AR505_0018	ISO4G1_0062	ISO4G11_0794	TALC_01557	AOA80_08280 (pseudo)	AOA81_02425 (pseudo), AOA81_02420 (pseudo)	AUQ37_02065	MMALV_16800	MMINT_09980 , MMINT_19320	-	Mpt1_c14350
Orc1/cdc6 family replication initiation protein	AR505_0001	ISO4G1_0001	ISO4G11_0219	TALC_00001	AOA80_10380	AOA81_02520	AUQ37_01980	MMALV_00010	MMINT_00010	WP_019178385.1	Mpt1_c00010
	AR505_1205	ISO4G1_0957	ISO4G11_0812	TALC_00716	AOA80_00790	AOA81_06510	AUQ37_04975	MMALV_10400	MMINT_18840	WP_019178317.1	Mpt1_c06580
Replication factor A	AR505_1652	ISO4G1_0118	ISO4G11_1527	TALC_00172	AOA80_04020	AOA81_01805	AUQ37_00610	MMALV_01600	MMINT_01650	WP_019178149.1	Mpt1_c13130
Replication factor C large subunit	AR505_0801	ISO4G1_0811	ISO4G11_0324	TALC_00887	AOA80_06710 (pseudo)	AOA81_04590 (pseudo)	AUQ37_01645	MMALV_08210	MMINT_12650	-	Mpt1_c04630
Replication factor C small subunit	AR505_1202	ISO4G1_0958	ISO4G11_0212	TALC_00718	AOA80_10735	AOA81_06520	AUQ37_04990 (pseudo)	MMALV_10430	MMINT_08020	WP_019177244.1	Mpt1_c06560
DNA polymerase family B	AR505_0130	ISO4G1_1347	ISO4G11_1207	TALC_01432	AOA80_09935 (pseudo)	AOA81_02070	AUQ37_07865 (pseudo)	MMALV_15420	MMINT_13800	WP_019177962.1	Mpt1_c01120
DNA polymerase II large subunit	AR505_1438	ISO4G1_1214	ISO4G11_1300	TALC_00430	AOA80_10405 (pseudo)	AOA81_01285 (pseudo), AOA81_01280 (pseudo)	AUQ37_03010 (pseudo)	MMALV_03540	MMINT_14000	WP_026068874.1	Mpt1_c01600
DNA polymerase II small subunit	AR505_1816	ISO4G1_0014	ISO4G11_0825	TALC_00014	AOA80_00850	AOA81_02585	AUQ37_01920 (pseudo)	MMALV_00150	MMINT_17980	WP_026069074.1	Mpt1_c12240
DNA polymerase sliding clamp subunit PCNA family Pcn	AR505_1650	ISO4G1_0135	ISO4G11_0169	TALC_00192	AOA80_06120	AOA81_03770	AUQ37_00710	MMALV_01790	MMINT_17790	WP_019176118.1	Mpt1_c12830
DNA primase DnaG	AR505_1142	ISO4G1_0729	ISO4G11_0623	TALC_00677	AOA80_09290	AOA81_04960	AUQ37_05285	MMALV_09870	MMINT_11650	WP_019177096.1	Mpt1_c07250
DNA primase large subunit PriB	AR505_1782	ISO4G1_0045	ISO4G11_0864	TALC_00054	AOA80_08580 (pseudo)	AOA81_02770	AUQ37_08165 (pseudo)	MMALV_00630	MMINT_19050	-	Mpt1_c11830
				TALC_00052							
DNA primase small subunit PriA	AR505_0009	ISO4G1_0054	ISO4G11_0804	TALC_01569	AOA80_08210	AOA81_02475	AUQ37_02020	MMALV_16880	MMINT_19390	WP_019178400.1	Mpt1_c14490
Ribonuclease HII RnhB	AR505_0209	ISO4G1_0287	ISO4G11_1597	TALC_01342	AOA80_01230 (pseudo)	AOA81_03980	AUQ37_05620	MMALV_14320	MMINT_04050	WP_019177553.1	Mpt1_c09760
Flap structure-specific endonuclease Fen	AR505_0460	ISO4G1_0603	ISO4G11_1503	TALC_00518	AOA80_06840	AOA81_05715 (pseudo)	AUQ37_08015 (pseudo)	MMALV_04650	MMINT_12970	WP_019176843.1	Mpt1_c03850

ATP-dependent DNA ligase	AR505_1277	ISO4G1_1019	ISO4G11_1358	TALC_01146	AOA80_08855	AOA81_02995	AUQ37_00360	MMALV_11800	MMINT_05290	WP_019176428.1	Mpt1_c07340
Genome segregation											
DNA topoisomerase I TopA	AR505_1299	ISO4G1_0592	ISO4G11_0062	TALC_01120	AOA80_10690	AOA81_05625	AUQ37_00475 (pseudo)	MMALV_11600	MMINT_08160	WP_019177234.1	Mpt1_c03970
DNA topoisomerase VI subunit A	AR505_0388	ISO4G1_0433	ISO4G11_0027	TALC_01216	AOA80_01455	AOA81_02825	AUQ37_03805	MMALV_12670	MMINT_14250	WP_019177592.1	Mpt1_c07830
DNA topoisomerase VI subunit B	AR505_0389	ISO4G1_0434	ISO4G11_0026	TALC_01215	AOA80_01450	AOA81_02830	AUQ37_03800 (pseudo)	MMALV_12660	MMINT_14240	WP_019177591.1	Mpt1_c07820
DNA gyrase subunit B GyrB	AR505_0033	ISO4G1_0073	ISO4G11_1004	-	AOA80_10545 (pseudo)	AOA81_02360	AUQ37_02145 (pseudo)	MMALV_16690	MMINT_18860	WP_019178436.1	Mpt1_c14200
DNA gyrase subunit A GyrA	AR505_0034	ISO4G1_0074	ISO4G11_1005	TALC_01544	AOA80_10555	AOA81_02365	AUQ37_02140 (pseudo)	MMALV_16680	MMINT_18850	-	Mpt1_c14190
Chromosome segregation and condensation protein ScpA	AR505_1610	ISO4G1_0176	ISO4G11_0129	TALC_00234	AOA80_09605	AOA81_01870	AUQ37_00940 (pseudo)	MMALV_02180	MMINT_16440	WP_019178109.1	Mpt1_c12420
Chromosome segregation and condensation protein ScpB	AR505_1609	ISO4G1_0177	ISO4G11_0128	TALC_00235	AOA80_09615	AOA81_01875	AUQ37_00950	MMALV_02190	MMINT_16450	WP_026069020.1	Mpt1_c12410
Chromosome segregation protein SMC	AR505_1611	ISO4G1_0175	ISO4G11_0130	TALC_00233	AOA80_09600 (pseudo)	AOA81_01860 , AOA81_01865	AUQ37_00935 (pseudo)	MMALV_02170	MMINT_16430	WP_026069021.1	Mpt1_c12430
Cell division											
Cell division protein FtsZ	AR505_0975	ISO4G1_0835	ISO4G11_0498	TALC_00964	AOA80_01585 , AOA80_01615	AOA81_06145 (pseudo)	AUQ37_08280	MMALV_09250	MMINT_17410 , MMINT_17400	WP_019176461.1	Mpt1_c05250 , Mpt1_c11940
CBS/parB domain-containing protein	AR505_0425	ISO4G1_0447	ISO4G11_0574	TALC_01172	AOA80_04760 (pseudo)	AOA81_01160 (pseudo)	AUQ37_02885	MMALV_12160	MMINT_13100	WP_019177577.1	-
ParA/MinD ATPase-like protein	AR505_1412	ISO4G1_0448	ISO4G11_1276	TALC_00452	AOA80_01375	AOA81_02885	AUQ37_00205	MMALV_03800	MMINT_13900	WP_019176627.1	-
Cell division GTPase	AR505_1792	ISO4G1_0038	ISO4G11_0855	TALC_00046	-	-	-	-	MMINT_11260	-	-
AAA family ATPase CDC48 subfamily protein	AR505_0052	ISO4G1_0020	ISO4G11_0833	TALC_00022	AOA80_05965	AOA81_02690	AUQ37_07920	MMALV_00240	MMINT_17110	WP_019176301.1	Mpt1_c14070
	AR505_1810	ISO4G1_0102	ISO4G11_1024	TALC_01524	AOA80_05565	AOA81_03445		MMALV_00250	MMINT_14960	WP_019178362.1	Mpt1_c12160
								MMALV_16470	MMINT_17620	WP_026069115.1	

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes.

Table A.4.20 Genes involved in cofactor biosynthesis in Methanomassiliicoccales

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Tetrapyrrole											
<i>gltX</i>	AR505_1121	ISO4G1_0936	ISO4G11_0692	TALC_00694	AOA80_09140	AOA81_05065	AUQ37_07065 (pseudo)	MMALV_10120	MMINT_12410	WP_019177132.1	Mpt1_c06970
<i>hemA</i>	AR505_1045	-	-	TALC_01207	AOA80_08475	-	AUQ37_03750	MMALV_12520	MMINT_17310	WP_026068749.1	Mpt1_c07070
<i>hemB</i>	AR505_1044	-	-	TALC_01208	AOA80_08480	-	AUQ37_03755	MMALV_12530	MMINT_17300	WP_026068750.1	Mpt1_c07060
<i>hemC</i>	AR505_1042	-	ISO4G11_0021	TALC_01210	AOA80_08490 (pseudo)	-	AUQ37_03765 (pseudo)	MMALV_12550	MMINT_17280	WP_026068751.1	Mpt1_c07040
<i>hemD</i>	AR505_1040	-	-	TALC_01212	AOA80_08500 (pseudo)	-	AUQ37_03775	MMALV_12570	MMINT_17260	WP_019176693.1	Mpt1_c07020
<i>hemL</i>	AR505_1043	-	-	TALC_01209	AOA80_08485	-	AUQ37_03760	MMALV_12540	MMINT_17290	WP_019176690.1	Mpt1_c07050
<i>corA</i>	AR505_1041	-	-	TALC_01211	AOA80_08495	-	AUQ37_03770	MMALV_12560	MMINT_17270	WP_019176692.1	Mpt1_c07030
<i>cysG</i>	AR505_1046	-	-	TALC_01249	AOA80_08470	AOA81_04390	AUQ37_06460	-	MMINT_17315	WP_019176687.1	Mpt1_c07080
Adenylosylcobalamin											
<i>cbiX</i>	AR505_0597	ISO4G1_0224	ISO4G11_0617	-	-	-	-	-	-	-	-
<i>cbiL</i>	AR505_0413	ISO4G1_0228	ISO4G11_0564	TALC_01192	-	-	AUQ37_00095	MMALV_12390	MMINT_01790	-	Mpt1_c07140
<i>cbiH</i>	AR505_0415	ISO4G1_0226	ISO4G11_0566	TALC_01190	-	-	AUQ37_00105	MMALV_12360	MMINT_01770	WP_026068753.1	Mpt1_c07120
<i>cbiF</i>	AR505_0414	ISO4G1_0227	ISO4G11_0545	TALC_01191	-	-	AUQ37_00100 (pseudo)	MMALV_12380	MMINT_01780	WP_019176698.1	Mpt1_c07130
<i>cbiG</i>	AR505_0379	ISO4G1_0230	ISO4G11_0036	TALC_01232	-	-	AUQ37_03850	MMALV_12760	MMINT_01810	WP_019176699.1	Mpt1_c07160
<i>cbiD</i>	AR505_0378	ISO4G1_0229	ISO4G11_0037	TALC_01233	-	-	-	MMALV_12770	MMINT_01800	WP_019176701.1	Mpt1_c07150
<i>cbiJ</i>	AR505_0380	ISO4G1_0231	ISO4G11_0035	TALC_01231	-	-	AUQ37_03845	MMALV_12750	MMINT_01820	-	Mpt1_c07170
<i>cobL</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cbiT</i>	-	-	-	-	-	-	-	-	-	WP_026068752.1	-
<i>cbiE</i>	-	-	-	-	-	-	-	-	-	WP_019176697.1	-
<i>cbiC</i>	AR505_0416	ISO4G1_0225	ISO4G11_0567	TALC_01189	-	-	AUQ37_00110	MMALV_12350	MMINT_01760	WP_019177037.1	Mpt1_c07110
<i>cbiA</i>	AR505_0381,	ISO4G1_0232	ISO4G11_0034	TALC_01230,	AOA80_08510	AOA81_06795, AOA81_03105	-	MMALV_12740,	MMINT_10700	WP_019177213.1,	Mpt1_c05110,
	AR505_0363	ISO4G1_0363	ISO4G11_0400	TALC_01250				MMALV_13200	MMINT_17215	WP_026068748.1	Mpt1_c08010
<i>fldA</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cobA</i>	AR505_0444	ISO4G1_1062	ISO4G11_0512	TALC_00413	AOA80_09520	-	AUQ37_03105	MMALV_03350	-	WP_019176716.1	Mpt1_c03460
<i>cbiP</i>	AR505_1136,	ISO4G1_0690	ISO4G11_0628	TALC_01049,	AOA80_04815, AOA80_04820	AOA81_03100	-	MMALV_09820,	MMINT_08250	WP_019177214.1	Mpt1_c06670, Mpt1_c06680
	AR505_1137	ISO4G1_0691	ISO4G11_0629	TALC_01050				MMALV_09830	MMINT_08260		
<i>cbiB</i>	AR505_1295	ISO4G1_0999	ISO4G11_0067	TALC_01124	AOA80_08005	AOA81_03075	AUQ37_00455	MMALV_11640	MMINT_06180	WP_026068706.1	Mpt1_c02260
<i>cobU</i>	-	-	-	-	-	-	-	-	-	-	-
<i>cobS/cobV</i>	AR505_1297	-	ISO4G11_0064	TALC_01122	AOA80_07990	AOA81_03085	-	MMALV_11620	MMINT_06160	WP_019176471.1	Mpt1_c02280
<i>cobC</i>	-	-	-	-	AOA80_01000 (pseudo)	-	-	-	-	-	-
NAD⁺ and NADP⁺											
<i>nadB</i>	-	-	-	-	-	-	-	-	-	WP_019176936.1	-
<i>nadA</i>	AR505_1155	-	ISO4G11_0606	TALC_00684	AOA80_09185	AOA81_05000	AUQ37_07135	MMALV_09980	MMINT_12200	WP_026068837.1	Mpt1_c06910
<i>pncB</i>	AR505_0471	ISO4G1_0593	ISO4G11_1490	TALC_00529	AOA80_10715	AOA81_05645	AUQ37_06315	MMALV_13500	MMINT_08070	WP_019177240.1	Mpt1_c03950

<i>nadC</i>	AR505_1654	-	ISO4G11_0173	TALC_00188	AOA80_06090	AOA81_03755	AUQ37_00685 (pseudo)	MMALV_01750	MMINT_17820	WP_019176124.1	Mpt1_c12890
<i>nadK</i>	AR505_0121	ISO4G1_1365	ISO4G11_0697	TALC_01451	AOA80_09810	AOA81_02005	AUQ37_07960	MMALV_15550	MMINT_02690	WP_019177988.1	Mpt1_c01280
<i>nadE</i>	AR505_0377	ISO4G1_0386	ISO4G11_0377	TALC_01235	AOA80_01555	AOA81_04445	AUQ37_04040 (pseudo)	MMALV_12810	MMINT_14860	WP_019177639.1	Mpt1_c07990
<i>nadM</i>	AR505_0616	ISO4G1_0899	ISO4G11_0619	TALC_00604	AOA80_10995	AOA81_05550 (pseudo)	-	MMALV_05730	MMINT_15265	WP_019176559.1	Mpt1_c02780
Riboflavin											
<i>ribK</i>	AR505_1679	ISO4G1_0106	ISO4G11_0942	TALC_00153	AOA80_05690	AOA81_01745	AUQ37_00550	MMALV_01480	MMINT_18460	WP_019178717.1	Mpt1_c13270
<i>ribB</i>	AR505_1180	ISO4G1_0933	ISO4G11_0234	TALC_00701	AOA80_10790	AOA81_05100	AUQ37_07045	MMALV_10180	MMINT_07940	WP_026068855.1	Mpt1_c07200
<i>ribL</i>	AR505_1181	ISO4G1_0932	ISO4G11_0233	TALC_00702	AOA80_10795	AOA81_05105	AUQ37_07040	MMALV_10190	MMINT_07930	WP_019177254.1	Mpt1_c07210
<i>ribC</i>	AR505_1182	ISO4G1_0931	ISO4G11_0232	TALC_00703	AOA80_10800	AOA81_05110	AUQ37_07035	MMALV_10200	MMINT_07920	WP_019177255.1	Mpt1_c07220
<i>ribH</i>	AR505_1183	ISO4G1_0930	ISO4G11_0231	TALC_00704	AOA80_10805	AOA81_05115	AUQ37_07030	MMALV_10210	MMINT_07910	WP_019177256.1	Mpt1_c07230
<i>ribD</i>	AR505_1602	ISO4G1_0188	ISO4G11_0120	TALC_00248	AOA80_01755	AOA81_01940	AUQ37_07835	MMALV_02330	MMINT_16300	WP_019178342.1	Mpt1_c11210
<i>ribA</i>	AR505_0210	ISO4G1_0288	ISO4G11_1596	TALC_01341	AOA80_01240	AOA81_03975	AUQ37_05625 (pseudo)	MMALV_14310	MMINT_04030	WP_019177554.1	Mpt1_c09750
Molybdenum cofactor											
<i>moaA</i> ₁	AR505_1263	-	ISO4G11_1699	TALC_00802	-	-	-	MMALV_15830	-	-	-
<i>moaA</i> ₂	AR505_1435	ISO4G1_1211	ISO4G11_1297	TALC_00433	AOA80_07265	AOA81_01255	AUQ37_02980	MMALV_03570	MMINT_13190	WP_026068867.1	Mpt1_c01630

*NCBI accession number is shown instead of locus_tag due to draft genome. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Glutamyl-tRNA synthetase (*gltX*). Glutamyl-tRNA reductase (*hemA*). Delta-aminolevulinic acid dehydratase (*hemB*). Porphobilinogen deaminase (*hemC*). Uroporphyrinogen III synthase (*hemD*). Glutamate-1-semialdehyde-2,1-aminomutase (*hemL*). Uroporphyrin-III C-methyltransferase (*corA*). Siroheme synthase (*cysG*). Sirohydrochlorin cobaltochelatase (*cbiX*). Cobalt-sirohydrochlorin (C²⁰)-methyltransferase (*cbiL*). Cobalt-precorrin-3 (C¹⁷)-methyltransferase (*cbiH*). Cobalt precorrin-4 (C¹¹)-methyltransferase (*cbiF*). Cobalt-precorrin 5A hydrolase (*cbiG*). Cobalt-precorrin-6A synthase (*cbiD*). Cobalt-precorrin-6A reductase (*cbiJ*). Precorrin-6B C^{5,15}-methyltransferase (*cobL*). Cobalt-precorrin-6B (C¹⁵)-methyltransferase (*cbiT*). Cobalt-precorrin-7 (C⁵)-methyltransferase (*cbiE*). Cobalt-precorrin-8 methylmutase (*cbiC*). Cobyrate *a,c*-diamide synthase (*cbiA*). Flavodoxin A (*fldA*). Cobalamin adenosyltransferase (*cobA*). Adenosyl-cobyrate synthase (*cbiP*). Adenosylcobinamide-phosphate synthase (*cbiB*). Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (*cobU*). Adenosylcobalamin synthase (*cobS*). Adenosyl-cobalamin (5'-phosphate) synthase (*cobV*). α -ribazole-5'-phosphate phosphatase (*cobC*). Aspartate oxidase (*nadB*). Quinolinate synthase (*nadA*). Nicotinate phosphoribosyltransferase (*pncB*). Quinolinate phosphoribosyltransferase (*nadC*). NAD kinase (*nadK*). NH₃-dependent NAD⁺ synthase (*nadE*). Nicotinamide-mononucleotide adenylyltransferase (*nadM*). Riboflavin kinase (*ribK*). 3,4-dihydroxy-2-butanone-4-phosphate synthase (*ribB*). FAD synthetase (*ribL*). Riboflavin synthase (*ribC*). 6,7-dimethyl-8-ribityllumazine synthase (*ribH*). Bifunctional diaminohydroxy phosphoribosylaminopyrimidine deaminase /5-amino-6-(5-phosphoribosylamino) uracil reductase (*ribD*). GTP cyclohydrolase II (*ribA*). Molybdopterin biosynthesis protein A (*moaA*).

Table A.4.21 Genes involved in secretion

	ISO4-H5	ISO4-G1	ISO4-G11 [#]	BRNA1	RumEnM1	RumEnM2	1R26	Mx1201	Mx1	B10*	MpT1
Signal recognition riboprotein subunits											
SRP54	AR505_0758	ISO4G1_0902	ISO4G11_0348	TALC_00918	AOA80_11290	AOA81_05835 (pseudo)	AUQ37_01505	MMALV_07830	MMINT_10970	WP_019177011.1	Mpt1_c04960
SRP19	AR505_1473	ISO4G1_1274	ISO4G11_0677	TALC_00338	AOA80_02415	AOA81_00415	AUQ37_03240	MMALV_03090	MMINT_04930	WP_019177450.1	Mpt1_c10520
Signal recognition receptor											
<i>ftsY</i>	AR505_0006	ISO4G1_0051	ISO4G11_0807	TALC_01572	AOA80_08185	AOA81_02495	AUQ37_02005	MMALV_16910	MMINT_19350	WP_019178395.1	Mpt1_c14550
Signal peptide cleavage											
Signal sequence peptidase SPI	AR505_1828	ISO4G1_0002	ISO4G11_0813	TALC_00002	AOA80_00795 (pseudo)	AOA81_02525	AUQ37_01975	MMALV_00030	MMINT_00020	WP_019178258.1	Mpt1_c12360
TFPP-like signal peptidase	-	-	-	-	-	-	-	-	-	-	-
Signal peptide peptidase SPP	-	-	-	-	-	-	-	-	-	-	-
Sec-independent protein translocase											
<i>tatC</i>	-	-	-	-	-	-	-	-	-	-	-
Sec61 translocon											
<i>secG</i>	AR505_0386	ISO4G1_0481	ISO4G11_0029	TALC_01224	AOA80_01490	AOA81_02815	AUQ37_03815	MMALV_12690	MMINT_06015	WP_019177600.1	Mpt1_c07850
<i>secY</i>	AR505_0241	ISO4G1_0319	ISO4G11_1567	TALC_01311	AOA80_08750 (pseudo)	AOA81_04135	AUQ37_05770	MMALV_14030	MMINT_04560	WP_019177507.1	Mpt1_c09390
<i>secE</i>	AR505_1799	ISO4G1_0032	ISO4G11_0848	TALC_00039	-	AOA81_02630	AUQ37_01800	MMALV_00430	MMINT_17390	WP_026069057.1	Mpt1_c12020

*NCBI accession number is shown instead of locus_tag due to draft genome. [#] Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Signal recognition particle protein (SRP54, SRP19). Signal recognition particle receptor (*ftsY*). Preprotein translocase (*secGYE*). Twin arginine protein translocation system (*tatC*).

Table A.5.1 T-test of spectra bins in sample (paired) and log transformed with p-value threshold of 0.05

Data transformation - Log							
Data scaling - Auto scaling		Data scaling - Pareto scaling					
Chemical shift	p.value	-log10(p)	FDR*	Chemical shift	p.value	-log10(p)	FDR*
0.618576	0.027484	1.5609	0.26061	0.618576	0.027484	1.5609	0.26061
0.628577	0.017632	1.7537	0.21773	0.628577	0.017632	1.7537	0.21773
0.638578	0.011383	1.9437	0.17372	0.638578	0.011383	1.9437	0.17372
0.878595	0.040705	1.3904	0.3226	0.878595	0.040705	1.3904	0.3226
0.888596	0.020211	1.6944	0.22433	0.888596	0.020211	1.6944	0.22433
0.898597	0.019024	1.7207	0.22433	0.898597	0.019024	1.7207	0.22433
0.958601	0.029485	1.5304	0.27467	0.958601	0.029485	1.5304	0.27467
1.04861	0.02035	1.6914	0.22433	1.04861	0.02035	1.6914	0.22433
1.05861	0.044553	1.3511	0.33797	1.05861	0.044553	1.3511	0.33797
1.17862	0.037261	1.4288	0.30364	1.17862	0.037261	1.4288	0.30364
1.47864	0.031946	1.4956	0.27918	1.47864	0.031946	1.4956	0.27918
1.75866	0.044437	1.3523	0.33797	1.75866	0.044437	1.3523	0.33797
2.10868	0.005681	2.2456	0.13115	2.10868	0.005681	2.2456	0.13115
2.11868	7.21E-05	4.1419	0.019151	2.11868	7.21E-05	4.1419	0.019151
2.12869	0.008258	2.0831	0.15019	2.12869	0.008258	2.0831	0.15019
2.13869	0.030346	1.5179	0.27782	2.13869	0.030346	1.5179	0.27782
2.14869	0.008075	2.0929	0.15019	2.14869	0.008075	2.0929	0.15019
2.15869	0.009218	2.0354	0.1579	2.15869	0.009218	2.0354	0.1579
2.16869	0.012009	1.9205	0.17714	2.16869	0.012009	1.9205	0.17714
2.17869	0.01145	1.9412	0.17372	2.17869	0.01145	1.9412	0.17372
2.3287	0.020701	1.684	0.22433	2.3287	0.020701	1.684	0.22433
2.3387	0.015524	1.809	0.20106	2.3387	0.015524	1.809	0.20106
2.3487	0.001564	2.8058	0.074874	2.3487	0.001564	2.8058	0.074874
2.3587	0.037636	1.4244	0.30364	2.3587	0.037636	1.4244	0.30364
2.3787	0.017502	1.7569	0.21773	2.3787	0.017502	1.7569	0.21773
2.39871	0.005456	2.2631	0.13115	2.39871	0.005456	2.2631	0.13115
2.46871	0.021927	1.659	0.22829	2.46871	0.021927	1.659	0.22829
2.47871	0.012356	1.9081	0.17733	2.47871	0.012356	1.9081	0.17733
2.48871	0.001371	2.8631	0.074874	2.48871	0.001371	2.8631	0.074874
2.49871	0.006868	2.1632	0.15019	2.49871	0.006868	2.1632	0.15019
2.63872	0.007569	2.121	0.15019	2.63872	0.007569	2.121	0.15019
2.64872	0.002787	2.5548	0.09867	2.64872	0.002787	2.5548	0.09867
2.65872	0.003385	2.4704	0.099858	2.65872	0.003385	2.4704	0.099858
2.66872	0.018192	1.7401	0.21955	2.66872	0.018192	1.7401	0.21955
2.67873	0.001583	2.8005	0.074874	2.67873	0.001583	2.8005	0.074874
2.68873	0.001521	2.818	0.074874	2.68873	0.001521	2.818	0.074874
2.76873	0.037741	1.4232	0.30364	2.76873	0.037741	1.4232	0.30364
2.77873	0.027188	1.5656	0.26061	2.77873	0.027188	1.5656	0.26061
2.78873	0.000195	3.7106	0.032031	2.78873	0.000195	3.7106	0.032031
2.79873	2.42E-05	4.6161	0.012854	2.79873	2.42E-05	4.6161	0.012854
2.80873	0.00114	2.9433	0.074874	2.80873	0.00114	2.9433	0.074874
2.81874	0.000241	3.6175	0.032031	2.81874	0.000241	3.6175	0.032031
2.84874	0.003661	2.4364	0.10136	2.84874	0.003661	2.4364	0.10136
2.85874	0.036325	1.4398	0.30364	2.85874	0.036325	1.4398	0.30364
2.89874	0.010108	1.9953	0.16773	2.89874	0.010108	1.9953	0.16773
2.90874	0.015144	1.8198	0.20106	2.90874	0.015144	1.8198	0.20106
2.92874	0.008485	2.0713	0.15019	2.92874	0.008485	2.0713	0.15019
2.94875	0.001841	2.7349	0.074874	2.94875	0.001841	2.7349	0.074874
2.99875	0.025107	1.6002	0.25638	2.99875	0.025107	1.6002	0.25638
3.00875	0.00791	2.1018	0.15019	3.00875	0.00791	2.1018	0.15019
3.01875	0.008201	2.0862	0.15019	3.01875	0.008201	2.0862	0.15019
3.02875	0.021636	1.6648	0.22829	3.02875	0.021636	1.6648	0.22829
3.59879	0.032072	1.4939	0.27918	3.59879	0.032072	1.4939	0.27918
3.88881	0.015477	1.8103	0.20106	3.88881	0.015477	1.8103	0.20106
5.18891	0.026876	1.5706	0.26061	5.18891	0.026876	1.5706	0.26061
5.22891	0.003343	2.4759	0.099858	5.22891	0.003343	2.4759	0.099858
5.24891	0.010487	1.9793	0.16875	5.24891	0.010487	1.9793	0.16875
5.78895	0.032889	1.483	0.28167	5.78895	0.032889	1.483	0.28167
6.06897	0.043671	1.3598	0.33797	6.06897	0.043671	1.3598	0.33797
7.72909	0.001365	2.8648	0.074874	7.72909	0.001365	2.8648	0.074874
7.8591	0.031981	1.4951	0.27918	7.8591	0.031981	1.4951	0.27918
8.17912	0.025848	1.5876	0.25896	8.17912	0.025848	1.5876	0.25896
8.18912	0.003208	2.4938	0.099858	8.18912	0.003208	2.4938	0.099858
8.23913	0.001974	2.7046	0.074874	8.23913	0.001974	2.7046	0.074874
8.24913	0.003818	2.4182	0.10136	8.24913	0.003818	2.4182	0.10136
8.25913	0.001873	2.7275	0.074874	8.25913	0.001873	2.7275	0.074874
8.32913	0.020533	1.6875	0.22433	8.32913	0.020533	1.6875	0.22433
8.59915	0.001268	2.897	0.074874	8.59915	0.001268	2.897	0.074874
8.60915	0.004463	2.3504	0.11285	8.60915	0.004463	2.3504	0.11285

8.70916	0.013543	1.8683	0.18924	8.70916	0.013543	1.8683	0.18924
---------	----------	--------	---------	---------	----------	--------	---------

*FDR: false discovery rate

Table A.5.2 T-test of spectra bins in control (paired) and log transformed with p-value threshold of 0.05

Data transformation - Log							
Data scaling - Auto scaling				Data scaling - Pareto scaling			
Chemical shift	p.value	-log10(p)	FDR*	Chemical shift	p.value	-log10(p)	FDR*
2.68873	0.044431	1.3523	0.58204	2.68873	0.044431	1.3523	0.49948
2.78873	0.008903	2.0505	0.35067	2.78873	0.008903	2.0505	0.27808
2.83874	0.048355	1.3156	0.59317	2.83874	0.048355	1.3156	0.50522
2.84874	0.022264	1.6524	0.4726	2.84874	0.022264	1.6524	0.40575
2.85874	0.021226	1.6731	0.4726	2.85874	0.021226	1.6731	0.40575
2.89874	0.002473	2.6068	0.14064	2.89874	0.002473	2.6068	0.10533
2.91874	0.019869	1.7018	0.4726	2.91874	0.019869	1.7018	0.40575
2.92874	0.030446	1.5165	0.4726	2.92874	0.030446	1.5165	0.40575
2.94875	0.012311	1.9097	0.43641	2.94875	0.012311	1.9097	0.34405
2.99875	0.027886	1.5546	0.4726	2.99875	0.027886	1.5546	0.40575
3.00875	0.042708	1.3695	0.58204	3.00875	0.042708	1.3695	0.493
3.02875	0.028912	1.5389	0.4726	3.02875	0.028912	1.5389	0.40575
3.03875	0.033688	1.4725	0.48744	3.03875	0.033688	1.4725	0.41601
3.04875	0.016086	1.7936	0.4726	3.04875	0.016086	1.7936	0.40575
3.05875	0.025489	1.5936	0.4726	3.05875	0.025489	1.5936	0.40575
3.08876	0.011244	1.9491	0.41959	3.08876	0.011244	1.9491	0.3317
3.09876	0.021254	1.6726	0.4726	3.09876	0.021254	1.6726	0.40575
3.10876	0.032959	1.482	0.48684	3.10876	0.032959	1.482	0.41601
3.59879	0.002777	2.5564	0.14064	3.59879	0.002777	2.5564	0.10533
3.6788	0.017958	1.7457	0.4726	3.6788	0.017958	1.7457	0.40575
3.7288	0.027635	1.5585	0.4726	3.7288	0.027635	1.5585	0.40575
3.77881	0.029032	1.5371	0.4726	3.77881	0.029032	1.5371	0.40575
3.79881	0.001418	2.8485	0.10051	3.79881	0.001418	2.8485	0.075273
3.80881	0.000131	3.8835	0.030905	3.80881	0.000131	3.8835	0.023146
3.81881	0.035005	1.4559	0.49637	3.81881	0.035005	1.4559	0.41778
3.86881	0.045151	1.3453	0.58204	3.86881	0.045151	1.3453	0.49948
3.88881	0.000933	3.0299	0.092066	3.88881	0.000933	3.0299	0.068952
3.89881	8.32E-05	4.0799	0.030905	3.89881	8.32E-05	4.0799	0.023146
3.90881	0.018015	1.7444	0.4726	3.90881	0.018015	1.7444	0.40575
3.93882	0.022965	1.6389	0.4726	3.93882	0.022965	1.6389	0.40575
3.97882	0.004121	2.385	0.18262	3.97882	0.004121	2.385	0.14589
3.98882	0.001165	2.9336	0.092066	3.98882	0.001165	2.9336	0.068952
4.00882	0.047788	1.3207	0.59317	4.00882	0.047788	1.3207	0.50522
4.07883	0.001717	2.7653	0.11064	4.07883	0.001717	2.7653	0.082866
4.10883	0.023896	1.6217	0.4726	4.10883	0.023896	1.6217	0.40575
4.11883	0.029976	1.5232	0.4726	4.11883	0.029976	1.5232	0.40575
5.26891	0.048524	1.314	0.59317	5.26891	0.048524	1.314	0.50522
5.32892	0.003118	2.5061	0.1474	5.37892	0.000863	3.0642	0.068952
5.34892	0.025055	1.6011	0.4726	5.38892	0.002643	2.5779	0.10533
5.37892	0.000863	3.0642	0.092066	6.06897	0.035405	1.4509	0.41778
5.38892	0.002643	2.5779	0.14064	6.10897	0.029042	1.537	0.40575
5.98897	0.019564	1.7085	0.4726	7.38907	0.024604	1.609	0.40575
6.10897	0.029042	1.537	0.4726	7.73909	0.01876	1.7268	0.40575
6.14898	0.040083	1.397	0.55723	7.98911	0.004858	2.3136	0.16122
6.27899	0.026223	1.5813	0.4726	8.18912	0.000108	3.967	0.023146
6.419	0.013273	1.877	0.44812	8.19913	0.017089	1.7673	0.40575
7.38907	0.024604	1.609	0.4726	8.22913	0.031329	1.5041	0.40575
7.73909	0.01876	1.7268	0.4726	8.23913	0.000502	3.2991	0.066676
7.98911	0.004858	2.3136	0.2026	8.24913	0.030878	1.5103	0.40575
8.18912	0.000108	3.967	0.030905	8.25913	0.000836	3.0775	0.068952
8.19913	0.017089	1.7673	0.4726	8.32913	0.001169	2.9323	0.068952
8.22913	0.031329	1.5041	0.4726				
8.23913	0.000502	3.2991	0.089027				
8.24913	0.030878	1.5103	0.4726				
8.25913	0.000836	3.0775	0.092066				
8.32913	0.001169	2.9323	0.092066				
8.54915	0.04449	1.3517	0.58204				
8.67916	0.019664	1.7063	0.4726				

*FDR: false discovery rate

Table A.5.03 Gene expression of ISO4-H5

Locus_tag	Product	Trt1	Trt2	Trt3	Trt4
AR505_0001	orc1/cdc6 family replication initiation protein	9	6	7	6
AR505_0002	hypothetical transmembrane protein	0	0	0	1
AR505_0003	conserved hypothetical protein	6	1	4	3
AR505_0004	acetyl-CoA C-acetyltransferase	2489	3104	3967	3119
AR505_0005*	adhesin-like protein	462*	152	153	76*
AR505_0006	signal recognition particle receptor FtsY	43	14	13	10
AR505_0007	prefoldin alpha subunit PfdA	142	61	55	65
AR505_0008	ribosomal protein LX	41	27	30	28
AR505_0009	DNA primase small subunit PriA	50	51	47	36
AR505_0010	transposase	44	32	23	23
AR505_0011	hydrolase, TatD family	38	12	8	15
AR505_0012	beta-lactamase domain-containing protein	127	190	166	109
AR505_0013	peptidase M48 family (4 TMHs)	123	147	89	141
AR505_0014	bifunctional hexulose-6-phosphate synthase/ribonuclease regulator	61	110	75	78
AR505_0015	arsenate reductase	149	301	190	150
AR505_0016	hypothetical protein	30	43	23	22
AR505_0017	hypothetical protein	34	15	48	21
AR505_0018	replicative DNA helicase Mcm	70	41	64	51
AR505_0019	hypothetical protein	21	10	18	12
AR505_0020	NMD3 family protein	42	22	37	12
AR505_0022	fumarate hydratase FumA	34	11	31	15
AR505_0023	fumarate hydratase FumB	59	61	30	44
AR505_0024*	hypothetical transmembrane protein	158*	167	113	71*
AR505_0025*	ATP-dependent DNA helicase	39	17*	33	59*
AR505_0026	hypothetical protein	281	397	384	319
AR505_0027	8-oxoguanine DNA-glycosylase Ogg	342	494	418	446
AR505_0028*	endonuclease IV	257	251*	423	597*
AR505_0029	hypothetical transmembrane protein	10	10	6	25
AR505_0030	ABC transporter permease protein	19	4	2	19
AR505_0031	ABC transporter ATP-binding protein	53	27	31	45
AR505_0032*	thiamine biosynthesis protein ThiC1	107*	161	131	241*
AR505_0033	DNA gyrase B subunit GyrB	41	21	27	41
AR505_0034	DNA gyrase A subunit GyrA	54	27	26	36
AR505_0035	hypothetical protein	47	21	7	12
AR505_0036	hypothetical protein	69	54	57	91
AR505_0037	phosphoribosylformylglycinamide cyclo-ligase PurM	91	90	68	78
AR505_0038*	ribosomal RNA large subunit methyltransferase J RrmJ	144	245*	113*	140
AR505_0039*	ATP-dependent DNA helicase	52*	43	25*	49
AR505_0040	CoB--CoM heterodisulfide reductase subunit D HdrD	316	444	335	465
AR505_0041	hypothetical protein	33	32	38	10
AR505_0042	hypothetical protein	23	70	67	80
AR505_0043	transcriptional regulator ArsR family	29	53	52	28
ISO4H5_0043*	tRNA 2'-O-methylase (pseudo)	170*	48*	65	71
ISO4H5_0044	tRNA 2'-O-methylase (pseudo)	68	12	18	16
AR505_0047	thioredoxin TrxA	58	73	71	120
AR505_0048	thioredoxin-disulfide reductase TrxB1	114	102	88	126
AR505_0049	XRE family transcriptional regulator	35	27	28	29
AR505_0050	hypothetical protein	23	45	51	17
AR505_0051	histone acetyltransferase ELP3 family	33	21	19	20
AR505_0052	AAA family ATPase CDC48 subfamily	72	53	53	58
AR505_0053	DNA-directed RNA polymerase subunit H RpoH	41	9	15	8
AR505_0054	DNA-directed RNA polymerase subunit B RpoB	77	34	55	56
AR505_0055	DNA-directed RNA polymerase subunit A' RpoA1	81	29	77	62
AR505_0056	DNA-directed RNA polymerase subunit A'' RpoA2	71	32	79	60
AR505_0057	ribosomal protein L30e Rpl30e	38	13	31	22
AR505_0058	transcription elongation factor NusA-like protein	134	151	148	124
AR505_0059*	radical SAM domain protein	77*	161	192*	177
AR505_0060	orotidine 5'-phosphate decarboxylase PyrF	103	194	121	90
AR505_0061	adhesin-like protein	99	58	77	65
AR505_0062	hypothetical protein	116	58	114	74
AR505_0063	hypothetical protein	4	2	1	0
AR505_0064	translin family DNA-binding protein	39	52	60	52
AR505_0065	tRNA pseudouridine synthase A TruA	18	6	11	14
AR505_0066	phosphoribosylamine--glycine ligase PurD	134	213	206	208
AR505_0067*	hydrogenase accessory protein HypB	79*	134	163*	136
AR505_0068	glutamyl-tRNA(Gln) amidotransferase subunit D GatD	70	78	88	95
AR505_0069	glutamyl-tRNA(Gln) amidotransferase subunit E GatE	81	59	62	87
AR505_0070	methyltransferase	163	151	173	341
AR505_0071	metallo-beta-lactamase domain-containing protein	42	54	59	54
AR505_0072*	hypothetical protein	126*	195	234	305*
AR505_0073	phosphoserine phosphatase SerB1	72	53	34	50

AR505_0074	MORN repeat-containing protein	29	15	17	21
AR505_0075	TraB family protein	30	50	37	23
AR505_0076	thymidylate synthase ThyX	40	51	54	42
AR505_0077	ribosomal protein S17e Rps17e	45	40	50	42
AR505_0078	fibronectin-binding protein FbpA	34	31	29	29
AR505_0079	hypothetical protein	45	52	46	60
AR505_0080*	hydrogenase expression/formation protein HypE	34*	84*	46	53
AR505_0081	UDP-glucose 4-epimerase GalE	74	104	100	128
AR505_0082	aldose 1-epimerase	63	97	81	105
AR505_0083	hypothetical protein	37	8	9	6
AR505_0084	adenine phosphoribosyltransferase Apt1	43	75	63	44
AR505_0085	bifunctional inositol-1 monophosphatase/fructose-1,6-bisphosphatase/ATP-NAD kinase	10	4	6	12
AR505_0086	hypothetical protein	90	111	131	122
AR505_0087	hypothetical protein	50	67	90	63
AR505_0088	hypothetical transmembrane protein	48	62	40	52
AR505_0089	hypothetical protein	29	35	45	43
AR505_0090	hypothetical protein	71	108	133	103
AR505_0091	glutamine synthetase GlnA	288	398	462	358
AR505_0092	thermosome subunit	1411	1184	1580	1369
AR505_0093*	molecular chaperone GrpE	309*	134	151	100*
AR505_0094*	chaperone protein DnaK	925*	302	420	275*
AR505_0095*	chaperone protein DnaJ	545*	176*	354	291
AR505_0096	hypothetical protein	138	30	36	35
AR505_0097	bifunctional inositol-1 monophosphatase/fructose-1,6-bisphosphatase/ATP-NAD kinase	122	129	88	97
AR505_0098*	pyridoxamine 5'-phosphate oxidase-related protein	395*	236	144*	153
AR505_0099	methyltransferase	79	93	64	57
AR505_0100	thiamine monophosphate synthase ThiE	100	36	34	31
AR505_0101	tyrosine lyase ThiH	50	42	24	24
AR505_0102	thiazole synthase ThiG	58	70	73	77
AR505_0103	thiamine biosynthesis protein ThiF1	112	145	132	110
AR505_0104	ThiS sulfur-carrier protein	42	33	55	27
AR505_0105	Fic family protein	21	10	13	9
AR505_0106	transposase	8	2	12	5
AR505_0107	transposase	7	0	5	7
AR505_0108	glutamate-5-semialdehyde dehydrogenase ProA	23	23	29	24
AR505_0109	glutamate 5-kinase ProB	33	52	34	33
AR505_0110	methyltransferase cognate corrinoid protein	31	23	18	24
AR505_0111	ABC transporter ATP-binding protein	3	3	4	2
AR505_0112	ABC transporter substrate-binding protein	45	9	8	12
AR505_0113	ABC transporter permease protein	66	48	43	40
AR505_0114*	Methylase involved in ubiquinone/menaquinone biosynthesis	103*	37	27*	47
AR505_0115	universal archaeal protein Kae1	147	185	174	175
AR505_0116	hypothetical protein	103	189	116	79
AR505_0117	ssDNA exonuclease RecJ	27	9	7	14
AR505_0118	ribosomal protein S15P Rps15p	745	448	370	377
AR505_0119	NUDIX domain-containing protein	20	23	19	16
AR505_0120	fibrillarin	39	74	66	88
AR505_0121	ATP-NAD kinase	64	112	110	89
AR505_0122	metal-dependent protease	57	57	41	59
AR505_0123	phosphoglucosamine mutase GlmM1	62	112	94	89
AR505_0124	hypothetical protein	351	415	663	677
AR505_0125	replication-associated recombination protein A	37	29	26	31
AR505_0126*	hypothetical transmembrane protein	118	172*	56*	92
AR505_0127	permease	22	28	12	16
AR505_0128	thiazole biosynthesis/tRNA modification protein ThiI	81	68	47	35
AR505_0129	ribosomal protein L15e Rpl15e	200	88	118	89
AR505_0130	DNA polymerase family B PolB	18	10	6	13
AR505_0131	translation-associated GTPase	29	32	33	16
AR505_0132	dimethyladenosine transferase KsgA	23	9	5	11
AR505_0133*	conserved hypothetical protein	132*	101	75	57*
AR505_0134	DNA-directed RNA polymerase subunit F RpoF	319	294	336	328
AR505_0135	ribosomal protein L21e Rpl21e	928	934	842	906
AR505_0136	hypothetical protein	88	69	85	74
AR505_0137	RNA-binding protein	35	14	6	2
AR505_0138	serine/threonine protein kinase RIO1 family	36	11	9	12
AR505_0139	translation initiation factor aIF-1A	146	90	110	54
AR505_0140	hypothetical protein	88	60	46	66
AR505_0141	phosphoribosylglycinamide formyltransferase PurN	125	249	194	169
AR505_0142	archaease	13	27	15	15
AR505_0143	L-aspartate dehydrogenase	20	29	9	19
AR505_0144	peptidase M24 family	12	18	24	18
AR505_0145	glutamate dehydrogenase GdhA	208	384	449	253
AR505_0146	hypothetical transmembrane protein	106	85	71	62

AR505_0147	transposase IS4 family	67	55	51	43
AR505_0148	hypothetical protein	45	94	63	89
AR505_0149	hypothetical protein	125	89	65	82
AR505_0150	2,3-dihydroxy-isovalerate:NADP ⁺ oxidoreductase IlvC	158	289	156	185
AR505_0151	transposase IS4 family	67	55	51	43
AR505_0152	acetolactate synthase large subunit IlvB1	76	101	77	83
AR505_0153	acetolactate synthase large subunit IlvB2	101	176	158	177
AR505_0154	glyceraldehyde-3-phosphate dehydrogenase Gap	108	115	101	141
AR505_0155	phosphoglycerate kinase Pgl	59	33	34	40
AR505_0156	hypothetical protein	39	10	18	22
AR505_0157	L-L-diaminopimelate aminotransferase DapC	18	5	2	2
AR505_0158	diaminopimelate epimerase DapF	16	3	6	3
AR505_0159	diaminopimelate decarboxylase LysA	35	13	12	11
AR505_0160	aspartate kinase Ask	20	5	7	6
AR505_0161	dihydrodipicolinate synthase DapA	23	10	4	7
AR505_0162	transcriptional regulator AsnC family	45	22	32	30
AR505_0163	mechanosensitive ion channel protein	127	172	131	141
AR505_0164	hypothetical protein	38	51	43	40
AR505_0165	radical SAM domain-containing protein	23	20	29	36
AR505_0166	thiamine-monophosphate kinase ThiL	109	131	197	172
AR505_0167*	conserved hypothetical protein	92*	220*	162	158
AR505_0168	CoB-CoM heterodisulfide reductase subunit D HdrD2	109	142	105	111
AR505_0169*	dihydropteroate synthase FolP	272	344*	228	161*
AR505_0170	hypothetical transmembrane protein	249	230	183	136
AR505_0171	hypothetical transmembrane protein	284	350	320	211
AR505_0172	hypothetical transmembrane protein	14	25	13	17
AR505_0173	thiazole biosynthesis adenylyltransferase ThiF	11	5	9	8
AR505_0174	hypothetical protein	8	1	10	7
AR505_0175	hypothetical protein	22	5	8	14
AR505_0176	hypothetical protein	52	30	20	30
AR505_0177	6-phospho 3-hexuloisomerase hxlB	49	61	19	47
AR505_0178	endonuclease IV	109	213	155	205
AR505_0179	ribosomal protein L18e Rpl18e	194	214	227	178
AR505_0180	ribosomal protein L13P Rpl13p	217	225	157	208
AR505_0181	ribosomal protein S9P Rps9p	602	754	512	740
AR505_0182	DNA-directed RNA polymerase subunit N RpoN	230	199	200	270
AR505_0183*	hypothetical protein	43	115*	63	21*
AR505_0184	hypothetical protein	81	97	64	46
AR505_0185	hypothetical transmembrane protein	13	7	11	10
AR505_0186	nitroreductase family protein	47	52	46	31
AR505_0187	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	95	121	83	95
AR505_0188	Kae1-associated kinase Bud32	51	119	125	100
AR505_0189*	DNA repair and recombination protein RadB	163*	95	74	60*
AR505_0190	bifunctional short chain isoprenyl diphosphate synthase IdsA/GGPS	173	63	61	74
AR505_0191	isopentenyl diphosphate delta-isomerase Fni	103	60	34	40
AR505_0192	isopentenyl phosphate kinase	55	33	25	27
AR505_0193	drug resistance MFS transporter	30	30	21	42
AR505_0194	hydrogenase assembly chaperone HypC/HupF	39	61	29	23
AR505_0195	alpha-NAC homolog	112	260	166	233
AR505_0196	hypothetical transmembrane protein	28	20	18	18
AR505_0197	hypothetical transmembrane protein	29	22	18	14
AR505_0198	alanyl-tRNA synthetase AlaS	92	139	123	117
AR505_0199*	transcriptional regulator AsnC family	72	45*	101*	45
AR505_0200	aspartate--tRNA synthetase AspS1	116	162	129	174
AR505_0201*	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit B GatB	72*	21*	34	25
AR505_0202	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit A GatA	56	13	17	15
AR505_0203	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit C GatC	27	10	8	9
AR505_0204	TPR repeat-containing protein	69	215	103	73
AR505_0205	ammonium transporter Amt	110	66	101	38
AR505_0206*	nitrogen regulatory protein P-II GlnK	104	86	131*	56*
AR505_0207	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	124	115	107	55
AR505_0208	sterol binding protein	44	49	36	42
AR505_0209	ribonuclease HII RnhB	27	49	32	19
AR505_0210	GTP cyclohydrolase RibA	106	99	79	108
AR505_0211	hypothetical protein	73	44	35	36
AR505_0212	CoA-disulfide reductase cdr	73	84	65	82
AR505_0213	transposase IS116/IS110/IS902 family	6	1	0	4
AR505_0214	hypothetical protein	2	0	0	0
AR505_0215	transposase IS605 OrfB family	77	133	137	104
AR505_0216	TIGR01210 family protein	123	152	136	153
AR505_0217	hypothetical protein	57	96	73	99
AR505_0218*	ribosomal protein L3P Rpl3p	436*	192*	196	255
AR505_0219	ribosomal protein L4P Rpl4p	291	124	126	173
AR505_0220*	ribosomal protein L23P Rpl23p	229*	62*	124	93
AR505_0221*	ribosomal protein L2P Rpl2p	237*	56*	201	121

AR505_0222*	ribosomal protein S19P Rps19p	253*	44*	303	134
AR505_0223*	ribosomal protein L22P Rpl22p	259*	70*	227	164
AR505_0224*	ribosomal protein S3P Rps3p	156*	41*	138	94
AR505_0225*	ribosomal protein L29P Rpl29p	235	81*	301*	177
AR505_0226*	translation initiation factor aSUII	298	65*	358*	163
AR505_0227*	ribonuclease P subunit P29	297*	61*	293	153
AR505_0228*	ribosomal protein S17P Rps17p	118*	20*	78	46
AR505_0229*	ribosomal protein L14e Rpl14e	214*	30*	173	103
AR505_0230*	ribosomal protein L24P Rpl24p	119*	19*	85	51
AR505_0231*	ribosomal protein S4e Rps4e	192*	58*	163	106
AR505_0232*	ribosomal protein L5P Rpl5p	133*	24*	85	66
AR505_0233*	ribosomal protein S8P Rps8p	161*	39*	112	43
AR505_0234*	ribosomal protein L6P Rpl6p	168	51*	178*	94
AR505_0235*	ribosomal protein L32e Rpl32e	251*	61*	186	96
AR505_0236*	ribosomal protein L19e Rpl19e	411*	117*	345	237
AR505_0237*	ribosomal protein L18P Rpl18p	284*	65*	232	157
AR505_0238*	ribosomal protein S5P Rps5p	340*	77*	331	183
AR505_0239*	ribosomal protein L30P Rpl30p	336*	68*	277	177
AR505_0240*	ribosomal protein L15P Rpl15p	389*	84*	318	128
AR505_0241*	preprotein translocase subunit SecY	180*	26*	114	56
AR505_0242*	hypothetical transmembrane protein	151*	18*	90	44
AR505_0243	tRNA pseudouridine synthase B TruB	22	9	19	17
AR505_0244	hypothetical protein	16	10	4	5
AR505_0245	hypothetical transmembrane protein	64	44	20	21
AR505_0246	hypothetical protein	52	44	38	19
AR505_0247	tryptophanyl-tRNA synthetase TrpS	25	29	18	18
AR505_0248	phenylalanyl-tRNA synthetase alpha subunit PheS	41	44	34	46
AR505_0249	hypothetical protein	21	18	11	26
AR505_0250	hypothetical protein	112	195	138	212
AR505_0251	uridylate kinase PyrH	94	161	121	182
AR505_0252	peptide chain release factor aRF1	33	21	27	36
AR505_0253	arginine-tRNA synthetase ArgS	54	26	48	54
AR505_0254	acetyltransferase	117	76	70	92
AR505_0255	hypothetical transmembrane protein	500	452	433	339
AR505_0256	hypothetical transmembrane protein	170	139	70	70
AR505_0257	5-formaminoimidazole-4-carboxamide-1-(beta)-D- ribofuranosyl 5'-monophosphate synthetase-like protein	253	264	186	213
AR505_0258	divalent cation transporter mgtE family	126	133	103	96
AR505_0259	phosphate uptake regulator PhoU	108	40	37	41
AR505_0260*	phosphate uptake regulator PhoU	123*	54	42*	70
AR505_0261	crcB protein CrcB	53	30	16	20
AR505_0262	adenylate kinase Adk	121	135	48	99
AR505_0263	FAD linked oxidase domain-containing protein	74	114	77	112
AR505_0264	peptidase M50 family (6 TMHs)	67	111	63	63
AR505_0265	phosphoadenosine phosphosulfate reductase	42	62	58	60
AR505_0266	hypothetical transmembrane protein	40	60	38	34
AR505_0267*	hypothetical protein	31	48*	22	11*
AR505_0268	pyruvoyl-dependent arginine decarboxylase PdaD	50	17	34	11
AR505_0269	hypothetical protein	34	24	32	31
AR505_0270*	peptidase M16 family	54*	96	63	130*
AR505_0271*	hydrogenase maturation protease HycI	154*	283	195	401*
AR505_0272	transcriptional regulator LysR family	23	13	35	32
AR505_0273*	CoB--CoM heterodisulfide reductase subunit C HdrC	93	79*	681*	166
AR505_0274*	CoB--CoM heterodisulfide reductase subunit B HdrB	182	110*	836*	279
AR505_0275*	TPR repeat-containing protein	13	8*	38*	16
AR505_0276	transposase IS605 OrfB family	83	99	129	57
AR505_0277	ribosomal protein S3Ae Rps3ae	132	85	115	75
AR505_0278	arsenite-activated ATPase ArsA	147	157	207	167
AR505_0279	hypothetical protein	254	309	277	244
AR505_0280	hypothetical protein	186	115	133	113
AR505_0281*	dihydroorotase PyrC	134*	82	80	59*
AR505_0282	hypothetical protein	103	76	80	84
AR505_0283	ribosomal protein L37e Rpl37e	62	70	46	77
AR505_0284	amidophosphoribosyltransferase PurF	44	17	11	24
AR505_0285	Na ⁺ -dependent transporter SNF family	25	8	5	14
AR505_0286	heat shock protein Hsp90	95	113	110	92
AR505_0287*	sodium/proline symporter PutP	141*	56	39	32*
AR505_0288*	hypothetical transmembrane protein	229	296	301*	141*
AR505_0289*	NADPH-dependent FMN reductase	339*	233	125	78*
AR505_0290	transposase IS605 OrfB family	103	87	88	58
AR505_0291	hypothetical protein	21	22	24	25
AR505_0292	hypothetical protein	44	27	46	35
AR505_0293	homoserine dehydrogenase metL	59	66	62	116
AR505_0294	amino acid-binding ACT domain-containing protein	43	66	47	49
AR505_0295	universal stress protein UspA	25	64	57	43

AR505_0296	MatE efflux family protein	47	17	14	22
AR505_0297	hypothetical protein	204	178	256	155
AR505_0298	Cob/MinD domain containing protein	333	294	194	239
AR505_0299*	cobalamin biosynthesis protein CbiX	316*	278	127*	207
AR505_0300	hypothetical protein	133	189	184	172
AR505_0301	adenine phosphoribosyltransferase Apt	155	159	142	143
AR505_0302	hypothetical transmembrane protein	15	38	23	17
AR505_0303	ABC transporter solute binding protein	89	55	78	72
AR505_0304	ABC transporter ATP binding protein	38	50	46	60
AR505_0305	ABC transporter permease protein	117	116	121	149
AR505_0306	hypothetical protein	14	12	16	1
AR505_0307	SAM-dependent methyltransferase	14	3	6	10
AR505_0308	ABC transporter ATP-binding protein	24	5	4	7
AR505_0309	ABC transporter permease protein	34	8	8	9
AR505_0310	ABC transporter solute-binding protein	139	44	67	55
AR505_0311	transporter DMT family	24	11	6	10
AR505_0312	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	46	52	48	93
AR505_0313	phage integrase	0	0	0	0
AR505_0314	hypothetical protein	0	0	0	0
AR505_0315	hypothetical protein	0	0	0	0
AR505_0316	hypothetical protein	0	0	0	0
AR505_0317	hypothetical protein	0	0	0	0
AR505_0318	hypothetical protein	0	0	0	0
AR505_0319	hypothetical protein	0	0	0	0
AR505_0320	hypothetical protein	0	0	0	0
AR505_0321	hypothetical protein	0	0	0	0
AR505_0322	hypothetical protein	0	0	0	0
AR505_0323	hypothetical protein	0	0	0	0
AR505_0324	hypothetical protein	0	0	0	0
AR505_0325	hypothetical protein	0	0	0	0
AR505_0326	hypothetical protein	0	0	0	0
AR505_0327	DNA-cytosine methyltransferase Dcm1	0	0	0	0
AR505_0328	hypothetical protein	0	0	0	0
AR505_0329	DNA mismatch endonuclease Vsr	0	0	0	0
AR505_0330	conserved hypothetical protein	0	0	0	0
AR505_0331	hypothetical protein	0	0	0	0
AR505_0332	MORN repeat-containing protein	0	0	0	0
AR505_0333	hypothetical protein	0	0	0	0
AR505_0334	hypothetical protein	0	0	0	0
AR505_0335	hypothetical protein	0	0	0	0
AR505_0336	conserved hypothetical protein	0	0	0	0
AR505_0337	hypothetical protein	0	0	0	0
AR505_0338	hypothetical protein	0	0	0	0
AR505_0339	DNA-cytosine methyltransferase Dcm2	0	0	0	0
AR505_0340	DNA-cytosine methyltransferase Dcm3	0	0	0	0
AR505_0341	hypothetical protein	0	0	0	0
AR505_0342	hypothetical protein	0	0	0	0
AR505_0343	hypothetical protein	0	0	0	0
AR505_0344	hypothetical protein	0	0	0	0
AR505_0345	hypothetical protein	0	0	0	0
AR505_0346	hypothetical protein	0	0	0	0
AR505_0347	hypothetical transmembrane protein	0	0	0	0
AR505_0348	hypothetical transmembrane protein	0	0	0	0
AR505_0349	hypothetical transmembrane protein	0	0	0	0
AR505_0350	hypothetical transmembrane protein	0	0	0	0
AR505_0351	hypothetical transmembrane protein	0	0	0	0
AR505_0352	hypothetical transmembrane protein	0	0	0	0
AR505_0353	adhesin-like protein	0	0	0	0
AR505_0354	adhesin-like protein	0	0	0	0
AR505_0355	adhesin-like protein	0	0	0	0
AR505_0356	hypothetical protein	0	0	0	0
AR505_0357	hypothetical protein	0	0	0	0
AR505_0358	hypothetical protein	0	0	0	0
AR505_0359*	nitrogenase iron protein NifH	84*	34*	57	68
AR505_0360	cobalamin biosynthesis protein CbiX	78	34	35	24
AR505_0361	cell wall biosynthesis protein Mur ligase family	73	28	28	21
AR505_0362	methanogenesis marker protein 13	67	16	27	13
AR505_0363	cobyrinic acid a,c-diamide synthase CbiA	27	5	11	8
AR505_0364	MFS transporter	8	3	2	8
AR505_0365	hypothetical transmembrane protein	176	289	260	155
AR505_0366	TPR repeat-containing protein	143	187	204	281
AR505_0367	TPR repeat-containing protein	60	53	72	68
AR505_0368	TPR repeat-containing protein	41	33	47	58
AR505_0369	sodium Bile acid symporter family	28	29	27	42
AR505_0370	TPR repeat-containing protein	74	76	36	34

AR505_0371	transposase IS605 OrfB family	43	52	38	30
AR505_0372	transposase	28	5	8	8
AR505_0373	TPR repeat-containing protein	31	20	23	13
AR505_0374	DNA polymerase III PolC	45	33	50	25
AR505_0375	hypothetical protein	70	87	115	102
AR505_0376*	N-carbamoyl-D-amino acid amidohydrolase AguB	38	64*	46	26*
AR505_0377*	NAD synthetase NadE	36*	107	129*	95
AR505_0378	cobalt-precorrin-5 (C1)-methyltransferase CbiD	10	3	1	7
AR505_0379	cobalt-precorrin 5A hydrolase CbiG	3	0	2	1
AR505_0380	precorrin-6x reductase CbiJ	15	4	3	12
AR505_0381	cobyrinic acid a,c-diamide synthase CbiA	110	58	71	61
AR505_0382	zinc transporter ZIP9	71	78	97	50
AR505_0383	nickel responsive transcriptional regulator NikR	13	9	7	4
AR505_0384*	hypothetical protein	4047	1276*	3195	4321*
AR505_0385*	transporter Na ⁺ /H ⁺ antiporter family	280*	134	78*	219
AR505_0386	hypothetical protein	21	44	19	21
AR505_0387	lysyl-tRNA synthetase LysS	33	38	35	59
AR505_0388*	DNA topoisomerase VI subunit A	43	21	21*	52*
AR505_0389	DNA topoisomerase VI subunit B	38	15	14	29
AR505_0390	hypothetical transmembrane protein	57	121	63	86
AR505_0391	formamidopyrimidine-DNA glycosylase MutM	3	5	2	8
AR505_0392	hypothetical transmembrane protein	33	22	8	26
AR505_0393	small GTP-binding protein	52	96	48	81
AR505_0394*	histidyl-tRNA synthetase HisS	44*	64	81	103*
AR505_0395	hypothetical protein	25	14	30	40
AR505_0396*	hypothetical protein	46	64*	59	16*
AR505_0397	threonyl-tRNA synthetase ThrS	31	38	19	34
AR505_0398	cobaltochelataze CobN	3	1	1	5
AR505_0399	hypothetical protein	3	4	2	0
AR505_0400	hypothetical protein	9	3	5	4
AR505_0401	hypothetical transmembrane protein	14	14	5	9
AR505_0402	nitrogen regulatory protein P-II	36	5	5	19
AR505_0403	hypothetical protein	29	43	22	73
AR505_0404	magnesium chelatase ChlD	4	1	0	4
AR505_0405	magnesium chelatase ChlI	4	1	3	1
AR505_0406	cobaltochelataze CobN	3	1	1	3
AR505_0407	adhesin-like protein	2	0	1	5
AR505_0408	ABC transporter permease protein	14	18	9	5
AR505_0409	ABC transporter permease protein	6	10	4	3
AR505_0410	ABC transporter ATP-binding protein	12	4	4	10
AR505_0411	ABC transporter permease protein	4	4	2	2
AR505_0412	ABC transporter ATP-binding protein	7	0	0	2
AR505_0413	precorrin-2 C20-methyltransferase CbiL	17	5	10	14
AR505_0414	precorrin-4 C11-methyltransferase CbiF	38	10	11	4
AR505_0415	precorrin-3B C17-methyltransferase CbiH	25	7	2	10
AR505_0416	precorrin-8X methylmutase CbiC	23	11	7	8
AR505_0417	ABC transporter ATP-binding protein	25	5	5	24
AR505_0418*	ABC transporter permease protein	70*	10	8*	11
AR505_0419	SelI repeat-containing protein	10	2	0	5
AR505_0420	ribonuclease H	18	7	5	10
AR505_0421	aspartate 1-decarboxylase PanD	123	123	117	163
AR505_0422	ABC transporter ATP-binding protein	6	4	3	5
AR505_0423	ABC transporter permease protein	7	1	6	8
AR505_0424	hypothetical transmembrane protein	4	1	2	6
AR505_0425	signal transduction protein with CBS domains	52	68	106	65
AR505_0426	ATPase (AAA+ superfamily)	6	4	4	1
AR505_0427	phosphoenolpyruvate synthase PpsA1	174	197	218	191
AR505_0428	HTH domain-containing protein	39	20	48	49
AR505_0429	pyruvate ferredoxin oxidoreductase gamma subunit PorC	240	291	146	181
AR505_0430	pyruvate ferredoxin oxidoreductase delta subunit PorD	414	387	147	197
AR505_0431	pyruvate ferredoxin oxidoreductase alpha subunit PorA	809	526	359	528
AR505_0432	pyruvate ferredoxin oxidoreductase beta subunit PorB	879	419	497	395
AR505_0433	hypothetical transmembrane protein	20	7	9	7
AR505_0434	hypothetical protein	54	31	16	11
AR505_0435	hypothetical protein	94	74	77	39
AR505_0436	aspartate carbamoyltransferase regulatory subunit PyrI	179	260	245	145
AR505_0437	aspartate carbamoyltransferase PyrB	119	161	188	121
AR505_0438	archaeosine tRNA-ribosyltransferase TgtA	26	24	19	36
AR505_0439	hypothetical transmembrane protein	90	37	40	55
AR505_0440	transposase IS4 family	12	9	6	10
AR505_0441	hypothetical transmembrane protein	60	57	38	46
AR505_0442	hypothetical protein	17	0	13	33
AR505_0443*	universal stress protein UspA	57*	62	182	475*
AR505_0444	cobyrinic acid a,c-diamide adenosyltransferase CobO	3	9	15	28
AR505_0445	cell division control protein Cdc48	25	35	25	29

AR505_0446	flavodoxin	24	18	6	24
AR505_0447	oxidoreductase DSBA family	39	61	64	62
AR505_0448	6-O-methylguanine DNA methyltransferase Ogt	57	64	65	43
AR505_0449	aminoacyl-histidine dipeptidase PepD	68	54	58	85
AR505_0450	hypothetical protein	37	40	32	62
AR505_0451	ferredoxin	192	181	587	506
AR505_0452	ferredoxin	354	410	1277	1079
AR505_0453	hypothetical protein	39	39	43	41
AR505_0454	hypothetical protein	78	41	44	52
AR505_0455	isoleucyl-tRNA synthetase IleS	75	52	62	72
AR505_0456*	transporter DMT family	402*	1463*	513	905
AR505_0457	transcriptional regulator LysR family	27	12	17	17
AR505_0458	thiazole biosynthesis adenylyltransferase ThiF3	47	49	45	59
AR505_0469	DNase TatD family	17	21	19	15
AR505_0460*	flap endonuclease Fen	72*	111	121	161*
AR505_0461*	ribulose-phosphate 3-epimerase Rpe	94*	170	224*	186
AR505_0462	transcriptional regulator ArsR family	75	76	56	56
AR505_0463	hypothetical protein	192	243	330	302
AR505_0464*	ribonuclease Z Rnz	109*	54	43*	57
AR505_0465*	HTH/CBS domain-containing protein	52*	20	12	4*
AR505_0466	S-adenosylmethionine synthetase MetK	62	124	47	101
AR505_0467	hypothetical protein	228	377	403	348
AR505_0468	ribosomal protein L40e Rpl40e	9	2	4	2
AR505_0469	hypothetical protein	35	41	31	32
AR505_0470*	phosphopyruvate hydratase Eno	48	55*	28	21*
AR505_0471	Quinolate phosphoribosyltransferase (decarboxylating) NadC	34	21	31	22
AR505_0472	hypothetical protein	34	9	26	3
AR505_0473	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase CobT	37	37	50	44
AR505_0474*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase ApgM	28*	42	72*	38
AR505_0475	hydrogenase maturation factor HypF	24	27	22	33
AR505_0476	ABC transporter solute-binding protein	6	1	0	0
AR505_0477	ABC transporter permease protein	41	22	31	44
AR505_0478	ABC transporter ATP-binding protein	7	3	2	5
AR505_0479	hypothetical protein	1	0	0	1
AR505_0480	hypothetical transmembrane protein	78	194	119	70
AR505_0481	methylthioadenosine phosphorylase MtnP	45	108	76	58
AR505_0482	hypothetical protein	8	1	0	0
AR505_0483	alcohol dehydrogenase	61	30	69	77
AR505_0484	hypothetical protein	95	53	100	52
AR505_0485*	PHP domain-containing protein	147*	67	54*	89
AR505_0486	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase HisE	33	29	32	30
AR505_0487	imidazoleglycerol-phosphate synthase cyclase subunit HisF	72	66	64	56
AR505_0488	imidazoleglycerol-phosphate dehydratase HisB	176	236	278	219
AR505_0489	amino acid-binding protein with ACT domain	12	3	32	8
AR505_0490	chorismate mutase AroH	68	141	88	60
AR505_0491	aspartate-semialdehyde dehydrogenase Asd	74	120	62	77
AR505_0492	hypothetical protein	21	10	7	14
AR505_0493	HipA-like protein	16	3	4	6
AR505_0494	ATP phosphoribosyltransferase HisG	120	144	123	142
AR505_0495	histidinol-phosphate aminotransferase HisC	84	53	56	66
AR505_0496	imidazole glycerol phosphate synthase glutamine amidotransferase subunit HisH	234	86	89	111
AR505_0497	phosphoribosylformimino-5- aminoimidazole carboxamide ribotide isomerase HisA	241	80	81	88
AR505_0498*	transposase IS605 OrfB family	53*	41	32	22*
AR505_0499	2-methylcitrate synthase/citrate synthase II PrpC/GltA1	47	72	37	70
AR505_0500	carbamoyl-phosphate synthase large subunit CarB1	13	4	8	12
AR505_0501	carbamoyl-phosphate synthase small subunit CarA1	12	4	5	5
AR505_0502	hypothetical protein	2	2	0	2
AR505_0503	carbamoyl-phosphate synthase large subunit CarB2	51	13	14	18
AR505_0504	carbamoyl-phosphate synthase small subunit CarA2	31	7	3	6
AR505_0505	ATPase (AAA+ superfamily)	6	5	3	3
AR505_0506	cell division protein pelota PelA	42	52	31	39
AR505_0507	transporter Na ⁺ /H ⁺ antiporter family	26	21	14	22
AR505_0508*	phospho-2-dehydro-3-deoxyheptonate aldolase/fructose-bisphosphate aldolase Fba	115*	338*	288	184
AR505_0509*	3-dehydroquinate synthase AroB1	112*	250*	185	128
AR505_0510	shikimate 5-dehydrogenase AroE	45	51	44	34
AR505_0511	shikimate kinase AroK	16	11	9	3
AR505_0512	3-phosphoshikimate 1-carboxyvinyltransferase AroA	56	53	36	59
AR505_0513	Fic family protein	5	4	5	5
AR505_0514	hypothetical protein	27	55	38	54

AR505_0515	prephenate dehydratase PheA	93	122	89	172
AR505_0516	transposase IS605 OrfB family	80	69	65	31
AR505_0517	ABC transporter ATP-binding protein	24	21	14	30
AR505_0518*	hypothetical protein	37	20*	45*	21
AR505_0519	hypothetical transmembrane protein	43	76	55	84
AR505_0520	ABC transporter ATP-binding protein	120	118	60	120
AR505_0521	ABC transporter permease protein	32	10	13	23
AR505_0522	ATPase (AAA+ superfamily)	14	9	2	11
AR505_0523	transposase IS605 OrfB family	29	28	39	19
AR505_0524	hypothetical protein	41	72	42	42
AR505_0525	transposase	27	10	11	20
AR505_0526	transporter RND family	23	28	46	61
AR505_0527	Fic family protein	19	8	4	7
AR505_0528	transposase	37	3	10	14
AR505_0529	hypothetical protein	32	14	5	16
AR505_0530	ATPase (AAA+ superfamily)	9	11	7	4
AR505_0531	isopropylmalate/isohomocitrate dehydrogenases LeuB	75	89	45	42
AR505_0532*	HTH domain-containing protein	167*	344*	216	239
AR505_0533	hypothetical protein	22	11	15	9
AR505_0534	hypothetical protein	23	23	8	15
AR505_0535	hypothetical protein	214	422	221	288
AR505_0536*	TPR repeat-containing protein	122	195*	88*	125
AR505_0537	SAM-dependent methyltransferase	11	7	6	4
AR505_0538	hypothetical transmembrane protein	22	15	16	7
AR505_0539	polysaccharide biosynthesis protein	33	10	8	16
AR505_0540	cell wall biosynthesis protein glycosyltransferase family	5	3	2	2
AR505_0541	NAD-dependent epimerase/dehydratase	11	4	2	2
AR505_0542	thiamine pyrophosphate-requiring enzymes	37	10	6	7
AR505_0543	CDP-glucose 4,6-dehydratase RfbG	13	2	3	3
AR505_0544	phosphoglycolate/pyridoxal phosphate phosphatase family	4	1	2	1
AR505_0545	4-hydroxy-2-oxovalerate aldolase DmpG	18	7	6	3
AR505_0546	Amidohydrolase family protein	33	58	29	37
AR505_0547	S-adenosyl-L-homocysteine hydrolase AhcY	47	60	53	46
AR505_0548	hypothetical transmembrane protein	141	148	111	123
AR505_0549*	glucose-1-phosphate cytidyltransferase RfbF	141	322*	241	115*
AR505_0550	glycosyl transferase GT2 family	15	11	11	5
AR505_0551	UDP-galactopyranose mutase Glf	17	15	11	7
AR505_0552	glucose-1-phosphate thymidyltransferase RfbA	19	28	24	8
AR505_0553	dTDP-glucose 4,6-dehydratase RfbB	11	12	11	12
AR505_0554	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC	30	10	13	4
AR505_0555	polysaccharide/polyol phosphate ABC transporter permease protein	10	6	4	3
AR505_0556	polysaccharide/polyol phosphate ABC transporter ATP-binding protein	18	7	6	3
AR505_0557	TPR repeat-containing protein	29	6	17	6
AR505_0558*	LPS biosynthesis protein LICD family	120*	75	71	45*
AR505_0559	glycosyl transferase GT8 family	22	8	17	3
AR505_0560	bifunctional phosphoglucose/phosphomannose isomerase	45	16	23	23
AR505_0561	glycosyl transferase GT2 family	33	14	19	13
AR505_0562	hypothetical protein	2	0	1	0
AR505_0563	hypothetical protein	3	5	9	2
AR505_0564	hypothetical protein	2	7	5	7
AR505_0565	hypothetical protein	18	10	15	7
AR505_0566	hypothetical protein	62	73	99	39
AR505_0567	hypothetical protein	5	4	8	5
AR505_0568	hypothetical protein	43	14	54	9
AR505_0569	hypothetical protein	7	8	0	8
AR505_0570	hypothetical protein	9	5	6	1
AR505_0571	hypothetical protein	13	4	2	6
AR505_0572	hypothetical transmembrane protein	21	16	17	8
AR505_0573	hypothetical protein	3	6	4	6
AR505_0574	transposase	46	16	13	20
AR505_0575	hypothetical transmembrane protein	41	44	38	14
AR505_0576	hypothetical protein	57	55	80	39
AR505_0577*	hypothetical protein	85*	240*	121	137
AR505_0578	ribonuclease III Rnc	10	15	18	7
AR505_0579	methionine adenosyltransferase MetK	286	208	323	397
AR505_0580	transposase IS605 OrfB family	44	36	37	20
AR505_0581	hypothetical protein	6	9	4	2
AR505_0582	hypothetical protein	105	126	77	72
AR505_0583	helicase SNF2 family	36	52	49	38
AR505_0584	hypothetical protein	152	109	157	109
AR505_0585	hypothetical protein	45	44	35	24
AR505_0586	hypothetical protein	160	225	146	123
AR505_0587	ATPase (AAA+ superfamily)	39	36	32	24
AR505_0588	hypothetical protein	12	15	10	7

AR505_0589	hypothetical transmembrane protein	3	8	8	5
AR505_0590	hypothetical transmembrane protein	27	36	26	21
AR505_0591	nitroreductase family protein	28	21	18	14
AR505_0592	aconitate hydratase 1 AcnA	35	42	36	37
AR505_0593	hypothetical transmembrane protein	166	65	34	36
AR505_0594*	adhesin-like protein	326*	57	41	26*
AR505_0595	Fic family protein	7	4	3	6
AR505_0596	hypothetical protein	32	39	32	17
AR505_0597	anaerobic cobalt chelatase CbiK	60	88	57	75
AR505_0598	polyphosphate:AMP phosphotransferase	12	27	21	29
AR505_0599	transcriptional regulator	18	14	9	22
AR505_0600	HTH domain-containing protein	525	223	387	222
AR505_0601*	hydroxymethylglutaryl-CoA synthase	672*	197	271	188*
AR505_0602*	acetyl-CoA acetyltransferase	1081*	337	480	277*
AR505_0603*	DNA-binding protein	529*	141	257	91*
AR505_0604	phosphoglycolate phosphatase	73	10	12	17
AR505_0605*	ABC transporter permease protein	142*	26*	38	66
AR505_0606	ABC transporter ATP-binding protein	35	8	9	14
AR505_0607	hypothetical protein	4	5	9	7
AR505_0608	hypothetical protein	20	33	15	33
AR505_0609*	low molecular weight phosphotyrosine protein phosphatase	35*	53	72	157*
AR505_0610	homoserine kinase ThrB	74	85	83	118
AR505_0611	threonine synthase ThrC	174	213	181	204
AR505_0612	Fic family protein	16	12	12	16
AR505_0613	helicase, superfamily II	16	13	10	13
AR505_0614	adhesin-like protein	51	61	39	42
AR505_0615	ATP-dependent protease S16 family	198	122	180	248
AR505_0616	nicotinamide-nucleotide adenyllyltransferase	56	40	52	45
AR505_0617	competence/damage-inducible protein CinA	29	11	16	5
AR505_0618	thiazole biosynthesis adenyllyltransferase ThiF4	21	1	17	11
AR505_0619*	hypothetical transmembrane protein	11*	660	349	727*
AR505_0620	sodium:solute symporter	79	471	365	623
AR505_0621	hypothetical transmembrane protein	22	46	62	70
AR505_0622	phosphoribosylaminoimidazolesuccinocarboxamide synthase PurC	965	1023	1061	1453
AR505_0623	hypothetical protein	19	33	25	18
AR505_0624	protein-tyrosine phosphatase	91	75	51	78
AR505_0625	hypothetical protein	49	33	29	50
AR505_0626	NAD(P)-dependent glycerol-1-phosphate dehydrogenase	81	96	91	71
AR505_0627	NADPH-dependent FMN reductase	281	364	468	435
AR505_0628	hypothetical protein	32	38	21	28
AR505_0629	hypothetical transmembrane protein	151	95	81	76
AR505_0630*	desulfoferrodoxin Dfx	171*	228	414*	226
AR505_0631*	2-isopropylmalate synthase LeuA	69*	175*	105	149
AR505_0632	3-isopropylmalate dehydratase large subunit LeuC	98	95	133	147
AR505_0633	3-isopropylmalate dehydratase small subunit LeuD	77	77	121	109
AR505_0634	3-isopropylmalate dehydrogenase LeuB	114	127	243	210
AR505_0635	hypothetical protein	34	6	19	17
AR505_0636*	pap2 family protein	83	37*	68	88*
AR505_0637	archaeosine tRNA-ribosyltransferase TgtA	81	46	63	82
AR505_0638	hypothetical protein	11	12	14	5
AR505_0639	transposase IS605 OrfB family	82	96	83	54
AR505_0640*	hypothetical protein	1639*	3634	2549	4169*
AR505_0641	TPR repeat-containing protein	111	63	60	104
AR505_0642	peptidyl-tRNA hydrolase	107	107	78	74
AR505_0643	thiamine monophosphate synthase ThiE2	84	60	52	70
AR505_0644	hydroxyethylthiazole kinase ThiM	37	40	30	17
AR505_0645	carbon starvation protein CstA	114	103	55	53
AR505_0646	adhesin-like protein	263	205	136	154
AR505_0647	hypothetical protein	361	312	307	217
AR505_0648	hypothetical protein	185	192	182	159
AR505_0649	hypothetical protein	6	6	2	2
AR505_0650	4-amino-2-methyl-5-hydroxymethylpyrimidine phosphate kinase ThiD	66	34	43	36
AR505_0651*	hypothetical protein	306	466*	291	216*
AR505_0652	hypothetical protein	10	1	3	1
AR505_0653	hypothetical protein	7	2	0	2
AR505_0654	adhesin-like protein	1863	2063	2046	1733
AR505_0655	hypothetical protein	131	105	52	58
AR505_0656	hypothetical transmembrane protein	60	48	22	27
AR505_0657	adhesin-like protein	123	117	124	84
AR505_0658	adhesin-like protein	114	89	91	60
AR505_0659	hypothetical transmembrane protein	615	557	664	370
AR505_0660*	adhesin-like protein	126*	108	101	51*
AR505_0661	hypothetical transmembrane protein	20	12	12	9
AR505_0662	GTPase subunit of restriction endonuclease	13	6	8	7

AR505_0663	McrBC 5-methylcytosine restriction system component	8	0	5	1
AR505_0664*	adhesin-like protein	111*	49*	83	92
AR505_0665	hypothetical protein	2553	1231	1882	2529
AR505_0666	adhesin-like protein	24	8	26	17
AR505_0667*	signal peptidase I	243	434*	182	156*
AR505_0668	adhesin-like protein	10	5	6	11
AR505_0669	integrase catalytic subunit	336	179	223	182
AR505_0670*	adhesin-like protein	310*	206	222	139*
AR505_0671	argininosuccinate lyase ArgH	145	102	125	129
AR505_0672	argininosuccinate synthase ArgG	210	290	260	392
AR505_0673	N-acetyl-gamma-glutamyl-phosphate reductase ArgC	29	37	37	73
AR505_0674	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein ArgJ	45	38	61	59
AR505_0675*	acetylglutamate kinase ArgB	29	15*	48*	34
AR505_0676	acetylornithine aminotransferase ArgD	14	14	15	20
AR505_0677	transposase IS605 OrfB family	102	104	124	39
AR505_0678*	citrate synthase	55*	56	111*	62
AR505_0679	CoB--CoM heterodisulfide reductase subunit B HdrB	24	21	24	35
AR505_0680	3-oxoadipate enol-lactonase PcaD	54	99	60	59
AR505_0681	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	13	38	24	18
AR505_0682	hypothetical transmembrane protein	30	40	25	35
AR505_0683	transglutaminase domain containing protein	72	92	72	55
AR505_0684	hypothetical protein	1	0	1	4
AR505_0685	peptidyl-prolyl cis-trans isomerase FKBP-type	176	461	370	511
AR505_0686	hypothetical protein	15	0	14	6
AR505_0687	hypothetical protein	316	353	371	196
AR505_0688	amidase	97	169	156	98
AR505_0689*	hypothetical transmembrane protein	150	235*	104*	148
AR505_0690	hypothetical protein	194	151	116	210
AR505_0691	hypothetical transmembrane protein	169	161	313	288
AR505_0692	anaerobic sulfatase maturase	71	62	37	37
AR505_0693	endoribonuclease L-PSP	41	30	32	20
AR505_0694	homoserine O-succinyltransferase Meta	44	43	26	21
AR505_0695	cysteine synthase CysK	65	83	52	67
AR505_0696*	transporter CDF family	97*	252	266*	173
AR505_0697	hypothetical protein	44	88	27	40
AR505_0698	hypothetical protein	46	94	54	52
AR505_0699	PHP domain-containing protein	30	26	23	30
AR505_0700	Rubredoxin	25	19	1	14
AR505_0701	ABC transporter ATP-binding protein	35	13	22	38
AR505_0702	peptidase C1A papain	37	37	46	43
AR505_0703	MATE efflux family protein	33	57	36	86
AR505_0704	adhesin-like protein	122	114	136	141
AR505_0705	AMP phosphorylase	74	56	81	100
AR505_0706	GMP synthase subunit A GuaA1	108	230	264	247
AR505_0707	hypothetical protein	15	29	33	27
AR505_0708	transposase	335	178	222	182
AR505_0709	methionyl-tRNA synthetase MetG1	32	27	75	93
AR505_0710	methionyl-tRNA synthetase beta subunit MetG	12	10	16	16
AR505_0711	php domain-containing protein	22	46	45	44
AR505_0712	ABC transporter ATP-binding protein	10	17	9	8
AR505_0713	ABC transporter permease protein	19	4	2	9
AR505_0714	ABC transporter permease protein	11	7	9	11
AR505_0715	ABC transporter solute-binding protein	6	3	5	4
AR505_0716	cobalamin (vitamin B12) biosynthesis protein CbiX	7	2	1	2
AR505_0717	ATPase (AAA+ superfamily)	4	5	5	4
AR505_0718	TfoX N-terminal domain protein	9	10	6	4
AR505_0719	hypothetical protein	9	18	6	17
AR505_0720	hypothetical protein	53	14	39	41
AR505_0721	CAAX amino terminal protease family	62	74	41	73
AR505_0722	von Willebrand factor type A domain protein	29	36	16	17
AR505_0723*	hypothetical transmembrane protein	207*	465*	322	342
AR505_0724	methanogenesis marker protein 16	12	6	9	3
AR505_0725	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	12	0	2	8
AR505_0726	ApbE family protein	16	8	5	4
AR505_0727	hypothetical protein	49	60	54	44
AR505_0728	dihydrodipicolinate reductase DapB	130	102	103	93
AR505_0729	bifunctional protein FolC	32	30	35	50
AR505_0730	hypothetical transmembrane protein	163	258	232	210
AR505_0731	hypothetical transmembrane protein	131	159	177	165
AR505_0732	NAD-dependent deacetylase SIR2 family	10	9	7	3
AR505_0733	macro domain protein	14	7	7	11
AR505_0734	transcriptional regulator HxIR family	8	12	15	8
AR505_0735	hypothetical protein	19	19	18	26
AR505_0736	asparagine synthase AsnB1	8	12	8	10

AR505_0737	Na ⁺ dependent transporter SBF family	22	25	14	26
AR505_0738	<i>O</i> -acetylhomoserine aminocarboxypropyltransferase/cysteine synthase MetC	23	37	23	27
AR505_0739	MFS transporter	37	37	27	23
AR505_0740*	TATA-box-binding protein Tbp	68*	258*	140	207
AR505_0741	hypothetical protein	5	2	1	2
AR505_0742	adenylosuccinate lyase PurB	66	86	58	82
AR505_0743	hypothetical transmembrane protein	43	28	20	16
AR505_0744	adhesin-like protein	132	138	167	112
AR505_0745	hypothetical protein	67	87	134	66
AR505_0746	mechanosensitive ion channel protein	128	102	112	82
AR505_0747	pyridoxamine 5'-phosphate oxidase PPOX	45	43	85	35
AR505_0748	hypothetical protein	48	83	66	80
AR505_0749*	trimethylamine permease	47	27*	119	1143*
AR505_0750*	hypothetical protein	33	27*	72	955*
AR505_0751	hypothetical transmembrane protein	11	10	7	190
AR505_0752	nitrate/sulfonate/bicarbonate ABC transporter ATPase NtrD	348	416	306	571
AR505_0753	nitrate/sulfonate/bicarbonate ABC transporter permease protein NtrB	454	663	409	827
AR505_0754*	nitrate/sulfonate/bicarbonate ABC transporter substrate-binding protein	295*	705	407	771*
AR505_0755	lipid A export permease/ATP-binding protein MsbA	27	26	21	16
AR505_0756	lipid A export permease/ATP-binding protein MsbA	19	10	17	6
AR505_0757	phosphoserine phosphatase SerB	276	257	139	174
AR505_0758	signal recognition particle SRP54 protein	45	28	47	31
AR505_0759	hypothetical protein	47	18	27	8
AR505_0760	hypothetical transmembrane protein	22	19	12	13
AR505_0761	inosine/xanthosine triphosphatase	41	13	18	13
AR505_0762	glycolate oxidase subunit GlcD2	14	7	16	13
AR505_0763	electron transfer flavoprotein beta subunit	7	2	3	11
AR505_0764	electron transfer flavoprotein alpha subunit	10	2	2	7
AR505_0765	phosphomethylpyrimidine kinase ThiD2	146	142	191	177
AR505_0766	peroxiredoxin AhpC	161	246	219	235
AR505_0767	phenylalanyl-tRNA synthetase subunit beta PheT	55	79	80	98
AR505_0768	hydroxymethylglutaryl-CoA reductase (NADPH) HmgA	61	85	85	120
AR505_0769	cobaltochelatase subunit	10	16	12	24
AR505_0770	cobaltochelatase subunit	128	27	33	29
AR505_0771	cobaltochelatase subunit	249	206	196	243
AR505_0772	trimethylamine:corrinoid methyltransferase MttB	6990	5817	7271	8763
AR505_0773	methyltransferase cognate corrinoid proteins MttC	4054	2553	4888	3917
AR505_0774	transcriptional regulator MarR family	57	24	18	16
AR505_0775	NADPH-dependent FMN reductase	57	28	36	22
AR505_0776	ribosomal protein S19e Rps19e	320	181	213	194
AR505_0777*	DNA-binding protein	213*	89*	102	148
AR505_0778	ribosomal protein L39e Rpl39e	332	151	198	216
AR505_0779	ribosomal protein L31e Rpl31e	178	62	108	69
AR505_0780	translation initiation factor aIF-6	55	23	35	46
AR505_0781	Zn-dependent hydrolase	306	73	76	130
AR505_0782	hypothetical transmembrane protein	113	170	130	123
AR505_0783	hypothetical protein	21	29	17	21
AR505_0784	transposase IS4 family	67	57	52	44
AR505_0785	peptidase M50 family (6 TMHs)	115	176	90	153
AR505_0786	methanogenesis marker protein 2	64	99	73	101
AR505_0787	hypothetical protein	11	9	8	12
AR505_0788	signal transduction histidine kinase	82	108	71	94
AR505_0789	hypothetical protein	106	133	84	109
AR505_0790	transcriptional regulator LytR family	112	140	117	85
AR505_0791	transcriptional regulator LytS family	89	171	104	86
AR505_0792	hypothetical protein	14	17	15	10
AR505_0793*	TPR repeat-containing protein	63	95*	58	39*
AR505_0794	hypothetical protein	10	1	2	2
AR505_0795	TPR repeat-containing protein	32	28	25	33
AR505_0796	isochorismatase hydrolase	27	34	33	16
AR505_0797	transcriptional regulator HxIR family	23	34	34	33
AR505_0798	ssDNA exonuclease RecJ2	47	37	38	72
AR505_0799*	<i>O</i> -acetylserine sulfhydrylase	20	15	13*	43*
AR505_0800	cysteine synthase A CysK	10	11	9	29
AR505_0801	HTH domain-containing protein	53	94	53	45
AR505_0802	adhesin-like protein	28	40	18	21
AR505_0803*	hypothetical protein	85*	47	54	27*
AR505_0804	hypothetical protein	45	24	47	29
AR505_0805	ATP-dependent DNA helicase	30	17	27	23
AR505_0806	MFS transporter	48	65	49	92
AR505_0807	adhesin-like protein	85	63	79	104
AR505_0808	hypothetical protein	128	112	79	131

AR505_0809*	tRNA-dihydrouridine synthase DusA	519*	165	126*	280
AR505_0810	transcription initiation factor TFIIB Tfb	763	1324	993	1101
AR505_0811	hypothetical protein	20	39	18	25
AR505_0812	Na/Pi-cotransporter	30	30	15	35
AR505_0813	hypothetical protein	0	0	0	2
AR505_0814	DNA repair helicase Rad3	54	42	40	35
AR505_0815*	Na ⁺ -dependent transporter SBF family	38*	97*	49	63
AR505_0816	adhesin-like protein	102	112	117	93
AR505_0817	hypothetical protein	25	29	73	55
AR505_0818	hypothetical protein	9	35	25	5
AR505_0819	hypothetical protein	292	438	461	313
AR505_0820	hypothetical protein	12	0	0	10
AR505_0821	hypothetical protein	7	15	11	12
AR505_0822	methanogenesis marker protein 16	64	82	74	67
AR505_0823*	hypothetical transmembrane protein	58*	38	32	22*
AR505_0824	HPr kinase	19	11	28	7
AR505_0825	flavodoxin	67	48	37	41
AR505_0826*	hypothetical transmembrane protein	79*	70	29*	58
AR505_0827*	wyosine biosynthesis protein TYW1	58*	22	32	16*
AR505_0828	replication factor C large subunit RfcL	41	52	39	48
AR505_0829	hypothetical transmembrane protein	33	37	21	29
AR505_0830*	amino acid/peptide transporter	58*	23*	31	39
AR505_0831	transcriptional regulator MarR family	43	0	2	2
AR505_0832	molybdate ABC transporter ATP-binding protein ModC	27	24	14	24
AR505_0833*	hypothetical protein	83*	142	187*	130
AR505_0834	hypothetical protein	40	49	39	32
AR505_0835	transporter Na ⁺ /H ⁺ antiporter family	84	69	61	54
AR505_0836	peptidyl-prolyl cis-trans isomerase	32	31	36	30
AR505_0837	cobalt ABC transporter ATP-binding protein CbiO	10	1	3	7
AR505_0838	cobalt ABC transporter ATP-binding protein CbiO	7	2	8	20
AR505_0839	cobalt ABC transporter, permease protein CbiQ	5	1	1	6
AR505_0840	cobalt transport protein CbiN	23	7	2	1
AR505_0841	cobalt transport protein CbiM	7	2	5	4
AR505_0842	hypothetical protein	224	291	349	244
AR505_0843	transcriptional regulator	14	16	22	8
AR505_0844	GNAT family acetyltransferase	28	48	34	32
AR505_0845	hypothetical protein	163	120	132	126
AR505_0846	hypothetical protein	6	3	1	3
AR505_0847	hypothetical protein	249	419	401	389
AR505_0848	hypothetical protein	287	457	473	312
AR505_0849	hypothetical protein	11	4	5	12
AR505_0850*	hypothetical protein	10	3*	18	140*
AR505_0851	adhesin-like protein	156	131	165	155
AR505_0852	hypothetical protein	477	648	703	813
AR505_0853	hypothetical protein	52	79	94	63
AR505_0854	cell division control protein Cdc48	7	7	10	7
AR505_0855	hypothetical protein	23	33	36	6
AR505_0856*	hypothetical transmembrane protein	137	549*	396	52*
AR505_0857	prevent-host-death family protein	128	236	212	254
AR505_0858	addiction module toxin, RelE/StbE family	101	174	122	89
AR505_0859*	transcriptional regulator TetR family	6152*	7818	14364	31275*
AR505_0860	transposase IS605 OrfB family	124	156	173	178
AR505_0861	hypothetical protein	72	150	199	224
AR505_0862	hypothetical protein	11	6	11	6
AR505_0863	ATPase	5	2	7	2
AR505_0864	hypothetical protein	19	9	12	9
AR505_0865	hypothetical protein	3	5	3	2
AR505_0866	hypothetical protein	9	5	4	5
AR505_0867	hypothetical protein	52	48	34	40
AR505_0868	hypothetical protein	9	5	5	10
AR505_0869	hypothetical protein	9	7	6	9
AR505_0870	hypothetical protein	62	83	44	55
AR505_0871	hypothetical protein	148	163	187	214
AR505_0872	hypothetical protein	3	3	1	0
AR505_0873	hypothetical protein	9	2	2	0
AR505_0874	adhesin-like protein	13	11	9	6
AR505_0875	hypothetical protein	5	5	4	7
AR505_0876	hypothetical protein	3	1	5	1
AR505_0877	hypothetical protein	15	12	7	4
AR505_0878	hypothetical protein	3	2	0	9
AR505_0879	hypothetical protein	3	0	0	0
AR505_0880	hypothetical protein	10	5	11	1
AR505_0881	hypothetical protein	9	5	6	1
AR505_0882	hypothetical protein	7	2	2	3
AR505_0883	hypothetical protein	3	3	3	3

AR505_0884	sulfurtransferase DndC	7	8	5	5
AR505_0885	DNA sulfur modification protein DndD	7	4	11	3
AR505_0886	type III restriction endonuclease	4	6	1	0
AR505_0887	hypothetical protein	12	3	6	3
AR505_0888	hypothetical protein	6	3	3	0
AR505_0889	hypothetical protein	29	15	17	11
AR505_0890	SMC domain-containing protein	1	1	1	1
AR505_0891	SMC domain-containing protein	3	3	0	0
AR505_0892	geranylgeranyl reductase family protein	6	14	11	8
AR505_0893	ATPase	2	4	5	0
AR505_0894	hypothetical protein	23	38	35	23
AR505_0895	ATPase	10	9	12	8
AR505_0896	hypothetical protein	475	98	72	110
AR505_0897*	hypothetical protein	166*	72	60	33*
AR505_0898	TPR repeat-containing protein	83	106	121	165
AR505_0899	TPR repeat-containing protein	51	51	54	36
AR505_0900	ATPase	7	9	4	2
AR505_0901	hypothetical protein	17	28	19	10
AR505_0902*	Fe-S oxidoreductase	43	87*	71	41*
AR505_0903*	transposase IS605 OrfB family	100*	139	223*	133
AR505_0904	GNAT family acetyltransferases	66	23	36	37
AR505_0905*	EamA-like transporter family	52	25*	33	68*
AR505_0906	hypothetical protein	94	67	66	55
AR505_0907	peptidase U62, modulator of DNA gyrase	83	121	110	145
AR505_0908	peptidase U62 modulator of DNA gyrase	82	96	96	92
AR505_0909*	cell surface protein	128	263*	114*	164
AR505_0910	hypothetical protein	133	220	154	136
AR505_0911	MFS transporter	76	61	47	40
AR505_0912	hypothetical transmembrane protein	54	36	44	37
AR505_0913	transposase IS605 OrfB family	97	136	156	148
AR505_0914	hypothetical protein	149	293	180	181
AR505_0915	NADPH-dependent FMN reductase	121	236	149	177
AR505_0916	hypothetical protein	171	234	162	245
AR505_0917	TPR repeat-containing protein	158	271	205	245
AR505_0918	CDP-alcohol phosphatidyltransferase	13	20	6	11
AR505_0919	proline-specific peptidases	57	72	67	52
AR505_0920	hypothetical protein	24	18	28	14
AR505_0921*	hypothetical protein	78	143*	76	56*
AR505_0922	DNA-directed RNA polymerase subunit K RpoK	8	2	2	8
AR505_0923	hypothetical transmembrane protein	12	2	5	12
AR505_0924*	pyridoxamine 5'-phosphate oxidase family protein	103*	140	211	267*
AR505_0925	hypothetical protein	106	233	136	159
AR505_0926	NfeD family protein	138	174	211	243
AR505_0927	SPFH domain / Band 7 family protein	141	250	270	256
AR505_0928	acyl carrier protein phosphodiesterase AcpD	8	15	17	16
AR505_0929	hypothetical protein	3	3	0	6
AR505_0930	hypothetical protein	8	23	13	31
AR505_0931*	phage integrase	19*	164*	81	111
AR505_0932*	fructose-bisphosphate aldolase Fba	3016	2045*	4228	5566*
AR505_0933	cardiolipin synthase	63	73	50	48
AR505_0934	hypothetical transmembrane protein	24	28	16	16
AR505_0935*	PHP domain-containing protein	30*	56	59	87*
AR505_0936	hypothetical protein	13	13	31	3
AR505_0937	nucleoside 2-deoxyribosyltransferase	11	12	7	7
AR505_0938	FeS assembly ATPase SufC	94	200	110	136
AR505_0939*	FeS assembly protein SufBD	40*	88*	37	57
AR505_0940	hypothetical transmembrane protein	15	11	6	14
AR505_0941	MFS transporter	7	3	3	3
AR505_0942*	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase GpmA	50	89	40*	104*
AR505_0943	GNAT family acetyltransferase	38	76	43	69
AR505_0944	amino acid carrier protein AgcS	83	53	49	59
AR505_0945	hypothetical protein	128	106	77	98
AR505_0946*	hypothetical protein	129	193*	150	70*
AR505_0947*	cobalamin biosynthesis protein CobW	48*	76	115*	65
AR505_0948*	hypothetical protein	841*	1131	1639*	1214
AR505_0949	methanol-cobalamin methyltransferase B subunit MtaB1	537	76	67	88
AR505_0950	methanol corrinoid protein MtaC1	421	85	38	40
AR505_0951	methanol-cobalamin methyltransferase B subunit MtaB2	440	451	1378	1395
AR505_0952	methanol corrinoid protein MtaC2	455	449	1441	1324
AR505_0953	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	50	94	109	101
AR505_0954*	hypothetical protein	147*	30*	46	45
AR505_0955	transcriptional regulator HxIR family	85	40	60	73
AR505_0956	hydroxylamine reductase Hcp	95	13	75	116
AR505_0957	HPP family protein	26	39	28	29

AR505_0958	viral recombinase YgaJ family	44	57	51	62
AR505_0959	hypothetical protein	74	140	127	168
AR505_0960*	Arylsulfotransferase AssT	66*	104	109	152*
AR505_0961	hypothetical protein	7	0	4	5
AR505_0962	Type II/IV secretion system protein	9	3	6	9
AR505_0963	hydroase HD superfamily	12	24	8	7
AR505_0964	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent NrdJ	237	310	182	181
AR505_0965	hypothetical protein	38	40	37	33
AR505_0966	hypothetical protein	13	9	20	5
AR505_0967	proteasome endopeptidase complex	177	150	232	170
AR505_0968	universal archaeal KH-domain/beta-lactamase-domain protein	38	18	31	20
AR505_0969	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	53	12	23	13
AR505_0970	oxidoreductase	44	14	31	26
AR505_0971	hypothetical protein	38	21	28	57
AR505_0972	leucyl-tRNA synthetase LeuS	31	42	35	59
AR505_0973	SAM-dependent methyltransferase	25	54	42	47
AR505_0974*	hypothetical protein	968	509*	790	1631*
AR505_0975*	cell division protein FtsZ	664*	308*	423	531
AR505_0976	NADPH-dependent FMN reductase	96	109	126	85
AR505_0977	hypothetical protein	6	1	2	0
AR505_0978	flavodoxin-like protein	133	156	148	192
AR505_0979	HTH domain-containing protein	11	10	10	2
AR505_0980	toxin-antitoxin system, toxin component, HipA family	22	2	6	9
AR505_0981	SAM-dependent methyltransferases	59	21	16	28
AR505_0982	transcriptional regulator ArsR family	25	7	14	5
AR505_0983	ATPase	21	7	5	8
AR505_0984	sugar fermentation stimulation protein SfsA	14	4	13	15
AR505_0985*	adhesin-like protein	198*	327	546*	422
AR505_0986	signal peptidase I	18	5	9	12
AR505_0987	hypothetical protein	245	359	188	353
AR505_0988*	hypothetical transmembrane protein	289	211*	390	599*
AR505_0989	adhesin-like protein	178	103	190	121
AR505_0990	hypothetical transmembrane protein	78	32	73	63
AR505_0991	adhesin-like protein	45	22	28	35
AR505_0992	adhesin-like protein	63	32	70	55
AR505_0993	hypothetical transmembrane protein	41	33	46	34
AR505_0994	hypothetical protein	18	11	4	18
AR505_0995	xanthine/uracil permease family protein	26	21	17	20
AR505_0996	acetyltransferase	6	7	8	10
AR505_0997	anthranilate phosphoribosyltransferase TrpD	39	31	34	32
AR505_0998	indolepyruvate ferredoxin oxidoreductase beta subunit IorB	52	25	57	19
AR505_0999	indolepyruvate ferredoxin oxidoreductase alpha subunit IorA	42	30	26	42
AR505_1000	short-chain dehydrogenase/reductase SDR	45	27	24	28
AR505_1001	peptidase U32 family	132	167	98	183
AR505_1002	conserved hypothetical	23	10	15	7
AR505_1003	conserved hypothetical	89	89	20	32
AR505_1004	hypothetical protein	41	37	24	15
AR505_1005	flagellin N-methylase FliB	12	15	14	5
AR505_1006	hypothetical transmembrane protein	105	112	55	55
AR505_1007	fic family protein	13	4	4	7
AR505_1008*	SAM-dependent methyltransferases	16*	42	34	89*
AR505_1009	phenylacetate-CoA ligase PaaF1	66	124	111	135
AR505_1010	amino acid-binding ACT domain-containing protein	51	80	59	41
AR505_1011	elongation factor Tu domain 2 protein	219	84	90	95
AR505_1012	transcriptional regulator XRE family	49	64	48	68
AR505_1013	hypothetical transmembrane protein	55	40	34	51
AR505_1014	ABC transporter ATP-binding protein	170	86	84	109
AR505_1015	ABC transporter permease protein	94	50	64	55
AR505_1016*	hypothetical protein	134*	41	21*	30
AR505_1017	phenylacetate-CoA ligase PaaF2	15	20	11	34
AR505_1018	hypothetical transmembrane protein	27	16	7	19
AR505_1019	Raf kinase inhibitor-like protein	30	48	42	28
AR505_1020	TPR repeat-containing protein	19	17	18	17
AR505_1021	2'-5' RNA ligase	11	5	15	130
AR505_1022*	hypothetical protein	38	22*	34	245*
AR505_1023	ATP/GTP-binding protein	2	6	4	2
AR505_1024	hypothetical transmembrane protein	9	7	13	9
AR505_1025	hypothetical transmembrane protein	1	0	1	11
AR505_1026	hypothetical transmembrane protein	10	28	11	7
AR505_1027*	cysteine desulfurase SufS subfamily SufS	33*	80*	44	44
AR505_1028	peptidyl-prolyl cis-trans isomerase	23	36	78	42
AR505_1029	dihydroorotate dehydrogenase PyrD	97	131	128	125
AR505_1030	dihydroorotate dehydrogenase electron transfer subunit PyrK	87	143	81	130
AR505_1031	hypothetical protein	10	10	1	8

AR505_1032*	adhesin-like protein	63*	157*	127	84
AR505_1033	adhesin-like protein	40	50	46	29
AR505_1034	MatE efflux family protein	45	46	38	38
AR505_1035	methylcobalamin:coenzyme M methyltransferase MtaA1	28	29	30	54
AR505_1036	hypothetical protein	9	5	6	7
AR505_1037	DNA polymerase IV	14	12	17	5
AR505_1038	hypothetical protein	122	213	204	253
AR505_1039*	NADPH-dependent FMN reductase	122*	194	207	284*
AR505_1040	uroporphyrinogen III synthase HemD	9	3	5	5
AR505_1041	uroporphyrin-III C-methyltransferase CorA	33	9	25	17
AR505_1042	porphobilinogen deaminase HemC	37	10	13	11
AR505_1043	glutamate-1-semialdehyde aminomutase HemL	41	14	24	16
AR505_1044	porphobilinogen synthase HemB	45	31	53	37
AR505_1045	glutamyl-tRNA reductase HemA	26	13	24	15
AR505_1046	siroheme synthase CysG	42	33	27	28
AR505_1047	rubredoxin	34	35	69	76
AR505_1048	TPR repeat-containing protein	60	62	106	89
AR505_1049	adhesin-like protein	6	5	6	20
AR505_1050	hypothetical protein	6	3	3	2
AR505_1051	hypothetical protein	23	17	24	21
AR505_1052	MFS transporter	104	104	114	224
AR505_1053*	hypothetical protein	115	143*	115	49*
AR505_1054	hypothetical protein	230	357	459	217
AR505_1055*	site-specific recombinase	97*	13	10*	29
AR505_1055	site-specific recombinase	103	18	18	29
AR505_1058	hypothetical protein	17	5	6	12
AR505_1059	FeS cluster assembly scaffold protein NifU	1	3	3	5
AR505_1060	cysteine desulfurase NifS	5	2	3	10
AR505_1061	hypothetical protein	13	2	12	6
AR505_1062*	thermosome subunit	578*	844	1243*	1007
AR505_1063	methylcobalamin:coenzyme M methyltransferase MtaA2	1002	1100	1206	1356
AR505_1064	methyltransferase cognate corrinoid protein	1571	1852	1811	1751
AR505_1065	MFS transporter	1117	1686	1296	1310
AR505_1066*	methylcobalamin:coenzyme M methyltransferase MtaA	52*	63	105	881*
AR505_1067	methyltransferase cognate corrinoid proteins	49	57	81	785
AR505_1068*	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	149	116*	222	1139*
AR505_1069	DNA repair photolyase	26	41	42	78
AR505_1070	conserved hypothetical protein	27	29	43	33
AR505_1071	exopolyphosphatase Ppx	43	21	24	19
AR505_1072	polyphosphate kinase Ppk	195	231	257	219
AR505_1073*	histidinol dehydrogenase HisD	155*	412*	307	384
AR505_1074	potassium uptake protein TrkA family	58	44	54	50
AR505_1075	potassium uptake protein TrkH family	30	14	19	30
AR505_1076	drug resistance transporter Bcr/CflA subfamily	33	18	13	18
AR505_1077	hypothetical protein	34	40	29	33
AR505_1078	hypothetical protein	32	46	27	38
AR505_1079	ATPase	66	129	77	111
AR505_1080	hypothetical protein	11	13	4	3
AR505_1081	small multidrug resistance protein	13	15	13	19
AR505_1082	small multidrug resistance protein	19	19	21	33
AR505_1083*	hypothetical protein	155*	77	104	53*
AR505_1084	exodeoxyribonuclease VII small subunit XseB	197	189	177	126
AR505_1085	exodeoxyribonuclease VII large subunit XseA	21	15	19	25
AR505_1086	phenylacetic acid degradation protein PaaD	19	20	18	16
AR505_1087	hypothetical protein	63	35	40	27
AR505_1088	hypothetical protein	87	60	101	75
AR505_1089	CRISPR-associated endonuclease Cas3-HD	11	3	2	2
AR505_1090	CRISPR type I-E/ECOLI-associated protein CasA/Cse1	16	4	7	4
AR505_1091	CRISPR type I-E/ECOLI-associated protein CasB/Cse2 complex	14	7	4	0
AR505_1092*	CRISPR-associated protein Cas7/Cse4/CasC	67*	12	21	10*
AR505_1093	CRISPR-associated protein Cas5/CasD	26	6	10	1
AR505_1094	CRISPR-associated protein Cas6/Cse3/CasE	27	3	3	4
AR505_1095	CRISPR-associated endonuclease Cas1	16	5	1	0
AR505_1096	hypothetical protein	80	81	49	23
AR505_1097*	hypothetical protein	79	101*	71	38*
AR505_1098	hypothetical protein	16	11	6	15
AR505_1099	transcriptional regulator MarR family	36	35	14	26
AR505_1100	K ⁺ -dependent Na ⁺ /Ca ²⁺ exchanger	48	43	17	23
AR505_1101	ABC transporter ATP-binding protein	25	16	19	13
AR505_1102	thymidylate kinase Tmk1	25	11	15	9
AR505_1103	hypothetical protein	18	14	13	10
AR505_1104	phosphoenolpyruvate synthase PpsA2	31	27	36	55
AR505_1105	conserved hypothetical protein	55	66	83	91
AR505_1106	dolichol kinase (7 TMHs)	27	28	15	20
AR505_1107*	hypothetical protein	28*	41	84*	60

AR505_1108*	conserved hypothetical protein	198*	524	740*	498
AR505_1109	hypothetical transmembrane protein	182	197	259	143
AR505_1110	hypothetical transmembrane protein	844	1058	838	639
AR505_1111	hypothetical protein	0	0	0	2
AR505_1112	hypothetical protein	36	25	31	28
AR505_1113	hypothetical protein	21	11	19	14
AR505_1114	conserved hypothetical protein	30	22	22	18
AR505_1115*	DEAD/DEAH box helicase domain-containing protein	57*	26	22*	34
AR505_1116	hypothetical protein	38	17	16	29
AR505_1117	ATP-dependent RNA helicase	34	15	17	28
AR505_1118*	MTA/SAH nucleosidase MtnN	35	61*	26*	45
AR505_1119	hypothetical protein	92	87	230	57
AR505_1120	aspartokinase beta subunit	33	42	50	52
AR505_1121	glutamyl-tRNA synthetase GltX	69	97	76	127
AR505_1122	hypothetical protein	69	49	58	53
AR505_1123	hypothetical protein	216	264	259	143
AR505_1124	hypothetical protein	15	13	17	5
AR505_1125	hypothetical protein	11	9	8	7
AR505_1126	hypothetical protein	79	130	99	62
AR505_1127*	hypothetical protein	42*	119*	73	96
AR505_1128	hypothetical protein	15	48	44	52
AR505_1129	hypothetical protein	87	83	45	49
AR505_1130	hypothetical protein	44	69	31	26
AR505_1131	hypothetical protein	23	15	10	11
AR505_1132	ATP-dependent DNA helicase UvrD/REP family	30	13	15	9
AR505_1133	cation-transporting P-type ATPase	91	89	60	71
AR505_1134	hypothetical protein	37	37	39	63
AR505_1135	hypothetical protein	47	26	19	35
AR505_1136	cobyric acid synthase CbiP	42	38	19	29
AR505_1137	cobyric acid synthase CbiP	24	18	13	22
AR505_1138*	transporter SDF family	21	34	18*	52*
AR505_1139	exonuclease	76	39	60	71
AR505_1140	hypothetical transmembrane protein	43	34	34	34
AR505_1141	hypothetical protein	134	81	95	90
AR505_1142	DNA primase DnaG	67	20	72	68
AR505_1143	ATP-dependent protease	102	89	93	89
AR505_1144	hypothetical protein	79	93	74	38
AR505_1145	TPR repeat-containing protein	27	20	34	10
AR505_1146*	ribosomal-protein-alanine acetyltransferase RimI	28	59*	29	22*
AR505_1147	phospholipase D/transphosphatidylase PID	10	7	9	8
AR505_1148	triose-phosphate isomerase TpiA	62	17	26	15
AR505_1149*	fructose 1,6-bisphosphatase Fbp	194*	156	159	93*
AR505_1150	aspartyl-tRNA synthetase AspS2	87	109	73	112
AR505_1151	tryptophan synthase beta subunit TrpB	75	87	213	93
AR505_1151	tryptophan synthase beta subunit TrpB	109	105	240	127
AR505_1154	archaeal Holliday junction resolvase Hjc	212	271	246	233
AR505_1155*	quinolinate synthetase A protein NadA	113	196*	98*	186
AR505_1156	adhesin-like protein	65	34	43	51
AR505_1157*	hypothetical protein	4*	48*	27	23
AR505_1158	anthranilate synthase component I TrpE	9	6	39	14
AR505_1159	anthranilate synthase component II TrpG	13	10	23	15
AR505_1160	anthranilate phosphoribosyltransferase TrpD2	9	8	78	17
AR505_1161	indole-3-glycerol phosphate synthase TrpC	11	6	28	11
AR505_1162	phosphoribosylanthranilate isomerase TrpF	8	9	9	5
AR505_1163	tryptophan synthase beta subunit TrpB	11	6	14	24
AR505_1164	tryptophan synthase alpha subunit TrpA	26	29	40	29
AR505_1165	NTPase	51	36	40	22
AR505_1166	N ² ,N ² -dimethylguanosine tRNA methyltransferase Trm1	13	1	5	9
AR505_1167	hypothetical protein	6	3	8	19
AR505_1168	adenylosuccinate synthase PurA	170	200	106	139
AR505_1169	signal transduction histidine kinase	15	4	9	11
AR505_1170*	signal transduction histidine kinase	20*	61	31	117*
AR505_1171*	hypothetical protein	33*	85	55	86*
AR505_1172	3-octaprenyl-4-hydroxybenzoate decarboxylase UbiD	45	52	67	61
AR505_1173	hypothetical transmembrane protein	16	7	6	7
AR505_1174	hypothetical protein	22	23	19	9
AR505_1175	hypothetical protein	30	31	18	17
AR505_1176	transcriptional regulator TetR family	158	334	324	134
AR505_1177*	MMPL domain-containing protein	69*	15	10*	19
AR505_1178*	radical SAM domain containing protein	364	459	250*	583*
AR505_1179	metal dependent transcriptional regulator	142	208	167	192
AR505_1180	3,4-dihydroxy-2-butanone-4-phosphate synthase RibB	83	135	151	173
AR505_1181	FAD synthase	45	67	69	114
AR505_1182	riboflavin synthase RibC	51	54	81	44
AR505_1183	6,7-dimethyl-8-ribityllumazine synthase RibH	56	77	102	67

AR505_1184	formate/nitrite transporter FdhC	90	81	59	45
AR505_1185*	hydrogenase nickel insertion protein HypA1	14*	15	34	1017*
AR505_1186	hypothetical transmembrane protein	23	47	13	26
AR505_1187*	conserved hypothetical	221	1091*	159*	474
AR505_1188*	hypothetical transmembrane protein	67	125*	45*	102
AR505_1189	flavoredoxin family protein	23	27	22	23
AR505_1190	hypothetical protein	39	8	4	14
AR505_1191	cysteinyI-tRNA synthetase CysS	67	104	73	102
AR505_1192	serine O-acetyltransferase CysE	211	338	380	314
AR505_1193	phosphoadenosine phosphosulfate reductase family protein	35	46	46	64
AR505_1194	SAM-dependent methyltransferase	3	5	3	2
AR505_1195	ABC transporter substrate-binding protein	16	11	6	7
AR505_1196	SAM-dependent methyltransferase	5	0	4	2
AR505_1197	ABC transporter permease protein	9	8	6	13
AR505_1198	ABC transporter ATP-binding protein	6	9	12	5
AR505_1199	alanine aminotransferase	116	103	121	172
AR505_1200	hypothetical transmembrane protein	213	161	197	202
AR505_1201	hypothetical protein	151	72	87	81
AR505_1202	hypothetical protein	180	143	93	112
AR505_1203	methanogenesis marker protein 8	115	145	194	154
AR505_1204	PP-loop domain-containing protein	151	137	101	89
AR505_1205	cdc6 family replication initiation protein Cdc6	44	36	51	58
AR505_1206	NIF3 family protein	33	59	52	44
AR505_1207	hypothetical transmembrane protein	49	35	33	33
AR505_1208	hypothetical transmembrane protein	19	17	21	24
AR505_1209	replication factor C small subunit	23	10	28	16
AR505_1210	hypothetical protein	19	22	40	24
AR505_1211	coenzyme F ₃₉₀ synthetase FtsA	38	30	74	34
AR505_1212	TPR repeat-containing protein	41	9	23	14
AR505_1213	TPR repeat-containing protein	109	57	92	72
AR505_1214	TPR repeat-containing protein	79	49	72	51
AR505_1215	hypothetical protein	13	8	12	6
AR505_1216*	TPR repeat-containing protein	63	98*	42*	51
AR505_1217	formate-tetrahydrofolate ligase	357	598	482	324
AR505_1218*	haloacid dehalogenase-like hydrolase	696	901*	490	311*
AR505_1219*	transposase IS605 OrfB family	99	124*	112	42*
AR505_1220*	hypothetical transmembrane protein	42	103*	69	26*
AR505_1221	hypothetical transmembrane protein	22	28	6	12
AR505_1222*	ferrous iron transport protein B FeoB	89*	43	16*	32
AR505_1223	ferrous iron transport protein A FeoA	70	24	16	23
AR505_1224*	hypothetical protein	100*	81	32*	50
AR505_1225	TPR repeat-containing protein	34	61	50	65
AR505_1226	transcriptional regulator ArsR family	14	12	44	45
AR505_1227*	heavy metal translocating P-type ATPase	46	26*	46	63*
AR505_1228	chaperone protein DnaK2	31	9	5	7
AR505_1229	transcriptional regulator	37	12	15	21
AR505_1230	hypothetical protein	29	5	8	21
AR505_1231	hypothetical protein	20	10	12	11
AR505_1232	chaperone protein DnaK3	43	25	25	39
AR505_1233*	pseudouridylyl synthase	48	87*	38*	63
AR505_1234	Pirin family protein	106	108	114	131
AR505_1235	peptidyl-prolyl cis-trans isomerase	16	6	8	0
AR505_1236	archaeal histone	10	8	2	1
AR505_1237	transcriptional regulator HxIR family	213	298	165	187
AR505_1238	hypothetical protein	292	170	205	412
AR505_1239	transposase	53	29	42	44
AR505_1240	cell wall/surface repeat-containing protein	94	76	68	58
AR505_1241	hypothetical protein	15	25	21	29
AR505_1242*	dimethylamine permease	29	17*	58	223*
AR505_1243	nucleotide pyrophosphatase MazG	12	35	31	28
AR505_1244	GNAT family acetyltransferases	16	17	13	11
AR505_1245	carbonic anhydrase Cab	23	16	16	9
AR505_1246	Na ⁺ -driven multidrug efflux pump	23	23	15	27
AR505_1247	anaerobic ribonucleoside-triphosphate reductase NrdD	34	27	20	19
AR505_1248	ATP-dependent chaperone protein ClpB	130	120	107	86
AR505_1249	hypothetical protein	132	109	105	86
AR505_1250	hypothetical protein	291	268	227	237
AR505_1251	DNA helicase	294	281	154	187
AR505_1252	hypothetical protein	904	710	395	589
AR505_1253	hypothetical protein	28	34	23	32
AR505_1254	hypothetical protein	58	131	40	41
AR505_1255	hypothetical protein	7	3	2	3
AR505_1256	hypothetical protein	73	77	122	82
AR505_1257*	NYN domain-containing protein	87*	127	229*	174
AR505_1258	hypothetical protein	16	23	29	14

AR505_1259	hypothetical protein	7	5	4	2
AR505_1260	hypothetical protein	13	48	30	40
AR505_1261	hypothetical protein	36	48	26	38
AR505_1262	hypothetical protein	32	22	18	9
AR505_1263*	molybdenum cofactor biosynthesis protein MoaA1	189*	24*	64	35
AR505_1264	hypothetical protein	76	13	10	6
AR505_1265	hypothetical protein	72	6	7	9
AR505_1266	hypothetical protein	18	3	10	0
AR505_1266*	hypothetical protein	283*	53	35	27*
AR505_1267	helicase	18	10	13	10
AR505_1268	dinitrogenase iron-molybdenum cofactor biosynthesis protein	26	22	11	29
AR505_1269	hypothetical transmembrane protein	51	52	42	64
AR505_1270	hypothetical protein	176	351	220	208
AR505_1271	heavy metal translocating P-type ATPase	440	747	447	550
AR505_1272	transporter MIP family	167	124	94	112
AR505_1273	TPR repeat-containing protein	56	51	39	60
AR505_1274*	tRNA pseudouridine synthase D TruD	73*	47	32*	56
AR505_1275	hypothetical protein	42	53	24	40
AR505_1276	hypothetical protein	6	17	15	25
AR505_1277	ATP-dependent DNA ligase DnII	65	91	76	114
AR505_1278	DEAD/DEAH box helicase domain-containing protein	61	65	51	44
AR505_1279	iron-sulfur cluster assembly protein	444	480	774	610
AR505_1280	carboxymuconolactone decarboxylase family protein	85	215	173	170
AR505_1281*	hypothetical protein	151*	51*	104	134
AR505_1282	acetyl-CoA synthetase AcsA	165	102	152	102
AR505_1283	hypothetical transmembrane protein	21	24	23	67
AR505_1284	diphthine synthase DphB	56	68	56	40
AR505_1285	SAM-dependent methyltransferase	15	9	10	10
AR505_1286	hypothetical protein	149	126	167	93
AR505_1287	deoxycytidine triphosphate deaminase Dcd	174	190	232	229
AR505_1288	oxidoreductase/nitrogenase component 1	21	9	11	23
AR505_1289	nitrogenase	12	3	4	12
AR505_1290	adhesin-like protein	5	5	3	6
AR505_1291	ABC transporter ATP-binding protein	5	1	2	0
AR505_1292	ABC transporter permease protein	10	3	3	4
AR505_1293	ABC transporter substrate-binding protein	5	2	1	0
AR505_1294	threonine-phosphate decarboxylase CobD	20	26	29	31
AR505_1295	Adenosylcobinamide-phosphate synthase CbiB	18	8	6	16
AR505_1296	adenosylcobinamide amidohydrolase CbiZ	28	32	14	17
AR505_1297*	adenosylcobalamin synthase CobS	115*	45	39	26*
AR505_1298	GTP:adenosylcobinamide-phosphate guanylyltransferase CobU	36	4	8	8
AR505_1299	DNA topoisomerase I TopA	15	5	11	20
AR505_1300*	hypothetical protein	138*	30*	30	76
AR505_1301*	hypothetical protein	320*	119	130*	215
AR505_1302	nickel-responsive transcriptional regulator NikR	87	69	78	59
AR505_1303	asparagine synthase (glutamine-hydrolyzing) AsnB	27	28	51	34
AR505_1304	bifunctional protein FolC2	38	47	54	50
AR505_1305	endonuclease III Nth	17	13	11	18
AR505_1306	hydrogenase nickel insertion protein HypA2	87	107	80	88
AR505_1307	hydrogenase expression/formation protein HypD	71	91	73	107
AR505_1308	hypothetical protein	58	43	71	76
AR505_1309	DNA alkylation repair enzyme	76	62	57	82
AR505_1310*	small multidrug resistance protein	30	11*	34	163*
AR505_1311*	small multidrug resistance protein	29	5*	30	99*
AR505_1312	hypothetical protein	329	417	284	393
AR505_1313*	hypothetical transmembrane protein	218*	488*	310	313
AR505_1314	HTH domain-containing protein	422	384	386	283
AR505_1315*	hypothetical protein	311	575*	370	273*
AR505_1316	1,4-dihydroxy-2-naphthoate octaprenyltransferase MenA	161	387	204	218
AR505_1317	ubiquinone/menaquinone biosynthesis methyltransferase	124	192	151	177
AR505_1318	peptidase M18 family	58	132	170	175
AR505_1319	hypothetical protein	6	14	14	10
AR505_1320	Methyltransferase corrinoid activation protein	208	227	259	228
AR505_1321	ATP-dependent RNA helicase	48	15	17	17
AR505_1322*	pyrrolysine biosynthesis protein PylD	179*	99	105	55*
AR505_1323*	pyrrolysine biosynthesis protein PylC	198*	107	127	90*
AR505_1324	pyrrolysine biosynthesis radical SAM protein PylB	137	126	144	104
AR505_1325*	pyrrolysine--tRNA ligase PylS	289*	769*	428	514
AR505_1326	hypothetical protein	146	220	145	281
AR505_1327	monomethylamine methyltransferase MtmB	38	42	29	35
AR505_1328*	monomethylamine methyltransferase MtmB	132	72*	145	559*
AR505_1329*	methyltransferase cognate corrinoid proteins	75	49*	76	291*
AR505_1330	methyltransferase cognate corrinoid proteins	16	12	18	45
AR505_1331	dimethylamine permease	17	6	11	17
AR505_1332*	dimethylamine:corrinoid methyltransferase MtbB	1183	1018*	2138	3030*

AR505_1333*	dimethylamine corrinoid protein	1800*	2213	3479	5257*
AR505_1334	TPR repeat-containing protein	50	65	57	57
AR505_1335*	conserved hypothetical protein	79	101	185*	73*
AR505_1336	YbaK/EbsC family protein	40	29	41	31
AR505_1337	DEAD/DEAH box helicase domain-containing protein	79	57	66	82
AR505_1338	NADPH-dependent FMN reductase	26	29	33	27
AR505_1339	valyl-tRNA synthetase ValS	62	65	63	79
AR505_1340	IMP dehydrogenase	298	319	402	530
AR505_1341	glycyl-tRNA synthetase GlyS	109	52	66	131
AR505_1342	CBS domain-containing protein	97	92	44	54
AR505_1343	universal stress protein UspA	56	54	63	51
AR505_1344	amidohydrolase	156	208	324	300
AR505_1345	hypothetical protein	11	4	5	9
AR505_1346	thioredoxin-disulfide reductase TrxB2	53	27	26	28
AR505_1347	hypothetical transmembrane protein	21	12	14	14
AR505_1348	hypothetical protein	277	514	421	283
AR505_1349	hypothetical protein	51	52	112	138
AR505_1350	hypothetical transmembrane protein	87	99	59	43
AR505_1351*	TPR repeat-containing protein	51	92*	40*	59
AR505_1352	alpha/beta hydrolase fold protein	110	130	69	84
AR505_1353	rubrerythrin Rbr	954	1175	1232	880
AR505_1354	hypothetical transmembrane protein	115	84	124	102
AR505_1355	hypothetical protein	48	19	52	14
AR505_1356	transposase IS4 family	67	55	51	43
AR505_1357	gliding motility-associated protein GldE	54	54	41	39
AR505_1358	exosome subunit	86	59	59	60
AR505_1359	hypothetical transmembrane protein	105	93	61	82
AR505_1360	hypothetical protein	10	7	19	7
AR505_1361	hypothetical protein	8	4	3	5
AR505_1362	hypothetical protein	20	12	14	0
AR505_1363	hypothetical protein	27	19	16	16
AR505_1364	hypothetical protein	17	7	8	9
AR505_1365	hypothetical protein	53	89	53	66
AR505_1366	hypothetical protein	3	0	0	4
AR505_1367	Archaeal ATPase	14	9	16	5
AR505_1368	hypothetical protein	11	7	9	6
AR505_1369*	ATP-dependent DNA helicase	73*	19*	31	32
AR505_1370	ribosomal protein S27e Rps27e	274	156	175	141
AR505_1371	ribosomal protein S24e Rps24e	1075	631	736	1011
AR505_1372	hypothetical protein	600	382	529	569
AR505_1373	DNA-directed RNA polymerase subunit E RpoE	219	231	187	292
AR505_1374	DNA-directed RNA polymerase RpoE	386	589	470	732
AR505_1375	deoxyhypusine synthase Dys	109	90	119	149
AR505_1376*	isopropylmalate/isohomocitrate dehydrogenase	80*	32*	56	60
AR505_1377	uroporphyrinogen decarboxylase	76	30	30	34
AR505_1378	small multidrug resistance protein	127	114	82	85
AR505_1379	small multidrug resistance protein	48	8	20	22
AR505_1380	hypothetical protein	27	25	28	44
AR505_1381	haloacid dehalogenase-like hydrolase	85	54	42	21
AR505_1382*	N-methylhydantoinase A/acetone carboxylase beta subunit	33	20*	34	60*
AR505_1383*	glycolate oxidase, subunit GlcD3	281*	491	489	691*
AR505_1384	hypothetical protein	21	5	16	21
AR505_1385*	methanogenesis marker protein 7	277*	77*	249	162
AR505_1386*	methanogenesis marker protein 17	381	118*	411*	209
AR505_1387*	methanogenesis marker protein 15	256	95*	298*	136
AR505_1388*	methanogenesis marker protein 5	101	48*	131*	53
AR505_1389	methanogenesis marker protein 6	102	53	66	47
AR505_1390	methanogenesis marker protein 3	136	70	111	71
AR505_1391	methyl-coenzyme M reductase C subunit McrC	114	84	126	84
AR505_1392	methyl-coenzyme M reductase component A2 AtwA	215	170	235	191
AR505_1393	hypothetical protein	77	71	121	156
AR505_1394	hypothetical protein	68	44	73	80
AR505_1395*	hypothetical protein	1683	999*	4926*	1831
AR505_1396*	methyl-coenzyme M reductase alpha subunit McrA	1696	953*	2883*	1328
AR505_1397	methyl-coenzyme M reductase gamma subunit McrG	1679	1197	1572	1386
AR505_1398	methyl-coenzyme M reductase operon protein D McrD	2009	1700	2096	2176
AR505_1399	methyl-coenzyme M reductase beta subunit McrB	1646	1891	1968	1870
AR505_1400*	hypothetical protein	158*	260	399	400*
AR505_1401*	ornithine carbamoyltransferase ArgF	136*	251	236	274*
AR505_1402*	ssDNA exonuclease RecJ3	141*	220	280	327*
AR505_1403	phosphoesterase	15	14	17	6
AR505_1404	methylcobalamin:coenzyme M methyltransferase MtaA3	1086	1016	994	513
AR505_1405	methanogenesis marker protein 1	49	18	20	30
AR505_1406	RNA-splicing ligase RtcB	178	263	316	309
AR505_1407	Metal-dependent phosphohydrolase HD superfamily	230	293	251	369

AR505_1408	RNA-binding protein	37	51	44	30
AR505_1409	hypothetical protein	163	203	188	282
AR505_1410	NADPH-dependent FMN reductase	55	116	89	116
AR505_1411	hypothetical protein	41	30	25	26
AR505_1412	cell division ATPase MinD	48	85	55	67
AR505_1413	dinitrogenase iron-molybdenum cofactor biosynthesis protein	44	39	21	51
AR505_1414	7-cyano-7-deazaguanosine biosynthesis protein QueE	34	23	28	19
AR505_1415	queuosine biosynthesis protein QueC	83	84	68	60
AR505_1416	6-pyruvoyl tetrahydropterin synthase QueD	102	91	166	94
AR505_1417	methanogenesis marker protein 4	68	73	65	54
AR505_1418	hypothetical transmembrane protein	39	3	6	14
AR505_1419	hypothetical transmembrane protein	66	9	3	22
AR505_1420	diphthine synthase DphB	21	13	12	17
AR505_1421	ribosomal protein L10e Rpl10e	208	240	198	181
AR505_1422	haloacid dehalogenase-like hydrolase	61	42	46	50
AR505_1423	transposase	335	178	222	182
AR505_1424	ribonuclease P subunit RPR2	55	37	39	40
AR505_1425	RNA-binding protein	37	36	37	18
AR505_1426*	seryl-tRNA synthetase SerS	144	78*	108	247*
AR505_1427	haloacid dehalogenase-like hydrolase	58	68	64	91
AR505_1428	hypothetical transmembrane protein	42	70	67	89
AR505_1429	aspartate/tyrosine/aromatic aminotransferase	62	116	116	111
AR505_1430	hypothetical protein	49	85	69	92
AR505_1431	mevalonate kinase Mvk	61	53	47	46
AR505_1432	hypothetical transmembrane protein	43	17	11	38
AR505_1433	geranylgeranyl reductase	232	97	92	111
AR505_1434	ferredoxin	65	34	41	43
AR505_1435*	molybdenum cofactor biosynthesis protein A MoaA	197*	97	114	93*
AR505_1436	hypothetical protein	12	3	8	11
AR505_1437*	GTPase	131*	221	303*	178
AR505_1438	DNA polymerase II large subunit DP2 PolD2	69	74	84	81
AR505_1439	DNA-directed RNA polymerase subunit D RpoD	174	88	141	139
AR505_1440	ribosomal protein S11P Rps11p	329	156	235	288
AR505_1441	ribosomal protein S4P Rps4p	169	112	101	107
AR505_1442*	ribosomal protein S13P Rps13p	134*	81	86	52*
AR505_1443	methionine aminopeptidase Map	95	166	108	138
AR505_1444	Sua5/YciO/YrdC/YwC family translation factor	61	121	89	113
AR505_1445	metallo-beta-lactamase domain protein	40	17	32	20
AR505_1446	hypothetical protein	332	245	414	354
AR505_1447	nitrogenase cofactor biosynthesis protein NifB	78	108	82	79
AR505_1448	alanyl-tRNA synthetase AlaS	45	30	33	42
AR505_1449	chorismate synthase AroC	25	41	35	40
AR505_1450	chorismate mutase AroH	126	147	114	128
AR505_1451	hypothetical transmembrane protein	69	91	33	45
AR505_1452	dihydroxy-acid dehydratase IlvD	131	123	80	109
AR505_1453	ribosomal protein S10P Rps10p	469	422	426	531
AR505_1454	translation elongation factor aEF-1 alpha	1244	1873	1689	2149
AR505_1455	translation elongation factor aEF-2	215	188	207	239
AR505_1456	ribosomal protein S7P Rps7p	153	144	105	177
AR505_1457	ribosomal protein S12P Rps12p	189	165	137	209
AR505_1458	transposase IS4 family protein	68	55	51	43
AR505_1459*	translation initiation factor aIF-2 alpha subunit	211*	444*	362	294
AR505_1460	MiaB-like tRNA modifying enzyme	54	26	24	52
AR505_1461	alpha-acetolactate decarboxylase BudA	48	110	50	87
AR505_1462	MFS transporter	141	96	125	125
AR505_1463	TPR repeat-containing protein	36	59	62	49
AR505_1464	L-2,4-diaminobutyrate decarboxylase	30	15	18	31
AR505_1465	2,4-diaminobutyrate 4-transaminase	80	139	104	162
AR505_1466	addiction module antitoxin RelB/DinJ	45	26	31	38
AR505_1467	hypothetical protein	40	4	8	6
AR505_1468	addiction module antitoxin RelB/DinJ	9	17	6	7
AR505_1469	conserved hypothetical protein	16	6	8	4
AR505_1470*	hypothetical transmembrane protein	53*	14	7*	28
AR505_1471	phosphodiesterase	29	52	44	32
AR505_1472*	ribosomal protein S8e Rps8e	260	381*	216	161*
AR505_1473	signal recognition particle SRP19 protein	24	34	11	28
AR505_1474	carbohydrate kinase YjeF family	16	9	8	5
AR505_1475	phosphoesterase	11	8	11	4
AR505_1476*	methyl-viologen-reducing hydrogenase alpha subunit MvhA	436	320*	1771*	861
AR505_1477*	methyl-viologen-reducing hydrogenase gamma subunit MvhG	515	364*	1870*	1014
AR505_1478*	methyl-viologen-reducing hydrogenase delta subunit	400	361*	2055*	1072
AR505_1479*	CoB--CoM heterodisulfide reductase subunit A HdrA	381	327*	1194*	748
AR505_1480	hypothetical transmembrane protein	10	1	13	24
AR505_1481*	hypothetical protein	214	171*	406	580*
AR505_1482	proteasome alpha subunit PsmA	182	206	193	176

AR505_1483	ribosome maturation protein SBDS	198	116	122	127
AR505_1484	exosome complex RNA-binding protein Rrp4	79	37	42	35
AR505_1485	exosome complex exonuclease Rrp41	103	34	49	28
AR505_1486	exosome complex RNA-binding protein Rrp42	153	52	76	49
AR505_1487	ribosomal protein L37Ae Rpl37ae	132	69	128	49
AR505_1488	DNA-directed RNA polymerase subunit P RpoP	70	47	49	43
AR505_1489*	hypothetical protein	175*	74	114	53*
AR505_1490*	prefoldin beta subunit PfdB	97	36*	72	186*
AR505_1491	ABC transporter ATP-binding protein	15	48	35	17
AR505_1492	ABC transporter permease protein	69	109	83	73
AR505_1493*	phosphoesterase DHHA1	78*	98	118	165*
AR505_1494	tyrosyl-tRNA synthetase TyrS	157	207	183	279
AR505_1495	Fic family protein	13	8	10	4
AR505_1496	adenine phosphoribosyltransferase Apt3	34	64	52	50
AR505_1497	hypothetical transmembrane protein	21	6	4	9
AR505_1498	MFS transporter	279	397	299	298
AR505_1499	thioesterase family protein	166	158	140	195
AR505_1500	DNA helicase	22	9	7	10
AR505_1501	nitrogenase iron protein NifH2	6	3	3	5
AR505_1502	oxidoreductase/nitrogenase component 1	4	4	0	3
AR505_1503	cobalamin biosynthesis protein CbiX	10	16	9	18
AR505_1504	ABC transporter permease protein	56	53	34	28
AR505_1505	ABC transporter ATP-binding protein	8	5	1	3
AR505_1506	iron chelate uptake ABC transporter permease	11	5	8	11
AR505_1507	iron chelate uptake ABC transporter permease inner membrane subunit	6	2	2	8
AR505_1508	ABC transporter ATP-binding protein	3	0	4	2
AR505_1509	adhesin-like protein	5	4	1	3
AR505_1510	copper ion binding protein	213	395	260	218
AR505_1511	copper translocating P-type ATPase	166	94	76	73
AR505_1512	4Fe-4S-binding-domain containing ABC transporter ATP-binding protein	84	58	58	58
AR505_1513	ribose 5-phosphate isomerase A RpiA	116	175	121	218
AR505_1514	ribosomal protein L44e Rpl44e	440	511	371	351
AR505_1515	ribosomal protein S27e Rps27e	154	189	143	181
AR505_1516	translation initiation factor aIF-2 alpha subunit	139	125	77	133
AR505_1517	conserved hypothetical protein	34	8	6	4
AR505_1518	prophage Lp3 helicase	15	3	3	3
AR505_1519	hypothetical protein	20	2	11	5
AR505_1520	hypothetical protein	7	6	1	5
AR505_1521	adhesin-like protein	8	5	7	6
AR505_1522	hypothetical transmembrane protein	11	4	9	16
AR505_1523	ABC transporter substrate-binding protein	10	3	5	3
AR505_1524	adhesin-like protein	13	4	7	16
AR505_1525	ABC transporter permease protein	24	11	14	20
AR505_1526	ABC transporter ATP-binding protein	10	5	8	3
AR505_1527	hypothetical protein	15	7	5	11
AR505_1528	hypothetical protein	2	2	0	1
AR505_1529	hypothetical protein	5	14	6	5
AR505_1530	hypothetical transmembrane protein	22	25	26	18
AR505_1531	ATP-dependent DNA helicase	11	5	7	3
AR505_1532	adhesin-like protein	37	15	24	29
AR505_1533	cell surface leucine-rich repeat containing protein	18	7	9	5
AR505_1534	adhesin-like protein	26	12	20	14
AR505_1535	hypothetical protein	35	37	40	21
AR505_1536	hypothetical transmembrane protein	13	14	12	2
AR505_1537	hypothetical protein	21	23	19	14
AR505_1538	hypothetical protein	17	24	24	27
AR505_1539	hypothetical transmembrane protein	8	19	16	23
AR505_1540	hypothetical protein	70	125	138	73
AR505_1541	hypothetical protein	17	22	0	11
AR505_1542	hypothetical protein	61	49	40	32
AR505_1543*	phage integrase	54	20*	37	57*
AR505_1544	virulence-associated E family protein	13	2	6	11
AR505_1545	hypothetical protein	10	3	5	4
AR505_1546	hypothetical transmembrane protein	4	2	2	4
AR505_1547	adhesin-like protein	5	3	3	3
AR505_1548	ABC transporter substrate-binding protein	11	4	4	13
AR505_1549	adhesin-like protein	13	2	8	15
AR505_1550	ABC transporter permease protein	35	6	5	9
AR505_1551*	ABC transporter ATP-binding protein	69*	39	31*	40
AR505_1552	Fic family protein	7	8	6	3
AR505_1553	hypothetical protein	13	5	10	13
AR505_1554	hypothetical protein	7	8	12	13
AR505_1555	hypothetical protein	22	6	11	7

AR505_1556	adhesin-like protein	23	8	11	12
AR505_1557	atpase	10	6	7	4
AR505_1558	nucleotidyltransferase	18	65	30	19
AR505_1559*	adhesin-like protein	35	28*	48	418*
AR505_1560	adhesin-like protein	9	7	6	2
AR505_1561	adhesin-like protein	19	14	15	8
AR505_1562	transposase	12	9	6	10
AR505_1563	transposase	35	3	10	14
AR505_1564	hypothetical protein	21	18	19	8
AR505_1565	hypothetical protein	575	1089	940	659
AR505_1566*	death-on-curing family protein	2163*	7422*	4528	3251
AR505_1567	hypothetical protein	26	31	37	30
AR505_1568	hypothetical protein	56	166	73	41
AR505_1569	hypothetical protein	27	51	32	38
AR505_1570	phage integrase	34	9	3	8
AR505_1571	hypothetical protein	17	32	23	26
AR505_1572	hypothetical protein	6	0	3	2
AR505_1573	hypothetical protein	1	0	0	0
AR505_1574	transposase	52	29	42	44
AR505_1575	methylcobalamin:coenzyme M methyltransferase MtaA4	55	67	81	68
AR505_1576	MFS transporter	24	17	13	25
AR505_1577	hypothetical protein	78	73	107	88
AR505_1578*	excinuclease ABC A subunit UvrA	64*	31*	45	33
AR505_1579	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	34	18	50	15
AR505_1580	hypothetical protein	13	16	14	8
AR505_1581*	cytosine deaminase	37*	45	39	75*
AR505_1582	hydrolase beta-lactamase family	51	91	102	66
AR505_1583*	tRNA nucleotidyltransferase Cca	68	138*	54*	108
AR505_1584	hypothetical transmembrane protein	66	126	72	54
AR505_1585	DNA repair and recombination protein Rada	326	380	472	320
AR505_1586	N ² ,N ² -dimethylguanosine tRNA methyltransferase Trm	45	47	48	56
AR505_1587*	prenyltransferase UbiA	107	142*	73	59*
AR505_1588	geranylgeranylgeranyl phosphate synthase GGGPS	128	125	82	60
AR505_1589	hypothetical protein	42	36	14	8
AR505_1590	hypothetical protein	57	28	36	24
AR505_1591	hypothetical protein	44	12	10	10
AR505_1592	hypothetical protein	167	81	92	138
AR505_1593	ATPase	34	63	43	30
AR505_1594	conserved hypothetical protein	26	17	30	22
AR505_1595	NCAIR mutase (PurE)-related proteins	146	116	221	243
AR505_1596	conserved hypothetical protein	124	105	114	94
AR505_1597	hypothetical protein	123	148	103	34
AR505_1597	hypothetical protein	79	81	100	120
AR505_1598*	hypothetical protein	54*	110*	88	87
AR505_1599	aldehyde dehydrogenase	55	75	96	104
AR505_1600	hypothetical protein	10	4	3	10
AR505_1601*	RNA 3'-phosphate cyclase RtcA	141*	198	291*	231
	Bifunctional diaminohydroxyphosphoribosylaminopyrimidine				
AR505_1602	deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	40	30	44	33
	RibD				
AR505_1603*	translation initiation factor aIF-2 beta subunit	61*	43	37	27*
AR505_1604	ribulose-5-phosphate 4-epimerase and related epimerases and	26	25	40	29
	aldolases				
AR505_1605	C/D box methylation guide ribonucleoprotein complex aNOP56	68	37	60	29
	subunit				
AR505_1606	translation initiation factor aIF-5A	238	186	193	185
AR505_1607	agmatinase SpeB	83	37	35	41
AR505_1608	phosphoglucomutase	110	151	160	184
AR505_1609	chromosome segregation and condensation protein ScpB	111	61	60	83
AR505_1610	chromosome segregation and condensation protein ScpA	124	69	87	97
AR505_1611	chromosome segregation protein SMC	73	40	36	47
AR505_1612	signal peptidase I	52	29	29	32
AR505_1613	haloacid dehalogenase-like hydrolase	96	51	56	82
AR505_1614	uracil-DNA glycosylase Ung	28	15	19	28
AR505_1615	orotate phosphoribosyltransferase PyrE	92	105	90	61
AR505_1616	hypothetical transmembrane protein	61	130	77	73
AR505_1617	DNA/RNA-binding protein	79	72	52	66
AR505_1618	geranylgeranyl reductase	66	59	39	41
AR505_1619	octaprenyl-diphosphate synthase IspB	53	74	55	33
AR505_1620	hypothetical protein	553	937	1394	1120
AR505_1621	radical SAM domain protein	23	13	9	21
AR505_1622*	F ₄₂₀ H ₂ dehydrogenase subunit N FpoN	538	210	705*	86*
AR505_1623*	F ₄₂₀ H ₂ dehydrogenase subunit M FpoM	359	150	411*	50*
AR505_1624*	F ₄₂₀ H ₂ dehydrogenase subunit L FpoL	541	232	589*	86*
AR505_1625*	F ₄₂₀ H ₂ dehydrogenase subunit K FpoK	404*	99	355	63*

AR505_1626*	hypothetical transmembrane protein	453*	181	439	66*
AR505_1627	NADH:ubiquinone oxidoreductase J FpoJ	770	315	825	105
AR505_1628*	NADH:quinone oxidoreductase I FpoI	633*	214	546	82*
AR505_1629*	NADH dehydrogenase subunit H FpoH	376*	149	289	60*
AR505_1630*	NADH dehydrogenase subunit D FpoD	721*	317	468	134*
AR505_1631*	NADH dehydrogenase subunit C FpoC	765*	437	519	135*
AR505_1632*	NADH dehydrogenase subunit B FpoB	373*	230	261	69*
AR505_1633	NADH dehydrogenase subunit A FpoA	588	536	527	142
AR505_1634	NADP oxidoreductase coenzyme F ₄₂₀ dependent	71	67	62	71
AR505_1635*	Fe-S oxidoreductase	107*	53	74	48*
AR505_1636	undecaprenyl pyrophosphate synthetase UppS	50	43	52	32
AR505_1637	methanogenesis marker protein 11	196	310	224	272
AR505_1638	RNA 2'-phosphotransferase Tpt1/KptA	198	354	259	240
AR505_1639	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase FOLD	147	189	172	153
AR505_1640*	phage integrase	194*	94*	120	110
AR505_1641	AMP phosphorylase DeoA	186	163	184	151
AR505_1642	ribulose bisphosphate carboxylase RbcL	137	130	143	122
AR505_1643	ribose-1,5-bisphosphate isomerase E2b2	96	124	144	122
AR505_1644	hypothetical protein	36	55	52	60
AR505_1645	Met-10+ like-protein	47	61	33	59
AR505_1646	geranylgeranyl reductase family protein	48	16	29	16
AR505_1647	transaldolase	82	57	116	51
AR505_1648*	transketolase subunit B	120	65*	170*	87
AR505_1649	transketolase subunit A	257	202	360	289
AR505_1650	proliferating cell nuclear antigen PcnA	261	367	465	384
AR505_1651	transcription factor S Tfs	268	466	474	347
AR505_1652	adhesin-like protein	145	143	135	178
AR505_1653*	RNA-metabolising metallo-beta-lactamase	82	57*	99	125*
AR505_1654	quinolinate phosphoribosyltransferase (decarboxylating) NadC	31	11	20	23
AR505_1655	hypothetical protein	29	41	28	57
AR505_1656	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase PurH	125	157	159	143
AR505_1657	ribosomal protein L11 methyltransferase PrmA	51	30	38	57
AR505_1658*	exosome complex RNA-binding protein Csl4	161*	94	124	69*
AR505_1659	hypothetical protein	59	37	32	24
AR505_1660	thiamine biosynthesis ATP pyrophosphatase ThiI	156	240	63	203
AR505_1661*	hypothetical protein	87	170*	56*	88
AR505_1662	DEAD/DEAH box helicase domain-containing protein	27	6	10	13
AR505_1663	hypothetical protein	24	4	21	9
AR505_1664	phosphoglycerate dehydrogenase SerA	33	28	36	44
AR505_1665	phosphoserine aminotransferase	17	26	19	26
AR505_1666	aspartate aminotransferase	96	259	263	212
AR505_1667*	5-formaminoimidazole-4-carboxamide-1-(beta)-D- ribofuranosyl 5'-monophosphate-formate ligase PurP	116*	460*	365	302
AR505_1668	OB fold nucleic acid binding domain-containing protein	108	49	74	49
AR505_1669	hypothetical protein	174	105	120	130
AR505_1670	hypothetical protein	101	123	101	93
AR505_1671	ribosomal protein S2P Rps2p	53	22	24	21
AR505_1672	hypothetical protein	105	196	148	155
AR505_1673	HTH domain-containing protein	164	221	237	188
AR505_1674*	proteasome-activating nucleotidase	39	18*	31	52*
AR505_1675*	radical SAM domain-containing proteinB	85	114*	50*	89
AR505_1676	GTPase	49	90	62	39
AR505_1677	hypothetical transmembrane protein	361	520	563	376
AR505_1678	hypothetical transmembrane protein	587	466	618	353
AR505_1679	riboflavin kinase	47	39	31	30
AR505_1680	phosphoribosylformylglycinamide synthase I PurQ	202	113	137	171
AR505_1681	phosphoribosylformylglycinamide synthase II PurL	233	119	205	182
AR505_1682	phosphoribosylformylglycinamide synthase PurS	79	80	124	85
AR505_1683	tRNA methyltransferase subunit	40	28	11	18
AR505_1684	prolyl-tRNA synthetase ProS	112	131	89	92
AR505_1685	ribose-phosphate diphosphokinase Prs	130	201	131	127
AR505_1686	sulfate permease SulP	27	25	24	36
AR505_1687	hypothetical protein Ta0304	46	41	40	16
AR505_1688	GHMP kinase	99	70	68	58
AR505_1689	bifunctional phosphopantothenate-cysteine ligase/phosphopantothenoylcysteine decarboxylase CoaBC	49	29	30	28
AR505_1690	thymidylate kinase Tmk2	43	51	35	55
AR505_1691	TOPRIM domain-containing protein	12	9	12	10
AR505_1692*	transposase IS605 OrfB family	50*	97	118*	80
AR505_1693	hypothetical protein	102	129	232	347
AR505_1694*	hypothetical protein	60*	102	122*	81
AR505_1695	Metal-dependent hydrolases beta-lactamase family	30	44	26	34
AR505_1696*	CBS domain-containing protein	59	86*	50	29*

AR505_1697	phage integrase family protein	42	11	17	19
AR505_1698	hypothetical protein	13	6	5	12
AR505_1699	hypothetical protein	8	6	0	2
AR505_1700	hypothetical protein	2	4	1	5
AR505_1701	hypothetical protein	11	12	16	32
AR505_1702	hypothetical protein	3	4	3	0
AR505_1703	transposase	27	10	11	20
AR505_1704	hypothetical protein	8	4	4	1
AR505_1705	ABC transporter ATP-binding protein	14	11	9	6
AR505_1706	ABC transporter permease protein	18	5	7	8
AR505_1707	adhesin-like protein	17	9	11	12
AR505_1708	ABC transporter substrate-binding protein	13	2	7	6
AR505_1709	hypothetical transmembrane protein	17	8	14	12
AR505_1710	hypothetical transmembrane protein	16	11	13	7
AR505_1711	hypothetical transmembrane protein	17	13	18	10
AR505_1712	hypothetical transmembrane protein	81	48	69	87
AR505_1713	Listeria-Bacteroides repeat domain containing protein	16	9	10	9
AR505_1714	transposase IS4 family	12	9	6	10
AR505_1715	adhesin-like protein	29	34	24	21
AR505_1716	hypothetical protein	95	69	83	68
AR505_1717	hypothetical protein	97	114	115	130
AR505_1718*	hypothetical protein	38	63	82*	17*
AR505_1719*	hypothetical protein	41*	71	116*	62
AR505_1720	hypothetical protein	11	7	16	20
AR505_1721	hypothetical protein	109	141	129	120
AR505_1722	hypothetical protein	250	230	183	229
AR505_1723*	hypothetical protein	295*	429	517	594*
AR505_1724	hypothetical protein	1	2	5	8
AR505_1725	conserved hypothetical protein	102	81	59	109
AR505_1726	hypothetical protein	95	138	83	91
AR505_1727	hypothetical protein	29	24	23	28
AR505_1728	hypothetical protein	10	6	6	9
AR505_1729	resolvase domain-containing protein	7	2	5	11
AR505_1730	hypothetical protein	0	0	0	2
AR505_1731	hypothetical protein	31	8	3	15
AR505_1732	hypothetical protein	134	136	168	158
AR505_1733	hypothetical protein	29	81	54	59
AR505_1734	hypothetical protein	6	3	0	6
AR505_1735	hypothetical protein	8	0	4	7
AR505_1736	hypothetical protein	30	9	9	17
AR505_1737	hypothetical protein	44	19	11	15
AR505_1738	ATPase	111	43	50	121
AR505_1739	hypothetical transmembrane protein	4	7	6	8
AR505_1740	Fic family protein	4	0	1	1
AR505_1741*	adhesin-like protein	171*	294	454*	230
AR505_1742	hypothetical protein	5	10	9	14
AR505_1743	5'-nucleotidase SurE	160	180	144	197
AR505_1744	GNAT family acetyltransferases	127	359	290	336
AR505_1745	prephenate dehydrogenase TyrA	75	149	75	173
AR505_1746	hypothetical protein	162	80	91	142
AR505_1747	hypothetical transmembrane protein	5	10	2	3
AR505_1748	peptidylprolyl isomerase	69	122	93	119
AR505_1749	hypothetical transmembrane protein	55	63	22	23
AR505_1750	hypothetical transmembrane protein	82	45	38	33
AR505_1751	hypothetical protein	44	21	18	23
AR505_1752	translation initiation factor aIF-2 gamma subunit	107	67	69	67
AR505_1753	ribosomal protein S6e Rps6e	55	57	48	52
AR505_1754	phosphoheptose isomerase GmhA	94	124	143	80
AR505_1755*	translation initiation factor aIF-2	178*	327	374*	290
AR505_1756	nucleoside diphosphate kinase Ndk	187	59	99	67
AR505_1757	ribosomal protein L24e Rpl24e	233	89	110	47
AR505_1758*	ribosomal protein S28e Rps28e	205*	92	87	49*
AR505_1759*	ribosomal protein L7Ae Rpl7ae	466*	268	221	50*
AR505_1760*	hypothetical transmembrane protein	56*	26	36	24*
AR505_1761	adhesin-like protein	103	127	129	131
AR505_1762	hypothetical transmembrane protein	45	44	30	24
AR505_1763	glycosyl transferase GT2 family	17	14	8	11
AR505_1764	cell wall teichoic acid glycosylation protein	21	14	11	13
AR505_1765	transposase IS605 OrfB family	123	120	135	62
AR505_1766*	hypothetical protein	194*	182	151	60*
AR505_1767	branched-chain-amino-acid aminotransferase IlvE	136	210	170	128
AR505_1768	acetolactate synthase small subunit IlvN	82	159	161	109
AR505_1769	bifunctional phosphoglucose/phosphomannose isomerase	121	165	154	138
AR505_1770	histidinol-phosphate phosphatase	18	3	8	9
AR505_1771	L-threonine kinase PduX	54	40	45	25

AR505_1772	UDP- <i>N</i> -acetylglucosamine diphosphorylase/glucosamine-1-phosphate <i>N</i> -acetyltransferase GlmU	31	28	29	28
AR505_1773	hypothetical protein	28	34	37	50
AR505_1774	translation elongation factor aEF-1 beta	236	289	250	151
AR505_1775*	transposase IS605 OrfB family	53	52	80*	32*
AR505_1776	Group II Intron-encoding maturase	20	5	14	19
AR505_1777	transposase IS605 OrfB family	9	4	1	1
AR505_1778	glycosyl transferase GT2 family	26	7	9	12
AR505_1779	hypothetical transmembrane protein	48	54	55	51
AR505_1780*	malate dehydrogenase Mdh	37	28*	35	60*
AR505_1781	Fe-S oxidoreductase	36	13	10	11
AR505_1782*	DNA primase large subunit PriB	128	187*	93*	102
AR505_1783	CDP-diacylglycerol-serine <i>O</i> -phosphatidyltransferase PssA	206	311	166	167
AR505_1784	adenylate kinase Adk	45	36	40	45
AR505_1785	ribokinase RbsK	42	53	66	66
AR505_1786	glycosyl transferase family protein	21	22	18	22
AR505_1787	glycosyl transferase family protein	30	5	14	14
AR505_1788	adenosylhomocysteinase AhcY2	26	16	11	18
AR505_1789	hypothetical protein	20	14	17	13
AR505_1790	hypothetical protein	20	36	20	29
AR505_1791	RNA methyltransferase TrmH family	49	44	28	26
AR505_1792	cell division protein FtsZ2	66	56	23	48
AR505_1793	hypothetical protein	12	0	4	3
AR505_1794	ribosomal protein L12P Rpl12p	207	60	196	185
AR505_1795*	acidic ribosomal protein P0 RplPO	970*	290*	712	595
AR505_1796*	ribosomal protein L1P Rpl1p	685*	252*	507	393
AR505_1797	ribosomal protein L11P Rpl11p	305	215	278	284
AR505_1798	ribosomal protein L24 family	351	326	270	361
AR505_1799	protein translocase subunit Sss1	543	595	364	664
AR505_1800	hypothetical protein	73	90	68	57
AR505_1801	hypothetical protein	185	274	164	175
AR505_1802	GMP synthase subunit A GuaA	400	238	209	312
AR505_1803	GMP synthase subunit B GuaAb	207	105	113	142
AR505_1804	phosphoribosylaminoimidazole carboxylase PurE	118	103	144	147
AR505_1805	hypothetical transmembrane protein	351	652	727	388
AR505_1806	hypothetical protein	59	105	64	50
AR505_1807	transcription initiation factor TFIIB Tfb2	25	16	17	35
AR505_1808	tRNA intron endonuclease EndA	75	72	76	76
AR505_1809	transcriptional regulator ArsR family	443	187	217	264
AR505_1810*	AAA family ATPase CDC48 subfamily	647*	243	235*	427
AR505_1811*	transcriptional regulator	115*	169	290*	198
AR505_1812	hypothetical protein	34	27	61	27
AR505_1813	CAAX amino terminal protease family protein	68	69	45	40
AR505_1814	sugar phosphate isomerase/epimerase	100	104	70	52
AR505_1815	hypothetical protein	104	163	158	93
AR505_1816	DNA polymerase II small subunit DP1 PolD	48	73	63	40
AR505_1817*	hypothetical protein	163*	26*	86	54
AR505_1818*	A ₁ A ₀ ATP synthase subunit D	402*	57	188	64*
AR505_1819*	A ₁ A ₀ ATP synthase subunit B	353*	40*	131	44
AR505_1820*	A ₁ A ₀ ATP synthase subunit A	449*	48*	118	55
AR505_1821*	A ₁ A ₀ ATP synthase subunit F	211*	29*	44	33
AR505_1822*	A ₁ A ₀ ATP synthase subunit C	522*	56	132	37*
AR505_1823*	A ₁ A ₀ ATP synthase subunit E	395*	71	150	55*
AR505_1824*	A ₁ A ₀ ATP synthase subunit K	600*	92	172	66*
AR505_1825*	A ₁ A ₀ ATP synthase subunit I	722*	189	193	107*
AR505_1826*	A ₁ A ₀ ATP synthase subunit H	660*	261	220	151*
AR505_1827*	CMP/dCMP deaminase	64*	216*	149	92
AR505_1828	signal peptidase I	12	18	23	12

Trt1: ISO4-H5 enrichment culture with high H₂ on methanol. Trt2: ISO4-H5 enrichment culture +FD1 with high H₂ on methanol. Trt3: ISO4-H5 enrichment culture +FD1 with low H₂ on methanol. Trt4: ISO4-H5 enrichment culture +FD1 with low H₂ on monomethylamine. *: Significantly differentially expressed genes between two conditions by both Kruskal-Wallis test and Benjamini-Hochberg test of $q < 0.05$ and above two fold difference in expression were marked with *, the pair of conditions are highlighted with black background and white letter.

Table A.5.4 Gene expression of *Succinivibrio dextrinsolvens* H5

Locus_tag	Product	Trt1	Trt2	Trt3	Trt4
T508DRAFT_00001	hypothetical protein	0	35	0	0
T508DRAFT_00002	transposase	1	10	0	7
T508DRAFT_00003	Na ⁺ /H ⁺ -dicarboxylate symporters	35	16	6	11
T508DRAFT_00004	cysteine synthase A	76	54	2	0
T508DRAFT_00005	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	17	8	0	9
T508DRAFT_00006	large conductance mechanosensitive channel protein	107	87	0	0
T508DRAFT_00007	D-alanyl-D-alanine carboxypeptidase	5	11	0	0
T508DRAFT_00008	thioredoxin-disulfide reductase	113	54	0	24
T508DRAFT_00009	NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding	13	47	0	26
T508DRAFT_00010	hypothetical protein	90	56	0	0
T508DRAFT_00011	activator of osmoprotectant transporter ProP	19	0	10	0
T508DRAFT_00012	C-terminal peptidase (prc)	53	0	10	6
T508DRAFT_00013	aminopeptidase N, Escherichia coli type	65	19	0	0
T508DRAFT_00014	protein of unknown function (DUF2835)	43	0	0	0
T508DRAFT_00015	dihydroorotate oxidase A (EC 1.3.3.1)	71	39	22	35
T508DRAFT_00016	protein of unknown function (DUF1379)	1487	1285	887	761
T508DRAFT_00020	predicted periplasmic or secreted lipoprotein	113	47	0	14
T508DRAFT_00021	hypothetical protein	63	67	7	11
T508DRAFT_00022	murein endopeptidase	26	13	0	0
T508DRAFT_00023	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	17	0	0	27
T508DRAFT_00024	N-acetylglutamate kinase (EC 2.7.2.8)	5	0	0	0
T508DRAFT_00025	N-acetylglutamate synthase and related acetyltransferases	0	0	0	0
T508DRAFT_00026	transaminase, acetylornithine/succinylornithine family	35	4	0	1
T508DRAFT_00027	predicted P-loop ATPase fused to an acetyltransferase	39	68	0	45
T508DRAFT_00028	lysophospholipase	33	7	0	2
T508DRAFT_00029	succinyldiaminopimelate desuccinylase (EC 3.5.1.18)	48	0	0	8
T508DRAFT_00030	predicted Na ⁺ -dependent transporter	16	17	0	0
T508DRAFT_00031	ABC-type Fe ³⁺ transport system, permease component	13	2	0	0
T508DRAFT_00032	predicted integral membrane protein	51	43	18	73
T508DRAFT_00033	hypothetical protein	228	143	0	157
T508DRAFT_00034	hypothetical protein	2	0	0	0
T508DRAFT_00035	uncharacterised conserved protein related to MYG1 family	43	11	0	68
T508DRAFT_00036	tRNA-U20a,U20b-dihydrouridine synthase	0	22	0	11
T508DRAFT_00037	hypothetical protein	19	69	37	48
T508DRAFT_00038*	integral membrane protein, TerC family	93*	33	7*	63
T508DRAFT_00039	phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	65	36	0	12
T508DRAFT_00040	imidazoleglycerol phosphate synthase, cyclase subunit	61	0	0	31
T508DRAFT_00041	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)	83	0	0	0
T508DRAFT_00042	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	57	0	0	24
T508DRAFT_00043	imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	29	3	0	4
T508DRAFT_00044	histidinol-phosphate aminotransferase	46	40	0	6
T508DRAFT_00045	histidinol dehydrogenase	45	10	0	9
T508DRAFT_00046	ATP phosphoribosyltransferase	66	7	23	15
T508DRAFT_00047	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	41	73	10	11
T508DRAFT_00048	dsulfide bond formation protein DsbB	53	70	65	17
T508DRAFT_00049	sodium/proton antiporter, NhaB family (TC 2.A.34.1.1)	67	70	5	11
T508DRAFT_00050	hypothetical protein	54	55	0	0
T508DRAFT_00051	predicted permease	39	25	0	6
T508DRAFT_00052	TerB-C domain	15	5	3	7
T508DRAFT_00053	beta-N-acetylglucosaminidase	39	15	0	0
T508DRAFT_00054	trigger factor	294	22	0	0
T508DRAFT_00055	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP	47	5	0	19
T508DRAFT_00056	endopeptidase Clp ATP-binding regulatory subunit (clpX)	63	42	49	25
T508DRAFT_00057	hypothetical protein	51	18	10	16
T508DRAFT_00058	conserved hypothetical protein (putative transposase or invertase)	13	30	13	0
T508DRAFT_00059	ATP-dependent protease La	31	5	2	0
T508DRAFT_00060	hypothetical protein	17	31	0	0
T508DRAFT_00061	Parvulin-like peptidyl-prolyl isomerase	37	38	0	23
T508DRAFT_00062	protein of unknown function (DUF1036)	45	33	0	0
T508DRAFT_00063	hypothetical protein	78	0	0	41
T508DRAFT_00064	predicted transcriptional regulator	116	51	86	0
T508DRAFT_00065	putative NADH-flavin reductase	10	11	0	0
T508DRAFT_00066	predicted divalent heavy-metal cations transporter	45	18	0	0
T508DRAFT_00067	predicted ATPase (AAA+ superfamily)	48	4	29	16
T508DRAFT_00068	uncharacterized protein, YigZ family	53	9	22	108
T508DRAFT_00069	protein of unknown function (DUF3625)	112	37	0	46
T508DRAFT_00070	transglycosylase SLT domain	101	167	18	95
T508DRAFT_00071	universal stress protein UspA and related nucleotide-binding proteins	59	36	17	26

T508DRAFT_00072	tRNA s(2)C-32 sulfurtransferase (EC 2.8.1.4)	28	63	32	49
T508DRAFT_00073	protein of unknown function (DUF1703)/predicted AAA-ATPase	24	3	8	1
T508DRAFT_00074	hypothetical protein	42	37	22	32
T508DRAFT_00075	hypothetical protein	113	79	244	55
T508DRAFT_00076	hypothetical protein	14	27	0	69
T508DRAFT_00077	hypothetical protein	337	420	350	410
T508DRAFT_00078	predicted restriction endonuclease	13	5	24	20
T508DRAFT_00079	CRISPR-associated endoribonuclease Cas2	12	0	0	0
T508DRAFT_00080	CRISPR-associated endonuclease Cas1	49	33	39	44
T508DRAFT_00081	CRISPR-associated protein Cas4, subtype PREFRAN	5	0	0	0
T508DRAFT_00082	CRISPR-associated protein Cpf1, subtype PREFRAN	16	8	7	1
T508DRAFT_00083	protein of unknown function (DUF1703)/predicted AAA-ATPase	16	1	0	0
T508DRAFT_00084	DNA helicase/exodeoxyribonuclease V, gamma subunit (EC 3.1.11.5)	6	6	0	5
T508DRAFT_00085	ATP-dependent exoDNase (exonuclease V) beta subunit (contains helicase and exonuclease domains)	5	3	0	2
T508DRAFT_00086	DNA helicase/exodeoxyribonuclease V, alpha subunit (EC 3.1.11.5)	40	81	5	61
T508DRAFT_00087	addiction module antidote protein, HigA family	54	11	0	0
T508DRAFT_00088	hypothetical protein	0	0	0	0
T508DRAFT_00089	short-chain alcohol dehydrogenase of unknown specificity	88	99	42	52
T508DRAFT_00090	predicted ATPase (AAA+ superfamily)	23	36	6	0
T508DRAFT_00091	dihydropteroate synthase (EC 2.5.1.15)	13	10	0	0
T508DRAFT_00092	hypothetical protein	3	11	0	0
T508DRAFT_00093	Type I restriction-modification system methyltransferase subunit	10	4	0	4
T508DRAFT_00094	DNA-binding protein, YbaB/EbfC family	95	0	0	0
T508DRAFT_00095	DNA replication and repair protein RecR	11	0	0	0
T508DRAFT_00096	molecular chaperone, HSP90 family	97	20	0	1
T508DRAFT_00097	adenylate kinase (EC 2.7.4.3)	205	496	0	110
T508DRAFT_00098	hypothetical protein	95	75	0	26
T508DRAFT_00099	phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	32	43	0	2
T508DRAFT_00100	uracil-xanthine permease	40	60	21	34
T508DRAFT_00101	Rubryerythrin	598	142	132	99
T508DRAFT_00102	Fe ²⁺ /Zn ²⁺ uptake regulation proteins	91	127	96	0
T508DRAFT_00103*	arabinose efflux permease	73	47	9*	106*
T508DRAFT_00104	arabinose efflux permease	30	38	17	11
T508DRAFT_00105	sodium/pantothenate symporter	30	45	0	32
T508DRAFT_00106	predicted membrane protein	0	0	0	0
T508DRAFT_00107	UDP-glucose pyrophosphorylase (EC 2.7.7.9)	50	0	0	9
T508DRAFT_00108	intracellular septation protein A	17	37	0	4
T508DRAFT_00109	hypothetical protein	75	20	17	54
T508DRAFT_00110	alpha-L-glutamate ligase-related protein	24	3	0	0
T508DRAFT_00111	7 transmembrane helices usually fused to an inactive transglutaminase/Inactive transglutaminase fused to 7 transmembrane helices	28	92	8	21
T508DRAFT_00112	uncharacterised protein conserved in archaea	13	21	0	0
T508DRAFT_00113	oxygen-sensitive ribonucleoside-triphosphate reductase	0	46	48	0
T508DRAFT_00114	hypothetical protein	81	81	85	0
T508DRAFT_00115	NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporters	127	26	6	10
T508DRAFT_00116	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	81	0	0	8
T508DRAFT_00117	folylpolyglutamate synthase/dihydrofolate synthase	20	18	11	0
T508DRAFT_00118	sporulation related domain	9	6	0	0
T508DRAFT_00119	dinuclear metal center protein, YbgI/SA1388 family	21	7	0	15
T508DRAFT_00120	GTP cyclohydrolase I (EC 3.5.4.16)	14	0	0	0
T508DRAFT_00121	glycosyltransferases involved in cell wall biogenesis	10	14	0	0
T508DRAFT_00122	predicted membrane protein	14	0	0	0
T508DRAFT_00123	tRNA pseudouridine(38-40) synthase	18	91	0	58
T508DRAFT_00124	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	46	8	0	0
T508DRAFT_00127	glycosidases	89	45	0	19
T508DRAFT_00128	sulfur relay protein, TusE/DsrC/DsvC family	421	114	63	87
T508DRAFT_00130	hypothetical protein	83	111	0	14
T508DRAFT_00131*	aspartate ammonia-lyase	744*	102	99	28*
T508DRAFT_00132*	anaerobic C ₄ -dicarboxylate membrane transporter family protein	1179*	205	171	10*
T508DRAFT_00133	predicted Na ⁺ -dependent transporter	134	97	20	32
T508DRAFT_00134	GTP cyclohydrolase II	72	49	0	51
T508DRAFT_00135	homocysteine S-methyltransferase (EC 2.1.1.10)	30	44	0	0
T508DRAFT_00136	amino acid carrier protein	19	7	0	7
T508DRAFT_00137	tRNA-guanine transglycosylase (EC 2.4.2.29)	12	0	0	31
T508DRAFT_00138	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	7	5	0	0
T508DRAFT_00139	Tir chaperone protein (CesT) family	10	39	0	0
T508DRAFT_00140	hypothetical protein	96	135	6	41
T508DRAFT_00141	von Willebrand factor type A domain	43	33	19	8
T508DRAFT_00142	predicted hydrolase of alkaline phosphatase superfamily	75	55	0	19
T508DRAFT_00143	thioredoxin domain-containing protein	125	28	0	20
T508DRAFT_00144	PAP2 superfamily	32	95	0	0
T508DRAFT_00145	biotin synthase (EC 2.8.1.6)	25	22	0	0

T508DRAFT_00146	predicted permease	16	31	16	0
T508DRAFT_00147	putative Zn-dependent protease, contains TPR repeats	20	11	0	0
T508DRAFT_00148	pantothenate synthetase (EC 6.3.2.1)	58	21	0	0
T508DRAFT_00149	L-aspartate 1-decarboxylase (EC 4.1.1.11)	58	55	0	0
T508DRAFT_00150	regulatory inactivation of DnaA Hda protein	28	0	0	0
T508DRAFT_00151	uncharacterised protein conserved in bacteria (DUF2066)	29	28	0	18
T508DRAFT_00152	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	32	0	0	0
T508DRAFT_00153	arginine decarboxylase (EC 4.1.1.19)	114	21	0	7
T508DRAFT_00154	agmatinase	59	15	0	0
T508DRAFT_00155	PAS domain S-box/diguanylate cyclase (GGDEF) domain	120	67	20	21
T508DRAFT_00156	4Fe-4S dicluster domain	49	0	0	0
T508DRAFT_00157	pyrroline-5-carboxylate reductase	21	10	0	5
T508DRAFT_00158	predicted integral membrane protein	37	0	0	0
T508DRAFT_00159	DNA topoisomerase IV subunit A (EC 5.99.1.3)	36	23	0	6
T508DRAFT_00160	uncharacterised protein conserved in bacteria	72	206	66	130
T508DRAFT_00161	outer membrane protein and related peptidoglycan-associated (lipo)proteins	31	4	0	0
T508DRAFT_00162	acetyltransferase (isoleucine patch superfamily)	3	0	0	0
T508DRAFT_00163	hydrolases of the alpha/beta superfamily	55	21	9	24
T508DRAFT_00164	hypothetical protein	81	0	0	0
T508DRAFT_00165*	transcriptional regulator	430*	171	20	9*
T508DRAFT_00166	hypothetical protein	44	9	0	0
T508DRAFT_00167	conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	28	0	0	0
T508DRAFT_00168	DNA-directed RNA polymerase subunit alpha (EC 2.7.7.6)	82	26	8	40
T508DRAFT_00169	LSU ribosomal protein L17P	387	24	36	0
T508DRAFT_00170	DNA-directed RNA polymerase subunit alpha (EC 2.7.7.6)	335	24	0	17
T508DRAFT_00171	SSU ribosomal protein S4P	323	39	0	0
T508DRAFT_00172*	30S ribosomal protein S11	319*	31	34	0*
T508DRAFT_00173*	30S ribosomal protein S13	622*	204	86	0*
T508DRAFT_00175	protein translocase subunit secY/secE1 alpha	155	84	4	9
T508DRAFT_00176	LSU ribosomal protein L15P	457	44	0	14
T508DRAFT_00177	LSU ribosomal protein L30P	316	0	0	0
T508DRAFT_00178	ribosomal protein S5, bacterial/organelle type	445	13	0	0
T508DRAFT_00179*	ribosomal protein L18, bacterial type	663*	228	172	0*
T508DRAFT_00180	LSU ribosomal protein L6P	482	55	0	21
T508DRAFT_00181	ribosomal protein S8	404	67	0	0
T508DRAFT_00182	ribosomal protein S14	140	71	0	0
T508DRAFT_00183	ribosomal protein L5	813	45	61	0
T508DRAFT_00184	ribosomal protein L24, bacterial/organelle	416	101	59	59
T508DRAFT_00185	LSU ribosomal protein L14P	562	77	0	0
T508DRAFT_00186	SSU ribosomal protein S17P	131	0	0	2
T508DRAFT_00187	LSU ribosomal protein L29P	1084	25	25	50
T508DRAFT_00188	ribosomal protein L16, bacterial/organelle	1472	63	11	0
T508DRAFT_00189	ribosomal protein S3, bacterial type	385	7	0	0
T508DRAFT_00190	ribosomal protein L22, bacterial type	149	77	22	21
T508DRAFT_00191	SSU ribosomal protein S19P	226	0	0	1
T508DRAFT_00192	ribosomal protein L2, bacterial/organelle	464	26	12	0
T508DRAFT_00193	LSU ribosomal protein L23P	362	41	0	0
T508DRAFT_00194	50S ribosomal protein L4, bacterial/organelle	752	21	0	0
T508DRAFT_00195	50S ribosomal protein L3, bacterial	1184	109	0	0
T508DRAFT_00196	SSU ribosomal protein S10P	486	93	0	0
T508DRAFT_00197	predicted membrane-associated, metal-dependent hydrolase	19	29	0	0
T508DRAFT_00198	uncharacterised protein conserved in bacteria	37	24	0	0
T508DRAFT_00199	orotate phosphoribosyltransferase (EC 2.4.2.10)	102	22	0	0
T508DRAFT_00200	TIGR00255 family protein	19	5	4	0
T508DRAFT_00201	predicted ATP-dependent endonuclease of the OLD family	68	14	0	6
T508DRAFT_00202	cysteinyI-tRNA synthetase (EC 6.1.1.16)	33	14	0	0
T508DRAFT_00203	peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	202	211	28	23
T508DRAFT_00204	UDP-2,3-diacetylglucosamine hydrolase (EC 3.6.1.54)	10	36	0	0
T508DRAFT_00205	DNA polymerase I (EC 2.7.7.7)	28	15	0	12
T508DRAFT_00206	hypothetical protein	11	0	0	0
T508DRAFT_00207	conserved hypothetical integral membrane protein	76	15	0	25
T508DRAFT_00208	thioredoxin	51	171	26	115
T508DRAFT_00209	integral membrane protein, PqiA family	34	43	5	10
T508DRAFT_00210	paraquat-inducible protein B	21	15	0	0
T508DRAFT_00211	uncharacterised protein conserved in bacteria	234	1	0	9
T508DRAFT_00212	SseB protein C-terminal domain/SseB protein N-terminal domain	33	29	7	34
T508DRAFT_00213	D-alanine--D-alanine ligase	64	11	16	0
T508DRAFT_00214	transcription termination factor rho	41	20	0	0
T508DRAFT_00215	TRAP-type C ₄ -dicarboxylate transport system, periplasmic component	85	101	122	49
T508DRAFT_00216	Lactoylglutathione lyase and related lyases	66	48	0	110
T508DRAFT_00217	ATP-dependent DNA helicase UvrD (EC 3.6.1.-)	99	252	36	126
T508DRAFT_00218	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	7	0	0	0

T508DRAFT_00219	site-specific recombinase XerC	9	0	0	0
T508DRAFT_00220	diaminopimelate epimerase (EC 5.1.1.7)	24	23	0	42
T508DRAFT_00221	diaminopimelate decarboxylase	13	28	0	33
T508DRAFT_00222	prokaryotic lipoprotein-attachment site	0	6	0	0
T508DRAFT_00223	adenylate cyclase	30	53	3	17
T508DRAFT_00224	uncharacterised enzyme of heme biosynthesis	61	12	11	0
T508DRAFT_00225	heme biosynthesis-associated TPR protein	38	49	40	12
T508DRAFT_00226	ABC-type metal ion transport system, periplasmic component/surface antigen	15	0	0	5
T508DRAFT_00227	methionine-R-sulfoxide reductase/methionine-S-sulfoxide reductase	20	16	0	10
T508DRAFT_00228	protein of unknown function (DUF4026)/uncharacterised protein conserved in bacteria (DUF2314)	9	0	0	73
T508DRAFT_00229	hypothetical protein	58	134	0	0
T508DRAFT_00230*	outer membrane protein and related peptidoglycan-associated (lipo)proteins	1328*	232	29*	51
T508DRAFT_00231	hypothetical protein	48	59	74	27
T508DRAFT_00232	hypothetical protein	168	94	88	17
T508DRAFT_00233	addiction module antitoxin, RelB/DinJ family	52	91	135	320
T508DRAFT_00234	toxin-antitoxin system, toxin component, Txe/YoeB family	260	268	338	340
T508DRAFT_00235	outer membrane protein and related peptidoglycan-associated (lipo)proteins	968	574	407	985
T508DRAFT_00236	transcriptional regulator	542	251	165	684
T508DRAFT_00237	NADPH-dependent FMN reductase	13	15	0	0
T508DRAFT_00238	esterase/lipase	42	0	14	0
T508DRAFT_00239	uncharacterised homolog of gamma-carboxymuconolactone decarboxylase subunit	112	17	31	43
T508DRAFT_00240	hypothetical protein	247	106	151	288
T508DRAFT_00241*	threonine ammonia-lyase, biosynthetic, long form	199*	22*	80	134
T508DRAFT_00242	dihydroxy-acid dehydratase	113	37	42	92
T508DRAFT_00243	branched-chain amino acid aminotransferase, group I	162	34	0	64
T508DRAFT_00244	1-acyl- <i>sn</i> -glycerol-3-phosphate acyltransferase	44	17	11	15
T508DRAFT_00245	hypothetical protein	114	288	0	50
T508DRAFT_00246	protein-disulfide isomerase	114	26	14	39
T508DRAFT_00247	phytoene/squalene synthetase	48	52	0	20
T508DRAFT_00248	acyl-CoA hydrolase	129	75	16	60
T508DRAFT_00249	transcriptional regulator, TetR family	45	206	20	46
T508DRAFT_00250	RND family efflux transporter, MFP subunit	164	245	37	92
T508DRAFT_00251	The (largely Gram-negative bacterial) hydrophobe/Amphiphile Efflux-1 (HAE1) Family	78	34	7	17
T508DRAFT_00252	hypothetical protein	136	51	29	39
T508DRAFT_00253	predicted membrane protein	14	0	0	30
T508DRAFT_00254	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	20	51	0	0
T508DRAFT_00255	flavodoxin, long chain	349	622	157	11
T508DRAFT_00256	Na ⁺ -dependent transporters of the SNF family	111	81	20	41
T508DRAFT_00257	outer membrane protein (porin)	47	7	11	47
T508DRAFT_00258	protein of unknown function (DUF1703)/predicted AAA-ATPase	55	68	20	14
T508DRAFT_00259	cation/multidrug efflux pump	33	56	73	48
T508DRAFT_00260	RND family efflux transporter, MFP subunit	107	290	216	97
T508DRAFT_00261	transcriptional regulator, TetR family	13	0	0	0
T508DRAFT_00262	ABC-type sugar transport system, periplasmic component	1459	220	7	85
T508DRAFT_00263	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	65	0	0	0
T508DRAFT_00264	monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)	28	7	0	0
T508DRAFT_00265	monosaccharide ABC transporter membrane protein, CUT2 family (TC 3.A.1.2.-)	54	39	0	0
T508DRAFT_00266	L-arabinose isomerase	60	0	4	0
T508DRAFT_00267	tripartite ATP-independent periplasmic transporter solute receptor, DctP family	145	20	0	14
T508DRAFT_00268	TRAP-type C ₄ -dicarboxylate transport system, small permease component	225	267	115	60
T508DRAFT_00269	transposase and inactivated derivatives	629	407	148	121
T508DRAFT_00270	hypothetical protein	21	0	0	0
T508DRAFT_00271	hypothetical protein	18	56	31	20
T508DRAFT_00272	thiol:disulfide interchange protein	53	0	0	20
T508DRAFT_00273	hypothetical protein	11	50	0	91
T508DRAFT_00274	methyl-accepting chemotaxis protein	68	22	12	22
T508DRAFT_00275	protein affecting phage T7 exclusion by the F plasmid	22	20	0	25
T508DRAFT_00276	positive regulator of sigma(E), RseC/MucC	27	6	19	0
T508DRAFT_00277	inosine-uridine nucleoside N-ribohydrolase	44	54	0	9
T508DRAFT_00278	single stranded DNA-binding protein (ssb)	161	19	14	0
T508DRAFT_00279	predicted ATPase (AAA+ superfamily)	105	39	14	27
T508DRAFT_00280	putative efflux protein, MATE family	21	21	5	39
T508DRAFT_00281*	co-chaperonin GroES (HSP10)	827*	114*	249	553
T508DRAFT_00282	chaperonin GroL	1537	478	218	488

T508DRAFT_00283	predicted transcriptional regulators	127	0	20	68
T508DRAFT_00284	hydrolases of the alpha/beta superfamily	56	24	0	0
T508DRAFT_00285	uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	51	10	0	21
T508DRAFT_00286	hypothetical protein	40	0	0	0
T508DRAFT_00287	predicted Zn-dependent hydrolases of the beta-lactamase fold	7	0	0	9
T508DRAFT_00288	acetyltransferase (GNAT) domain	63	0	0	0
T508DRAFT_00289	3-methyl-2-oxobutanoate hydroxymethyltransferase	36	11	0	0
T508DRAFT_00290	uncharacterized conserved protein	14	0	0	0
T508DRAFT_00291	methyl-accepting chemotaxis protein	23	17	7	0
T508DRAFT_00292	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	54	27	30	14
T508DRAFT_00293	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	21	62	32	13
T508DRAFT_00294	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	41	111	21	37
T508DRAFT_00295	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	20	8	0	0
T508DRAFT_00296	hypothetical protein	2109	1552	1072	2945
T508DRAFT_00297	transcriptional regulator, HxlR family	191	155	60	195
T508DRAFT_00298	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	29	11	0	7
T508DRAFT_00299	putative NADPH-quinone reductase (modulator of drug activity B)	118	46	0	0
T508DRAFT_00300	uncharacterised membrane protein	28	14	0	28
T508DRAFT_00301	transposase, IS605 OrfB family, central region	8	7	8	0
T508DRAFT_00302	ABC-type sugar transport system, periplasmic component	91	42	30	13
T508DRAFT_00303*	ATP-binding cassette protein, ChvD family	189*	52	4*	40
T508DRAFT_00304	hypothetical protein	18	0	0	0
T508DRAFT_00305	transcriptional regulator, TetR family	48	0	0	45
T508DRAFT_00306	RND family efflux transporter, MFP subunit	20	14	10	20
T508DRAFT_00307	ABC-type multidrug transport system, ATPase component	20	4	0	26
T508DRAFT_00308	ABC-type multidrug transport system, permease component	5	0	15	20
T508DRAFT_00309	ABC-type multidrug transport system, permease component	33	5	0	0
T508DRAFT_00310	hypothetical protein	8	25	15	0
T508DRAFT_00311	conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	19	4	0	0
T508DRAFT_00312	flagellin and related hook-associated proteins	191	90	0	15
T508DRAFT_00313	alpha-acetolactate decarboxylase	46	7	0	13
T508DRAFT_00314	methyl-accepting chemotaxis protein	68	107	52	35
T508DRAFT_00315	anaerobic C ₄ -dicarboxylate membrane transporter family protein	36	19	0	0
T508DRAFT_00316	SsrA-binding protein	18	75	0	0
T508DRAFT_00317	sulfate permease and related transporters (MFS superfamily)	141	40	28	18
T508DRAFT_00319	protein of unknown function (DUF1703)/predicted AAA-ATPase	204	62	38	43
T508DRAFT_00320	hypothetical protein	37	74	50	8
T508DRAFT_00321	clostripain family protein	21	26	5	7
T508DRAFT_00322	hypothetical protein	9	1	0	26
T508DRAFT_00323	hypothetical protein	0	0	0	0
T508DRAFT_00324	hypothetical protein	20	37	0	0
T508DRAFT_00325	hypothetical protein	54	0	0	14
T508DRAFT_00326	protein of unknown function (DUF1653)	221	257	40	327
T508DRAFT_00327	adenine deaminase (EC 3.5.4.2)	70	78	44	120
T508DRAFT_00328	hypothetical protein	61	63	85	79
T508DRAFT_00329	hypothetical protein	63	11	9	10
T508DRAFT_00330	Type II secretory pathway, component PulF	10	0	0	0
T508DRAFT_00331	predicted permeases	35	7	0	11
T508DRAFT_00332	camphor resistance protein CrcB	33	17	0	2
T508DRAFT_00333	serine phosphatase RsbU, regulator of sigma subunit	24	9	4	11
T508DRAFT_00334	serine phosphatase RsbU, regulator of sigma subunit	55	19	9	7
T508DRAFT_00335	predicted redox protein, regulator of disulfide bond formation	176	309	106	98
T508DRAFT_00336	formate/nitrite family of transporters	29	2	16	21
T508DRAFT_00337	transposase and inactivated derivatives	1	20	0	2
T508DRAFT_00338	transposase, IS605 OrfB family, central region	4	38	0	10
T508DRAFT_00339	5'-nucleotidase, lipoprotein e(P4) family	132	49	56	0
T508DRAFT_00340	peptide chain release factor 3	48	51	36	32
T508DRAFT_00341	Mg-dependent DNase	148	451	152	288
T508DRAFT_00342	phosphoserine phosphatase SerB	2	0	13	68
T508DRAFT_00343	DNA repair protein Rada	32	7	22	0
T508DRAFT_00344	regulator of sigma D	151	122	90	59
T508DRAFT_00345	HAD-superfamily hydrolase, subfamily IIB	40	20	0	32
T508DRAFT_00346	ABC-type uncharacterized transport system, permease and ATPase components	65	34	36	113
T508DRAFT_00347	hypothetical protein	28	3	0	0
T508DRAFT_00348	membrane proteins related to metalloendopeptidases	48	164	46	12
T508DRAFT_00349	uncharacterised protein conserved in bacteria	1	0	0	0
T508DRAFT_00350	predicted permeases	52	5	3	18

T508DRAFT_00351	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	35	4	0	0
T508DRAFT_00352	IMP cyclohydrolase (EC 3.5.4.10)/ phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	48	7	0	5
T508DRAFT_00353	bacterial nucleoid DNA-binding protein	31	171	0	0
T508DRAFT_00354*	phosphoglucomutase, alpha-D-glucose phosphate-specific	212*	36	4*	16
T508DRAFT_00355	hypothetical protein	35	20	0	0
T508DRAFT_00356	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	19	24	0	0
T508DRAFT_00357	D-alanyl-D-alanine carboxypeptidase	23	50	0	0
T508DRAFT_00358	amino acid carrier protein	41	15	10	13
T508DRAFT_00359	uncharacterized domain HDIG	43	12	5	0
T508DRAFT_00360	uncharacterised membrane-associated protein	16	13	0	21
T508DRAFT_00361	predicted rRNA methylase (SpoU class)	9	0	0	0
T508DRAFT_00362	DNA segregation ATPase FtsK/SpoIIIE and related proteins	29	16	0	3
T508DRAFT_00363	periplasmic chaperone LolA	28	0	0	0
T508DRAFT_00364	ATPase related to the helicase subunit of the Holliday junction resolvase	52	57	17	36
T508DRAFT_00365	hypothetical protein	6210	4367	2540	2851
T508DRAFT_00366	3-deoxy-D-manno-octulosonic-acid transferase	193	152	49	43
T508DRAFT_00367	putative NADPH-quinone reductase (modulator of drug activity B)	72	18	22	0
T508DRAFT_00368	lipopolysaccharide kinase (Kdo/WaaP) family	34	15	0	15
T508DRAFT_00369*	ADP-heptose:LPS heptosyltransferase	259*	71	20*	86
T508DRAFT_00370	phosphopantetheine adenylyltransferase (EC 2.7.7.3)	818	658	85	220
T508DRAFT_00371	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18)	96	41	54	42
T508DRAFT_00373	uncharacterised protein conserved in bacteria	12	9	27	14
T508DRAFT_00374	tripartite tricarboxylate transporter TctB family	11	73	75	43
T508DRAFT_00375	uncharacterised protein conserved in bacteria	57	36	0	9
T508DRAFT_00376	Na/Pi-cotransporter	14	28	5	6
T508DRAFT_00377	glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	83	29	12	103
T508DRAFT_00378	glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	94	45	53	72
T508DRAFT_00379	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	43	65	49	47
T508DRAFT_00380	DNA replication and repair protein RecF	20	24	60	33
T508DRAFT_00381	DNA polymerase III, beta subunit	28	79	44	108
T508DRAFT_00382	ATPase involved in DNA replication initiation	27	55	26	43
T508DRAFT_00383	ribosomal protein L34, bacterial type	85	0	0	0
T508DRAFT_00384	ribonuclease P protein component, eubacterial	49	0	22	35
T508DRAFT_00385	protein translocase subunit yidC	23	28	0	38
T508DRAFT_00386	tRNA modification GTPase trmE	9	4	0	0
T508DRAFT_00387	uncharacterised protein conserved in bacteria	82	0	52	11
T508DRAFT_00388	paraquat-inducible protein B	89	107	22	19
T508DRAFT_00389	uncharacterised paraquat-inducible protein A	71	43	8	27
T508DRAFT_00390	anaerobic ribonucleoside-triphosphate reductase activating protein	110	51	0	10
T508DRAFT_00391	oxygen-sensitive ribonucleoside-triphosphate reductase	21	46	0	52
T508DRAFT_00392	ribonucleoside-triphosphate reductase class III catalytic subunit (EC 1.17.4.2)	36	42	23	24
T508DRAFT_00393	uncharacterised protein conserved in bacteria	17	11	0	0
T508DRAFT_00394	translation elongation factor P (EF-P)	78	139	30	40
T508DRAFT_00395	predicted acetyltransferase	61	28	0	15
T508DRAFT_00396	glucose-inhibited division protein A	20	3	22	0
T508DRAFT_00397	16S rRNA m(7)G-527 methyltransferase (EC 2.1.1.170)	32	0	0	0
T508DRAFT_00398	ATPases involved in chromosome partitioning	45	0	0	0
T508DRAFT_00399	ParB/RepB/Spo0J family partition protein	44	12	0	5
T508DRAFT_00400	hypothetical protein	110	28	0	79
T508DRAFT_00401	ATP synthase F ₀ subcomplex A subunit	15	9	0	0
T508DRAFT_00402	ATP synthase, F ₀ subunit C	90	20	39	0
T508DRAFT_00403	ATP synthase F ₀ subcomplex B subunit	52	19	0	0
T508DRAFT_00404	ATP synthase, F ₁ delta subunit	19	6	0	0
T508DRAFT_00405	proton translocating ATP synthase, F ₁ alpha subunit	41	13	12	0
T508DRAFT_00406	ATP synthase, F ₁ gamma subunit	34	18	0	22
T508DRAFT_00407	ATP synthase F ₁ subcomplex beta subunit	89	29	0	0
T508DRAFT_00408	ATP synthase, F ₁ epsilon subunit (delta in mitochondria)	50	0	0	0
T508DRAFT_00409	amino acid permeases	80	49	33	47
T508DRAFT_00410	L-serine ammonia-lyase (EC 4.3.1.17)	53	13	12	9
T508DRAFT_00411	RNA methyltransferase, RsmD family	47	0	0	0
T508DRAFT_00412	signal recognition particle-docking protein FtsY	1	7	0	0
T508DRAFT_00413*	RNA polymerase, sigma 32 subunit, RpoH	35	192*	11*	61
T508DRAFT_00414	predicted P-loop-containing kinase	149	7	15	0
T508DRAFT_00415	PTS IIA-like nitrogen-regulatory protein PtsN	91	16	0	72
T508DRAFT_00416	ribosomal subunit interface protein	73	87	58	31
T508DRAFT_00417	predicted metal-dependent hydrolase of the TIM-barrel fold	4	0	0	7
T508DRAFT_00418	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	11	6	12	0
T508DRAFT_00419	putative NADPH-quinone reductase (modulator of drug activity B)	40	10	3	0
T508DRAFT_00420	uncharacterised protein conserved in bacteria	15	24	0	0

T508DRAFT_00421	predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	4	13	0	0
T508DRAFT_00422	uncharacterised conserved protein	42	75	0	45
T508DRAFT_00423	transcriptional regulator, TetR family	114	226	47	55
T508DRAFT_00424	RNA polymerase, sigma 54 subunit, RpoN/SigL	94	46	3	31
T508DRAFT_00425	ABC-type (unclassified) transport system, ATPase component	64	2	0	15
T508DRAFT_00426	lipopolysaccharide transport periplasmic protein LptA	70	7	0	0
T508DRAFT_00427	uncharacterised protein conserved in bacteria	47	0	23	60
T508DRAFT_00428	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family	59	56	0	8
T508DRAFT_00429	ABC-type transport system involved in resistance to organic solvents, ATPase component	22	35	14	0
T508DRAFT_00430	conserved hypothetical integral membrane protein	8	20	0	0
T508DRAFT_00431	ABC-type transport system involved in resistance to organic solvents, periplasmic component	0	13	0	0
T508DRAFT_00432	ABC-type transport system involved in resistance to organic solvents, auxiliary component	8	9	0	0
T508DRAFT_00433	predicted NTP binding protein (contains STAS domain)	64	25	0	0
T508DRAFT_00434	uncharacterised protein conserved in bacteria	68	61	0	29
T508DRAFT_00435	protein of unknown function (DUF2750)	140	144	0	14
T508DRAFT_00436	excinuclease ABC, A subunit	48	16	10	15
T508DRAFT_00437	single stranded DNA-binding protein (ssb)	11	117	0	0
T508DRAFT_00438	rod shape-determining protein MreB	91	71	19	12
T508DRAFT_00439	rod shape-determining protein MreC	11	16	0	23
T508DRAFT_00440	rod shape-determining protein MreD	3	14	0	0
T508DRAFT_00441	MAF protein	3	69	0	0
T508DRAFT_00442	microcin-processing peptidase 2. Unknown type peptidase. MEROPS family U62	23	0	0	0
T508DRAFT_00443	6-phosphogluconate dehydratase (EC 4.2.1.12)	57	10	0	26
T508DRAFT_00444	carbohydrate kinase, thermoresistant glucokinase family	42	50	0	0
T508DRAFT_00445	TRAP-type C ₄ -dicarboxylate transport system, small permease component	3	0	0	77
T508DRAFT_00446	TRAP transporter, DctM subunit	36	13	7	20
T508DRAFT_00447	tripartite ATP-independent periplasmic transporter solute receptor, DctP family	166	7	0	10
T508DRAFT_00448	predicted Na ⁺ -dependent transporter	32	18	0	7
T508DRAFT_00449	predicted Na ⁺ -dependent transporter	64	77	21	86
T508DRAFT_00450*	predicted Zn-dependent proteases and their inactivated homologs	53*	331*	106	108
T508DRAFT_00451	flagellar basal body-associated protein	100	186	19	26
T508DRAFT_00452	glycerol-3-phosphate acyltransferase (EC 2.3.1.15)	35	97	45	98
T508DRAFT_00453	cation diffusion facilitator family transporter	71	49	9	0
T508DRAFT_00454	serine O-acetyltransferase (EC 2.3.1.30)	43	33	0	0
T508DRAFT_00455	PTS system, fructose-specific, IIB component/PTS system, fructose subfamily, IIA component/PTS system, fructose subfamily, IIC component	94	33	12	45
T508DRAFT_00456	hypothetical protein	70	0	0	0
T508DRAFT_00457	ATP-dependent protease HslVU, ATPase subunit	27	12	0	0
T508DRAFT_00458	ATP-dependent protease HslVU, peptidase subunit	20	0	0	0
T508DRAFT_00459	hypothetical protein	14	0	18	0
T508DRAFT_00460	arginyl-tRNA synthetase (EC 6.1.1.19)	50	4	0	18
T508DRAFT_00461	replication restart DNA helicase PriA	39	18	0	0
T508DRAFT_00462	LSU ribosomal protein L31P	250	408	144	187
T508DRAFT_00463	malic enzyme	301	127	65	36
T508DRAFT_00464	transposase, IS4 family	40	14	67	0
T508DRAFT_00465	tRNA (uracil-5-)-methyltransferase	146	53	28	19
T508DRAFT_00466	glutamate racemase (EC 5.1.1.3)	10	9	17	0
T508DRAFT_00467	uncharacterised protein conserved in bacteria	174	0	48	0
T508DRAFT_00468	acetolactate synthase, small subunit (EC 2.2.1.6)	1	0	0	0
T508DRAFT_00469	acetolactate synthase, large subunit (EC 2.2.1.6)	39	15	6	0
T508DRAFT_00470	suppressor of fused protein (SUFU)	22	18	0	0
T508DRAFT_00471	acetolactate synthase, small subunit (EC 2.2.1.6)	32	14	0	7
T508DRAFT_00472	acetolactate synthase, large subunit (EC 2.2.1.6)	58	23	15	27
T508DRAFT_00473	putative protein-S-isoprenylcysteine methyltransferase	8	13	0	0
T508DRAFT_00474	FAD/FMN-containing dehydrogenases	16	8	0	0
T508DRAFT_00480	haloacid dehalogenase-like hydrolase	83	85	43	38
T508DRAFT_00481	hypothetical protein	0	0	0	0
T508DRAFT_00482	protein involved in cell division	18	43	77	47
T508DRAFT_00483	tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB	25	19	7	20
T508DRAFT_00484	phosphate starvation-inducible protein PhoH, predicted ATPase	10	9	0	0
T508DRAFT_00485	probable rRNA maturation factor YbeY	5	0	0	0
T508DRAFT_00486	putative Mg ²⁺ and Co ²⁺ transporter CorC	19	0	0	0
T508DRAFT_00487	apolipoprotein N-acyltransferase	38	42	11	0
T508DRAFT_00488	hypothetical protein	25	3	14	24
T508DRAFT_00489	uncharacterised protein conserved in bacteria	29	8	0	0
T508DRAFT_00490	leucyl-tRNA synthetase (EC 6.1.1.4)	63	18	0	3
T508DRAFT_00491	rare lipoprotein B	65	15	14	0
T508DRAFT_00492	DNA polymerase III, delta subunit (EC 2.7.7.7)	48	9	49	35

T508DRAFT_00493	nicotinate-nucleotide adenyllyltransferase (EC 2.7.7.18)	10	8	0	21
T508DRAFT_00494	iojap-like ribosome-associated protein	76	0	2	0
T508DRAFT_00495	rRNA large subunit m3Psi methyltransferase RlmH	30	37	20	49
T508DRAFT_00496	penicillin-binding protein 2	13	7	0	13
T508DRAFT_00497	rod shape-determining protein RodA	15	0	0	0
T508DRAFT_00498	lytic murein transglycosylase B	3	37	0	0
T508DRAFT_00499	rare lipoprotein A	24	2	0	8
T508DRAFT_00500	penicillin-binding protein 6. serine peptidase. MEROPS family S11	33	13	0	0
T508DRAFT_00501	uncharacterised conserved protein	17	49	0	0
T508DRAFT_00502	uncharacterised membrane protein	11	50	0	0
T508DRAFT_00503	DNA adenine methylase (dam)	15	16	0	15
T508DRAFT_00504	predicted neuraminidase (sialidase)	45	63	10	39
T508DRAFT_00505	uncharacterized protein, YhcH/YjgK/YiaL family	61	62	0	23
T508DRAFT_00506	TRAP transporter, 4TM/12TM fusion protein	43	0	6	0
T508DRAFT_00507	TRAP transporter solute receptor, TAXI family	107	42	0	0
T508DRAFT_00508	transcriptional regulator, DeoR family	43	37	92	208
T508DRAFT_00509	uncharacterised protein conserved in bacteria	12	0	0	0
T508DRAFT_00510	4-hydroxythreonine-4-phosphate dehydrogenase	51	7	10	0
T508DRAFT_00511	dihydrodipicolinate synthase	38	12	0	2
T508DRAFT_00512	alcohol dehydrogenase, class IV	88	8	0	25
T508DRAFT_00513	DNA adenine methylase (dam)	51	32	18	0
T508DRAFT_00514	ribosomal protein L9	116	0	65	0
T508DRAFT_00515	SSU ribosomal protein S18P	229	203	31	53
T508DRAFT_00516	SSU ribosomal protein S6P	762	247	0	158
T508DRAFT_00517	23S rRNA Gm-2251 2'-O-methyltransferase (EC 2.1.1.185)	24	0	0	42
T508DRAFT_00518	ribonuclease R	24	6	6	0
T508DRAFT_00519	putative oxygen-independent coproporphyrinogen III oxidase	4	1	0	1
T508DRAFT_00520	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	21	35	0	11
T508DRAFT_00521	pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	12	8	0	10
T508DRAFT_00522	uncharacterised protein conserved in bacteria	35	101	35	15
T508DRAFT_00523	permease	36	7	0	15
T508DRAFT_00524	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED/beta-phosphoglucosylase family hydrolase	74	0	0	0
T508DRAFT_00525*	glycogen/starch/alpha-glucan phosphorylases	348*	44	27	3*
T508DRAFT_00526	flagellar biosynthetic protein FlhB	12	0	5	18
T508DRAFT_00527	DNA topoisomerase IV, B subunit, proteobacterial	44	6	0	14
T508DRAFT_00528	hypothetical protein	163	0	13	0
T508DRAFT_00529	hypothetical protein	92	0	0	0
T508DRAFT_00530	signal transduction histidine kinase	71	58	8	8
T508DRAFT_00531	response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	28	0	24	0
T508DRAFT_00532	predicted esterase	18	19	0	0
T508DRAFT_00533	predicted phosphohydrolases	40	31	0	0
T508DRAFT_00534	nudix-type nucleoside diphosphatase, YffH/AdpP family	23	8	0	38
T508DRAFT_00535	dihydroorotase and related cyclic amidohydrolases	47	1	24	25
T508DRAFT_00536	tryptophanyl-tRNA synthetase (EC 6.1.1.2)	54	46	0	13
T508DRAFT_00537	phosphoglycolate phosphatase	0	0	0	0
T508DRAFT_00538	ribulose-phosphate 3-epimerase	31	0	0	0
T508DRAFT_00539	AAA domain/Sporulation related domain	51	42	0	0
T508DRAFT_00540	3-dehydroquinate synthase (EC 4.2.3.4)	14	21	0	0
T508DRAFT_00541	shikimate kinase (EC 2.7.1.71)	50	23	0	5
T508DRAFT_00542	membrane-associated phospholipid phosphatase	19	28	26	0
T508DRAFT_00543	nucleoside H ⁺ symporter	52	25	29	38
T508DRAFT_00544	penicillin-binding protein, 1A family	21	9	0	7
T508DRAFT_00545	hypothetical protein	94	362	158	243
T508DRAFT_00546	type VI secretion ATPase, ClpV1 family	49	40	33	10
T508DRAFT_00547	type VI secretion protein, VC_A0111 family	7	0	31	0
T508DRAFT_00548	type VI secretion protein, VC_A0110 family	25	21	11	0
T508DRAFT_00549	type VI secretion system lysozyme-like protein	16	0	0	42
T508DRAFT_00550	type VI secretion system effector, Hcp1 family	897	706	563	138
T508DRAFT_00551	type VI secretion protein, EvpB/VC_A0108 family	262	82	66	15
T508DRAFT_00552	type VI secretion protein, VC_A0107 family	90	71	38	17
T508DRAFT_00553	uncharacterised protein conserved in bacteria	58	117	70	17
T508DRAFT_00554	type VI secretion system effector, Hcp1 family	234	475	503	23
T508DRAFT_00555	hypothetical protein	33	17	44	12
T508DRAFT_00556	hypothetical protein	9	37	63	38
T508DRAFT_00557	hypothetical protein	20	78	0	0
T508DRAFT_00558	hypothetical protein	21	0	95	19
T508DRAFT_00559	hypothetical protein	11	0	0	0
T508DRAFT_00560	uncharacterised protein conserved in bacteria	7	0	0	0
T508DRAFT_00561	hypothetical protein	121	18	0	0
T508DRAFT_00562	hypothetical protein	22	62	59	0
T508DRAFT_00563	hypothetical protein	67	37	70	0
T508DRAFT_00564	asparaginyl-tRNA synthetase (EC 6.1.1.22)	45	29	0	6

T508DRAFT_00565	predicted AAA-ATPase	34	0	0	17
T508DRAFT_00566	EamA-like transporter family	29	0	7	22
T508DRAFT_00567	anthranilate synthase, component I (EC 4.1.3.27)	11	29	6	21
T508DRAFT_00568	glutamine amidotransferase of anthranilate synthase or aminodeoxychorismate synthase	82	36	51	5
T508DRAFT_00569	predicted nucleotidyltransferases	15	0	0	0
T508DRAFT_00570	predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	6	0	0	0
T508DRAFT_00571	protein of unknown function (DUF1703)/predicted AAA-ATPase	3	21	6	6
T508DRAFT_00572	protein of unknown function (DUF1703)/predicted AAA-ATPase	10	20	0	0
T508DRAFT_00573	metal-dependent hydrolases of the beta-lactamase superfamily II	36	53	0	4
T508DRAFT_00574	anthranilate phosphoribosyltransferase	137	164	43	106
T508DRAFT_00575	indole-3-glycerol phosphate synthase (EC 4.1.1.48)	37	13	18	13
T508DRAFT_00576	tryptophan synthase, beta chain (EC 4.2.1.20)	65	45	56	12
T508DRAFT_00577	tryptophan synthase, alpha chain (EC 4.2.1.20)	52	66	16	15
T508DRAFT_00578	phosphoserine phosphatase	69	25	9	0
T508DRAFT_00579	predicted membrane protein, putative toxin regulator	21	0	0	0
T508DRAFT_00580	hypothetical protein	0	37	0	0
T508DRAFT_00581	TonB family C-terminal domain	49	31	0	7
T508DRAFT_00582	biopolymer transport protein	12	36	0	0
T508DRAFT_00583	biopolymer transport proteins	5	0	0	17
T508DRAFT_00584	flavodoxin	16	0	0	0
T508DRAFT_00585	putative heme iron utilization protein	6	0	0	0
T508DRAFT_00586	ATPase components of various ABC-type transport systems, contain duplicated ATPase	0	6	0	0
T508DRAFT_00587	cobalt transport protein	2	1	0	0
T508DRAFT_00588	hypothetical protein	0	15	0	0
T508DRAFT_00589	outer membrane receptor for ferrienterochelin and colicins	0	5	0	6
T508DRAFT_00590	putative heme utilization radical SAM enzyme HutW	7	7	0	0
T508DRAFT_00591	protein of unknown function (DUF1703)/predicted AAA-ATPase	8	29	8	0
T508DRAFT_00592*	sugar phosphate permease	195*	69	17*	45
T508DRAFT_00593	hypothetical protein	5	48	0	0
T508DRAFT_00594	helix-turn-helix	94	209	42	101
T508DRAFT_00595	hypothetical protein	42	16	0	19
T508DRAFT_00596	predicted transcriptional regulator	27	54	18	27
T508DRAFT_00597	lecithin retinol acyltransferase	17	0	0	0
T508DRAFT_00598	ATPase involved in DNA replication initiation	21	5	0	0
T508DRAFT_00599	hypothetical protein	43	47	0	0
T508DRAFT_00600	zinc-ribbon domain	60	15	15	13
T508DRAFT_00601	hypothetical protein	35	0	0	0
T508DRAFT_00602	hypothetical protein	270	311	69	270
T508DRAFT_00603	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	45	3	5	7
T508DRAFT_00604	histidinol-phosphate aminotransferase	36	12	18	0
T508DRAFT_00605	diguanylate cyclase (GGDEF) domain	10	35	0	20
T508DRAFT_00606	diguanylate cyclase (GGDEF) domain	12	18	0	0
T508DRAFT_00607	diguanylate cyclase (GGDEF) domain	34	45	0	20
T508DRAFT_00608	hypothetical protein	97	7	0	0
T508DRAFT_00609	cysteine desulfurase NifS	134	88	63	165
T508DRAFT_00610	modular FeS cluster scaffolding protein NifU	53	0	0	1
T508DRAFT_00611	transcriptional regulators	50	16	0	0
T508DRAFT_00612	copper-(or silver)-translocating P-type ATPase	9	5	0	4
T508DRAFT_00613	hypothetical protein	0	0	0	0
T508DRAFT_00614	conserved hypothetical protein (putative transposase or invertase)	15	22	0	36
T508DRAFT_00615	hypothetical protein	39	0	0	0
T508DRAFT_00616	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase	52	89	38	18
T508DRAFT_00617	hypothetical protein	15	27	40	95
T508DRAFT_00618	ferrous iron transporter FeoB	21	11	0	4
T508DRAFT_00619	Fe ²⁺ transport system protein A	69	193	73	32
T508DRAFT_00620	Na ⁺ /serine symporter	40	9	0	0
T508DRAFT_00621	predicted ATPase (AAA+ superfamily)	39	0	0	0
T508DRAFT_00622	threonine synthase	112	45	31	105
T508DRAFT_00623	homoserine kinase (EC 2.7.1.39)	25	5	0	0
T508DRAFT_00624	aspartate kinase (EC 2.7.2.4)	38	3	5	0
T508DRAFT_00625	hypothetical protein	63	42	79	67
T508DRAFT_00626	triosephosphate isomerase (EC 5.3.1.1)	281	115	50	12
T508DRAFT_00627	6-phosphofructokinase (EC 2.7.1.11)	207	195	25	51
T508DRAFT_00628	hypothetical protein	27	0	0	0
T508DRAFT_00629	FOG: TPR repeat, SEL1 subfamily	16	33	0	0
T508DRAFT_00630	FOG: TPR repeat, SEL1 subfamily	48	18	35	0
T508DRAFT_00631	FOG: TPR repeat, SEL1 subfamily	77	98	51	56
T508DRAFT_00632	bacterial surface protein 26-residue repeat	68	33	0	24
T508DRAFT_00634	hypothetical protein	17	0	0	22
T508DRAFT_00635	hemolysin activation/secretion protein	3	15	0	8
T508DRAFT_00636	filamentous hemagglutinin family N-terminal domain	17	0	4	5
T508DRAFT_00637	glucokinase, proteobacterial type	77	41	21	0

T508DRAFT_00638	transposase and inactivated derivatives	42	10	11	0
T508DRAFT_00639	transposase DDE domain	28	72	0	25
T508DRAFT_00640	anion transporter	43	47	9	46
T508DRAFT_00641	bacteriophage protein gp37	39	26	0	56
T508DRAFT_00642	protein of unknown function (DUF1703)/predicted AAA-ATPase	13	6	0	8
T508DRAFT_00643*	transposase and inactivated derivatives	412*	191	49*	211
T508DRAFT_00644	RNA polymerase sigma factor, sigma-70 family	88	76	46	63
T508DRAFT_00645	DNA-binding regulatory protein, YebC/PmpR family	108	20	0	12
T508DRAFT_00646	aspartyl-tRNA synthetase, bacterial type	48	9	0	11
T508DRAFT_00647*	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	246	566*	435	83*
T508DRAFT_00648	protein of unknown function (DUF1311)	12	101	24	25
T508DRAFT_00649	aspartate racemase	267	0	0	68
T508DRAFT_00650	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)	214	22	14	44
T508DRAFT_00653	L-aspartate oxidase (EC 1.4.3.16)	151	18	0	16
T508DRAFT_00654	RNA polymerase, sigma-24 subunit, RpoE	2226	3652	2944	2701
T508DRAFT_00655	negative regulator of sigma E activity	312	743	483	465
T508DRAFT_00656	sigma E regulatory protein, MucB/RseB	0	30	0	0
T508DRAFT_00657	GTP-binding protein LepA	28	9	0	0
T508DRAFT_00658	signal peptidase I, bacterial type	3	32	0	17
T508DRAFT_00659	ribonuclease III, bacterial	69	11	0	0
T508DRAFT_00660	GTP-binding protein Era	27	67	0	0
T508DRAFT_00661	DNA replication and repair protein RecO	71	39	0	60
T508DRAFT_00662	23S rRNA (uracil-5-)-methyltransferase RumA	23	0	0	4
T508DRAFT_00663	(p)ppGpp synthetase, RelA/SpoT family	17	23	0	5
T508DRAFT_00664	CTP synthase (EC 6.3.4.2)	39	16	0	9
T508DRAFT_00665	septum formation initiator	0	0	0	18
T508DRAFT_00666	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	4	0	0	4
T508DRAFT_00667	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	4	0	0	19
T508DRAFT_00668	predicted membrane protein	10	9	0	0
T508DRAFT_00669	membrane proteins related to metalloendopeptidases	18	14	0	0
T508DRAFT_00670	RNA polymerase, sigma 38 subunit, RpoS	37	31	0	20
T508DRAFT_00671	DNA mismatch repair protein MutS	18	10	0	21
T508DRAFT_00672	hypothetical protein	259	289	118	192
T508DRAFT_00673	uncharacterised protein conserved in bacteria	86	88	18	41
T508DRAFT_00674	protein RecA	165	29	66	92
T508DRAFT_00675	uncharacterised protein conserved in bacteria	20	0	0	16
T508DRAFT_00676	alanyl-tRNA synthetase (EC 6.1.1.7)	31	13	4	2
T508DRAFT_00677	carbon storage regulator, CsrA	38	0	0	63
T508DRAFT_00681	primary replicative DNA helicase (EC 3.6.1.-)	8	0	0	0
T508DRAFT_00682	alanine racemase	101	16	0	50
T508DRAFT_00683	nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)	691	55	19	12
T508DRAFT_00684	bacterial peptide chain release factor 2 (bRF-2)	30	9	0	0
T508DRAFT_00685	lysyl-tRNA synthetase, class II (EC 6.1.1.6)	55	28	0	0
T508DRAFT_00686	dihydrodipicolinate synthase	68	0	8	0
T508DRAFT_00687	tRNA (guanine-N7-)-methyltransferase (EC 2.1.1.33)	27	9	0	0
T508DRAFT_00688	predicted phosphotransferase related to Ser/Thr protein kinases	18	47	0	9
T508DRAFT_00689	nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)	6	10	0	0
T508DRAFT_00690	DnaJ-class molecular chaperone with C-terminal Zn finger domain	25	41	0	0
T508DRAFT_00691	DnaJ-domain-containing proteins 1	29	9	8	28
T508DRAFT_00692	cytosine/adenosine deaminases	181	100	0	59
T508DRAFT_00693	predicted ATPase (AAA+ superfamily)	14	0	0	10
T508DRAFT_00694*	ribosomal large subunit pseudouridine synthase A (EC 5.4.99.-)	318*	131	40	10*
T508DRAFT_00695	beta-barrel assembly machine subunit BamD	77	26	0	53
T508DRAFT_00696	ribosomal large subunit pseudouridine synthase D (EC 5.4.99.-)	32	16	19	20
T508DRAFT_00697	uncharacterized protein, YfiH family	14	0	19	13
T508DRAFT_00698	ATP-dependent chaperone ClpB	263	320	222	399
T508DRAFT_00699	uncharacterized protein conserved in bacteria	202	48	55	156
T508DRAFT_00700	uncharacterized protein conserved in bacteria	71	42	33	16
T508DRAFT_00701	protein of unknown function (DUF1703)/predicted AAA-ATPase	31	44	12	10
T508DRAFT_00702	hypothetical protein	64	150	85	55
T508DRAFT_00703	RloB-like protein	60	17	36	0
T508DRAFT_00704	predicted ATPases	167	94	50	75
T508DRAFT_00705	hypothetical protein	11	24	0	0
T508DRAFT_00706	hypothetical protein	121	25	21	46
T508DRAFT_00707	hypothetical protein	102	21	9	12
T508DRAFT_00708	hypothetical protein	35	18	0	0
T508DRAFT_00709	macrocin-O-methyltransferase (TylF)	29	0	7	7
T508DRAFT_00710	asparagine synthase (glutamine-hydrolyzing)	26	10	0	0
T508DRAFT_00711	cytidyltransferase-like domain	31	0	0	0

T508DRAFT_00712	thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]	9	0	0	0
T508DRAFT_00713	predicted AAA-ATPase	32	39	16	27
T508DRAFT_00714	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	129	112	135	79
T508DRAFT_00715	transketolase, N-terminal subunit	68	109	38	46
T508DRAFT_00716	transketolase subunit B (EC 2.2.1.1)	64	72	30	37
T508DRAFT_00717	isopropylmalate/homocitrate/citramalate synthases	32	43	3	8
T508DRAFT_00718	hypothetical protein	142	22	35	15
T508DRAFT_00719	coenzyme F ₃₉₀ synthetase	40	8	0	10
T508DRAFT_00720	acyl-CoA reductase (LuxC)	33	32	10	10
T508DRAFT_00721	hypothetical protein	42	1	0	0
T508DRAFT_00722	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	92	37	33	107
T508DRAFT_00723	hypothetical protein	165	90	23	64
T508DRAFT_00724	flagellar biosynthetic protein FlhS	83	76	0	80
T508DRAFT_00725	hypothetical protein	44	0	0	12
T508DRAFT_00726	protein of unknown function (DUF1703)/predicted AAA-ATPase	12	29	0	47
T508DRAFT_00727	phosphoribosylformylglycinamide synthase, single chain form	47	20	10	34
T508DRAFT_00728	hypothetical protein	6387	4814	1162	1695
T508DRAFT_00729	hypothetical protein	22	98	0	0
T508DRAFT_00730*	acetyl-CoA carboxylase, biotin carboxylase subunit	103*	30	12	6*
T508DRAFT_00731	acetyl-CoA carboxylase, biotin carboxyl carrier protein	10	7	0	0
T508DRAFT_00732	3-dehydroquinate dehydratase (EC 4.2.1.10)	80	101	34	0
T508DRAFT_00733	transcriptional regulator	56	18	0	18
T508DRAFT_00734	uncharacterised conserved protein	15	14	0	0
T508DRAFT_00735	arabinose efflux permease	60	66	0	0
T508DRAFT_00736	glycine/serine hydroxymethyltransferase	116	99	35	36
T508DRAFT_00737	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26)	14	5	0	0
T508DRAFT_00738	riboflavin synthase alpha chain (EC 2.5.1.9)	79	23	0	0
T508DRAFT_00739	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)	121	58	0	88
T508DRAFT_00740	NusB antitermination factor	1	0	0	0
T508DRAFT_00741	thiamine-monophosphate kinase	39	26	0	31
T508DRAFT_00742	FKBP-type peptidyl-prolyl cis-trans isomerases 1	39	66	0	10
T508DRAFT_00743	predicted ATPase (AAA+ superfamily)	6	25	2	18
T508DRAFT_00744	hypothetical protein	86	19	32	35
T508DRAFT_00745	tyrosine recombinase XerD	63	26	0	16
T508DRAFT_00746	hypothetical protein	40	24	0	0
T508DRAFT_00747	dephospho-CoA kinase	27	0	0	12
T508DRAFT_00748	uncharacterised protein conserved in bacteria	40	7	0	0
T508DRAFT_00749	uncharacterised protein conserved in bacteria	13	1	0	51
T508DRAFT_00750	organic solvent tolerance protein OstA	31	11	0	8
T508DRAFT_00751	periplasmic chaperone for outer membrane proteins SurA	52	44	7	8
T508DRAFT_00752	dimethyladenosine transferase	59	14	11	8
T508DRAFT_00753	16S RNA G1207 methylase RsmC	115	37	60	57
T508DRAFT_00754	lactate dehydrogenase and related dehydrogenases	55	13	0	19
T508DRAFT_00755	predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	3	0	0	0
T508DRAFT_00756	hypothetical protein	27	0	0	18
T508DRAFT_00757	glucose-1-phosphate adenylyltransferase	161	79	26	16
T508DRAFT_00758	glycogen synthase (ADP-glucose)	54	98	13	22
T508DRAFT_00759	hypothetical protein	15	55	0	18
T508DRAFT_00760	Tir chaperone protein (CesT) family	14	0	0	70
T508DRAFT_00761	Tir chaperone protein (CesT) family	19	17	0	0
T508DRAFT_00762	transcriptional regulator, TetR family	5	0	0	0
T508DRAFT_00763	Aldo/keto reductases, related to diketogulonate reductase	71	0	0	0
T508DRAFT_00764	Aldo/keto reductases, related to diketogulonate reductase	13	0	13	0
T508DRAFT_00765	Aldo/keto reductases, related to diketogulonate reductase	24	28	0	41
T508DRAFT_00766	transcriptional regulator	49	45	6	75
T508DRAFT_00767	flavodoxins	10	0	0	0
T508DRAFT_00768	flavodoxins	8	0	0	0
T508DRAFT_00769	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	14	4	0	12
T508DRAFT_00770	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	19	6	0	0
T508DRAFT_00771	ATP/ADP translocase	23	14	0	27
T508DRAFT_00772	aldo/keto reductases, related to diketogulonate reductase	39	2	14	0
T508DRAFT_00773	protein of unknown function (DUF1703)/predicted AAA-ATPase	30	33	0	8
T508DRAFT_00774	transcriptional regulator, RpiR family	37	0	0	10
T508DRAFT_00775	N-acetylglucosamine-6-phosphate deacetylase	17	61	33	0
T508DRAFT_00776	superfamily II DNA and RNA helicases	38	22	15	0
T508DRAFT_00777	uncharacterised conserved protein	29	0	41	0
T508DRAFT_00778	thymidylate synthase (EC 2.1.1.45)	175	118	3	0

T508DRAFT_00779	phosphoenolpyruvate-protein phosphotransferase	52	28	0	5
T508DRAFT_00780	NTP pyrophosphohydrolases including oxidative damage repair enzymes	101	83	64	0
T508DRAFT_00781	DNA mismatch repair protein MutH	6	14	0	0
T508DRAFT_00782*	hypothetical protein	994*	434	159	69*
T508DRAFT_00784	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	127	77	38	33
T508DRAFT_00785	membrane-associated phospholipid phosphatase	158	39	26	36
T508DRAFT_00786	ribosomal protein L19, bacterial type	112	20	0	0
T508DRAFT_00787	tRNA (guanine-N ₁)-methyltransferase	101	16	11	0
T508DRAFT_00788	16S rRNA processing protein RimM	99	25	0	0
T508DRAFT_00789	SSU ribosomal protein S16P	96	14	0	0
T508DRAFT_00790	signal recognition particle subunit FFH/SRP54 (srp54)	18	19	0	17
T508DRAFT_00791	ABC-type metal ion transport system, permease component	11	0	0	0
T508DRAFT_00792	ABC-type metal ion transport system, ATPase component	12	14	0	21
T508DRAFT_00793	ABC-type metal ion transport system, periplasmic component/surface antigen	40	0	24	0
T508DRAFT_00794	acetylornithine deacetylase/succinyl-diaminopimelate desuccinylase and related deacylases	16	86	30	28
T508DRAFT_00795	putative efflux protein, MATE family	59	154	90	61
T508DRAFT_00796	hypothetical protein	2681	20720	14625	8836
T508DRAFT_00797	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	247	626	617	191
T508DRAFT_00798	Sel1 repeat	48	178	52	166
T508DRAFT_00799	transposase and inactivated derivatives	444	127	0	0
T508DRAFT_00800	Isopentenylidiphosphate isomerase	37	8	0	31
T508DRAFT_00801	magnesium Mg ²⁺ and cobalt Co ²⁺ transport protein (corA)	70	26	15	0
T508DRAFT_00802	transcriptional regulators	35	12	18	0
T508DRAFT_00803	phosphate/sulphate permeases	66	120	0	42
T508DRAFT_00804	predicted membrane protein	4	30	0	0
T508DRAFT_00805	nucleoside permease	10	8	0	0
T508DRAFT_00806	uridine kinase (EC 2.7.1.48)	24	47	0	24
T508DRAFT_00807	bacterial nucleoid DNA-binding protein	102	21	36	0
T508DRAFT_00808	Na ⁺ /serine symporter	54	4	0	0
T508DRAFT_00809	hypothetical protein	601	175	86	58
T508DRAFT_00810	GGGtGRT protein	821	177	85	36
T508DRAFT_00811	hypothetical protein	23	37	0	27
T508DRAFT_00812	hypothetical protein	17	44	0	20
T508DRAFT_00813	addiction module antitoxin, RelB/DinJ family	0	0	0	36
T508DRAFT_00814	addiction module toxin, RelE/StbE family	0	89	24	0
T508DRAFT_00815	AraC-type DNA-binding domain-containing proteins	318	243	308	471
T508DRAFT_00816	sugar (glycoside-Pentoside-Hexuronide) transporter	81	7	6	24
T508DRAFT_00817	glycosidases	36	28	0	27
T508DRAFT_00818	Na ⁺ /H ⁺ antiporter NhaD and related arsenite permeases	22	36	8	31
T508DRAFT_00819	predicted N6-adenine-specific DNA methylase	17	16	0	13
T508DRAFT_00820	ATPase components of ABC transporters with duplicated ATPase domains	12	5	0	7
T508DRAFT_00821	predicted metal-dependent phosphoesterases (PHP family)	37	12	0	22
T508DRAFT_00822	serine phosphatase RsbU, regulator of sigma subunit	73	45	4	4
T508DRAFT_00823	Abi-like protein	46	0	0	0
T508DRAFT_00824	diacylglycerol kinase	48	0	0	0
T508DRAFT_00825	tRNA-adenosine deaminase (EC 3.5.4.-)	20	0	0	0
T508DRAFT_00826*	uncharacterised protein conserved in bacteria	179*	34	35	0*
T508DRAFT_00827	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/YrdC/YwlC family	10	29	0	0
T508DRAFT_00828	hypothetical protein	38	36	46	21
T508DRAFT_00829	hypothetical protein	95	259	250	120
T508DRAFT_00830	aspartate-ammonia ligase (EC 6.3.1.1)	270	145	50	59
T508DRAFT_00831	hypothetical protein	41	10	26	0
T508DRAFT_00832	diguanylate cyclase (GGDEF) domain	29	11	0	0
T508DRAFT_00833	diguanylate cyclase (GGDEF) domain	25	49	0	22
T508DRAFT_00834	collagenase and related proteases	61	33	20	14
T508DRAFT_00835	DNA recombination-dependent growth factor C	33	13	0	0
T508DRAFT_00836	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	53	8	0	3
T508DRAFT_00837	phosphoserine aminotransferase apoenzyme (EC 2.6.1.52)	110	65	30	59
T508DRAFT_00838	acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	14	89	33	42
T508DRAFT_00839	ribonuclease D	13	24	0	0
T508DRAFT_00840	transporter, SSS family	111	31	0	20
T508DRAFT_00841	HNH endonuclease	83	158	265	176
T508DRAFT_00842	putative NADH-flavin reductase	35	130	47	51
T508DRAFT_00843	predicted permeases	26	70	16	12
T508DRAFT_00844	phosphotransferase system IIA components	37	53	0	0
T508DRAFT_00845	transcriptional regulator	99	464	186	293
T508DRAFT_00846	putative NADPH-quinone reductase (modulator of drug activity B)	64	83	0	17

T508DRAFT_00847	transporter, NhaC family (TC 2.A.35)	57	28	10	19
T508DRAFT_00848	antimicrobial peptide resistance and lipid A acylation protein PagP	161	303	132	86
T508DRAFT_00849	SprA-related family	86	16	0	55
T508DRAFT_00850	ribose-phosphate pyrophosphokinase	41	23	13	27
T508DRAFT_00851	predicted ATPase (AAA+ superfamily)	13	7	23	60
T508DRAFT_00852	ABC-type spermidine/putrescine transport system, permease component II	121	35	9	40
T508DRAFT_00853	ABC-type spermidine/putrescine transport system, permease component I	28	51	0	0
T508DRAFT_00854	spermidine/putrescine ABC transporter ATP-binding subunit	62	20	0	0
T508DRAFT_00855	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	39	72	44	42
T508DRAFT_00856	Abi-like protein	470	303	114	93
T508DRAFT_00857*	hypothetical protein	6644*	4720	1142*	1823
T508DRAFT_00858	BON domain protein	3	0	0	0
T508DRAFT_00859	L-glutamine synthetase (EC 6.3.1.2)	47	22	6	19
T508DRAFT_00860	acetyltransferases	36	57	0	0
T508DRAFT_00861	peroxidase	23	0	19	45
T508DRAFT_00862	thioredoxin-disulfide reductase	44	26	31	10
T508DRAFT_00863	carbamoyl-phosphate synthase, large subunit	74	33	15	43
T508DRAFT_00864	carbamoyl-phosphate synthase, small subunit	9	0	0	9
T508DRAFT_00865	outer membrane protein	13	0	0	8
T508DRAFT_00866	uncharacterised protein conserved in bacteria	16	2	0	0
T508DRAFT_00867	predicted ATP-dependent protease	30	3	0	0
T508DRAFT_00868	DJ-1 family protein	210	26	0	0
T508DRAFT_00869	protein of unknown function (DUF2819)	39	41	5	4
T508DRAFT_00870	protein of unknown function (DUF2636)	96	87	0	0
T508DRAFT_00873	excinuclease ABC subunit B	18	61	2	7
T508DRAFT_00874	uncharacterised protein conserved in bacteria	277	213	0	36
T508DRAFT_00875	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	53	8	0	0
T508DRAFT_00876*	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	280*	53	12	0*
T508DRAFT_00877	predicted signal-transduction protein containing cAMP-binding and CBS domains	197	25	0	7
T508DRAFT_00878	ribonuclease, Rne/Rng family	127	3	0	4
T508DRAFT_00879	protein of unknown function (DUF1703)/predicted AAA-ATPase	42	40	6	15
T508DRAFT_00880	pseudouridine synthase, RluA family	23	6	0	39
T508DRAFT_00881	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	139	435	200	99
T508DRAFT_00882	hypothetical protein	97	44	27	0
T508DRAFT_00883	predicted metal-binding, possibly nucleic acid-binding protein	11	0	0	53
T508DRAFT_00884	ribosomal protein L32	258	0	0	24
T508DRAFT_00885	phosphate:acyl-[acyl carrier protein] acyltransferase	30	33	0	12
T508DRAFT_00886	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	129	20	0	0
T508DRAFT_00887	[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39)	57	7	0	0
T508DRAFT_00888	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	121	103	35	0
T508DRAFT_00889	acyl carrier protein	352	143	0	0
T508DRAFT_00890	beta-ketoacyl-acyl-carrier-protein synthase II	149	58	0	16
T508DRAFT_00891*	conjugative transfer signal peptidase TraF	291*	113	20*	36
T508DRAFT_00892	transcriptional regulator, RpiR family	110	8	14	28
T508DRAFT_00893	diaminopimelate dehydrogenase (EC 1.4.1.16)	84	74	0	23
T508DRAFT_00895	predicted DNA alkylation repair enzyme	26	33	0	0
T508DRAFT_00896	transcriptional regulator, LacI family	14	5	0	11
T508DRAFT_00897	L-ribulose 5-phosphate 4-epimerase (EC 5.1.3.4)	89	53	31	37
T508DRAFT_00898	predicted nucleoside-diphosphate sugar epimerase	31	35	0	0
T508DRAFT_00899	phosphate acetyltransferase	146	37	9	19
T508DRAFT_00900	uncharacterised protein conserved in bacteria	17	0	0	0
T508DRAFT_00901	monosaccharide ABC transporter substrate-binding protein, CUT2 family (TC 3.A.1.2.-)	1217	60	17	0
T508DRAFT_00902	ABC-type sugar transport system, ATPase component	18	5	0	0
T508DRAFT_00903	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	14	4	0	0
T508DRAFT_00904	monosaccharide ABC transporter membrane protein, CUT2 family (TC 3.A.1.2.-)	15	0	0	30
T508DRAFT_00905	hypothetical protein	299	287	103	50
T508DRAFT_00906	transposase and inactivated derivatives	1	8	0	4
T508DRAFT_00907	maltoporin (phage lambda and maltose receptor)	82	48	3	8
T508DRAFT_00908	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)	14	18	0	18
T508DRAFT_00909	sugar (pentulose and hexulose) kinases	45	15	6	0
T508DRAFT_00910	phosphoesterase, MJ0936 family	0	0	0	0
T508DRAFT_00911	uncharacterized protein, YhcH/YjgK/YiaL family	0	35	0	0
T508DRAFT_00913	hypothetical protein	9	0	0	0
T508DRAFT_00914*	malate dehydrogenase (NAD) (EC 1.1.1.37)	699*	174	16*	71
T508DRAFT_00915	aconitase (EC 4.2.1.3)	30	27	0	25

T508DRAFT_00916	negative regulator of beta-lactamase expression	13	23	3	6
T508DRAFT_00917	UDP-3- <i>O</i> -[3-hydroxymyristoyl] <i>N</i> -acetylglucosamine deacetylase (EC 3.5.1.108)	116	278	64	321
T508DRAFT_00918*	cell division protein FtsZ	308*	219	69	22*
T508DRAFT_00919*	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	45	28	107*	7*
T508DRAFT_00920	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	46	31	107	17
T508DRAFT_00921	cell division protein FtsZ	174	66	13	7
T508DRAFT_00922	cell division protein FtsA	76	15	7	7
T508DRAFT_00923	cell division septal protein	26	49	13	47
T508DRAFT_00924	UDP- <i>N</i> -acetylmuramate--L-alanine ligase (EC 6.3.2.8)	23	0	0	7
T508DRAFT_00925	UDP- <i>N</i> -acetylglucosamine- <i>N</i> -acetylmuramylpentapeptide <i>N</i> -acetylglucosamine transferase	9	4	0	0
T508DRAFT_00926	cell division-specific peptidoglycan biosynthesis regulator FtsW	18	0	0	0
T508DRAFT_00927	UDP- <i>N</i> -acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	22	0	0	0
T508DRAFT_00928	phospho- <i>N</i> -acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	18	21	0	7
T508DRAFT_00929	UDP- <i>N</i> -acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)	78	11	0	2
T508DRAFT_00930	UDP- <i>N</i> -acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	8	5	0	17
T508DRAFT_00931	peptidoglycan synthetase FtsI (EC 2.4.1.129)	14	28	0	4
T508DRAFT_00932	cell division protein	65	6	1	16
T508DRAFT_00933	16S rRNA (cytosine(1402)- <i>N</i> (4))-methyltransferase	53	32	16	18
T508DRAFT_00934	mraZ protein	110	53	18	19
T508DRAFT_00935	TRAP transporter solute receptor, TAXI family	48	32	0	0
T508DRAFT_00936	predicted ATPase (AAA+ superfamily)	25	49	5	25
T508DRAFT_00937	aspartate racemase (EC 5.1.1.13)	84	89	56	25
T508DRAFT_00938	protein involved in cell division	18	25	0	0
T508DRAFT_00939	AraC-type DNA-binding domain-containing proteins	43	85	8	58
T508DRAFT_00940	arabinose efflux permease	22	114	0	22
T508DRAFT_00941	lactoylglutathione lyase and related lyases	31	42	0	0
T508DRAFT_00942	TRAP transporter, 4TM/12TM fusion protein	40	91	21	60
T508DRAFT_00944	probable <i>S</i> -adenosylmethionine-dependent methyltransferase, YraL family	14	7	0	0
T508DRAFT_00945	D-alanyl-D-alanine dipeptidase	4	46	27	15
T508DRAFT_00946	putative lipoprotein	194	116	51	97
T508DRAFT_00947	hypothetical protein	359	757	506	225
T508DRAFT_00948	stringent starvation protein B	17	180	0	27
T508DRAFT_00949	YolD-like protein	40	0	13	0
T508DRAFT_00950	Nucleotidyltransferase/DNA polymerase involved in DNA repair	72	113	25	38
T508DRAFT_00951	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	31	23	27	28
T508DRAFT_00952	methyl-accepting chemotaxis protein	316	183	154	137
T508DRAFT_00953*	ribosomal protein S9	584*	241	106	0*
T508DRAFT_00954	LSU ribosomal protein L13P	205	35	5	0
T508DRAFT_00955	sugar fermentation stimulation protein	16	12	7	0
T508DRAFT_00956	hypothetical protein	0	36	53	0
T508DRAFT_00957	mannitol-1-phosphate/altronate dehydrogenases	32	30	1	12
T508DRAFT_00958	D-mannonate dehydratase (EC 4.2.1.8)	14	8	4	0
T508DRAFT_00959	glucuronate isomerase	38	0	0	6
T508DRAFT_00960	TRAP transporter, DctM subunit	18	31	0	6
T508DRAFT_00961	TRAP-type C ₄ -dicarboxylate transport system, small permease component	43	9	0	28
T508DRAFT_00962	tripartite ATP-independent periplasmic transporter solute receptor, DctP family	52	56	12	0
T508DRAFT_00963	entner-Doudoroff aldolase	88	144	56	0
T508DRAFT_00964	sugar kinases, ribokinase family	22	30	46	0
T508DRAFT_00965	transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains	6	16	0	8
T508DRAFT_00966	tagaturonate reductase (EC 1.1.1.58)	53	39	4	7
T508DRAFT_00967	putative C-S lyase	26	73	0	26
T508DRAFT_00968	protein of unknown function (DUF3737)	29	6	0	0
T508DRAFT_00969	hypothetical protein	470	558	0	309
T508DRAFT_00970*	<i>N</i> -acetylglucosamine-6-phosphate deacetylase	628*	3366*	789	2399
T508DRAFT_00971	hypothetical protein	166	226	193	100
T508DRAFT_00972	periplasmic serine protease, Do/DeqQ family	345	181	157	235
T508DRAFT_00973	molecular chaperone (small heat shock protein)	1873	1241	1350	2470
T508DRAFT_00974	macrophage migration inhibitory factor (MIF)	43	41	0	0
T508DRAFT_00975	predicted hydrolase of the alpha/beta superfamily	168	54	42	40
T508DRAFT_00976	trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	59	52	29	50
T508DRAFT_00977	Type I restriction-modification system methyltransferase subunit	70	89	18	34
T508DRAFT_00978	OAH/OAS sulfhydrylase	66	37	22	45
T508DRAFT_00979	superoxide dismutase	469	831	557	1254

T508DRAFT_00980	hypothetical protein	177	102	34	0
T508DRAFT_00981	glucose-binding protein/galactose-binding protein	133	99	3	46
T508DRAFT_00982	ABC-type sugar transport system, periplasmic component	96	44	5	48
T508DRAFT_00983*	tRNA(Ile)-lysine synthetase, N-terminal domain/tRNA(Ile)-lysine synthetase, C-terminal domain	194*	556	496	1062*
T508DRAFT_00984	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	30	98	79	35
T508DRAFT_00985	RNase HII (EC 3.1.26.4)	33	28	0	14
T508DRAFT_00986	lipid-A-disaccharide synthase (EC 2.4.1.182)	36	21	0	17
T508DRAFT_00987	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine acyltransferase (EC 2.3.1.129)	O-43	21	0	0
T508DRAFT_00988	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	71	0	0	0
T508DRAFT_00989	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.191)	70	14	9	13
T508DRAFT_00990	periplasmic chaperone for outer membrane proteins Skp	72	43	0	0
T508DRAFT_00991	beta-barrel assembly machine subunit BamA	59	13	11	17
T508DRAFT_00992	RIP metalloprotease RseP	22	0	0	0
T508DRAFT_00993	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	22	0	0	11
T508DRAFT_00994	CDP-diglyceride synthetase	10	13	0	0
T508DRAFT_00995	undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	42	14	0	0
T508DRAFT_00996	ribosome recycling factor	22	0	0	0
T508DRAFT_00997	uridylate kinase (EC 2.7.4.22)	140	0	0	72
T508DRAFT_00998	translation elongation factor Ts (EF-Ts)	129	0	0	12
T508DRAFT_00999	ribosomal protein S2, bacterial type	479	24	14	32
T508DRAFT_01000	metal-dependent hydrolases of the beta-lactamase superfamily III	53	12	9	45
T508DRAFT_01001	methionine aminopeptidase, type I (EC 3.4.11.18)	39	40	0	44
T508DRAFT_01002	UTP--GlnB (protein PII) uridylyltransferase, GlnD	59	45	22	19
T508DRAFT_01003	hypothetical protein	16	19	0	14
T508DRAFT_01004	predicted ATPase (AAA+ superfamily)	23	53	0	0
T508DRAFT_01005*	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, F subunit	299*	92	31	0*
T508DRAFT_01006	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, E subunit	110	0	0	0
T508DRAFT_01007	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, D subunit	115	0	0	0
T508DRAFT_01008	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, C subunit	191	21	5	22
T508DRAFT_01009	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, B subunit	206	78	22	41
T508DRAFT_01010	NADH:ubiquinone oxidoreductase, Na ⁺ -translocating, A subunit	169	0	0	13
T508DRAFT_01011	Major Facilitator superfamily	31	28	0	20
T508DRAFT_01012	uncharacterised protein conserved in bacteria	17	0	0	0
T508DRAFT_01013	1-deoxy-D-xylulose-5-phosphate synthase (EC 2.2.1.7)	11	10	0	0
T508DRAFT_01014	geranylgeranyl pyrophosphate synthase	31	6	10	12
T508DRAFT_01015	exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	33	0	0	0
T508DRAFT_01016	phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)	47	7	3	0
T508DRAFT_01017	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)	35	7	0	0
T508DRAFT_01018	hypothetical protein	180	245	538	46
T508DRAFT_01019	ABC-type transport system, involved in lipoprotein release, permease component	31	22	0	13
T508DRAFT_01020	lipoprotein releasing system, ATP-binding protein	12	11	0	15
T508DRAFT_01021	ABC-type transport system, involved in lipoprotein release, permease component	16	59	0	35
T508DRAFT_01022	predicted acyltransferases	6	93	0	93
T508DRAFT_01023	protein of unknown function (DUF1703)/predicted AAA-ATPase	62	37	6	43
T508DRAFT_01024*	hypothetical protein	78*	425*	531	156
T508DRAFT_01025	L-asparaginase, type II	1314	47	53	0
T508DRAFT_01026	flagellar hook-basal body complex protein FliE	44	10	0	0
T508DRAFT_01027	flagellar basal-body M-ring protein/flagellar hook-basal body protein (fliF)	20	7	0	5
T508DRAFT_01028	flagellar motor switch protein FliG	38	42	9	0
T508DRAFT_01029	flagellar biosynthesis/type III secretory pathway protein	43	37	1	0
T508DRAFT_01030	flagellar protein export ATPase FliI	10	5	0	0
T508DRAFT_01031	flagellar export protein FliJ	19	0	0	0
T508DRAFT_01032	hypothetical protein	45	39	0	0
T508DRAFT_01033	flagellar hook-length control protein	28	0	0	8
T508DRAFT_01034	flagellar basal body-associated protein	174	58	56	80
T508DRAFT_01035	flagellar motor switch protein FliM	81	38	46	14
T508DRAFT_01036	flagellar motor switch protein FliN	17	18	34	26
T508DRAFT_01037	flagellar biogenesis protein	70	56	0	54
T508DRAFT_01038	flagellar biosynthetic protein FliP	17	18	11	12
T508DRAFT_01039	flagellar biosynthetic protein FliQ	0	0	0	0
T508DRAFT_01040	flagellar biosynthetic protein FliR	57	34	0	10
T508DRAFT_01041	transcriptional regulator	29	49	3	41
T508DRAFT_01042	putative hydrolase, CocE/NonD family	17	3	7	20
T508DRAFT_01043	predicted Rossmann fold nucleotide-binding protein	47	27	100	29
T508DRAFT_01044	enzyme related to GTP cyclohydrolase I	45	0	0	13
T508DRAFT_01045	16S rRNA m(3)U-1498 methyltransferase (EC 2.1.1.193)	25	0	0	0
T508DRAFT_01046	endonuclease I	28	6	7	0
T508DRAFT_01047	hypothetical protein	22	59	25	14
T508DRAFT_01048	pyridoxal/pyridoxine/pyridoxamine kinase	33	12	46	32

T508DRAFT_01049	predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	12	28	1	0
T508DRAFT_01050	transcriptional regulator	76	15	0	17
T508DRAFT_01051	hypothetical protein	161	56	16	60
T508DRAFT_01052	transcriptional regulator, DeoR family	4	12	19	3
T508DRAFT_01053	hypothetical protein	23	0	0	0
T508DRAFT_01054	prevent-host-death family protein	18	31	38	49
T508DRAFT_01055	PIN domain	19	63	8	0
T508DRAFT_01056	H ⁺ /gluconate symporter and related permeases	211	112	80	189
T508DRAFT_01057	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	104	62	23	11
T508DRAFT_01058	uncharacterised protein conserved in bacteria	39	44	0	0
T508DRAFT_01059	uncharacterised NAD(FAD)-dependent dehydrogenases	33	10	0	3
T508DRAFT_01060	transcriptional regulator, ArsR family	69	168	99	219
T508DRAFT_01061	methionine adenosyltransferase (EC 2.5.1.6)	202	503	486	441
T508DRAFT_01062	fructose-6-phosphate aldolase, TalC/MipB family	55	9	0	16
T508DRAFT_01063	transketolase (EC 2.2.1.1)	97	10	7	0
T508DRAFT_01064	predicted hydrolases of HD superfamily	12	12	0	14
T508DRAFT_01065	Na ⁺ /proline symporter	80	18	28	59
T508DRAFT_01066	hypothetical protein	0	0	0	0
T508DRAFT_01067	ABC-type sugar transport system, periplasmic component	2	7	0	0
T508DRAFT_01068	phosphoglycerate kinase (EC 2.7.2.3)	359	140	43	44
T508DRAFT_01069	fructose-bisphosphate aldolase (EC 4.1.2.13)	288	104	9	44
T508DRAFT_01070	flagellar capping protein	40	48	56	47
T508DRAFT_01071	aspartate kinase (EC 2.7.2.4)	46	53	7	0
T508DRAFT_01072	predicted branched-chain amino acid permease (azaleucine resistance)	26	0	0	15
T508DRAFT_01073	predicted membrane protein	37	0	0	0
T508DRAFT_01074	hypothetical protein	6	0	0	14
T508DRAFT_01075	Zn-dependent protease with chaperone function	40	10	30	40
T508DRAFT_01076	cell division topological specificity factor MinE	40	0	0	0
T508DRAFT_01077	septum site-determining protein MinD	87	43	0	0
T508DRAFT_01078	septum formation inhibitor	40	0	11	0
T508DRAFT_01079	amino acid carrier protein	23	47	0	0
T508DRAFT_01080	hypothetical protein	12	57	0	0
T508DRAFT_01081	hypothetical protein	159	18	0	0
T508DRAFT_01082	amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.1.3.-)	34	18	19	0
T508DRAFT_01083	amine acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine family	15	20	0	0
T508DRAFT_01084	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	14	0	0	11
T508DRAFT_01085	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	19	52	53	45
T508DRAFT_01086	hypothetical protein	19	0	42	0
T508DRAFT_01087	carbohydrate ABC transporter ATP-binding protein, CUT1 family (TC 3.A.1.1.-)	26	15	13	47
T508DRAFT_01088	ABC-type maltose transport systems, permease component	22	0	0	0
T508DRAFT_01089	ABC-type sugar transport systems, permease components	9	9	0	22
T508DRAFT_01090	maltose-binding periplasmic proteins/domains	69	25	0	10
T508DRAFT_01091	AraC-type DNA-binding domain-containing proteins	149	236	94	81
T508DRAFT_01092	iron (metal) dependent repressor, DtxR family	112	96	34	80
T508DRAFT_01093	Fe ²⁺ /Zn ²⁺ uptake regulation proteins	345	416	111	213
T508DRAFT_01094	hypothetical protein	44	0	0	0
T508DRAFT_01095	hypothetical protein	10	5	0	0
T508DRAFT_01096	quinolinate synthetase (EC 2.5.1.72)	3	13	0	18
T508DRAFT_01097	hypothetical protein	14	0	20	0
T508DRAFT_01098	Sel1 repeat	9	17	0	0
T508DRAFT_01099	carbon starvation protein, predicted membrane protein	13	5	0	7
T508DRAFT_01100	7-keto-8-aminopelargonate synthetase and related enzymes	109	16	0	0
T508DRAFT_01101	uncharacterised protein conserved in bacteria	230	45	0	85
T508DRAFT_01102	biotin biosynthesis protein BioC	320	28	0	20
T508DRAFT_01105	phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	65	24	0	8
T508DRAFT_01106	adenosylmethionine-8-amino-7-oxononanoate aminotransferase apoenzyme (EC 2.6.1.62)	16	12	0	0
T508DRAFT_01107	dethiobiotin synthase	11	9	0	0
T508DRAFT_01108	protein of unknown function (DUF1703)/predicted AAA-ATPase	7	16	18	0
T508DRAFT_01109	carbon starvation protein, predicted membrane protein	226	105	0	18
T508DRAFT_01110	flagellin and related hook-associated proteins	37	5	0	47
T508DRAFT_01111	uncharacterised lipoprotein	56	27	11	0
T508DRAFT_01112	hypothetical protein	88	26	0	0
T508DRAFT_01113	glutaminyl-tRNA synthetase (EC 6.1.1.18)	45	29	8	8
T508DRAFT_01114	uncharacterised protein conserved in bacteria	195	131	86	52
T508DRAFT_01115	acetyltransferase (isoleucine patch superfamily)	75	42	0	29
T508DRAFT_01116	protein-(glutamine-N5) methyltransferase, release factor-specific	69	169	0	20
T508DRAFT_01117	bacterial peptide chain release factor 1 (BRF-1)	70	51	0	19

T508DRAFT_01118*	hypothetical protein	722*	3180*	2249	3409
T508DRAFT_01119	hypothetical protein	173	219	138	204
T508DRAFT_01120	hypothetical protein	24	21	12	11
T508DRAFT_01121	membrane protein involved in colicin uptake	7	25	0	6
T508DRAFT_01122	uncharacterised conserved protein	5	4	0	0
T508DRAFT_01123	hypothetical protein	9	0	0	6
T508DRAFT_01124	ABC-type antimicrobial peptide transport system, ATPase component	16	0	0	16
T508DRAFT_01125	von Willebrand factor type A domain	13	0	0	8
T508DRAFT_01126	SelI repeat	13	62	0	41
T508DRAFT_01127	putative bacterial virulence factor	39	8	0	7
T508DRAFT_01128	uncharacterised protein conserved in bacteria, putative virulence factor	21	10	0	0
T508DRAFT_01130	transposase and inactivated derivatives	617	393	167	137
T508DRAFT_01131	phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	46	95	61	52
T508DRAFT_01132	ABC-type molybdate transport system, periplasmic component	14	26	0	0
T508DRAFT_01133	putative SAM-dependent methyltransferase	45	59	0	0
T508DRAFT_01134	shikimate 5-dehydrogenase	15	0	0	14
T508DRAFT_01135	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/YrdC/YwlC family	31	14	0	0
T508DRAFT_01136	phosphoribosylaminoimidazole carboxylase, PurE protein	53	0	13	0
T508DRAFT_01137	Zn-finger domain associated with topoisomerase type I	11	0	0	0
T508DRAFT_01138	peptide deformylase	29	25	0	0
T508DRAFT_01139	methionyl-tRNA formyltransferase (EC 2.1.2.9)	20	3	0	10
T508DRAFT_01140	16S rRNA cytosine ⁹⁶⁷ -C ⁵ methyltransferase (EC 2.1.1.176)	14	10	4	0
T508DRAFT_01141	K ⁺ transport systems, NAD-binding component	22	0	0	0
T508DRAFT_01142	Trk-type K ⁺ transport systems, membrane components	72	44	0	0
T508DRAFT_01143	1,4-dihydroxy-2-naphthoate prenyltransferase (EC 2.5.1.74)	11	0	9	0
T508DRAFT_01144	1,4-dihydroxy-2-naphthoate octaprenyltransferase	63	0	0	0
T508DRAFT_01145	exoribonuclease II	13	5	13	0
T508DRAFT_01146	acetyltransferases	98	105	63	22
T508DRAFT_01147	oligopeptidase A (EC:3.4.24.70). metallo peptidase. MEROPS family M03A	69	52	30	4
T508DRAFT_01148	Xaa-Pro aminopeptidase	31	30	0	6
T508DRAFT_01149	phosphatidylserine/phosphatidylglycerophosphate/cardioplin synthases and related enzymes	11	0	7	11
T508DRAFT_01150	ATP-dependent DNA helicase RecG (EC 3.6.1.-)	11	13	0	4
T508DRAFT_01151	hypothetical protein	14	54	25	36
T508DRAFT_01152	predicted membrane protein	38	139	126	7
T508DRAFT_01153	D-alanyl-D-alanine carboxypeptidase	63	32	11	101
T508DRAFT_01154	GTP-binding protein TypA/BipA	107	59	23	60
T508DRAFT_01155	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)	44	15	10	14
T508DRAFT_01156	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	40	17	7	0
T508DRAFT_01157	ABC-type metal ion transport system, periplasmic component/surface antigen	24	0	10	0
T508DRAFT_01158	ABC-type metal ion transport system, ATPase component	21	0	0	8
T508DRAFT_01159	ABC-type metal ion transport system, permease component	12	41	0	55
T508DRAFT_01160	aspartate/tyrosine/aromatic aminotransferase	14	28	0	9
T508DRAFT_01161	2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketoisovalerate family	17	100	0	0
T508DRAFT_01162	2-oxoacid:acceptor oxidoreductase, delta subunit, pyruvate/2-ketoisovalerate family	39	26	0	17
T508DRAFT_01163	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	5	4	0	20
T508DRAFT_01164	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	9	22	34	0
T508DRAFT_01165	coenzyme F ₃₉₀ synthetase	43	19	12	11
T508DRAFT_01166	methyltransferase, TIGR00027 family	20	6	0	0
T508DRAFT_01167	cystathionine gamma-lyase (EC 4.4.1.1)	7	13	19	0
T508DRAFT_01168	cysteine synthase	13	13	0	0
T508DRAFT_01169	putative efflux protein, MATE family	48	16	31	5
T508DRAFT_01170	protein of unknown function (DUF3334)	83	69	52	20
T508DRAFT_01171	ribosome biogenesis GTP-binding protein YsxC/EngB	12	33	0	0
T508DRAFT_01172	guanylate kinase (EC 2.7.4.8)	27	1	0	23
T508DRAFT_01173	DNA-directed RNA polymerase, omega subunit	93	116	43	0
T508DRAFT_01174	(p)ppGpp synthetase, RelA/SpoT family	36	63	0	12
T508DRAFT_01175	lysophospholipase	18	6	0	0
T508DRAFT_01176	putative GTPases (G3E family)	28	25	0	0
T508DRAFT_01177	hypothetical protein	66	170	0	36
T508DRAFT_01178	ribosomal protein L25 (general stress protein Ctc)	174	141	39	0
T508DRAFT_01179	uncharacterised protein conserved in bacteria	9	0	0	0
T508DRAFT_01180	periplasmic serine proteases (ClpP class)	31	7	0	15
T508DRAFT_01181	DNA topoisomerase I, bacterial	20	15	2	31
T508DRAFT_01182	ABC-type multidrug transport system, ATPase and permease components	21	7	11	24

T508DRAFT_01183	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	16	15	0	1
T508DRAFT_01184	acetyltransferases, including <i>N</i> -acetylases of ribosomal proteins	46	37	7	30
T508DRAFT_01185	predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	20	0	20	0
T508DRAFT_01186*	hypothetical protein	58	217*	9*	30
T508DRAFT_01187	gucoase-1-phosphate thymidyltransferase (EC 2.7.7.24)	11	13	0	0
T508DRAFT_01188	dTDP-4-dehydrorhamnose 3,5-epimerase	21	0	0	0
T508DRAFT_01189	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	47	18	0	0
T508DRAFT_01190	predicted ATPase	18	18	20	43
T508DRAFT_01191	predicted membrane protein	10	27	15	14
T508DRAFT_01192	membrane carboxypeptidase/penicillin-binding protein PbpC	26	42	6	11
T508DRAFT_01193	large extracellular alpha-helical protein	16	11	2	0
T508DRAFT_01194	methyl-accepting chemotaxis protein	105	141	93	56
T508DRAFT_01195	exodeoxyribonuclease I subunit C (EC 3.1.11.1)	67	43	12	37
T508DRAFT_01196	domain of unknown function (DUF4250)	8	0	0	0
T508DRAFT_01197	formate-dependent phosphoribosylglycinamide formyltransferase (EC 6.3.4.-)	83	32	0	0
T508DRAFT_01198	protein-tyrosine-phosphatase	13	0	0	32
T508DRAFT_01199	ABC-type sugar transport system, periplasmic component	124	130	87	102
T508DRAFT_01200	3-oxoacyl-(acyl-carrier-protein) synthase	340	225	154	279
T508DRAFT_01201	3-oxoacyl-(acyl-carrier-protein) reductase, putative	21	0	11	0
T508DRAFT_01202	predicted 3-hydroxylacyl-(acyl carrier protein) dehydratase	42	0	0	0
T508DRAFT_01203	3-oxoacyl-(acyl-carrier-protein) synthase	33	45	0	0
T508DRAFT_01204	protein of unknown function (DUF3261)	14	0	0	0
T508DRAFT_01205	predicted exporter	10	0	0	17
T508DRAFT_01206	outer membrane lipoprotein carrier protein LolA	9	40	0	0
T508DRAFT_01207	predicted thioesterase	12	0	0	0
T508DRAFT_01208	predicted acyltransferase	11	43	0	0
T508DRAFT_01209	glycosyltransferases involved in cell wall biogenesis	13	22	0	0
T508DRAFT_01210	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	8	12	0	0
T508DRAFT_01211	acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	13	10	0	0
T508DRAFT_01212	predicted membrane protein	220	102	39	22
T508DRAFT_01213	acyl carrier protein	17	33	0	0
T508DRAFT_01214	acyl carrier protein	81	0	0	0
T508DRAFT_01215	1-acyl- <i>sn</i> -glycerol-3-phosphate acyltransferase	4	7	0	0
T508DRAFT_01216	beta-ketoacyl synthase, N-terminal domain	22	0	0	41
T508DRAFT_01217	<i>O</i> -methyltransferase	10	2	0	0
T508DRAFT_01218	protein of unknown function (DUF1703)/predicted AAA-ATPase	41	10	0	0
T508DRAFT_01219	superfamily II DNA/RNA helicases, SNF2 family	16	10	2	0
T508DRAFT_01220	transposase	25	52	14	0
T508DRAFT_01221	EspA-like secreted protein	106	121	111	123
T508DRAFT_01222	hypothetical protein	2	6	0	0
T508DRAFT_01223	anti-anti-sigma factor	58	0	0	0
T508DRAFT_01224	soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	55	51	73	32
T508DRAFT_01225	type III secretion system ATPase, FliI/YscN (EC 3.6.3.15)	64	81	25	30
T508DRAFT_01226	type III secretion apparatus protein, HrpE/YscL family	53	152	31	0
T508DRAFT_01227	hypothetical protein	36	6	15	0
T508DRAFT_01228	type III secretion apparatus lipoprotein, YscJ/HrcJ family	84	86	81	54
T508DRAFT_01229	predicted ATPase	32	0	0	6
T508DRAFT_01230	TRAP transporter solute receptor, TAXI family	37	15	7	11
T508DRAFT_01231	Na ⁺ /glutamate symporter	70	90	111	98
T508DRAFT_01232	hypothetical protein	10	38	0	12
T508DRAFT_01233	hypothetical protein	37	9	0	0
T508DRAFT_01234	Tir chaperone protein (CesT) family	5	0	0	0
T508DRAFT_01235	Tir chaperone protein (CesT) family	14	0	0	2
T508DRAFT_01236	type III secretion system major needle protein, YscF/MxiH/PrgI family	36	72	0	29
T508DRAFT_01237	hypothetical protein	95	110	120	0
T508DRAFT_01238	thioredoxin domain-containing protein	24	59	0	0
T508DRAFT_01239	type III secretion apparatus protein, YscD/HrpQ family	18	20	0	0
T508DRAFT_01240	type III secretion outer membrane pore, YscC/HrcC family	37	11	21	20
T508DRAFT_01241	hypothetical protein	22	0	0	0
T508DRAFT_01242	hypothetical protein	120	57	62	32
T508DRAFT_01243	uncharacterised conserved protein	251	215	156	56
T508DRAFT_01244	type III secretion low calcium response chaperone LcrH/SycD	180	51	30	10
T508DRAFT_01245	type III secretion protein, HrcV family	46	14	8	14
T508DRAFT_01246	hypothetical protein	4	34	38	0
T508DRAFT_01247	hypothetical protein	20	0	19	0
T508DRAFT_01248	hypothetical protein	115	201	51	0
T508DRAFT_01249	TyeA	116	150	41	20
T508DRAFT_01250	Type III secretion protein, YscU/HrpY family	11	0	0	0
T508DRAFT_01251	Type III secretion protein YscO	0	0	31	0
T508DRAFT_01252*	hypothetical protein	120	390*	228	53*
T508DRAFT_01253	Stage II sporulation protein E (SpoIIIE)/HAMP domain	18	25	4	31

T508DRAFT_01254	Stage II sporulation protein E (SpoIIE)	2	27	10	5
T508DRAFT_01255	anti-sigma regulatory factor (Ser/Thr protein kinase)	72	176	157	81
T508DRAFT_01256	anti-anti-sigma factor	38	82	180	48
T508DRAFT_01257	prolipoprotein diacylglycerol transferase	24	12	0	25
T508DRAFT_01258	hypothetical protein	31	0	0	0
T508DRAFT_01259	hypothetical protein	8	0	0	0
T508DRAFT_01260	type III secretion protein SpaR/YscT/HrcT	14	28	0	25
T508DRAFT_01261	type III secretion protein, HrpO family	15	74	0	0
T508DRAFT_01262	hypothetical protein	11	0	0	0
T508DRAFT_01263	ribosomal protein L20	231	491	39	57
T508DRAFT_01264	LSU ribosomal protein L35P	301	36	0	0
T508DRAFT_01266	translation initiation factor IF-3	470	14	19	0
T508DRAFT_01267	threonyl-tRNA synthetase (EC 6.1.1.3)	40	43	12	5
T508DRAFT_01269	rhodanese-related sulfurtransferase	41	64	0	21
T508DRAFT_01270	TRAP transporter, 4TM/12TM fusion protein	54	13	8	4
T508DRAFT_01271	TRAP transporter solute receptor, TAXI family	117	26	0	0
T508DRAFT_01272	amidophosphoribosyltransferase (EC 2.4.2.14)	17	16	0	0
T508DRAFT_01273	uncharacterised membrane protein, required for colicin V production	17	0	0	0
T508DRAFT_01274	seryl-tRNA synthetase (EC 6.1.1.11)	61	11	0	7
T508DRAFT_01275	hypothetical protein	45	21	0	0
T508DRAFT_01276	protein of unknown function (DUF1703)/predicted AAA-ATPase	108	15	0	0
T508DRAFT_01277	protein of unknown function (DUF1703)/predicted AAA-ATPase	28	9	0	0
T508DRAFT_01278	hypothetical protein	0	0	0	0
T508DRAFT_01279	FOG: EAL domain	10	50	6	13
T508DRAFT_01280	O-6-methylguanine DNA methyltransferase	131	16	0	14
T508DRAFT_01281*	23S rRNA (uracil-5-)-methyltransferase RumA	43	74*	10*	22
T508DRAFT_01282	outer membrane lipoprotein	379	363	28	263
T508DRAFT_01284	DNA primase, catalytic core	82	372	44	165
T508DRAFT_01285	uncharacterised protein conserved in bacteria with an aminopeptidase-like domain	147	13	0	0
T508DRAFT_01286	methionyl-tRNA formyltransferase	136	6	0	16
T508DRAFT_01287	Bis(5'nucleosyl)-tetraphosphatase, ApaH	400	0	0	138
T508DRAFT_01288	dihydrofolate reductase	94	65	5	0
T508DRAFT_01289	Obg family GTPase CgtA	95	0	13	0
T508DRAFT_01290	ribosomal protein L27	52	8	0	2
T508DRAFT_01291	LSU ribosomal protein L21P	195	61	0	66
T508DRAFT_01292	geranylgeranyl pyrophosphate synthase	87	34	16	23
T508DRAFT_01293	sodium--glutamate symport carrier (gltS)	60	0	11	20
T508DRAFT_01294	adenylosuccinate synthetase (EC 6.3.4.4)	33	59	11	0
T508DRAFT_01295	HflC protein	63	53	0	0
T508DRAFT_01296	protease FtsH subunit HflK	36	54	8	0
T508DRAFT_01297	GTP-binding protein HflX (EC 3.1.5.-)	22	34	0	0
T508DRAFT_01298	RNA chaperone Hfq	139	6	0	0
T508DRAFT_01299	sugar kinases, ribokinase family	105	0	0	35
T508DRAFT_01300	transcriptional regulator, LacI family	23	0	0	0
T508DRAFT_01301	MFS transporter, sugar porter (SP) family	84	0	16	0
T508DRAFT_01302	protein of unknown function (DUF2786)	46	90	32	36
T508DRAFT_01303	carboxylesterase type B	8	36	18	16
T508DRAFT_01304	tRNA dimethylallyltransferase	13	3	0	18
T508DRAFT_01305	DNA mismatch repair protein MutL	16	1	4	0
T508DRAFT_01306	N-acetylmuramoyl-L-alanine amidase	13	3	6	11
T508DRAFT_01307	tRNA threonylcarbamoyl adenosine modification protein YjeE	28	0	0	0
T508DRAFT_01308	yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-terminal region	70	61	44	11
T508DRAFT_01309	hypothetical protein	20	0	0	0
T508DRAFT_01310	transcriptional regulator/sugar kinase	144	195	156	34
T508DRAFT_01311	single-stranded-DNA-specific exonuclease RecJ	12	13	6	14
T508DRAFT_01312	hypothetical protein	49	35	0	0
T508DRAFT_01313	uncharacterised membrane protein	40	40	5	35
T508DRAFT_01314	acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	18	0	0	0
T508DRAFT_01315	1,4-Dihydroxy-2-naphthoyl-CoA synthase (EC 4.1.3.36)	41	0	0	18
T508DRAFT_01316	uncharacterized domain I	24	13	0	1
T508DRAFT_01317	Lhr-like helicases	7	5	0	14
T508DRAFT_01318	P-loop domain of unknown function (DUF2791)	51	13	0	17
T508DRAFT_01319	hypothetical protein	20	7	50	11
T508DRAFT_01320	uncharacterised protein conserved in bacteria	53	23	22	26
T508DRAFT_01321	FOG: TPR repeat, SEL1 subfamily	5	89	10	50
T508DRAFT_01322	ribosomal protein L11 methyltransferase	17	34	0	0
T508DRAFT_01323	hypothetical protein	71	95	16	10
T508DRAFT_01327	hypothetical protein	337	98	0	0
T508DRAFT_01328	TRAP-type C ₄ -dicarboxylate transport system, small permease component	0	0	0	0
T508DRAFT_01329	TRAP transporter, DctM subunit	2	27	0	0
T508DRAFT_01330	endonuclease I	15	0	0	0

T508DRAFT_01331	outer membrane protein and related peptidoglycan-associated (lipo)proteins	28	2	17	0
T508DRAFT_01332	deoxycytidylate deaminase	47	67	0	25
T508DRAFT_01333	arabinose efflux permease	52	36	22	12
T508DRAFT_01334	beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	31	9	0	2
T508DRAFT_01335	ABC-type sugar transport system, periplasmic component	33	206	175	92
T508DRAFT_01336	domain of unknown function (DUF4432)	151	162	126	58
T508DRAFT_01337	transcriptional regulator/sugar kinase	52	0	0	0
T508DRAFT_01338	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	309	0	0	0
T508DRAFT_01339	monosaccharide ABC transporter substrate-binding protein, CUT2 family (TC 3.A.1.2.-)	1596	8	0	7
T508DRAFT_01340	monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)	63	4	0	0
T508DRAFT_01341	monosaccharide ABC transporter membrane protein, CUT2 family (TC 3.A.1.2.-)	83	21	0	0
T508DRAFT_01342	sugar (pentulose and hexulose) kinases	47	0	0	6
T508DRAFT_01343	hypothetical protein	28	0	0	0
T508DRAFT_01344	threonine dehydrogenase and related Zn-dependent dehydrogenases	42	0	0	0
T508DRAFT_01345	mannitol-1-phosphate/altronate dehydrogenases	122	29	0	36
T508DRAFT_01346	hypothetical protein	6	33	0	25
T508DRAFT_01347	conserved hypothetical protein (putative transposase or invertase)	5	6	0	0
T508DRAFT_01348	methyl-accepting chemotaxis protein	40	44	56	45
T508DRAFT_01349	PAS domain S-box	12	0	0	6
T508DRAFT_01350	glycerate kinase	15	5	0	30
T508DRAFT_01351	hypothetical protein	3	29	0	0
T508DRAFT_01352	dihydrodipicolinate synthase	50	21	29	24
T508DRAFT_01353	2-hydroxy-3-oxopropionate reductase	37	13	12	0
T508DRAFT_01354	gluconate transporter	26	8	5	17
T508DRAFT_01355	D-glucarate dehydratase (EC 4.2.1.40)	37	27	24	5
T508DRAFT_01356	altronate dehydratase	41	12	0	13
T508DRAFT_01357	aldo/keto reductases, related to diketogulonate reductase	239	183	21	31
T508DRAFT_01358	transcriptional regulators	63	20	0	0
T508DRAFT_01359	thioredoxin	2230	2212	2089	2588
T508DRAFT_01360	lipid A 3-O-deacylase (PagL)	366	229	48	393
T508DRAFT_01361	hypothetical protein	12	0	0	0
T508DRAFT_01362	ABC-type transport system involved in Fe-S cluster assembly, permease component	35	2	0	12
T508DRAFT_01363	ABC-type transport system involved in Fe-S cluster assembly, ATPase component	7	0	0	0
T508DRAFT_01364	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	50	3	0	20
T508DRAFT_01365	transcriptional regulator, LacI family	27	56	35	65
T508DRAFT_01366	predicted dehydrogenases and related proteins	61	19	0	0
T508DRAFT_01367	sugar phosphate isomerases/epimerases	103	43	35	101
T508DRAFT_01368	ABC-type sugar transport system, periplasmic component	45	7	0	22
T508DRAFT_01369	ABC-type sugar transport system, ATPase component	135	19	8	27
T508DRAFT_01370	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	259	73	0	130
T508DRAFT_01371	flagellar hook protein FlgE	72	68	22	75
T508DRAFT_01372	transposase, IS605 OrfB family, central region	35	30	39	45
T508DRAFT_01373	protein of unknown function (DUF1703)/predicted AAA-ATPase	37	21	0	12
T508DRAFT_01374	tRNA pseudouridine(55) synthase	12	20	0	13
T508DRAFT_01375	lipid-A-disaccharide kinase (EC 2.7.1.130)	24	31	0	0
T508DRAFT_01376	3-deoxy-D-manno-octulosonate cytidyltransferase	8	0	0	0
T508DRAFT_01377	N-formylmethionyl-tRNA deformylase	25	1	0	0
T508DRAFT_01378	hypothetical protein	95	0	137	51
T508DRAFT_01379	RNAse T (EC 3.1.13.-)	67	9	12	0
T508DRAFT_01380	hypothetical protein	162	148	17	23
T508DRAFT_01381	HAD-superfamily subfamily IB hydrolase, TIGR01490	185	247	78	40
T508DRAFT_01382	predicted AAA-ATPase	68	4	29	9
T508DRAFT_01384	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)	83	63	0	0
T508DRAFT_01385*	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	530*	273	22	0*
T508DRAFT_01386	hypothetical protein	129	49	0	0
T508DRAFT_01387*	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	726*	49	29	16*
T508DRAFT_01388*	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	957	60	61	7*
T508DRAFT_01389	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	768	30	36	9
T508DRAFT_01390	2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketoisovalerate family	416	53	0	31
T508DRAFT_01391	transcriptional regulator/sugar kinase	12	7	0	0
T508DRAFT_01392	predicted transcriptional regulator	17	6	0	0

T508DRAFT_01393	drug resistance transporter, Bcr/CflA subfamily	22	58	0	27
T508DRAFT_01394	protein-disulfide isomerase	103	162	0	14
T508DRAFT_01395	hypothetical protein	333	200	0	78
T508DRAFT_01396	ABC-type xylose transport system, periplasmic component	31	27	73	41
T508DRAFT_01397	OmpA family	2	27	0	0
T508DRAFT_01398	SelI repeat	53	72	54	66
T508DRAFT_01399	L-fucose isomerase and related proteins	278	164	8	41
T508DRAFT_01400	ammonium transporter (TC 1.A.11)	25	6	0	0
T508DRAFT_01401	nitrogen regulatory protein P-II family	8	0	0	0
T508DRAFT_01402	putative efflux protein, MATE family	48	42	7	13
T508DRAFT_01403	spermidine/putrescine-binding periplasmic protein	107	71	26	23
T508DRAFT_01404*	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	127*	61	11*	37
T508DRAFT_01405	uncharacterised protein conserved in bacteria	26	18	20	17
T508DRAFT_01406	formate acetyltransferase 1	354	14	0	4
T508DRAFT_01407	pyruvate formate-lyase 1-activating enzyme	114	144	0	78
T508DRAFT_01408	predicted ATPase (AAA+ superfamily)	24	16	0	0
T508DRAFT_01409	DDE_Tnp_1-associated	2778	2430	782	1292
T508DRAFT_01410*	hypothetical protein	8709*	6323	1109*	1910
T508DRAFT_01411	outer membrane protein (porin)	33	20	0	0
T508DRAFT_01412*	alpha-1,4-glucan:alpha-1,4-glucan 6-glycosyltransferase	122*	17	5*	24
T508DRAFT_01413	4-alpha-glucanotransferase	76	20	16	27
T508DRAFT_01414	glyceraldehyde-3-phosphate dehydrogenase, type I	1324	651	150	200
T508DRAFT_01415	methyl-accepting chemotaxis protein	52	10	0	11
T508DRAFT_01416	Tir chaperone protein (CesT) family	49	13	50	0
T508DRAFT_01417	hypothetical protein	30	37	16	43
T508DRAFT_01418	Tir chaperone protein (CesT) family	29	20	0	27
T508DRAFT_01419	hypothetical protein	27	27	19	14
T508DRAFT_01420	TRAP transporter solute receptor, TAXI family	6	7	0	11
T508DRAFT_01421	Na ⁺ /glutamate symporter	17	26	0	40
T508DRAFT_01422	Tir chaperone protein (CesT) family	92	55	103	0
T508DRAFT_01423	methyl-accepting chemotaxis protein	54	58	34	33
T508DRAFT_01424	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	65	22	0	0
T508DRAFT_01425	monosaccharide ABC transporter substrate-binding protein, CUT2 family (TC 3.A.1.2.-)	128	63	45	23
T508DRAFT_01426	N-acetylneuraminate synthase (EC 2.5.1.56)	29	7	0	17
T508DRAFT_01427	Zn-dependent protease with chaperone function	18	8	0	0
T508DRAFT_01428	hypothetical protein	6	0	0	6
T508DRAFT_01429	prephenate dehydrogenase	3	20	0	1
T508DRAFT_01430	surface lipoprotein	16	5	19	23
T508DRAFT_01431	membrane protein involved in colicin uptake	33	13	4	4
T508DRAFT_01432	uncharacterised homolog of the cytoplasmic domain of flagellar protein FhlB	48	0	0	0
T508DRAFT_01433	protein of unknown function (DUF1703)/predicted AAA-ATPase	82	112	72	95
T508DRAFT_01434	hypothetical protein	81	99	24	0
T508DRAFT_01435	Winged helix-turn helix/DDE superfamily endonuclease	199	84	31	60
T508DRAFT_01436	hypothetical protein	6162	4355	2560	2812
T508DRAFT_01437	transcriptional regulators	0	0	0	0
T508DRAFT_01438	Cupin domain	27	67	0	0
T508DRAFT_01439	pyrimidine reductase, riboflavin biosynthesis	46	23	4	65
T508DRAFT_01441	diguanylate cyclase (GGDEF) domain	28	28	24	0
T508DRAFT_01442	hypothetical protein	40	75	11	0
T508DRAFT_01443	polyphosphate:nucleotide phosphotransferase, PPK2 family	28	77	0	17
T508DRAFT_01444	endoglucanase Y	98	117	44	94
T508DRAFT_01445	cellulose synthase subunit D	28	3	0	0
T508DRAFT_01446	tetratricopeptide repeat/cellulose synthase operon protein C C-terminus (BCSC_C)	22	4	0	5
T508DRAFT_01447	bacterial cellulose synthase subunit	13	5	5	28
T508DRAFT_01448	cellulose synthase catalytic subunit (UDP-forming)	9	6	0	4
T508DRAFT_01449	ATPases involved in chromosome partitioning	9	0	9	12
T508DRAFT_01450	hypothetical protein	31	15	0	0
T508DRAFT_01451	cellulose synthase operon protein YhjU	92	66	4	27
T508DRAFT_01452	protein of unknown function (DUF3260)	16	0	0	11
T508DRAFT_01453	hypothetical protein	38	63	0	25
T508DRAFT_01454	protein of unknown function (DUF2819)	13	14	0	19
T508DRAFT_01455	cellulose synthase operon protein C C-terminus (BCSC_C)	6	2	3	0
T508DRAFT_01456	endoglucanase Y	13	6	0	14
T508DRAFT_01457	bacterial cellulose synthase subunit	23	11	0	0
T508DRAFT_01458	cellulose synthase catalytic subunit (UDP-forming)	21	2	0	4
T508DRAFT_01459	YhjQ protein	16	0	0	0
T508DRAFT_01460	hypothetical protein	0	20	0	0
T508DRAFT_01461	3-deoxy-8-phosphooctulonate synthase	100	59	45	0
T508DRAFT_01462	hypothetical protein	9	26	0	0
T508DRAFT_01463	hypothetical protein	29	18	0	0

T508DRAFT_01464	pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)	175	84	12	186
T508DRAFT_01465*	predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	157*	55	4*	12
T508DRAFT_01466	formyltetrahydrofolate deformylase	201	214	182	210
T508DRAFT_01467	citrate synthase (EC 2.3.3.1)	31	51	9	0
T508DRAFT_01468	hypothetical protein	76	95	8	14
T508DRAFT_01469	Tir chaperone protein (CesT) family	19	14	0	0
T508DRAFT_01470	hypothetical protein	21	0	0	0
T508DRAFT_01471	Tir chaperone protein (CesT) family	0	0	0	0
T508DRAFT_01472	hypothetical protein	0	0	0	0
T508DRAFT_01473	hypothetical protein	0	0	0	0
T508DRAFT_01474	hypothetical protein	100	61	34	8
T508DRAFT_01475	hypothetical protein	49	0	0	0
T508DRAFT_01476	helix-turn-helix domain	72	0	0	0
T508DRAFT_01477	predicted <i>O</i> -methyltransferase	14	17	15	0
T508DRAFT_01478	Tir chaperone protein (CesT) family	11	14	0	0
T508DRAFT_01479	hypothetical protein	49	89	26	40
T508DRAFT_01480	hypothetical protein	159	0	0	0
T508DRAFT_01481	TIGR04076 family protein	127	55	1	61
T508DRAFT_01482	Tir chaperone protein (CesT) family	34	89	0	0
T508DRAFT_01483	hypothetical protein	53	76	37	27
T508DRAFT_01484	hypothetical protein	42	16	9	16
T508DRAFT_01485	hypothetical protein	205	67	34	336
T508DRAFT_01486	hypothetical protein	31	22	3	7
T508DRAFT_01487	Tir chaperone protein (CesT) family	47	34	0	0
T508DRAFT_01488	transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs	70	64	26	34
T508DRAFT_01489	lysine efflux permease	134	88	0	70
T508DRAFT_01490	hypothetical protein	20	0	65	30
T508DRAFT_01491	hypothetical protein	0	12	0	0
T508DRAFT_01492	putative oligopeptide transporter, OPT family	26	12	5	5
T508DRAFT_01493	permeases	15	6	0	14
T508DRAFT_01494	arabinose efflux permease	18	23	6	18
T508DRAFT_01495	uncharacterised host factor I protein	234	28	0	27
T508DRAFT_01496	rfaE bifunctional protein, domain I/rfaE bifunctional protein, domain II	86	75	8	24
T508DRAFT_01497	KpsF/GutQ family protein	11	23	0	12
T508DRAFT_01498	hypothetical protein	23	0	0	0
T508DRAFT_01501	preprotein translocase, SecA subunit	49	7	0	0
T508DRAFT_01504	phosphatidylserine decarboxylase precursor	50	68	20	0
T508DRAFT_01505	succinate dehydrogenase subunit A (EC 1.3.5.1)	833	124	84	78
T508DRAFT_01506*	succinate dehydrogenase and fumarate reductase iron-sulfur protein	252*	31	29	0*
T508DRAFT_01507*	fumarate reductase subunit C	329*	97	59	0*
T508DRAFT_01508	succinate dehydrogenase subunit D (EC 1.3.5.1)	420	101	87	114
T508DRAFT_01509*	pyruvate kinase	318*	78	9*	187
T508DRAFT_01510	flagellar biosynthetic protein FlhS	261	32	172	59
T508DRAFT_01511	uncharacterised flagellar protein FlaG	258	167	229	304
T508DRAFT_01512	hypothetical protein	0	0	0	0
T508DRAFT_01513	flagellar hook-associated protein 3	20	4	9	13
T508DRAFT_01514	flagellar hook-associated protein FlgK	4	3	0	8
T508DRAFT_01515	muramidase (flagellum-specific)	14	1	0	0
T508DRAFT_01516	response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	31	33	50	8
T508DRAFT_01517	UDP- <i>N</i> -acetylglucosamine 4,6-dehydratase	26	35	0	12
T508DRAFT_01518	UDP-4-keto-6-deoxy- <i>N</i> -acetylglucosamine 4-aminotransferase	17	13	0	43
T508DRAFT_01519	pseudaminic acid CMP-transferase	17	13	0	13
T508DRAFT_01520	pseudaminic acid biosynthesis-associated protein PseG	73	12	8	18
T508DRAFT_01521	uracil-DNA glycosylase (EC 3.2.2.-)	20	0	19	27
T508DRAFT_01522	predicted membrane protein	284	315	195	297
T508DRAFT_01523	chorismate mutase (EC 5.4.99.5)	104	45	0	0
T508DRAFT_01524	hypothetical protein	155	10	0	29
T508DRAFT_01525	hypothetical protein	199	97	27	86
T508DRAFT_01526	hypothetical protein	204	224	305	209
T508DRAFT_01527*	glutamate dehydrogenase (NADP) (EC 1.4.1.4)	122*	82	6*	79
T508DRAFT_01528	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	87	66	41	23
T508DRAFT_01529	protein of unknown function (DUF1703)/predicted AAA-ATPase	11	7	0	8
T508DRAFT_01530	short-chain dehydrogenases of various substrate specificities	19	14	0	12
T508DRAFT_01531	dihydrodipicolinate reductase (EC 1.3.1.26)	26	0	0	0
T508DRAFT_01532	acetyltransferases	26	0	0	0
T508DRAFT_01533	DNA repair protein RecN	10	22	0	0
T508DRAFT_01534	predicted sugar kinase	62	83	0	0
T508DRAFT_01535	hypothetical protein	10	0	50	0
T508DRAFT_01536	ribosome-binding factor A	28	18	0	0
T508DRAFT_01537*	translation initiation factor IF-2	83*	22	3*	8

T508DRAFT_01538	NusA antitermination factor	48	20	0	23
T508DRAFT_01539	uncharacterised protein conserved in bacteria	68	20	0	0
T508DRAFT_01540	membrane protein TerC, possibly involved in tellurium resistance	23	15	8	10
T508DRAFT_01541	pseudouridine synthase	21	15	0	0
T508DRAFT_01542	uncharacterised protein conserved in bacteria	38	0	66	0
T508DRAFT_01543	5,10-methenyltetrahydrofolate synthetase	70	12	0	0
T508DRAFT_01544	protein translocase subunit SecG	36	2	0	0
T508DRAFT_01545	phosphoglucosamine mutase (EC 5.4.2.10)	14	19	7	0
T508DRAFT_01546	dihydropteroate synthase and related enzymes	27	26	0	0
T508DRAFT_01547	membrane protease FtsH catalytic subunit (EC 3.4.24.-)	61	36	0	0
T508DRAFT_01548	23S rRNA Um-2552 2'-O-methyltransferase (EC 2.1.1.166)	64	66	0	16
T508DRAFT_01549	putative RNA-binding protein, YhbY family	408	57	0	0
T508DRAFT_01550	transcription elongation factor GreA	129	12	0	31
T508DRAFT_01551	chaperone protein DnaJ	201	196	112	105
T508DRAFT_01552	chaperone protein DnaK	641	290	257	384
T508DRAFT_01553	molecular chaperone GrpE (heat shock protein)	18	23	0	48
T508DRAFT_01554	small protein A (tmRNA-binding)	23	6	0	0
T508DRAFT_01555	hypothetical protein	71	24	0	11
T508DRAFT_01556	polyphosphate kinase 1	76	37	6	23
T508DRAFT_01557	uncharacterised conserved protein	38	29	0	18
T508DRAFT_01558	uncharacterised protein conserved in bacteria	6	0	0	0
T508DRAFT_01559	hypothetical protein	175	67	88	90
T508DRAFT_01560	tRNA threonylcarbamoyl adenosine modification protein YeaZ	28	0	0	0
T508DRAFT_01561	Rad3-related DNA helicases	19	0	0	0
T508DRAFT_01562	collagenase and related proteases	12	2	0	9
T508DRAFT_01563	uncharacterised conserved protein	93	26	17	0
T508DRAFT_01564	dihydroxyacetone kinase DhaM subunit (EC 2.7.1.121)	121	252	29	108
T508DRAFT_01565	hypothetical protein	19	75	149	53
T508DRAFT_01566	diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	55	8	36	22
T508DRAFT_01567	hypothetical protein	38	9	0	0
T508DRAFT_01568	ATPase components of ABC transporters with duplicated ATPase domains	17	0	4	11
T508DRAFT_01569	inorganic pyrophosphatase/exopolyphosphatase	111	29	0	7
T508DRAFT_01570	SSU ribosomal protein S12P methylthiotransferase (EC 2.-.-.-)	18	5	0	5
T508DRAFT_01571	xanthine phosphoribosyltransferase	27	20	0	19
T508DRAFT_01572	xanthine permease	34	35	6	42
T508DRAFT_01573	protein of unknown function (DUF1703)/predicted AAA-ATPase	33	50	21	14
T508DRAFT_01574	methyl-accepting chemotaxis protein	33	74	14	19
T508DRAFT_01575	predicted phosphohydrolases	19	5	0	38
T508DRAFT_01576	predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	23	33	0	22
T508DRAFT_01577	hypothetical protein	4	0	0	2
T508DRAFT_01578	hypothetical protein	25	40	0	18
T508DRAFT_01579	hypothetical protein	46	93	0	0
T508DRAFT_01580	protein of unknown function (DUF1703)/predicted AAA-ATPase	38	29	0	0
T508DRAFT_01581	peptidase T	31	36	0	1
T508DRAFT_01582	putative p-aminobenzoyl-glutamate transporter	32	28	10	5
T508DRAFT_01583	enolase (EC 4.2.1.11)	65	34	15	11
T508DRAFT_01584	FimV C-terminal domain	69	30	28	17
T508DRAFT_01585	aspartate-semialdehyde dehydrogenase	34	84	33	60
T508DRAFT_01586	hypothetical protein	11	0	0	44
T508DRAFT_01587	glucose-binding protein/galactose-binding protein	89	72	78	17
T508DRAFT_01588	outer membrane protein and related peptidoglycan-associated (lipo)proteins	289	285	80	85
T508DRAFT_01589	ribosomal protein L33, bacterial type	236	80	0	0
T508DRAFT_01590	LSU ribosomal protein L28P	277	50	0	49
T508DRAFT_01591	phosphopantothenate-cysteine ligase (EC 6.3.2.5)/phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)	179	281	109	250
T508DRAFT_01592	deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	229	304	181	206
T508DRAFT_01593	argininosuccinate lyase	60	61	28	64
T508DRAFT_01594	argininosuccinate synthase (EC 6.3.4.5)	142	23	0	6
T508DRAFT_01595	ornithine carbamoyltransferase	57	0	0	16
T508DRAFT_01596	NTP pyrophosphohydrolases including oxidative damage repair enzymes	56	40	5	46
T508DRAFT_01597	heat shock protein Hsp15	30	0	0	0
T508DRAFT_01598	disulfide bond chaperones of the HSP33 family	52	0	0	0
T508DRAFT_01599	glycerol kinase (EC 2.7.1.30)	56	0	0	0
T508DRAFT_01600	transketolase, C-terminal subunit	50	0	9	0
T508DRAFT_01601	transketolase, N-terminal subunit	132	34	0	11
T508DRAFT_01602	L-fucose isomerase and related proteins	70	3	0	7
T508DRAFT_01603	PTS system, glucose subfamily, IIA component	97	28	0	0
T508DRAFT_01604	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	130	0	0	0
T508DRAFT_01605	ABC-type sugar transport system, ATPase component	104	0	0	0

T508DRAFT_01606	predicted periplasmic lipoprotein	120	0	0	0
T508DRAFT_01607	ABC-type sugar transport system, periplasmic component	1073	73	0	0
T508DRAFT_01608	2'-5' RNA ligase	37	0	0	0
T508DRAFT_01609	AraC-type DNA-binding domain-containing proteins	2	13	0	0
T508DRAFT_01610	ABC-type ribose transport system, auxiliary component	19	8	0	0
T508DRAFT_01611	sugar kinases, ribokinase family	70	5	10	11
T508DRAFT_01612	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)	192	327	83	79
T508DRAFT_01613	predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	47	33	0	0
T508DRAFT_01614	hypothetical protein	45	78	58	27
T508DRAFT_01615	transcription elongation factor GreB	29	75	38	63
T508DRAFT_01616	phosphoenolpyruvate carboxykinase (ATP)	460	283	59	75
T508DRAFT_01617	thioredoxin-like proteins and domains	124	113	14	82
T508DRAFT_01618	hypothetical protein	0	0	0	0
T508DRAFT_01619	hypothetical protein	34	0	0	0
T508DRAFT_01620	glycerol-3-phosphate dehydrogenase	102	14	0	12
T508DRAFT_01621	protein translocase subunit SecB	133	13	0	0
T508DRAFT_01622	rhodanese-related sulfurtransferase	95	5	0	0
T508DRAFT_01623*	phosphoglycerate mutase (EC 5.4.2.1)	495*	184	27*	94
T508DRAFT_01624	outer membrane protein (porin)	64	16	0	16
T508DRAFT_01625	protein of unknown function (DUF1703)/predicted AAA-ATPase	7	18	31	6
T508DRAFT_01626	hypothetical protein	7	0	0	0
T508DRAFT_01627	hypothetical protein	3	7	0	0
T508DRAFT_01628	uncharacterised conserved protein	6	18	0	0
T508DRAFT_01629	rhodanese-related sulfurtransferase	28	15	0	0
T508DRAFT_01630	protein of unknown function (DUF1703)/predicted AAA-ATPase	48	45	0	28
T508DRAFT_01631	Ca ²⁺ /Na ⁺ antiporter	47	22	0	0
T508DRAFT_01632	putative NADH-flavin reductase	0	0	0	0
T508DRAFT_01633	predicted transcriptional regulator	27	11	0	0
T508DRAFT_01634	transposase	8	0	0	0
T508DRAFT_01635	predicted ATPase (AAA+ superfamily)	49	83	12	23
T508DRAFT_01636	hypothetical protein	18	0	0	0
T508DRAFT_01637	ribose-5-phosphate isomerase (EC 5.3.1.6)	25	0	0	40
T508DRAFT_01638	tyrosyl-tRNA synthetase (EC 6.1.1.1)	110	0	0	0
T508DRAFT_01639	predicted molecular chaperone distantly related to HSP70-fold metalloproteases	62	31	7	0
T508DRAFT_01640	predicted phosphohydrolases	29	26	0	35
T508DRAFT_01641	alpha-galactosidase	54	25	37	8
T508DRAFT_01642	competence/damage-inducible protein CinA C-terminal domain	110	385	235	177
T508DRAFT_01643	predicted ATPase (AAA+ superfamily)	61	24	31	16
T508DRAFT_01644	protein of unknown function (DUF2802)	62	51	9	59
T508DRAFT_01645	hypothetical protein	28	48	0	18
T508DRAFT_01646	ABC-type metal ion transport system, permease component	9	0	0	20
T508DRAFT_01647	ABC-type metal ion transport system, ATPase component	21	0	0	0
T508DRAFT_01648	ABC-type metal ion transport system, periplasmic component/surface antigen	28	8	0	40
T508DRAFT_01649	glycine/D-amino acid oxidases (deaminating)	14	8	0	7
T508DRAFT_01650	ABC-type metal ion transport system, periplasmic component/surface antigen	69	56	9	26
T508DRAFT_01651	predicted permease, DMT superfamily	50	31	3	27
T508DRAFT_01652	hypothetical protein	22	0	0	0
T508DRAFT_01653	monosaccharide ABC transporter membrane protein, CUT2 family (TC 3.A.1.2.-)	31	16	0	21
T508DRAFT_01654	monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)	27	1	0	8
T508DRAFT_01655	ABC-type sugar transport system, periplasmic component	148	14	0	18
T508DRAFT_01656	phosphatidylglycerophosphatase (EC 3.1.3.27)	6	11	0	0
T508DRAFT_01659	ABC-type xylose transport system, periplasmic component	2477	35	22	0
T508DRAFT_01660	ABC-type sugar transport system, ATPase component	328	18	0	0
T508DRAFT_01661	multiple monosaccharide ABC transporter membrane protein	168	20	0	12
T508DRAFT_01662	xylulokinase (EC 2.7.1.17)	46	17	0	4
T508DRAFT_01663	transcriptional regulator, LacI family	30	8	10	11
T508DRAFT_01665	SSU ribosomal protein S15P	278	52	0	41
T508DRAFT_01666	polyribonucleotide nucleotidyltransferase	187	9	3	0
T508DRAFT_01667	Na ⁺ -dependent transporters of the SNF family	16	7	0	14
T508DRAFT_01668	Na ⁺ -dependent transporters of the SNF family	20	24	0	37
T508DRAFT_01669	Na ⁺ -dependent transporters of the SNF family	43	30	0	12
T508DRAFT_01670	soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	24	40	0	0
T508DRAFT_01672	predicted permease, DMT superfamily	72	78	34	2
T508DRAFT_01673	hypothetical protein	298	79	2	22
T508DRAFT_01674	ABC-type Mn ²⁺ /Zn ²⁺ transport systems, permease components	149	20	0	54
T508DRAFT_01675	ABC-type Mn/Zn transport systems, ATPase component	106	44	0	0
T508DRAFT_01676	ABC-type metal ion transport system, periplasmic component/surface adhesin	64	0	13	7

T508DRAFT_01677	hypothetical protein	43	0	0	0
T508DRAFT_01678	Holliday junction endonuclease RuvC (EC 3.1.22.4)	49	57	0	32
T508DRAFT_01679	Holliday junction DNA helicase subunit RuvA	30	0	0	5
T508DRAFT_01680	Holliday junction DNA helicase subunit RuvB	0	1	0	0
T508DRAFT_01681	tol-pal system-associated acyl-CoA thioesterase	11	25	0	0
T508DRAFT_01682	TolQ protein	18	0	0	9
T508DRAFT_01683	cell division and transport-associated protein TolR (TC 2.C.1.2.1)	15	0	0	0
T508DRAFT_01684	TolA protein	29	0	0	0
T508DRAFT_01685	tol-pal system beta propeller repeat protein TolB	66	37	2	0
T508DRAFT_01686	peptidoglycan-associated lipoprotein	59	91	9	16
T508DRAFT_01687	tol-pal system protein YbgF	70	35	0	11
T508DRAFT_01688	ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA	34	4	7	17
T508DRAFT_01689	hypothetical protein	9	0	0	0
T508DRAFT_01692	hypothetical protein	267	30	45	100
T508DRAFT_01693	sortase and related acyltransferases	0	84	0	67
T508DRAFT_01694	nitroreductase	4	14	0	0
T508DRAFT_01695	TIGR04076 family protein	61	42	0	0
T508DRAFT_01696	stress responsive A/B Barrel domain	69	59	0	9
T508DRAFT_01697	predicted dehydrogenases and related proteins	21	7	0	0
T508DRAFT_01698	phosphoglycerate dehydrogenase and related dehydrogenases	108	0	0	0
T508DRAFT_01699	predicted oxidoreductase	261	77	17	27
T508DRAFT_01700	esterase/lipase	56	82	57	52
T508DRAFT_01701	ribosomal protein S21	174	49	83	0
T508DRAFT_01702	D-tyrosyl-tRNA(Tyr) deacylase	61	82	60	23
T508DRAFT_01703	hypothetical protein	120	132	45	14
T508DRAFT_01704	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	39	37	13	8
T508DRAFT_01705	dihydroneopterin aldolase	15	0	0	0
T508DRAFT_01706	2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine diphosphokinase	60	0	0	0
T508DRAFT_01707	undecaprenyl-diphosphatase UppP	62	38	0	0
T508DRAFT_01708	glutathione peroxidase	50	67	0	0
T508DRAFT_01709	aspartate racemase	67	8	0	0
T508DRAFT_01710	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	19	17	0	0
T508DRAFT_01711	tRNA nucleotidyltransferase/poly(A) polymerase	16	6	0	12
T508DRAFT_01712	type II secretion system protein A	63	43	46	59
T508DRAFT_01713	hypothetical protein	45	16	25	0
T508DRAFT_01714	Cupin domain	39	0	25	0
T508DRAFT_01715	sugar (pentulose and hexulose) kinases	42	7	7	18
T508DRAFT_01716	transcriptional regulator, contains sigma factor-related N-terminal domain	38	5	0	0
T508DRAFT_01717	ABC-type sugar transport system, ATPase component	19	34	6	17
T508DRAFT_01718	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	51	24	0	31
T508DRAFT_01719	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	34	0	0	10
T508DRAFT_01720	ABC-type sugar transport system, periplasmic component	226	32	35	24
T508DRAFT_01721	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	61	16	9	5
T508DRAFT_01722	chemotaxis signal transduction protein	199	386	316	192
T508DRAFT_01723	hypothetical protein	81	3	0	0
T508DRAFT_01724	thiamine biosynthesis protein ThiC	65	111	19	102
T508DRAFT_01726	predicted amidohydrolase	75	44	0	20
T508DRAFT_01727	uncharacterised conserved protein	30	30	0	0
T508DRAFT_01728	protein of unknown function (DUF1703)/predicted AAA-ATPase	34	8	0	19
T508DRAFT_01729	aspartate-semialdehyde dehydrogenase, gamma-proteobacterial	60	56	0	6
T508DRAFT_01730	hypothetical protein	5	0	0	0
T508DRAFT_01731	uncharacterized domain	6	34	0	10
T508DRAFT_01732	outer membrane lipoprotein involved in outer membrane biogenesis	7	7	0	0
T508DRAFT_01733	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	10	0	0	0
T508DRAFT_01734	ribose-phosphate pyrophosphokinase	30	0	0	36
T508DRAFT_01735	hypothetical protein	43	26	7	2
T508DRAFT_01736	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	26	0	0	0
T508DRAFT_01737	predicted transcriptional regulators	34	0	0	0
T508DRAFT_01738	predicted hydrolase of the alpha/beta superfamily	31	12	14	9
T508DRAFT_01739	phenolic acid decarboxylase	95	37	2	21
T508DRAFT_01740	membrane-associated lipoprotein involved in thiamine biosynthesis	86	32	18	25
T508DRAFT_01741	uncharacterised protein conserved in bacteria	57	20	37	64
T508DRAFT_01742	prolyl-tRNA synthetase (EC 6.1.1.15)	71	25	12	5
T508DRAFT_01743	flagellar basal-body P-ring protein	34	5	0	0
T508DRAFT_01744	flagellar basal body L-ring protein	1	0	0	0
T508DRAFT_01745	flagellar basal-body rod protein FlgG, Gram-negative bacteria	21	6	0	0
T508DRAFT_01746	flagellar basal-body rod protein FlgF	30	0	0	0
T508DRAFT_01747	flagellar hook capping protein	67	61	0	20
T508DRAFT_01748	predicted ATPase (AAA+ superfamily)	38	36	0	5

T508DRAFT_01749	flagellar basal-body rod protein FlgC	56	140	9	22
T508DRAFT_01750	flagellar basal-body rod protein FlgB	24	4	0	0
T508DRAFT_01751	methylase of chemotaxis methyl-accepting proteins	68	56	23	34
T508DRAFT_01752	flagella basal body P-ring formation protein FlgA	41	9	40	8
T508DRAFT_01753	anti-sigma-28 factor, FlgM family	36	63	73	98
T508DRAFT_01754	AAA domain (dynein-related subfamily)	49	46	19	15
T508DRAFT_01755	hypothetical protein	6156	4449	2560	2812
T508DRAFT_01756	hypothetical protein	357	139	0	1
T508DRAFT_01758	predicted permeases	82	58	65	86
T508DRAFT_01759	AraC-type DNA-binding domain-containing proteins	125	49	0	37
T508DRAFT_01760	predicted permeases	33	37	7	0
T508DRAFT_01761	DNA polymerase III, gamma/tau subunits	11	0	0	0
T508DRAFT_01762	thymidylate kinase (EC 2.7.4.9)	14	0	0	0
T508DRAFT_01763	conserved hypothetical protein, YceG family	18	4	0	0
T508DRAFT_01764	diguanylate cyclase (GGDEF) domain	22	17	21	0
T508DRAFT_01765	valyl-tRNA synthetase (EC 6.1.1.9)	54	4	0	7
T508DRAFT_01766	hypothetical protein	155	21	37	0
T508DRAFT_01767	OAH/OAS sulfhydrylase	72	82	13	98
T508DRAFT_01768	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	19	0	0	0
T508DRAFT_01769	lipoprotein signal peptidase	28	35	0	0
T508DRAFT_01770	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	65	10	0	0
T508DRAFT_01771	riboflavin kinase/FMN adenylyltransferase	59	49	0	9
T508DRAFT_01772	SSU ribosomal protein S20P	196	204	108	153
T508DRAFT_01773	AraC-type DNA-binding domain-containing proteins	101	86	62	0
T508DRAFT_01774	DDE superfamily endonuclease	1315	1705	1639	681
T508DRAFT_01775*	ribosomal S4P (gammaproteobacterial)	317*	950*	550	694
T508DRAFT_01776	protein of unknown function (DUF1703)/predicted AAA-ATPase	8	6	0	5
T508DRAFT_01777	predicted AAA-ATPase	227	257	192	159
T508DRAFT_01778*	predicted AAA-ATPase	310*	169	39*	147
T508DRAFT_01779	predicted AAA-ATPase	226	139	111	67
T508DRAFT_01780	hypothetical protein	54	81	14	107
T508DRAFT_01781	flagellin and related hook-associated proteins	101	157	123	86
T508DRAFT_01782	predicted permease, DMT superfamily	97	165	32	77
T508DRAFT_01783	protein of unknown function (DUF2846)	16	17	16	24
T508DRAFT_01784	methionyl-tRNA synthetase (EC 6.1.1.10)	66	12	0	16
T508DRAFT_01785	hypothetical protein	8	0	0	0
T508DRAFT_01786	hypothetical protein	17	22	0	6
T508DRAFT_01787	transcription-repair coupling factor	44	13	12	9
T508DRAFT_01788	glycosidases	17	17	0	28
T508DRAFT_01789	fumarase, class I, homodimeric (EC 4.2.1.2)	226	217	113	53
T508DRAFT_01790	hypothetical protein	133	72	72	62
T508DRAFT_01791	chorismate synthase (EC 4.2.3.5)	175	122	37	22
T508DRAFT_01792	protein-(glutamine-N5) methyltransferase, ribosomal protein L3-specific	22	25	0	0
T508DRAFT_01793	protein of unknown function (DUF1107)	97	151	330	159
T508DRAFT_01794	phosphohistidine phosphatase, SixA	41	59	0	0
T508DRAFT_01795	DNA-binding protein H-NS	54	14	18	116
T508DRAFT_01796	orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	483	493	88	321
T508DRAFT_01797	predicted N-acetylglucosaminyl transferase	24	27	0	14
T508DRAFT_01798	predicted membrane protein	80	84	40	0
T508DRAFT_01799	bacterial nucleoid DNA-binding protein	1518	1538	1733	1191
T508DRAFT_01800	amidohydrolase	20	28	0	0
T508DRAFT_01801	ABC-type metal ion transport system, ATPase component	35	12	0	0
T508DRAFT_01802	ABC-type metal ion transport system, permease component	30	0	0	35
T508DRAFT_01803	ABC-type metal ion transport system, periplasmic component/surface antigen	122	12	0	0
T508DRAFT_01804	galactose mutarotase and related enzymes	14	78	0	11
T508DRAFT_01805*	ribosomal protein S1	259*	28	8*	14
T508DRAFT_01806	cytidylate kinase (EC 2.7.4.14)	52	23	0	0
T508DRAFT_01807	transposase and inactivated derivatives	33	0	0	145
T508DRAFT_01808	SH3 domain of the SH3b1 type	19	24	54	6
T508DRAFT_01809	uncharacterised protein conserved in bacteria	23	15	14	6
T508DRAFT_01810	uncharacterised protein conserved in bacteria	93	84	49	10
T508DRAFT_01811	uncharacterised protein conserved in bacteria	72	104	143	43
T508DRAFT_01812	hypothetical protein	79	47	97	24
T508DRAFT_01813	histidinol phosphatase and related hydrolases of the PHP family	19	13	0	27
T508DRAFT_01814	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	10	11	0	29
T508DRAFT_01815	putative methyltransferase, YaeB/AF_0241 family	4	0	0	0
T508DRAFT_01816	hypothetical protein	2	0	0	0
T508DRAFT_01817	glutamyl-tRNA synthetase, bacterial family	26	0	0	0
T508DRAFT_01818	Aldo/keto reductases, related to diketogulonate reductase	20	9	0	0
T508DRAFT_01819	phosphoenolpyruvate--protein phosphotransferase (EC 2.7.3.9)	17	4	0	6
T508DRAFT_01820	uncharacterised protein conserved in bacteria	31	4	0	6
T508DRAFT_01822	integrase	12	5	7	6

T508DRAFT_01823	transcriptional regulator, AlpA family	47	35	0	58
T508DRAFT_01824	hypothetical protein	185	904	197	752
T508DRAFT_01825	hypothetical protein	15	5	0	0
T508DRAFT_01826	hypothetical protein	80	22	47	48
T508DRAFT_01827	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	28	9	13	49
T508DRAFT_01832*	type I secretion outer membrane protein, TolC family	108	150*	76	0*
T508DRAFT_01833	transposase IS66 family	98	10	0	14
T508DRAFT_01834	hypothetical protein	9	17	0	0
T508DRAFT_01835	uncharacterised membrane protein, possible Na ⁺ channel or pump	12	63	0	0
T508DRAFT_01836	hypothetical protein	25	0	0	0
T508DRAFT_01837	hypothetical protein	62	117	43	29
T508DRAFT_01838	methyl-accepting chemotaxis protein	19	32	0	0
T508DRAFT_01839	maltose-binding periplasmic proteins/domains	87	43	25	17
T508DRAFT_01840	SH3 domain protein	45	26	0	0
T508DRAFT_01841	uncharacterised conserved protein	26	0	0	21
T508DRAFT_01842	glutamine synthetase adenyllyltransferase	19	8	0	0
T508DRAFT_01843	hypothetical protein	45	58	0	36
T508DRAFT_01844	lipid A biosynthesis lauroyl (or palmitoleoyl) acyltransferase	17	33	6	19
T508DRAFT_01845	transcriptional regulator, LacI family	26	15	0	0
T508DRAFT_01846	UDP-glucose-4-epimerase galE	42	0	0	0
T508DRAFT_01847	galactose-1-phosphate uridylyltransferase, family 1	83	14	32	10
T508DRAFT_01848	galactokinase	79	29	0	0
T508DRAFT_01849	AmmeMemoRadiSam system protein A	23	55	113	21
T508DRAFT_01850	AmmeMemoRadiSam system radical SAM enzyme	40	18	33	0
T508DRAFT_01851	bacterial nucleoid DNA-binding protein	298	140	63	157
T508DRAFT_01852	putative NADPH-quinone reductase (modulator of drug activity B)	214	119	0	70
T508DRAFT_01853	uncharacterised conserved protein	120	127	64	91
T508DRAFT_01854	chemotaxis signal transduction protein	7	180	132	59
T508DRAFT_01855	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	164	95	104	17
T508DRAFT_01856	hypothetical protein	12	28	0	23
T508DRAFT_01857	hydroxyethylthiazole kinase, sugar kinase family	13	7	14	37
T508DRAFT_01858	uncharacterised conserved protein	0	0	0	22
T508DRAFT_01859	thiamine monophosphate synthase	2	0	15	2
T508DRAFT_01860	transposase and inactivated derivatives	46	0	0	142
T508DRAFT_01861	hypothetical protein	206	64	4	48
T508DRAFT_01862	hypothetical protein	42	0	0	0
T508DRAFT_01863	glycogen debranching enzyme GlgX	12	0	15	16
T508DRAFT_01864	periplasmic serine proteases (ClpP class)	40	7	10	8
T508DRAFT_01865	membrane protease subunits, stomatin/prohibitin homologs	34	14	0	0
T508DRAFT_01866	membrane protein implicated in regulation of membrane protease activity	8	0	0	37
T508DRAFT_01867	hypothetical protein	9	0	0	0
T508DRAFT_01868	methyl-accepting chemotaxis protein	226	212	143	102
T508DRAFT_01869	hypothetical protein	33	67	32	15
T508DRAFT_01870	inosine-5'-monophosphate dehydrogenase	60	7	8	0
T508DRAFT_01871	GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit/GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit	22	17	14	0
T508DRAFT_01872	DNA-binding protein, stimulates sugar fermentation	7	0	0	0
T508DRAFT_01873	putative zinc- or iron-chelating domain	31	14	0	0
T508DRAFT_01874	Tir chaperone protein (CesT) family	285	222	49	29
T508DRAFT_01875	hypothetical protein	36	15	0	0
T508DRAFT_01876	RND family efflux transporter, MFP subunit	14	15	0	31
T508DRAFT_01877	The (largely Gram-negative bacterial) hydrophobe/Amphiphile Efflux-1 (HAE1) Family	5	8	0	6
T508DRAFT_01878	nitroreductase	8	56	0	0
T508DRAFT_01879	flavodoxin	77	490	30	126
T508DRAFT_01880	DNA polymerase I - 3'-5' exonuclease and polymerase domains	83	16	0	0
T508DRAFT_01882	uncharacterised conserved protein	17	0	0	22
T508DRAFT_01883	AAA domain/domain of unknown function (DUF4143)	62	31	0	14
T508DRAFT_01884	hypothetical protein	20	8	0	6
T508DRAFT_01885	DNA polymerase III, subunit gamma and tau	47	9	0	0
T508DRAFT_01886	adenine phosphoribosyltransferase (EC 2.4.2.7)	50	0	0	6
T508DRAFT_01887	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	34	30	14	0
T508DRAFT_01888	outer membrane protein (porin)	152	88	8	42
T508DRAFT_01889	uncharacterised protein conserved in bacteria	100	19	9	0
T508DRAFT_01890	glycosyltransferases involved in cell wall biogenesis	37	0	12	0
T508DRAFT_01891	glycosyltransferases involved in cell wall biogenesis	68	14	41	0
T508DRAFT_01892	methyl-accepting chemotaxis protein	115	247	150	109
T508DRAFT_01893	excinuclease ABC subunit C	15	33	11	16
T508DRAFT_01894	lipoprotein, YaeC family	178	713	135	171
T508DRAFT_01895	predicted ATPase (AAA+ superfamily)	118	197	75	106

T508DRAFT_01896	ABC-type metal ion transport system, permease component	9	0	6	0
T508DRAFT_01897	ABC-type metal ion transport system, ATPase component	13	8	37	6
T508DRAFT_01898	cobalamin-5'-phosphate synthase (EC 2.7.8.26)	158	156	87	95
T508DRAFT_01899	hypothetical protein	36	11	28	18
T508DRAFT_01900	uncharacterised phage-associated protein	51	18	23	21
T508DRAFT_01901	hypothetical protein	27	18	0	51
T508DRAFT_01902	hypothetical protein	0	0	0	35
T508DRAFT_01903	hypothetical protein	52	265	250	208
T508DRAFT_01904	protein of unknown function (DUF1703)/predicted AAA-ATPase	13	7	0	0
T508DRAFT_01905	predicted AAA-ATPase	0	0	0	0
T508DRAFT_01906	protein of unknown function (DUF1703)/predicted AAA-ATPase	34	21	2	0
T508DRAFT_01907	hypothetical protein	195	88	152	188
T508DRAFT_01908	flagellar hook-basal body protein	63	83	27	57
T508DRAFT_01909	queuosine biosynthesis protein QueC	104	30	0	0
T508DRAFT_01910	electron transport complex, RnfABCDGE type, E subunit	40	38	0	85
T508DRAFT_01911	electron transport complex, RnfABCDGE type, G subunit	11	0	0	0
T508DRAFT_01912	electron transport complex, RnfABCDGE type, D subunit	40	16	18	18
T508DRAFT_01913	electron transport complex, RnfABCDGE type, C subunit	44	11	20	11
T508DRAFT_01914	electron transport complex, RnfABCDGE type, B subunit	106	25	0	73
T508DRAFT_01915	predicted NADH:ubiquinone oxidoreductase, subunit RnfA	34	0	0	0
T508DRAFT_01916	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18)/endonuclease III (EC 3.2.2.-)	35	13	0	36
T508DRAFT_01917*	uncharacterised conserved protein	242*	85	4*	57
T508DRAFT_01918	phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	32	26	3	10
T508DRAFT_01919	hydrolase, TatD family	2	15	0	0
T508DRAFT_01920	glycosyltransferase involved in LPS biosynthesis	4	6	0	0
T508DRAFT_01921	hypothetical protein	23	16	0	0
T508DRAFT_01922	hypothetical protein	57	14	0	25
T508DRAFT_01923	ADP-heptose:LPS heptosyltransferase	39	42	7	24
T508DRAFT_01924	hypothetical protein	92	15	0	0
T508DRAFT_01925	hypothetical protein	11	0	0	0
T508DRAFT_01926	hypothetical protein	345	101	0	0
T508DRAFT_01927	MFS/sugar transport protein	42	28	0	0
T508DRAFT_01928	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	49	75	14	32
T508DRAFT_01929	UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23)/glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	23	4	7	0
T508DRAFT_01930	prolipoprotein diacylglycerol transferase	10	37	0	15
T508DRAFT_01931	hypothetical protein	9	13	0	0
T508DRAFT_01932	phosphopantetheinyl transferase	25	21	10	0
T508DRAFT_01933	DNA-directed DNA polymerase III (polc)	31	1	4	6
T508DRAFT_01934	TRAP-type C ₄ -dicarboxylate transport system, periplasmic component	28	18	23	2
T508DRAFT_01935	glucose-6-phosphate isomerase	230	170	73	102
T508DRAFT_01936	transcriptional regulator	6	24	8	0
T508DRAFT_01937	ketol-acid reductoisomerase (EC 1.1.1.86)	194	0	0	0
T508DRAFT_01938	ADP-ribose pyrophosphatase	22	0	0	0
T508DRAFT_01939	ATP-dependent DNA helicase Rep (EC 3.6.1.-)	10	0	0	7
T508DRAFT_01940	DNA primase (bacterial type)	46	28	0	20
T508DRAFT_01941	dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1	27	0	0	0
T508DRAFT_01944	hypothetical protein	16	32	0	26
T508DRAFT_01945	predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	219	316	110	129
T508DRAFT_01946	hypothetical protein	0	18	0	0
T508DRAFT_01947	dipeptidase	75	27	0	14
T508DRAFT_01948	dipeptidase	30	9	10	13
T508DRAFT_01949	DNA replication protein	19	0	0	38
T508DRAFT_01950	RNAse H-fold protein YqgF	21	8	0	0
T508DRAFT_01951	uncharacterised protein conserved in bacteria	16	9	0	0
T508DRAFT_01952	flagellar biosynthesis protein FlhA	15	8	0	10
T508DRAFT_01953	flagellar biosynthetic protein FlhF	171	220	134	169
T508DRAFT_01954	ATPases involved in chromosome partitioning	104	169	65	88
T508DRAFT_01955	RNA polymerase sigma factor, FlhA/WhiG family	111	115	71	106
T508DRAFT_01956*	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	103	12	288*	0*
T508DRAFT_01957	chemotaxis protein	226	182	158	120
T508DRAFT_01958	chemotaxis protein histidine kinase and related kinases	109	142	129	47
T508DRAFT_01959	chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain	162	66	99	9
T508DRAFT_01960	flagellar motor component	80	29	26	0
T508DRAFT_01961	flagellar motor protein	27	24	9	33
T508DRAFT_01962	ATPases involved in chromosome partitioning	33	22	8	13
T508DRAFT_01963	CheW-like domain	19	10	5	0
T508DRAFT_01964	chemotaxis signal transduction protein	136	160	171	31
T508DRAFT_01965	outer membrane protein (porin)	126	156	77	227

T508DRAFT_01966	plasmid replication region DNA-binding N-term	1564	1693	692	1242
T508DRAFT_01967	aspartate carbamoyltransferase, regulatory subunit	17	36	0	48
T508DRAFT_01968	aspartate carbamoyltransferase (EC 2.1.3.2)	26	23	18	52
T508DRAFT_01969	transcriptional regulator, TetR family	66	14	10	32
T508DRAFT_01970	hypothetical protein	1072	540	242	47
T508DRAFT_01971	hypothetical protein	2662	1917	87	419
T508DRAFT_01973	hypothetical protein	13	27	0	0
T508DRAFT_01974	ribosomal-protein-alanine acetyltransferase	65	217	18	76
T508DRAFT_01975	NAD(P) transhydrogenase, alpha subunit	160	50	14	12
T508DRAFT_01976	NAD/NADP transhydrogenase beta subunit	122	29	31	51
T508DRAFT_01977	hypothetical protein	132	237	73	117
T508DRAFT_01978	PTS system, glucose subfamily, IIA component	24	78	26	8
T508DRAFT_01979	phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	27	12	7	9
T508DRAFT_01980	uncharacterised protein involved in cysteine biosynthesis	2	17	0	20
T508DRAFT_01981	cell division protein	58	10	19	46
T508DRAFT_01982	DNA ligase, NAD-dependent	68	19	0	39
T508DRAFT_01983	transglycosylase SLT domain	47	10	0	28
T508DRAFT_01984	ribonuclease HI	64	53	0	0
T508DRAFT_01985	DNA polymerase III, epsilon subunit, Proteobacterial	23	20	0	0
T508DRAFT_01986	phosphoheptose isomerase	18	0	0	0
T508DRAFT_01987	phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	44	29	0	5
T508DRAFT_01988	AraC-type DNA-binding domain-containing proteins	20	25	0	0
T508DRAFT_01989	hypothetical protein	150	80	15	134
T508DRAFT_01990	hypothetical protein	204	368	0	0
T508DRAFT_01992	monosaccharide ABC transporter substrate-binding protein, CUT2 family (TC 3.A.1.2.-)	102	82	0	70
T508DRAFT_01993	ribosome-associated GTPase EngA	115	239	146	134
T508DRAFT_01994	beta-barrel assembly machine subunit BamB	30	10	0	7
T508DRAFT_01995	uncharacterised protein conserved in bacteria	41	17	0	10
T508DRAFT_01996	histidyl-tRNA synthetase (EC 6.1.1.21)	36	8	0	0
T508DRAFT_01997	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.17.4.3)	33	0	0	0
T508DRAFT_01998	domain of unknown function (DUF4115)/helix-turn-helix domain	10	16	0	0
T508DRAFT_01999	23S rRNA m(2)A-2503 methyltransferase (EC 2.1.1.192)	60	27	30	24
T508DRAFT_02000	NAD-dependent protein deacetylases, SIR2 family	118	273	136	202
T508DRAFT_02001	leucyl aminopeptidase	16	11	0	0
T508DRAFT_02002	cysteine sulfinatase desulfinate/cysteine desulfurase and related enzymes	1	24	0	8
T508DRAFT_02003	predicted transcriptional regulators	0	0	0	6
T508DRAFT_02004	lipoprotein NlpI, contains TPR repeats	18	11	0	12
T508DRAFT_02005	protein-export membrane protein, SecD/SecF family	79	0	0	0
T508DRAFT_02006	protein-export membrane protein, SecD/SecF family	32	0	0	0
T508DRAFT_02007	preprotein translocase, YajC subunit	23	0	23	0
T508DRAFT_02008	hypothetical protein	31	0	0	13
T508DRAFT_02009	hypothetical protein	0	0	0	0
T508DRAFT_02010	hypothetical protein	25	94	0	0
T508DRAFT_02011	hypothetical protein	43	27	0	0
T508DRAFT_02012	hypothetical protein	66	40	0	0
T508DRAFT_02013*	ATPase, P-type (transporting), HAD superfamily, subfamily IC/heavy metal translocating P-type ATPase	78*	15	3*	16
T508DRAFT_02014*	hypothetical protein	128*	844*	440	201
T508DRAFT_02015	ATP dependent PIM1 peptidase. serine peptidase. MEROPS family S16	34	30	17	8
T508DRAFT_02016	predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	86	136	12	0
T508DRAFT_02017	hypothetical protein	21	31	0	9
T508DRAFT_02018	NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporters with a unique C-terminal domain	49	27	3	4
T508DRAFT_02019	ATP-dependent helicase HrpA	32	16	3	0
T508DRAFT_02020	hypothetical protein	36	20	0	0
T508DRAFT_02021	hypothetical protein	38	51	11	37
T508DRAFT_02022	hypothetical protein	63	63	11	0
T508DRAFT_02023	phosphotransferase System HPr (HPr) Family	44	5	39	30
T508DRAFT_02024	bacterial nucleoid DNA-binding protein	41	18	0	0
T508DRAFT_02025	hypothetical protein	6696	4540	2728	2934
T508DRAFT_02026	hypothetical protein	56	47	0	34
T508DRAFT_02027	phage-related protein	24	0	0	0
T508DRAFT_02028	predicted transcriptional regulator with C-terminal CBS domains	151	113	71	24
T508DRAFT_02029	uncharacterized protein TIGR03905	1738	1053	517	1144
T508DRAFT_02030	nitroreductase	304	92	81	151
T508DRAFT_02031	galactose mutarotase and related enzymes	56	36	0	22
T508DRAFT_02032	predicted permeases	38	10	0	25
T508DRAFT_02033	3-isopropylmalate dehydratase, small subunit	114	0	1	10
T508DRAFT_02034	3-isopropylmalate dehydratase, large subunit	54	0	9	13
T508DRAFT_02035	3-isopropylmalate dehydrogenase	44	1	0	7
T508DRAFT_02036	2-isopropylmalate synthase (EC 2.3.3.13)	45	13	3	7

T508DRAFT_02037	superfamily II DNA and RNA helicases	34	12	0	0
T508DRAFT_02038	tRNA and rRNA cytosine-C ⁵ -methylases	68	22	0	0
T508DRAFT_02039	domain of unknown function (DUF4357)	12	25	0	0
T508DRAFT_02040	aspartate/tyrosine/aromatic aminotransferase	34	17	9	0
T508DRAFT_02041	D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	51	41	9	0
T508DRAFT_02042	uncharacterised paraquat-inducible protein B	53	8	0	13
T508DRAFT_02043	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	48	8	0	30
T508DRAFT_02044	predicted permeases	68	27	0	4
T508DRAFT_02047	transposase IS66 family	38	25	0	10
T508DRAFT_02048	hypothetical protein	36	68	23	11
T508DRAFT_02049	hypothetical protein	78	123	60	31
T508DRAFT_02050	hypothetical protein	14	0	0	0
T508DRAFT_02051	predicted membrane protein	79	0	0	0
T508DRAFT_02052	glyoxalase-like domain	7	24	0	0
T508DRAFT_02053	hypothetical protein	247	106	35	68
T508DRAFT_02054	hypothetical protein	273	165	131	181
T508DRAFT_02055	hypothetical protein	19	5	51	72
T508DRAFT_02056	predicted ATPase (AAA+ superfamily)	20	8	3	0
T508DRAFT_02057	predicted acyltransferases	42	5	0	0
T508DRAFT_02058	nicotinamide mononucleotide transporter PnuC	61	4	0	0
T508DRAFT_02059	thiamine pyrophosphokinase	19	7	0	0
T508DRAFT_02060	ADP-ribose pyrophosphatase	13	35	0	0
T508DRAFT_02061	transcriptional regulator, Spx/MgsR family	6	0	0	0
T508DRAFT_02062	calcineurin-like phosphoesterase	28	0	0	8
T508DRAFT_02063	nicotinate phosphoribosyltransferase	60	50	0	17
T508DRAFT_02064	Type IV secretory pathway, VirD4 components	4	0	0	12
T508DRAFT_02065	hypothetical protein	8	0	0	0
T508DRAFT_02066	hypothetical protein	14	0	8	5
T508DRAFT_02067	putative helicase	23	6	0	2
T508DRAFT_02068	hypothetical protein	335	98	0	0
T508DRAFT_02069	hypothetical protein	52	72	0	0
T508DRAFT_02070	glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41)	76	161	15	48
T508DRAFT_02071	glutamate 5-kinase (EC 2.7.2.11)	26	9	0	0
T508DRAFT_02072	alpha/beta hydrolase of unknown function (DUF1100)	21	14	0	0
T508DRAFT_02073	integral membrane protein MviN	16	23	0	14
T508DRAFT_02074	hypothetical protein	39	14	0	0
T508DRAFT_02075	universal stress protein UspA and related nucleotide-binding proteins	65	116	112	30
T508DRAFT_02076	transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs	62	29	14	49
T508DRAFT_02077	pyridoxal 5'-phosphate synthase, synthase subunit Pdx1	41	35	35	34
T508DRAFT_02078	pyridoxal phosphate synthase yaaE subunit	28	30	13	71
T508DRAFT_02079	Xaa-His dipeptidase	62	3	0	0
T508DRAFT_02080	glycosidases	162	432	344	258
T508DRAFT_02081	hypothetical protein	863	3038	2344	796
T508DRAFT_02082	outer membrane protein (porin)	31	101	114	19
T508DRAFT_02083	hypothetical protein	14	49	0	0
T508DRAFT_02084	DNA replication protein	10	15	0	10
T508DRAFT_02085	transposase and inactivated derivatives	78	58	27	33
T508DRAFT_02086	hypothetical protein	1071	1128	966	2070
T508DRAFT_02087	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	32	19	0	6
T508DRAFT_02088	WxcM-like, C-terminal	96	0	0	27
T508DRAFT_02089	uncharacterised oxidoreductases, Fe-dependent alcohol dehydrogenase family	29	53	22	8
T508DRAFT_02090	isopropylmalate/homocitrate/citramalate synthases	29	0	0	0
T508DRAFT_02091	transketolase, N-terminal subunit	36	14	0	0
T508DRAFT_02092	transketolase, C-terminal subunit	131	74	10	0
T508DRAFT_02093*	hypothetical protein	5652*	1840	599*	778
T508DRAFT_02094*	hypothetical protein	3544*	1260	190*	658
T508DRAFT_02095	domain of unknown function (DUF4277)	1440	665	229	455
T508DRAFT_02096	GDP-mannose 4,6-dehydratase	128	61	9	54
T508DRAFT_02097	mannose-1-phosphate guanylyltransferase	22	10	6	19
T508DRAFT_02098	phosphomannose isomerase	26	20	0	12
T508DRAFT_02099	NTP pyrophosphohydrolases including oxidative damage repair enzymes	0	34	0	0
T508DRAFT_02100	phosphomannomutase	21	43	7	18
T508DRAFT_02101	transposase DDE domain	961	673	56	205
T508DRAFT_02102	preprotein translocase, SecE subunit, bacterial	22	10	0	0
T508DRAFT_02103	transcription antitermination protein nusG	30	23	0	36
T508DRAFT_02104	LSU ribosomal protein L11P	301	127	0	0
T508DRAFT_02105	ribosomal protein L1, bacterial/chloroplast	414	79	0	0
T508DRAFT_02106	LSU ribosomal protein L10P	180	24	0	0
T508DRAFT_02107	LSU ribosomal protein L12P	182	35	0	0
T508DRAFT_02108	DNA-directed RNA polymerase, beta subunit	135	26	6	4

T508DRAFT_02109	DNA-directed RNA polymerase subunit beta' (EC 2.7.7.6)	84	9	0	5
T508DRAFT_02110	reactive intermediate/imine deaminase	63	58	23	37
T508DRAFT_02111	uncharacterised conserved protein involved in intracellular sulfur reduction	25	0	0	0
T508DRAFT_02112	hypothetical protein	9	0	0	0
T508DRAFT_02113	hypothetical protein	0	0	0	0
T508DRAFT_02114	SSU ribosomal protein S12P	323	43	0	5
T508DRAFT_02115	ribosomal protein S7, bacterial/organelle	343	41	0	20
T508DRAFT_02116	translation elongation factor 2 (EF-2/EF-G)	361	28	6	19
T508DRAFT_02117	hypothetical protein	64	0	0	0
T508DRAFT_02118	IS66 Orf2 like protein	38	41	0	0
T508DRAFT_02119	hypothetical protein	15	0	0	0
T508DRAFT_02120	cysteine sulfinase desulfurase/cysteine desulfurase and related enzymes	36	40	17	7
T508DRAFT_02121	hypothetical protein	9	0	7	46
T508DRAFT_02122	TIGR02688 family protein	14	6	0	8
T508DRAFT_02123	hypothetical protein	22	0	11	0
T508DRAFT_02124	hypothetical protein	24	33	0	26
T508DRAFT_02125	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes	16	0	0	0
T508DRAFT_02126	hypothetical protein	17	2	0	10
T508DRAFT_02127	membrane-associated phospholipid phosphatase	33	2	0	0
T508DRAFT_02128	transposase and inactivated derivatives	37	14	0	0
T508DRAFT_02129*	translation elongation factor TU	2034*	313	56	47*
T508DRAFT_02130	fructose-1,6-bisphosphatase, class II	78	88	0	18
T508DRAFT_02131	site-specific recombinase XerD	62	38	19	22
T508DRAFT_02132	site-specific recombinase XerD	113	109	36	89
T508DRAFT_02133	site-specific recombinase XerD	62	37	0	53
T508DRAFT_02134	retron-type reverse transcriptase	74	16	0	13
T508DRAFT_02137	superinfection exclusion protein B	80	41	13	0
T508DRAFT_02138	nitrogen regulatory protein P-II family	103	125	0	28
T508DRAFT_02139	uncharacterised protein conserved in bacteria	31	26	0	0
T508DRAFT_02140	5-ribosylhomocysteine lyase (EC 4.4.1.21)/quorum-sensing autoinducer 2 (AI-2) synthesis protein LuxS	33	0	0	0
T508DRAFT_02141	D-alpha,beta-D-heptose 1,7-bisphosphate phosphatase (EC 3.1.3.-)	63	32	0	24
T508DRAFT_02142	murein lipoprotein	89	304	28	34
T508DRAFT_02143*	tyrosine lyase ThiH	133*	52	21*	63
T508DRAFT_02144	thiazole-phosphate synthase	58	31	0	0
T508DRAFT_02145	thiamine biosynthesis protein ThiS	73	0	0	0
T508DRAFT_02146	dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	26	0	0	0
T508DRAFT_02147	thiamine-phosphate pyrophosphorylase	27	17	0	22
T508DRAFT_02150	hypothetical protein	25	57	30	99
T508DRAFT_02151	hypothetical protein	53	0	0	0
T508DRAFT_02152*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	96	86	14*	167*
T508DRAFT_02153	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (EC 2.5.1.54)	43	28	8	34
T508DRAFT_02154	exodeoxyribonuclease III	101	2	0	16
T508DRAFT_02155	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	62	9	0	19
T508DRAFT_02156	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	22	6	0	17
T508DRAFT_02157	peptidase T	69	24	0	18
T508DRAFT_02158	ABC-type antimicrobial peptide transport system, ATPase component	40	31	6	4
T508DRAFT_02159	RND family efflux transporter, MFP subunit	46	78	17	10
T508DRAFT_02160	predicted SAM-dependent methyltransferases	15	3	0	0
T508DRAFT_02161	Zn-dependent hydrolases, including glyoxylases	14	0	0	0
T508DRAFT_02162	addiction module antitoxin, RelB/DinJ family	55	0	0	0
T508DRAFT_02163	hypothetical protein	152	104	0	49
T508DRAFT_02164	uncharacterised protein conserved in bacteria	340	897	273	986
T508DRAFT_02165	uncharacterised protein conserved in bacteria	126	58	0	77
T508DRAFT_02166	hypothetical protein	38	96	0	10
T508DRAFT_02167	protein of unknown function (DUF3990)	56	24	0	19
T508DRAFT_02168	transposase and inactivated derivatives	380	113	100	30
T508DRAFT_02169	universal stress protein UspA and related nucleotide-binding proteins	102	104	62	58
T508DRAFT_02170	hypothetical protein	56	170	35	27
T508DRAFT_02171	RND family efflux transporter, MFP subunit	43	28	14	0
T508DRAFT_02172	The (largely Gram-negative bacterial) hydrophobe/Amphiphile Efflux-1 (HAE1) Family	39	37	0	9
T508DRAFT_02173*	flagellin and related hook-associated proteins	151*	77	34	14*
T508DRAFT_02174	predicted GTPase, probable translation factor	30	64	19	19
T508DRAFT_02175	peptidyl-tRNA hydrolase	8	0	12	0
T508DRAFT_02176	2-amino-4-hydroxy-6-hydroxymethylhydropteridine diphosphokinase	0	0	0	0
T508DRAFT_02177	poly(A) polymerase	27	4	0	9
T508DRAFT_02178	glutamyl- and glutaminytRNA synthetases	14	0	0	0
T508DRAFT_02179	transcriptional regulator, TraR/DksA family	81	66	0	0
T508DRAFT_02180	penicillin-binding protein 1B	14	4	0	5

T508DRAFT_02181	methionine synthase II (cobalamin-independent)	9	4	0	21
T508DRAFT_02182	hypothetical protein	272	115	0	94
T508DRAFT_02183	adenylosuccinate lyase	25	10	0	12
T508DRAFT_02184	uncharacterised protein involved in purine metabolism	51	35	0	0
T508DRAFT_02185	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	28	6	0	0
T508DRAFT_02186	ADP-ribose pyrophosphatase	21	114	0	0
T508DRAFT_02187	predicted membrane protein	24	0	0	35
T508DRAFT_02188	hypothetical protein	180	271	208	86
T508DRAFT_02189	multidrug resistance efflux pump	47	14	0	0
T508DRAFT_02190	ABC-type multidrug transport system, permease component	21	29	2	26
T508DRAFT_02191	FOG: TPR repeat, SEL1 subfamily	26	5	7	0
T508DRAFT_02192	isocitrate dehydrogenase (NADP) (EC 1.1.1.42)	54	20	0	0
T508DRAFT_02193	predicted membrane protein	35	23	0	12
T508DRAFT_02194	bacterial translation initiation factor 1 (bIF-1)	82	26	0	0
T508DRAFT_02195	3-oxoacyl-(acyl-carrier-protein) synthase	84	22	0	12
T508DRAFT_02196	pseudouridine synthase	29	11	0	0
T508DRAFT_02197	hypothetical protein	26	82	0	0
T508DRAFT_02201	hypothetical protein	67	16	0	21
T508DRAFT_02202	region found in RelA / SpoT proteins	144	42	31	70
T508DRAFT_02203	predicted Zn-dependent hydrolases of the beta-lactamase fold	536	60	45	26
T508DRAFT_02204	transcriptional regulators	209	0	0	0
T508DRAFT_02205	uncharacterised protein conserved in bacteria	319	31	0	12
T508DRAFT_02206	cobalamin biosynthesis protein CobD/CbiB	299	44	20	21
T508DRAFT_02207	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	252	66	16	54
T508DRAFT_02208	glucose-1-phosphate adenylyltransferase	190	222	51	14
T508DRAFT_02209	deoxyguanosinetriphosphate triphosphohydrolase, putative	23	12	0	6
T508DRAFT_02210	glycerol-3-phosphate acyltransferase (EC 2.3.1.15)	24	0	0	0
T508DRAFT_02211	hypothetical protein	103	52	90	224
T508DRAFT_02212	FKBP-type peptidyl-prolyl cis-trans isomerases 2	177	190	87	112
T508DRAFT_02213	tRNA sulfurtransferase ThiI/thiazole biosynthesis domain	32	17	5	0
T508DRAFT_02214	uracil phosphoribosyltransferase (EC 2.4.2.9)	19	0	0	0
T508DRAFT_02215	hypothetical protein	107	71	0	0
T508DRAFT_02216	hypothetical protein	41	0	0	0
T508DRAFT_02217	predicted ATPase (AAA+ superfamily)	62	36	19	38
T508DRAFT_02218*	hypothetical protein	260*	563	548	897*
T508DRAFT_02219	hypothetical protein	904	1500	1520	1277
T508DRAFT_02220	Flp pilus assembly protein, ATPase CpaF	17	8	0	0
T508DRAFT_02221	Type IV secretory pathway, VirB2 components (pilins)	0	9	0	0
T508DRAFT_02222	Type IV secretory pathway, TrbD component	20	0	0	0
T508DRAFT_02223	Type IV secretory pathway, VirB4 components	6	0	0	0
T508DRAFT_02224	Type IV secretory pathway, TrbF components	0	10	0	0
T508DRAFT_02225	Type IV secretory pathway, VirB9 components	4	26	15	0
T508DRAFT_02226	Type IV secretory pathway, VirB10 components	7	0	0	0
T508DRAFT_02227	hypothetical protein	0	0	0	0
T508DRAFT_02228	TrbL/VirB6 plasmid conjugal transfer protein	8	0	0	0
T508DRAFT_02229	putative transposase DNA-binding domain	54	15	0	51
T508DRAFT_02230	Altronate dehydratase	38	21	0	7
T508DRAFT_02231	transposase	9	0	0	10
T508DRAFT_02232	transposase and inactivated derivatives	0	17	0	0
T508DRAFT_02233	ABC-type xylose transport system, periplasmic component	59	43	0	11
T508DRAFT_02234	predicted acetyltransferase	51	97	20	0
T508DRAFT_02235	transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains	8	11	10	0
T508DRAFT_02236	tripartite ATP-independent periplasmic transporter solute receptor, DctP family	91	464	375	119
T508DRAFT_02237	TRAP-type C ₄ -dicarboxylate transport system, small permease component	22	24	75	0
T508DRAFT_02238	TRAP transporter, DctM subunit	99	158	9	16
T508DRAFT_02239	threonine dehydrogenase and related Zn-dependent dehydrogenases	14	23	5	9
T508DRAFT_02240	mannitol-1-phosphate/altronate dehydrogenases	7	23	0	0
T508DRAFT_02241	DDE_Tnp_1-associated	2778	2430	782	1292
T508DRAFT_02242	domain of unknown function (DUF4411)	53	0	0	32
T508DRAFT_02243	predicted Zn peptidase	20	6	12	33
T508DRAFT_02244	hypothetical protein	11	0	0	0
T508DRAFT_02245	hypothetical protein	3	0	0	0
T508DRAFT_02246	phosphomannomutase	13	5	6	5
T508DRAFT_02247	AAA domain	27	0	0	0
T508DRAFT_02248	hypothetical protein	22	0	55	0
T508DRAFT_02249	hypothetical protein	53	103	0	58
T508DRAFT_02250	hypothetical protein	10	9	0	0
T508DRAFT_02251	hypothetical protein	31	0	0	0
T508DRAFT_02252	hypothetical protein	372	227	22	410
T508DRAFT_02253	bacterial transferase hexapeptide (six repeats)/Hexapeptide repeat of succinyl-transferase	164	0	36	0
T508DRAFT_02254	hypothetical protein	813	63	88	16

T508DRAFT_02255*	transposase DDE domain	1881*	556	149*	357
T508DRAFT_02256	glycosyltransferases, probably involved in cell wall biogenesis	34	14	11	0
T508DRAFT_02257*	transposase DDE domain	1695*	948	97*	604
T508DRAFT_02258*	hypothetical protein	1571*	697	151*	470
T508DRAFT_02259	glycosyltransferase	27	33	14	85
T508DRAFT_02260	hypothetical protein	66	9	0	22
T508DRAFT_02261	hypothetical protein	34	140	0	0
T508DRAFT_02262	hypothetical protein	70	35	0	0
T508DRAFT_02263	hypothetical protein	25	25	0	17
T508DRAFT_02264*	Permeases of the drug/metabolite transporter (DMT) superfamily	530*	181	113*	322
T508DRAFT_02265	uncharacterised protein conserved in bacteria	66	0	30	51
T508DRAFT_02266	hypothetical protein	11	0	0	0
T508DRAFT_02267	chemotaxis signal transduction protein	53	171	165	10
T508DRAFT_02268	TIGR04076 family protein	7	67	0	38
T508DRAFT_02269	membrane-associated phospholipid phosphatase	42	49	57	0
T508DRAFT_02270	ABC-type sugar transport system, auxiliary component	47	0	0	24
T508DRAFT_02271	rubrerythrin	24	42	0	0
T508DRAFT_02272	cation diffusion facilitator family transporter	51	47	17	36
T508DRAFT_02273	predicted ester cyclase	4	0	20	0
T508DRAFT_02274	hypothetical protein	5709	5273	846	3054
T508DRAFT_02275	hypothetical protein	7	9	0	0
T508DRAFT_02276	uncharacterised protein conserved in bacteria	43	0	0	0
T508DRAFT_02277	predicted transcriptional regulator	16	0	0	0
T508DRAFT_02278	PAS domain S-box	38	0	0	0
T508DRAFT_02279	response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	32	12	15	0
T508DRAFT_02280*	transcriptional regulator, IclR family	532*	379	31*	62
T508DRAFT_02282	acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	42	21	21	0
T508DRAFT_02283*	hypothetical protein	71*	21	15	0*
T508DRAFT_02284	hypothetical protein	10	31	0	0
T508DRAFT_02285	uncharacterised protein conserved in bacteria	53	0	0	0
T508DRAFT_02286	flagellar biosynthesis/type III secretory pathway chaperone	80	23	35	61
T508DRAFT_02287	aldo/keto reductases, related to diketogulonate reductase	42	59	0	9
T508DRAFT_02288	tRNA-U16,U17-dihydrouridine synthase	36	11	0	0
T508DRAFT_02289	glycine/serine hydroxymethyltransferase	230	20	0	0
T508DRAFT_02290	membrane proteins related to metalloendopeptidases	54	136	73	67
T508DRAFT_02291	arginine degradation protein (predicted deacylase)	41	20	26	16
T508DRAFT_02292	Abi-like protein	42	30	56	52
T508DRAFT_02293	hypothetical protein	2447	2271	708	1246
T508DRAFT_02294	DDE_Tnp_1-associated	2776	2430	782	1292
T508DRAFT_02295	predicted UDP-glucose 6-dehydrogenase	17	15	9	63
T508DRAFT_02296	phosphonopyruvate decarboxylase (EC 4.1.1.82)	61	8	0	18
T508DRAFT_02297	CTP:phosphocholine cytidyltransferase involved in choline phosphorylation for cell surface LPS epitopes	25	24	0	0
T508DRAFT_02298	methyltransferase domain	22	29	0	0
T508DRAFT_02299	2-aminoethylphosphonate aminotransferase	13	30	0	0
T508DRAFT_02300	phosphoenolpyruvate mutase (EC 5.4.2.9)	15	5	1	38
T508DRAFT_02301*	hypothetical protein	8490*	5171	891*	3785
T508DRAFT_02302*	translation elongation factor TU	2091*	379	57	47*
T508DRAFT_02305	pantothenate kinase (EC 2.7.1.33)	268	162	44	197
T508DRAFT_02306	birA, biotin-[acetyl-CoA-carboxylase] ligase region	38	82	3	15
T508DRAFT_02307	UDP-N-acetylmuramate dehydrogenase (EC 1.1.1.158)	37	42	36	9
T508DRAFT_02308	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	35	0	0	29
T508DRAFT_02309	homoserine O-succinyltransferase (EC 2.3.1.46)	18	9	0	0
T508DRAFT_02312	hypothetical protein	83	0	0	0
T508DRAFT_02313	metal-dependent hydrolases of the beta-lactamase superfamily III	74	39	19	5
T508DRAFT_02314	hypothetical protein	48	51	7	0
T508DRAFT_02315	hypothetical protein	75	53	0	17
T508DRAFT_02316	hypothetical protein	46	46	0	20
T508DRAFT_02317	hypothetical protein	42	27	0	87
T508DRAFT_02318	protein of unknown function (DUF2971)	13	15	2	0
T508DRAFT_02319	hypothetical protein	47	10	8	50
T508DRAFT_02320*	hypothetical protein	8440*	5161	891*	3761
T508DRAFT_02321	outer membrane protein (porin)	963	2442	852	752
T508DRAFT_02322*	outer membrane protein (porin)	688*	289	139	29*
T508DRAFT_02323*	outer membrane protein (porin)	3829*	744	591	55*
T508DRAFT_02324	predicted hydrolase of alkaline phosphatase superfamily	23	28	0	21
T508DRAFT_02325*	hypothetical protein	8763*	4823	1211*	2346
T508DRAFT_02326	hypothetical protein	71	76	32	83
T508DRAFT_02327	sodium/proline symporter	43	15	6	33
T508DRAFT_02328	NAD synthase	50	27	5	4
T508DRAFT_02329	Type II secretory pathway, pullulanase PulA and related glycosidases	60	9	0	38
T508DRAFT_02330	hypothetical protein	180	437	94	344
T508DRAFT_02331*	hypothetical protein	6670*	4755	1124*	1827
T508DRAFT_02338	exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	14	21	0	6

T508DRAFT_02339	hypothetical protein	15	8	0	13
T508DRAFT_02340	predicted ATPase (AAA+ superfamily)	14	83	0	0
T508DRAFT_02341	Na ⁺ /H ⁺ -dicarboxylate symporters	110	0	0	74
T508DRAFT_02342	transposase	17	44	0	3
T508DRAFT_02343	Na ⁺ /H ⁺ -dicarboxylate symporters	4	0	0	0
T508DRAFT_02344	hypothetical protein	19	6	0	0
T508DRAFT_02345	hypothetical protein	43	58	0	2
T508DRAFT_02346	type III secretion system apparatus protein YscQ/HrcQ	11	17	0	43
T508DRAFT_02347	type III secretion apparatus protein, YscR/HrcR family	1	0	0	0
T508DRAFT_02348	hypothetical protein	48	33	0	0
T508DRAFT_02349	hypothetical protein	425	584	488	487
T508DRAFT_02350	hypothetical protein	125	272	95	42
T508DRAFT_02351	protein involved in catabolism of external DNA	39	36	20	3
T508DRAFT_02352	FOG: EAL domain	38	18	0	30
T508DRAFT_02353	transposase and inactivated derivatives	693	365	74	225
T508DRAFT_02354	Miro-like protein	196	115	126	27
T508DRAFT_02355	hypothetical protein	102	0	16	0
T508DRAFT_02356	Recombinational DNA repair ATPase (RecF pathway)	24	0	9	23
T508DRAFT_02357	hypothetical protein	12	0	0	0
T508DRAFT_02358	predicted transcriptional regulators	67	16	0	41
T508DRAFT_02359	hypothetical protein	0	0	0	0
T508DRAFT_02360	hypothetical protein	25	57	30	99
T508DRAFT_02361	hypothetical protein	144	76	15	134
T508DRAFT_02362	hypothetical protein	216	413	3	0
T508DRAFT_02363	site-specific recombinase XerD	37	50	0	23
T508DRAFT_02364	site-specific recombinase XerD	26	47	5	0
T508DRAFT_02365	site-specific recombinase XerD	37	64	16	47
T508DRAFT_02366*	FOG: transposase and inactivated derivatives	1250*	355	24*	405
T508DRAFT_02367	membrane protein involved in the export of O-antigen and teichoic acid	54	49	14	51
T508DRAFT_02368	hypothetical protein	63	45	0	48
T508DRAFT_02369	hypothetical protein	42	23	0	0
T508DRAFT_02370	glycosyltransferases involved in cell wall biogenesis	47	11	0	0
T508DRAFT_02371	DDE superfamily endonuclease	31	30	8	6
T508DRAFT_02372	small-conductance mechanosensitive channel	15	35	6	7
T508DRAFT_02373	flagellin and related hook-associated proteins	53	18	0	8
T508DRAFT_02374	ATPases involved in chromosome partitioning	172	322	91	192
T508DRAFT_02375	spermidine/putrescine-binding periplasmic protein	53	22	6	10
T508DRAFT_02376	hypothetical protein	0	8	25	0
T508DRAFT_02377	DNA replication protein	555	548	205	725
T508DRAFT_02378	hypothetical protein	396	346	18	369
T508DRAFT_02379	plasmid replication region DNA-binding N-term	887	531	211	826
T508DRAFT_02380	uncharacterised conserved protein	10	40	0	56
T508DRAFT_02381	hypothetical protein	33	67	0	13
T508DRAFT_02382	uncharacterised membrane protein (homolog of Drosophila rhomboid)	78	87	41	70
T508DRAFT_02383	ADP-L-glycero-D-manno-heptose-6-epimerase	91	44	18	10
T508DRAFT_02384	lipopolysaccharide heptosyltransferase II	204	318	80	280
T508DRAFT_02385	aspartate/tyrosine/aromatic aminotransferase	28	24	18	0
T508DRAFT_02386	putative efflux protein, MATE family	60	17	13	5
T508DRAFT_02387	ABC-type multidrug transport system, ATPase and permease components	38	43	0	36
T508DRAFT_02388	uncharacterised protein conserved in bacteria (DUF2333)	87	41	0	10
T508DRAFT_02389	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	21	0	0	0
T508DRAFT_02390	hypothetical protein	37	69	0	28
T508DRAFT_02391	transposase	42	0	0	0
T508DRAFT_02392	hypothetical protein	219	299	164	363
T508DRAFT_02393	DNA replication protein	29	31	12	0
T508DRAFT_02394	hypothetical protein	91	146	0	0
T508DRAFT_02395	protein of unknown function (DUF1703)/predicted AAA-ATPase	15	22	3	4
T508DRAFT_02396	hypothetical protein	67	83	47	27
T508DRAFT_02397	DNA replication protein	91	181	14	106
T508DRAFT_02398	uncharacterised protein involved in chromosome partitioning	44	73	0	15
T508DRAFT_02399	transposase IS66 family	61	37	0	39
T508DRAFT_02400	transposase	75	3	0	7
T508DRAFT_02401	transposase	18	16	6	5
T508DRAFT_02402	nucleoside-diphosphate-sugar epimerases	39	0	0	0
T508DRAFT_02403	glycosyltransferase	38	38	9	8
T508DRAFT_02404*	hypothetical protein	45*	10	14	0*
T508DRAFT_02405	hypothetical protein	14	0	0	0
T508DRAFT_02407	predicted ATPase (AAA+ superfamily)	30	65	10	8
T508DRAFT_02408	hypothetical protein	0	0	0	0
T508DRAFT_02409	transposase IS66 family	794	270	130	134
T508DRAFT_02410*	hypothetical protein	460*	313	18*	130
T508DRAFT_02411	hypothetical protein	83	65	0	65
T508DRAFT_02412	hypothetical protein	34	0	0	0

T508DRAFT_02413	zeta toxin	152	32	0	12
T508DRAFT_02414	DDE superfamily endonuclease	5517	4920	2658	5227
T508DRAFT_02415	hypothetical protein	70	0	19	10
T508DRAFT_02416	acetate kinase	32	28	8	9
T508DRAFT_02418*	flagellin and related hook-associated proteins	138*	60	11*	116
T508DRAFT_02419	transposase and inactivated derivatives	548	284	77	70
T508DRAFT_02420	FOG: TPR repeat, SEL1 subfamily	18	50	3	0
T508DRAFT_02421	hypothetical protein	0	45	0	0
T508DRAFT_02422	2-keto-3-deoxy-6-phosphogluconate aldolase	35	101	15	19
T508DRAFT_02423	SAF domain	0	0	0	0
T508DRAFT_02424	predicted AAA-ATPase	22	9	6	15
T508DRAFT_02425	IS66 Orf2 like protein	44	4	32	80
T508DRAFT_02426	hypothetical protein	8	9	0	0
T508DRAFT_02427	transposase IS66 family	208	159	45	131
T508DRAFT_02428*	flagellin and related hook-associated proteins	288	105*	153	463*
T508DRAFT_02429	transposase	21	5	7	12
T508DRAFT_02431	predicted transcriptional regulator with C-terminal CBS domains	42	0	33	29
T508DRAFT_02432	phage-related protein	39	20	0	27

Trt1: ISO4-H5 enrichment culture with high H₂ on methanol. Trt2: ISO4-H5 enrichment culture +FD1 with high H₂ on methanol. Trt3: ISO4-H5 enrichment culture +FD1 with low H₂ on methanol. Trt4: ISO4-H5 enrichment culture +FD1 with low H₂ on monomethylamine. *: Significantly differentially expressed genes between two conditions by both Kruskal-Wallis test and Benjamini-Hochberg test of $q < 0.05$ and above two fold difference in expression were marked with *, the pair of conditions are highlighted with black background and white letter.

Table A.5.5 Gene expression of *Ruminococcus flavefaciens* FD1

Locus_tag	Predicted gene product	Trt2	Trt3	Trt4
FD1_0001	response regulator	56	784	51
FD1_0002	hypothetical protein	44	610	0
FD1_0003	hypothetical protein	15	367	0
FD1_0004	LysR family transcriptional regulator	31	0	0
FD1_0005	lysozyme M1 (1,4-beta-N-acetylmuramidase)	900	958	23
FD1_0006*	pseudouridine synthase	2949*	890	47*
FD1_0007	prephenate dehydrogenase	994	316	0
FD1_0008	beta-lactamase	57	7	0
FD1_0009	N-acetylmuramoyl-L-alanine amidase	0	0	0
FD1_0010	cell surface protein	0	0	0
FD1_0011	hypothetical protein	0	0	0
FD1_0012	peptidase C11	16	3	8
FD1_0013	sirohydrochlorin cobaltochelata	0	0	0
FD1_0014	hypothetical protein	0	0	0
FD1_0015	iron ABC transporter substrate-binding protein	3	0	0
FD1_0016	proposed F ₄₂₀ -0 ABC transporter, permease protein	4	0	0
FD1_0017	proposed F ₄₂₀ -0 ABC transporter, ATP-binding protein	0	0	0
FD1_0018	carboxylate/amino acid/amine transporter	0	0	0
FD1_0019	hypothetical protein	0	0	0
FD1_0020	hypothetical protein	21	3	0
FD1_0021	phosphate regulon transcriptional regulatory protein PhoB	0	8	0
FD1_0022	phosphate regulon sensor kinase PhoR	5	0	0
FD1_0023	peptide ABC transporter ATP-binding protein	0	0	0
FD1_0024	cell division protein FtsX	0	0	0
FD1_0025	ATP-dependent Clp protease ClpS	0	0	0
FD1_0026	ATP-dependent Clp protease ClpA	14	6	0
FD1_0027	leucyl/phenylalanyl-tRNA--protein transferase	56	0	0
FD1_0028	hypothetical protein	0	0	0
FD1_0029	N-acetyltransferase GCN5	23	0	0
FD1_0030	hypothetical protein	312	35	0
FD1_0031	CopG family transcriptional regulator	0	24	0
FD1_0032	hypothetical protein	10	3	0
FD1_0033	thiamine biosynthesis protein ThiH	0	8	0
FD1_0034	hypothetical protein	86	2	0
FD1_0035	sporulation protein, YlmC/YmxH family	0	0	0
FD1_0036	30S ribosomal protein S2	24	0	0
FD1_0037	elongation factor Ts	23	0	0
FD1_0038	magnesium chelatase	44	0	0
FD1_0039	hypothetical protein	25	0	0
FD1_0040*	transglutaminase-like protein	172*	19	0*
FD1_0041*	hypothetical protein	761*	129	16*
FD1_0042*	50S ribosomal protein L11 methyltransferase	353*	108	0*
FD1_0043	hypothetical protein	164	59	13
FD1_0044	50S ribosomal protein L21	13	8	0
FD1_0045*	hypothetical protein	105*	39	0*
FD1_0046	50S ribosomal protein L27	236	0	0
FD1_0047	GTPase CgtA	71	0	0
FD1_0048**	ribonuclease III	31**	0**	0
FD1_0049	transcriptional regulator	11	27	0
FD1_0050	hypothetical protein	42	28	0
FD1_0051	GNAT family acetyltransferase	161	11	0
FD1_0052**	GNAT family acetyltransferase	35**	0**	0
FD1_0053	hypothetical transmembrane protein	92	0	0
FD1_0054	hypothetical protein	38	20	0
FD1_0055	hypothetical protein	49	15	0
FD1_0056	hypothetical protein RF007C_05955	16	0	0
FD1_0057	NADH-quinone oxidoreductase, E subunit	93	17	0

FD1_0058*	NADH-quinone oxidoreductase, F subunit	124*	31	12*
FD1_0059*	NADH-quinone oxidoreductase, G subunit	113*	14	0*
FD1_0060	rubrerythrin	28	0	0
FD1_0061	glycerol-3-phosphate acyltransferase	60	0	0
FD1_0062	thioredoxin reductase	8	0	0
FD1_0063	peptidase M16	19	0	0
FD1_0064	hypothetical protein	49	0	0
FD1_0065	hypothetical protein	159	0	0
FD1_0066	hypothetical protein	45	19	0
FD1_0067	hypothetical protein	39	0	0
FD1_0068	hypothetical protein	31	0	0
FD1_0069	multi-sensor signal transduction histidine kinase	542	28	0
FD1_0070	transcriptional regulator	35	0	0
FD1_0071	hypothetical protein	51	8	13
FD1_0072*	hypothetical protein	196*	36	0*
FD1_0073	hypothetical protein	90	34	29
FD1_0074	MarR family transcriptional regulator	160	22	0
FD1_0075	hypothetical protein	83	38	0
FD1_0076	transglutaminase domain protein	68	5	0
FD1_0077*	hypothetical protein	2461*	91*	282
FD1_0078	glycoside hydrolase family 9	88	4	0
FD1_0079	AraC family transcriptional regulator	63	0	0
FD1_0080	hypothetical protein	84	5	0
FD1_0081	LytTR family transcriptional regulator	0	0	0
FD1_0082	hypothetical protein	0	0	0
FD1_0083	accessory protein regulator B	0	0	0
FD1_0084	cyclic lactone autoinducer peptide	0	0	0
FD1_0085	MATE efflux family protein	0	0	0
FD1_0086	cystathionine beta-lyase	0	0	0
FD1_0087	hypothetical protein	0	0	0
FD1_0088	hypothetical protein	0	0	0
FD1_0089	hypothetical protein	0	0	0
FD1_0090	type II restriction enzyme methylase subunit	0	0	0
FD1_0091	glycoside hydrolase family 3	0	0	0
FD1_0092	metal ABC transporter substrate-binding protein	0	0	0
FD1_0093	sulfonate ABC transporter ATP-binding protein	0	0	0
FD1_0094	ABC transporter permease	0	0	0
FD1_0095	ABC transporter permease	0	0	0
FD1_0096	methyltransferase	0	0	0
FD1_0097	cystathionine gamma-synthase	0	0	0
FD1_0098	cysteine synthase	0	8	0
FD1_0099	LysR family transcriptional regulator	0	0	0
FD1_0100	pyruvate ferredoxin oxidoreductase subunit gamma	0	0	0
FD1_0101	pyruvate ferredoxin oxidoreductase subunit delta	0	0	0
FD1_0102	pyruvate ferredoxin oxidoreductase alpha subunit	0	0	0
FD1_0103	pyruvate ferredoxin oxidoreductase beta subunit	0	0	0
FD1_0104	coenzyme F ₃₉₀ synthetase	2	0	0
FD1_0105	aminotransferase, class I/II	0	0	0
FD1_0106	stage II sporulation protein E	6	0	0
FD1_0107	1,4-alpha-glucan branching protein	156	175	0
FD1_0108*	glucose-1-phosphate adenyllyltransferase	116*	54	0*
FD1_0109*	glucose-1-phosphate adenyllyltransferase	181*	86	0*
FD1_0110*	glycogen/starch synthase	213*	68	0*
FD1_0111	hypothetical protein	59	23	0
FD1_0112	nicotinamide mononucleotide transporter	23	9	0
FD1_0113	hypothetical protein	39	0	0
FD1_0114	hypothetical protein	0	0	0
FD1_0115	hypothetical protein	15	0	0
FD1_0116	type II restriction endonuclease Eco47II	63	0	0
FD1_0117	DNA (cytosine-5-)-methyltransferase	44	10	0
FD1_0118	hypothetical protein	0	0	0

FD1_0119	hypothetical protein	0	0	0
FD1_0120	plasmid recombination enzyme	6	0	0
FD1_0121	hypothetical protein	0	0	0
FD1_0122	hypothetical protein	0	0	0
FD1_0123	hypothetical protein	0	0	0
FD1_0124	GMP synthase (glutamine-hydrolyzing)	50	0	0
FD1_0125	hypothetical protein	74	0	15
FD1_0126	hypothetical protein	0	0	0
FD1_0127	hypothetical protein	11	0	64
FD1_0128	tRNA (guanine-N ₇ -)-methyltransferase	12	0	35
FD1_0129	sodium:calcium symporter	9	8	0
FD1_0130	hypothetical protein	18	0	0
FD1_0131	helicase-exonuclease AddAB, AddB subunit	11	1	0
FD1_0132	helicase-exonuclease AddAB, AddA subunit	4	2	0
FD1_0133	serine-type D-Ala-D-Ala carboxypeptidase	885	1109	0
FD1_0134	serine-type D-Ala-D-Ala carboxypeptidase	780	1222	0
FD1_0135	hypothetical protein	0	0	0
FD1_0136	hypothetical protein	0	0	0
FD1_0137	hypothetical protein	0	0	0
FD1_0138	hypothetical protein	0	0	0
FD1_0139	glucose-6-phosphate isomerase(pseudogene)	0	0	0
FD1_0140	glucose-6-phosphate isomerase(pseudogene)	160	271	32
FD1_0141*	hypothetical protein	298*	187	0*
FD1_0142*	hypothetical protein	325*	143	0*
FD1_0143	50S ribosomal protein L32	195	0	0
FD1_0144	Fe-S oxidoreductase(pseudogene)	0	0	0
FD1_0145	Fe-S oxidoreductase(pseudogene)	8	0	0
FD1_0146	ribosome-associated GTPase EngA	24	12	0
FD1_0147	glycerol-3-phosphate acyltransferase	12	13	0
FD1_0148	asparagine synthase	21	4	0
FD1_0149	GNAT family acetyltransferase	10	0	0
FD1_0150	nucleoid-structuring protein H-NS(pseudogene)	10	0	0
FD1_0151	nucleoid-structuring protein H-NS(pseudogene)	6	0	0
FD1_0152	ACR YkgG family COG1556	0	0	0
FD1_0153	ribosomal subunit interface protein	22	6	0
FD1_0154	phosphoserine phosphatase	49	0	0
FD1_0155	glycerol-1-phosphate dehydrogenase	39	9	0
FD1_0156	HAD family hydrolase	185	0	0
FD1_0157	<i>N,N'</i> -diacetylchitobiose phosphorylase	24	0	0
FD1_0158	ABC-2 type transporter family protein	5	8	0
FD1_0159	multidrug ABC transporter ATP-binding protein	13	0	0
FD1_0160	Na ⁺ /Pi-cotransporter	24	9	0
FD1_0161	LL-diaminopimelate aminotransferase	62	5	0
FD1_0162	diaminopimelate epimerase	0	0	0
FD1_0163	hypothetical protein	22	9	0
FD1_0164	DNA polymerase III subunit gamma/tau	19	4	0
FD1_0165	DNA-binding protein, YbaB/EbfC family	39	0	0
FD1_0166	recombinase RecR	26	0	0
FD1_0167	hypothetical transmembrane protein	130	0	0
FD1_0168	phage terminase small subunit	46	0	44
FD1_0169	phage terminase, large subunit, PBSX family	30	0	0
FD1_0170	serine/threonine protein phosphatase	34	13	77
FD1_0171	phage capsid family	5	0	0
FD1_0172	hypothetical protein	11	0	0
FD1_0173	hypothetical protein	0	0	0
FD1_0174	hypothetical protein	0	0	0
FD1_0175	hypothetical protein	53	0	0
FD1_0176	hypothetical protein	17	0	0
FD1_0177	FeoA family protein	21	0	0
FD1_0178	transcriptional regulator	8	0	0
FD1_0179	hypothetical protein	0	0	0

FD1_0180	Cro/C1 family transcriptional regulator	10	0	0
FD1_0181	hypothetical protein	50	0	0
FD1_0182	hypothetical protein	22	0	0
FD1_0183	pyruvate-flavodoxin oxidoreductase	133	17	33
FD1_0184	stage V sporulation protein AC	53	69	0
FD1_0185	relaxase	0	7	0
FD1_0186	hypothetical protein	0	0	0
FD1_0187	hypothetical protein	0	0	0
FD1_0188	hypothetical protein	1	0	0
FD1_0189	hypothetical protein	0	0	0
FD1_0190	hypothetical protein	0	0	0
FD1_0191	resolvase	27	6	16
FD1_0192*	glycoside hydrolase family protein	351	505*	58*
FD1_0193	TetR family transcriptional regulator	0	5	0
FD1_0194	aldo/keto reductase	33	6	0
FD1_0195	flavodoxin	16	39	0
FD1_0196	DNA polymerase IV	29	9	0
FD1_0197	DeoR family transcriptional regulator	30	0	0
FD1_0198	transcriptional regulator	8	0	0
FD1_0199	endoribonuclease L-PSP	7	0	0
FD1_0200	competence protein TfoX	0	0	50
FD1_0201	hypothetical transmembrane protein	0	0	0
FD1_0202	type VI secretion system FHA domain protein	4	7	15
FD1_0203	protein serine/threonine phosphatase	0	0	0
FD1_0204	serine/threonine protein kinase	5	0	0
FD1_0205	hypothetical protein	0	0	0
FD1_0206	hypothetical protein	0	0	0
FD1_0207	adhesin-like protein	3	1	0
FD1_0208	hypothetical protein	0	0	0
FD1_0209	hypothetical protein	0	0	0
FD1_0210	type VII secretion protein EssC	3	1	0
FD1_0211	hypothetical protein	0	0	0
FD1_0212	WXG100 family type VII secretion target	0	0	0
FD1_0213	WXG100 family type VII secretion target	0	0	0
FD1_0214	bacterial Ig-like domain protein	4	0	8
FD1_0215	WXG100 family type VII secretion target	0	0	0
FD1_0216	beta-xylosidase	11	4	0
FD1_0217	mannan endo-1,4-beta-mannosidase	11	3	0
FD1_0218	glycoside hydrolase	1	0	0
FD1_0219	aspartate decarboxylase	0	53	0
FD1_0220	pantoate--beta-alanine ligase	31	0	0
FD1_0221	3-methyl-2-oxobutanoate hydroxymethyltransferase	26	18	0
FD1_0222	dockerin (pseudogene)	955	79	0
FD1_0223*	dockerin (pseudogene)	1064*	81	12*
FD1_0224	hypothetical protein	34	1	0
FD1_0225	glycerate dehydrogenase	10	3	0
FD1_0226	glutamate 5-kinase	46	0	0
FD1_0227	cytidine deaminase	38	11	0
FD1_0228	glutamate-5-semialdehyde dehydrogenase	27	0	0
FD1_0229	hypothetical protein	36	7	9
FD1_0230	DNA polymerase I	69	1	0
FD1_0231	hypothetical protein	8	0	0
FD1_0232	ribosomal-protein-alanine acetyltransferase	22	0	0
FD1_0233	tRNA threonylcarbamoyladenosine modification protein TsaD	40	5	0
FD1_0234	hypothetical protein	33	0	0
FD1_0235	hypothetical protein	155	33	0
FD1_0236	hypothetical protein	516	38	0
FD1_0237**	hypothetical protein	42**	0**	0
FD1_0238	hypothetical protein	1963	1237	0
FD1_0239	adhesin-like protein	23	1	0
FD1_0240	phosphopantothenoylcysteine decarboxylase	2	0	0

FD1_0241	chloramphenicol acetyltransferase CAT	15	0	0
FD1_0242	hypothetical protein	15	0	0
FD1_0243**	hypothetical protein	22**	0**	0
FD1_0244*	type III pantothenate kinase	702*	228	0*
FD1_0245	CAAX prenyl protease domain-containing protein	68	0	0
FD1_0246	rubredoxin	0	0	0
FD1_0247	diguanylate cyclase	7	0	0
FD1_0248	sugar ABC transporter substrate-binding protein	0	0	0
FD1_0249	diguanylate cyclase	9	0	0
FD1_0250	glycosyl hydrolase family 25	21	0	0
FD1_0251	mannose-6-phosphate isomerase	37	0	0
FD1_0252	glucokinase	52	0	0
FD1_0253	glycosyl hydrolase family 16	18	8	0
FD1_0254	AraC family transcriptional regulator	33	46	0
FD1_0255	50S ribosomal protein L10	95	0	0
FD1_0256	50S ribosomal protein L7/L12	60	20	0
FD1_0257	cysteine-rich secreted protein	113	46	0
FD1_0258	bifunctional tetrahydrofolate synthase FolC	34	6	0
FD1_0259	ECF transporter S component, folate family	113	0	0
FD1_0260	hypothetical protein	1	0	0
FD1_0261	phage shock operon rhodanese PspE	7	8	0
FD1_0262	Sell repeat protein	6	7	0
FD1_0263	hypothetical protein	4	0	0
FD1_0264	small multi-drug export	35	33	0
FD1_0265	NUDIX hydrolase	65	0	0
FD1_0266	amidase	0	0	0
FD1_0267	ribose-phosphate pyrophosphokinase	12	0	0
FD1_0268	nicotinate phosphoribosyltransferase	7	0	0
FD1_0269	phosphoglycerate mutase	15	0	0
FD1_0270	hypothetical protein	14	0	0
FD1_0271	NAD ⁺ synthetase	40	0	0
FD1_0272	hypothetical protein	6	100	0
FD1_0273**	RNA polymerase sigma-70 factor	0**	48**	0
FD1_0274	hypothetical protein	13	0	0
FD1_0275	ABC transporter ATP-binding protein	9	4	0
FD1_0276	precorrin-8X methylmutase	0	12	0
FD1_0277	cobyric acid synthase	6	0	0
FD1_0278	threonine-phosphate decarboxylase	10	16	0
FD1_0279	cobalamin biosynthesis protein CobD	0	0	0
FD1_0280	alpha-ribazole phosphatase	0	0	0
FD1_0281	hypothetical protein	20	22	0
FD1_0282	cobalamin-5-phosphate synthase	1	0	8
FD1_0283	cobinamide kinase/cobinamide phosphate guanylttransferase	40	0	30
FD1_0284	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	0	0	0
FD1_0285	cobyric acid a,c-diamide synthase	0	3	0
FD1_0286	precorrin-6x reductase	7	0	0
FD1_0287	precorrin-6x reductase	31	0	0
FD1_0288	precorrin-3B C17-methyltransferase	17	0	0
FD1_0289	cobalamin (vitamin B12) biosynthesis CbiG protein	24	0	0
FD1_0290	cobalt-precorrin-4 C(11)-methyltransferase	7	0	43
FD1_0291	cobalt-precorrin-6A synthase (pseudogene)	11	0	0
FD1_0292**	cobalt-precorrin-6A synthase (pseudogene)	22**	0**	0
FD1_0293	precorrin-2 C20-methyltransferase	26	0	0
FD1_0294	dimethyladenosine transferase	23	0	0
FD1_0295	hypothetical protein	0	0	0
FD1_0296	FAD-dependent dehydrogenase	4	4	0
FD1_0297	flavoprotein, HI0933 family	14	3	0
FD1_0298	small-conductance mechanosensitive channel	24	11	0
FD1_0299	CAAX prenyl protease domain-containing protein	0	0	0
FD1_0300	ABC-2 membrane transporter protein	5	0	0
FD1_0301	ABC-2 membrane transporter protein	8	27	0

FD1_0302	ABC-2 membrane transporter protein	18	0	0
FD1_0303	ABC-type multidrug transport system, ATPase component	0	0	0
FD1_0304	GntR family transcriptional regulator	0	0	0
FD1_0305	hypothetical protein	24	0	0
FD1_0306	hypothetical protein	42	0	0
FD1_0307	hypothetical protein	24	0	0
FD1_0308	sulfate permease	32	13	0
FD1_0309	RNA polymerase sigma factor	56	8	0
FD1_0310	hypothetical protein	33	15	0
FD1_0311	NUDIX hydrolase	35	0	0
FD1_0312	glycosyl hydrolase family 9	13	1	0
FD1_0313	fructose-bisphosphate aldolase	71	29	0
FD1_0314	alpha/beta hydrolase	2	0	0
FD1_0315	ABC transporter substrate-binding protein	191	11	0
FD1_0316	ABC transporter	126	39	0
FD1_0317	ABC transporter	60	0	0
FD1_0318	hypothetical protein	55	0	0
FD1_0319	peptide deformylase	324	12	0
FD1_0320	DtxR family transcriptional regulator	63	9	0
FD1_0321	hypothetical protein	48	3	0
FD1_0322*	UDP- <i>N</i> -acetylmuramoyl-L-alanine--D-glutamate ligase	51*	18	0*
FD1_0323	hypothetical protein	42	0	0
FD1_0324	peptidyl-prolyl cis-trans isomerase	14	0	0
FD1_0325	glutamyl-tRNA synthetase	5	0	0
FD1_0326	methionine--tRNA ligase	6	0	0
FD1_0327	cell surface protein	0	0	0
FD1_0328	glycoside hydrolase family 43	194	38	4
FD1_0329	hypothetical protein	0	0	0
FD1_0330	hypothetical protein	0	0	0
FD1_0331	hypothetical protein	0	0	0
FD1_0332	resolvase	0	0	0
FD1_0333*	RNA polymerase subunit sigma-24	481*	175	0*
FD1_0334	alpha/beta hydrolase	10	0	0
FD1_0335	hypothetical protein	0	0	0
FD1_0336	phosphoglycerate kinase	251	13	0
FD1_0337	hypothetical protein	48	0	0
FD1_0338*	triosephosphate isomerase	88*	15	0*
FD1_0339	hypothetical protein	91	0	0
FD1_0340	hypothetical protein	6	25	0
FD1_0341*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	64*	31	0*
FD1_0342	GCN5 family acetyltransferase	0	25	0
FD1_0343	polysaccharide deacetylase	11	38	0
FD1_0344	ApbE family lipoprotein	14	0	0
FD1_0345	hypothetical protein	13	15	0
FD1_0346	heptaprenyl diphosphate synthase	13	0	0
FD1_0347	hypothetical protein	0	0	0
FD1_0348	formate--tetrahydrofolate ligase	53	4	0
FD1_0349	hydrolase, P-loop family	66	3	0
FD1_0350	peptidase M22	21	15	0
FD1_0351	ribose 5-phosphate isomerase B	146	23	0
FD1_0352	acetyltransferase (GNAT) family protein	158	0	0
FD1_0353	uracil phosphoribosyltransferase	117	0	0
FD1_0354	pyridoxamine 5'-phosphate oxidase	15	0	0
FD1_0355	GNAT family acetyltransferase	6	0	0
FD1_0356	serine protease	18	0	0
FD1_0357	hypothetical protein	27	11	0
FD1_0358	chorismate synthase	9	0	0
FD1_0359	3-phosphoshikimate 1-carboxyvinyltransferase	24	0	0
FD1_0360	3-dehydroquinate synthase	0	7	0
FD1_0361	diguanylate cyclase	74	22	0
FD1_0362	calcium-transporting P-type ATPase	19	1	0

FD1_0363	<i>O</i> -acetylhomoserine aminocarboxypropyltransferase	4	0	0
FD1_0364	PhoB family transcriptional regulator	91	11	0
FD1_0365	histidine kinase	77	53	0
FD1_0366*	hypothetical protein	312*	111	17*
FD1_0367	5'-methylthioadenosine nucleosidase	61	47	0
FD1_0368	hypothetical protein	11	0	0
FD1_0369	hypothetical protein	49	0	0
FD1_0370	hypothetical protein	39	0	0
FD1_0371	copper-(or silver)-translocating P-type ATPase (pseudogene)	24	18	0
FD1_0372	copper-(or silver)-translocating P-type ATPase (pseudogene)	16	5	0
FD1_0373	hypothetical protein	138	0	0
FD1_0374	cellulase	29	0	0
FD1_0375	hypothetical protein	144	19	18
FD1_0376	hypothetical protein	107	0	0
FD1_0377	molybdenum cofactor biosynthesis protein	30	0	0
FD1_0378	hemolysin	2	0	0
FD1_0379	polar amino acid ABC transporter permease (pseudogene)	0	0	0
FD1_0380	polar amino acid ABC transporter permease (pseudogene)	0	0	0
FD1_0381	amino acid ABC transporter ATP-binding protein	0	0	0
FD1_0382	small GTP-binding protein domain	11	0	0
FD1_0383	hypothetical protein	74	0	0
FD1_0384	serine/threonine protein phosphatase	21	20	0
FD1_0385	FHA domain containing protein	23	4	0
FD1_0386	diguanylate cyclase	1	0	0
FD1_0387	ATPase of the PP-loop superfamily implicated in cell cycle control	5	0	0
FD1_0388	hypothetical protein	0	0	0
FD1_0389	excinuclease ABC subunit C	9	7	0
FD1_0390	peptidase U32	0	0	0
FD1_0391	hypothetical protein	13	1	0
FD1_0392	glycine--tRNA ligase	47	3	0
FD1_0393	hypothetical protein	1	0	0
FD1_0394	adenylosuccinate synthetase	82	52	21
FD1_0395	hypothetical protein	53	2	0
FD1_0396	hypothetical protein	63	54	0
FD1_0397	prepilin-type cleavage/methylation protein	38	37	10
FD1_0398	RNA polymerase subunit sigma-24	41	0	0
FD1_0399	hypothetical protein	8	0	0
FD1_0400	RNA polymerase sigma-70 factor	2	0	0
FD1_0401	hypothetical protein	6	18	0
FD1_0402	hypothetical transmembrane protein	15	0	0
FD1_0403	hypothetical protein	28	15	9
FD1_0404	hypothetical protein	0	0	0
FD1_0405	cobalamin biosynthesis protein CobQ	19	12	0
FD1_0406	2-oxoglutarate ferredoxin oxidoreductase, delta subunit	43	0	0
FD1_0407	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductase alpha subunit	41	0	0
FD1_0408**	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductase beta subunit	82**	7**	31
FD1_0409**	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductase gamma subunit	162**	15**	0
FD1_0410	hypothetical protein	0	0	0
FD1_0411	hypothetical protein	7	0	0
FD1_0412	gliding-associated ABC transporter substrate-binding component GldG	17	0	0
FD1_0413	gliding motility-associated ABC transporter permease protein GldF	12	0	0
FD1_0414	gliding motility-associated ABC transporter ATP- binding subunit GldA	10	10	0
FD1_0415	riboflavin biosynthesis protein RibF	15	0	0
FD1_0416	tRNA pseudouridine synthase B	6	0	0
FD1_0417	DHHA1 domain protein	15	10	35
FD1_0418	ribosome-binding factor A	0	15	26
FD1_0419	hypothetical protein	0	0	0
FD1_0420	translation initiation factor IF-2	8	0	6
FD1_0421	50S ribosomal protein L7ae	1	0	0

FD1_0422	hypothetical protein	33	0	0
FD1_0423	transcription termination factor NusA	12	0	0
FD1_0424	ribosome maturation factor RimP	20	0	0
FD1_0425	hypothetical protein	5	0	0
FD1_0426	hypothetical protein	74	7	0
FD1_0427	aspartate kinase	6	4	0
FD1_0428	hypothetical protein	0	0	0
FD1_0429* **	hypothetical protein	447**	2083*,**	0*
FD1_0430	hypothetical protein	117	248	77
FD1_0431**	carbohydrate binding module (family 6)/glycoside hydrolase 97	240**	21**	0
FD1_0432	hypothetical protein	61	0	0
FD1_0433	DNA alkylation repair protein	22	0	0
FD1_0434	hypothetical transmembrane protein(pseudogene)	24	0	0
FD1_0435	hypothetical transmembrane protein(pseudogene)	20	0	0
FD1_0436**	multidrug transporter	328**	5**	17
FD1_0437	AraC family transcriptional regulator	29	0	0
FD1_0438	magnesium transporter CorA	0	0	0
FD1_0439	threonyl-tRNA synthetase	65	0	0
FD1_0440	hypothetical protein	36	0	0
FD1_0441	hypothetical protein	74	0	0
FD1_0442	hypothetical protein	9	0	0
FD1_0443	hypothetical protein	35	0	0
FD1_0444	germination protease	0	3	0
FD1_0445	30S ribosomal protein S20	0	58	0
FD1_0446	hypothetical protein	0	5	0
FD1_0447	hypothetical protein	0	0	0
FD1_0448	ABC-F type ribosomal protection protein	0	0	0
FD1_0449	hypothetical protein	19	0	28
FD1_0450	hypothetical protein	0	0	0
FD1_0451*	hypothetical protein	300*	92	0*
FD1_0452	amidohydrolase	24	0	0
FD1_0453*	glycoside hydrolase family 9	8	26*	0*
FD1_0454* ***	hypothetical protein	536*,**	120**	0*
FD1_0455* ***	Fe-S oxidoreductase	241*,**	51**	0*
FD1_0456	peptidoglycan-binding lysin domain-containing protein (pseudogene)	14	0	0
FD1_0457	peptidoglycan-binding lysin domain-containing protein (pseudogene)	4	0	0
FD1_0458	glycoside hydrolase family 10	37	10	0
FD1_0459	hypothetical protein	0	0	0
FD1_0460	spore coat protein CotH	9	0	0
FD1_0461	spore coat protein CotH	7	4	0
FD1_0462	Type I secretion membrane fusion protein, HlyD	8	7	0
FD1_0463	peptide ABC transporter ATP-binding protein	0	0	0
FD1_0464	hypothetical protein	17	0	0
FD1_0465**	diguanylate cyclase	98*	5*	0
FD1_0466	hypothetical protein	41	0	0
FD1_0467* ***	transposase, partial	642*,**	91**	0*
FD1_0468	GCN5 family acetyltransferase	33	0	0
FD1_0469	hypothetical protein	8	0	0
FD1_0470	methyltransferase type 11	15	0	0
FD1_0471	adenylate kinase	11	33	0
FD1_0472**	hypothetical protein	38**	4**	0
FD1_0473	DNA-binding protein	26	22	0
FD1_0474	hypothetical protein	14	0	0
FD1_0475	restriction endonuclease subunit R (pseudogene)	4	0	0
FD1_0476	restriction endonuclease subunit R (pseudogene)	0	0	0
FD1_0477	restriction endonuclease subunit R (pseudogene)	0	0	0
FD1_0478	hypothetical protein	20	0	0
FD1_0479	phage integrase	26	0	0
FD1_0480*	hypothetical protein	1305	2210*	0*
FD1_0481*	hypothetical protein	1346	2295*	21*

FD1_0482	hypothetical protein	0	7	0
FD1_0483	modification methylase Sall	7	16	0
FD1_0484	type II restriction endonuclease Sall	5	0	0
FD1_0485	hypothetical protein	0	0	0
FD1_0486	Xre family DNA-binding protein	0	11	0
FD1_0487	hypothetical protein	8	8	0
FD1_0488	hypothetical protein	0	0	0
FD1_0489	hypothetical protein	0	0	0
FD1_0490	recombinase	0	7	0
FD1_0491	MerR family transcriptional regulator	17	0	0
FD1_0492	recombinase	106	67	0
FD1_0493	glyoxalase	0	0	0
FD1_0494	hypothetical protein	0	0	0
FD1_0495	glycosyl hydrolase family 3	84	0	10
FD1_0496	cellulase (glycosyl hydrolase family 5)	30	0	0
FD1_0497	bacterial extracellular solute-binding protein	17	0	0
FD1_0498*	von Willebrand factor type A	189*	125	0*
FD1_0499*	hypothetical protein	280*	122	0*
FD1_0500	cell division protein FtsH	6	0	0
FD1_0501	proline:sodium symporter	6	0	0
FD1_0502	glycosyl transferase	16	4	0
FD1_0503	CDP-glucose 4,6-dehydratase	21	4	0
FD1_0504	resolvase (partial, end of contig)	36	52	0
FD1_0505	hypothetical protein	24	0	0
FD1_0506	peptidase C14 caspase catalytic subunit p20	0	21	0
FD1_0507	hypothetical protein	0	0	0
FD1_0508	hypothetical protein	0	0	0
FD1_0509	hypothetical protein	0	0	0
FD1_0510	hypothetical protein	0	0	0
FD1_0511	signal peptidase	0	0	0
FD1_0512	sortase	13	26	0
FD1_0513	hypothetical protein	6	0	0
FD1_0514*	sortase	187*	81	0*
FD1_0515*	hypothetical protein	449*	375	15*
FD1_0516	glycerol-3-phosphate dehydrogenase	46	0	0
FD1_0517	6-phosphofructokinase	42	18	0
FD1_0518	UDP-galactose-4-epimerase	9	0	0
FD1_0519**	hypothetical protein	112**	11**	0
FD1_0520***	<i>N</i> -acetylglucosamine-1-phosphate uridyltransferase	33**	93*,**	0*
FD1_0521	hypothetical protein	68	0	0
FD1_0522	hypothetical protein	99	0	0
FD1_0523	heme ABC transporter ATP-binding protein	123	45	22
FD1_0524**	hypothetical protein	71**	10**	0
FD1_0525**	ATP-dependent chaperone protein ClpB	45**	8**	0
FD1_0526	colicin V production protein	33	7	29
FD1_0527	hypothetical protein	61	0	0
FD1_0528	tRNA pseudouridine synthase A	10	0	0
FD1_0529	bacterial membrane protein YfhO	19	0	0
FD1_0530	cobalt ECF transporter T component CbiQ	12	18	0
FD1_0531	cobalt ABC transporter ATP-binding protein	26	14	0
FD1_0532	cobalt transport protein ATP-binding subunit	25	30	21
FD1_0533	xylan 1,4-beta-xylosidase	46	0	0
FD1_0534	hypothetical protein	3	0	0
FD1_0535	acetyltransferase GNAT family	24	0	0
FD1_0536	SAM-dependent methyltransferase	72	14	0
FD1_0537**	phosphoglucosamine mutase	41**	4**	0
FD1_0538	hypothetical protein	55	0	0
FD1_0539	Holliday junction DNA helicase RuvB	23	20	0
FD1_0540	hypothetical protein	45	0	0
FD1_0541	SseB family protein	19	22	0
FD1_0542	Holliday junction DNA helicase RuvA	25	0	0

FD1_0543	crossover junction endodeoxyribonuclease RuvC	70	0	0
FD1_0544	prephenate dehydratase	8	0	0
FD1_0545	homocysteine methyltransferase	4	16	0
FD1_0546	hexosyltransferase	36	3	0
FD1_0547	hexosyltransferase	7	0	0
FD1_0548	phosphopantetheine-protein transferase	0	0	0
FD1_0549	preprotein translocase subunit SecE	14	0	0
FD1_0550	ribonuclease R	9	12	0
FD1_0551	hypothetical protein	5	0	0
FD1_0552	glycosyltransferase	23	0	0
FD1_0553	Crp/Fnr family transcriptional regulator	9	15	0
FD1_0554	hypothetical transmembrane protein	0	0	0
FD1_0555*	heat shock protein Hsp20	119	209*	0*
FD1_0556	2,5-diketo-D-gluconic acid reductase	74	17	0
FD1_0557	aldehyde oxidase (pseudogene)	0	0	0
FD1_0558	aldehyde oxidase (pseudogene)	0	0	0
FD1_0559	flavodoxin, partial	0	0	0
FD1_0560	flavodoxin	13	15	0
FD1_0561	hypothetical protein	0	28	0
FD1_0562*	hypothetical protein	400*	64	0*
FD1_0563*	esterase/lipase-like protein (pseudogene)	183*	33	0*
FD1_0564	esterase/lipase-like protein (pseudogene)	222	2	0
FD1_0565	hypothetical protein	159	40	0
FD1_0566	flavodoxin	122	94	0
FD1_0567*	transcriptional regulator, LysR family	225*	15	0*
FD1_0568***	transposase, partial	936*,**	143**	0*
FD1_0569	hypothetical protein	193	20	0
FD1_0570	transcription-repair coupling factor	17	0	0
FD1_0571	peptidyl-tRNA hydrolase	0	0	0
FD1_0572**	D-alanyl-D-alanine carboxypeptidase	152**	3**	0
FD1_0573	azaleucine resistance protein AzlC	41	0	0
FD1_0574	branched-chain amino acid ABC transporter	101	25	0
FD1_0575	hypothetical protein	341	0	0
FD1_0576**	GCN5 family acetyltransferase	228**	15**	0
FD1_0577***	tRNA-splicing ligase RtcB	292*,**	18**	0*
FD1_0578	conjugal transfer protein TraX	3	0	0
FD1_0579	cyclase	0	0	0
FD1_0580**	hypothetical protein	238**	25**	0
FD1_0581	hypothetical protein	0	0	0
FD1_0582	iron transporter FeoB	4	5	0
FD1_0583	GNAT family acetyltransferase	38	0	0
FD1_0584*	hypothetical protein	83*	48	0*
FD1_0585	hypothetical protein	47	0	0
FD1_0586**	flavodoxin	284**	22**	0
FD1_0587**	diguanylate cyclase	80**	0**	0
FD1_0588**	exodeoxyribonuclease III	135**	5**	0
FD1_0589**	hypothetical protein	180**	30**	0
FD1_0590*	hypothetical protein	199*	119	0*
FD1_0591*	hypothetical transmembrane protein	144*	81	0*
FD1_0592*	hypothetical transmembrane protein	455*	279	0*
FD1_0593*	XRE family transcriptional regulator	223*	129	0*
FD1_0594	hypothetical protein	146	135	0
FD1_0595	ECF subfamily RNA polymerase sigma-24 factor	0	0	0
FD1_0596	hypothetical protein	12	0	0
FD1_0597	cysteine proteinase	31	0	0
FD1_0598***	hypothetical protein	2785*,**	319**	11*
FD1_0599***	sugar ABC transporter permease	270*,**	46**	0*
FD1_0600***	sugar ABC transporter permease	171*,**	25**	0*
FD1_0601	stage III sporulation protein AA	32	0	0
FD1_0602	stage III sporulation protein AB	25	0	0
FD1_0603	stage III sporulation protein AC	25	0	0

FD1_0604	stage III sporulation protein AD	5	0	0
FD1_0605	stage III sporulation protein AE	9	0	0
FD1_0606	stage III sporulation protein AF	48	0	0
FD1_0607	stage III sporulation protein AG	41	0	0
FD1_0608	stage III sporulation protein AH	96	0	0
FD1_0609	alkaline shock protein 23	75	0	0
FD1_0610	transcription termination factor NusB	51	0	0
FD1_0611	peptidase M22	100	0	0
FD1_0612**	exodeoxyribonuclease VII large subunit	112**	10**	0
FD1_0613	exodeoxyribonuclease VII small subunit	61	0	0
FD1_0614	polyprenyl synthetase	92	11	0
FD1_0615***	1-deoxy-D-xylulose-5-phosphate synthase	139*,**	9**	0*
FD1_0616**	TlyA family rRNA methyltransferase/putative hemolysin	100**	8**	0
FD1_0617**	NAD ⁺ kinase	102**	7**	0
FD1_0618	ArgR family transcriptional regulator	98	0	0
FD1_0619***	DNA repair protein RecN	107*,**	13**	0*
FD1_0620	phosphoglycerate mutase	76	15	0
FD1_0621***	beta-galactosidase	239*,**	24**	0*
FD1_0622*	D-tyrosyl-tRNA ^{Tyr} deacylase	182*	76	0*
FD1_0623**	penicillin-binding protein 2	2500**	221**	0
FD1_0624	DNA-binding helix-turn-helix protein	0	0	0
FD1_0625	hypothetical protein	53	17	0
FD1_0626*	serine/threonine protein kinase	35*	17	0*
FD1_0627*	hypothetical protein	59*	27	0*
FD1_0628**	DNA mismatch repair protein MutS	44**	3**	0
FD1_0629	PadR family transcriptional regulator	2	0	0
FD1_0630	hypothetical transmembrane protein	8	24	0
FD1_0631	hypothetical protein	3	10	0
FD1_0632	phage shock protein C PspC	14	211	0
FD1_0633	phage shock protein C PspC	0	18	0
FD1_0634	hypothetical protein	21	21	0
FD1_0635**	1-phosphofructokinase	131**	7**	0
FD1_0636*	PTS fructose transporter subunit IIC	41*	11	0*
FD1_0637	PTS beta-glucoside transporter subunit IIABC	23	0	0
FD1_0638	phosphoenolpyruvate-protein phosphotransferase	0	0	0
FD1_0639*	adhesin-like protein	22	44*	0*
FD1_0640	pectate lyase/Amb allergen	82	20	0
FD1_0641**	sugar ABC transporter substrate-binding protein	181**	2**	0
FD1_0642	cellulosome protein CotH	44	0	7
FD1_0643	hypothetical transmembrane protein	18	0	0
FD1_0644	hypothetical transmembrane protein	0	0	0
FD1_0645	protein-export membrane protein SecD (partial, end of contig)	0	0	0
FD1_0646	hypothetical protein	25	0	0
FD1_0647	phosphomethylpyrimidine kinase	62	0	0
FD1_0648	glycosyl hydrolase family 88	19	15	0
FD1_0649	sugar ABC transporter permease	23	0	0
FD1_0650**	sugar ABC transporter permease	66**	7**	9
FD1_0651***	carbohydrate ABC transporter substrate-binding protein	163*,**	35**	9*
FD1_0652	Xaa-His dipeptidase	20	11	0
FD1_0653	sugar ABC transporter ATP-binding protein	597	667	183
FD1_0654	16S pseudouridylate synthase	5	0	0
FD1_0655**	hypothetical protein	115**	1**	0
FD1_0656	NrdR family transcriptional regulator	39	6	0
FD1_0657	sugar phosphate isomerase/epimerase	9	2	0
FD1_0658	ABC transporter ATP-binding protein	35	20	0
FD1_0659	small acid-soluble spore proteins alpha/beta type	87	0	0
FD1_0660	transcriptional regulator, y4mF family	50	18	26
FD1_0661	hypothetical protein	83	54	0
FD1_0662	eDD domain protein DegV family	43	11	0
FD1_0663	tRNA (cytidine ³⁴ -2'-O)-methyltransferase	95	0	0
FD1_0664***	hypothetical protein	483*,**	67**	0*

FD1_0665	Holliday junction resolvase YqgF	9	13	0
FD1_0666	hypothetical protein	55	0	0
FD1_0667	papain family cysteine protease	2	0	0
FD1_0668	dihydroorotate dehydrogenase, catalytic subunit	113	42	0
FD1_0669	dihydroorotate dehydrogenase B NAD ⁺ electron transfer subunit	16	29	0
FD1_0670	hypothetical transmembrane protein	40	0	0
FD1_0671	glycoside hydrolase	0	2	0
FD1_0672	hypothetical protein	16	0	0
FD1_0673	1,4-beta-xylanase (pseudogene)	73	0	0
FD1_0674	1,4-beta-xylanase (pseudogene)	72	17	0
FD1_0675	pectate lyase	723	265	10
FD1_0676	hypothetical protein	32	0	0
FD1_0677	potassium transporter TrkA	46	0	0
FD1_0678	Trk system potassium transporter TrkH	42	19	0
FD1_0679*	adhesin-like protein	117*	41	0*
FD1_0680	30S ribosomal protein S12	93	22	0
FD1_0681	30S ribosomal protein S7	24	0	0
FD1_0682	elongation factor G	52	15	6
FD1_0683***	elongation factor Tu	2692*,**	227**	17*
FD1_0684***	serine/threonine phosphatase	31**	223*,**	0*
FD1_0685	glycosyl transferase family 2	7	0	0
FD1_0686	hypothetical protein	19	0	0
FD1_0687	permease of the drug/metabolite transporter (DMT) superfamily	13	0	0
FD1_0688	BioY protein	0	0	0
FD1_0689	E1-E2 ATPase	15	29	0
FD1_0690	copper chaperone	0	299	0
FD1_0691**	hypothetical protein	194**	2497**	0
FD1_0692**	DNA-directed RNA polymerase subunit sigma	153**	2049**	0
FD1_0693***	acetate kinase	283*,**	42**	0*
FD1_0694	nucleotidyltransferase	25	0	0
FD1_0695	peptidase C39 like family protein	3	0	0
FD1_0696	haloacid dehalogenase	6	0	0
FD1_0697	tRNA (5-methylaminomethyl-2-thiouridylate)- methyltransferase	5	4	0
FD1_0698	hypothetical protein	0	0	0
FD1_0699	isochorismatase family hydrolase	7	0	0
FD1_0700	hypothetical protein	0	0	0
FD1_0701	methyltransferase	0	0	0
FD1_0702	ribosomal RNA small subunit methyltransferase I	0	0	0
FD1_0703	metal-dependent phosphoesterase (PHP family)	12	0	0
FD1_0704	hypothetical protein	0	0	0
FD1_0705	hypothetical protein	0	0	0
FD1_0706	AMP-dependent synthetase	11	3	0
FD1_0707	adhesin-like protein	9	23	0
FD1_0708	sodium:solute symporter (pseudogene)	0	0	0
FD1_0709	sodium:solute symporter (pseudogene)	9	2	0
FD1_0710	NADPH-dependent FMN reductase	0	0	0
FD1_0711	hypothetical protein	0	0	0
FD1_0712	relaxase/mobilization nuclease family protein	0	0	0
FD1_0713	hypothetical protein	0	0	0
FD1_0714	resolvase	0	0	0
FD1_0715	histidine kinase	0	0	0
FD1_0716	hypothetical transmembrane protein	0	0	0
FD1_0717	hypothetical protein	0	0	0
FD1_0718	hypothetical protein	0	0	0
FD1_0719	hypothetical protein	0	0	0
FD1_0720	relaxase/mobilization nuclease family protein (pseudogene)	0	0	0
FD1_0721**	relaxase/mobilization nuclease family protein (pseudogene)	422**	76**	84
FD1_0722***	hypothetical protein	711*,**	155**	31*
FD1_0723	growth inhibitor PemK	322	0	94
FD1_0724	hypothetical protein	236	117	0
FD1_0725	hypothetical protein	54	32	0

FD1_0726	DNA mismatch repair protein MutT (pseudogene)	27	2	0
FD1_0727	DNA mismatch repair protein MutT (pseudogene)	0	43	0
FD1_0728	hypothetical protein	0	5	0
FD1_0729	XRE family transcriptional regulator	14	0	0
FD1_0730	histidine kinase	9	0	0
FD1_0731	multidrug ABC transporter ATP-binding protein	6	0	0
FD1_0732	ABC transporter permease	23	5	0
FD1_0733***	hypothetical protein	249*,**	55**	0*
FD1_0734	acyl-CoA thioester hydrolase	56	0	0
FD1_0735	cardiolipin synthase	0	3	0
FD1_0736	cyclic diguanylate phosphodiesterase (EAL) domain protein	35	19	0
FD1_0737	GTP-binding protein YchF	45	0	0
FD1_0738	acetyltransferase (GNAT) family	0	9	0
FD1_0739	glutamine synthetase	13	0	0
FD1_0740**	response regulator receiver/ANTAR domain- containing protein	106**	16**	0
FD1_0741**	hypothetical transmembrane protein	383**	24**	0
FD1_0742***	RNA polymerase sigma factor, sigma-70 family protein	265*,**	12**	0*
FD1_0743***	glycoside hydrolase family 43	134*,**	38**	14*
FD1_0744***	citrate transporter	331*,**	19**	0*
FD1_0745**	hypothetical transmembrane protein	143**	10**	0
FD1_0746***	beta-galactosidase	50*,**	11**	0*
FD1_0747	hypothetical protein	16	0	0
FD1_0748**	alpha-N-arabinofuranosidase	67**	4**	6
FD1_0749	multidrug transporter MatE	0	3	35
FD1_0750	GTPase	11	0	0
FD1_0751	cobalamin biosynthesis protein CobW	28	0	0
FD1_0752	acylphosphatase	0	32	0
FD1_0753**	xylanase	186**	16**	13
FD1_0754**	glycerate kinase	243**	11**	0
FD1_0755	dihydrofolate reductase	141	0	0
FD1_0756	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	58	35	0
FD1_0757	dihydropteroate synthase	9	0	0
FD1_0758	metal-dependent phosphohydrolase	28	0	0
FD1_0759	RNA polymerase subunit sigma-24	0	15	0
FD1_0760	hypothetical transmembrane protein	15	3	20
FD1_0761**	oxidoreductase	42**	6**	0
FD1_0762	RNA methyltransferase	0	7	0
FD1_0763	diguanylate cyclase	56	18	0
FD1_0764	hypothetical transmembrane protein	15	9	0
FD1_0765	hypothetical protein	0	6	0
FD1_0766**	hypothetical protein	249**	44**	0
FD1_0767	hypothetical protein	22	12	0
FD1_0768	RNA polymerase subunit sigma-24	10	12	0
FD1_0769	adhesin-like protein	28	49	0
FD1_0770	hypothetical transmembrane protein	16	0	0
FD1_0771	hypothetical protein	105	0	0
FD1_0772	auxin efflux carrier (AEC) family protein (pseudogene)	9	0	0
FD1_0773	auxin efflux carrier (AEC) family protein (pseudogene)	72	0	0
FD1_0774	ribonuclease H	68	10	63
FD1_0775	cysteine desulfurase	0	0	0
FD1_0776	hypothetical protein	14	0	0
FD1_0777	FeS cluster assembly scaffold protein NifU	25	0	0
FD1_0778	hypothetical transmembrane protein	0	0	0
FD1_0779	phosphoglucosamine mutase	3	0	0
FD1_0780	hypothetical protein	0	0	0
FD1_0781	RNA polymerase subunit sigma-24	0	0	0
FD1_0782	hypothetical transmembrane protein	0	5	0
FD1_0783	hypothetical transmembrane protein	0	8	0
FD1_0784	RNA polymerase subunit sigma-24	0	0	0
FD1_0785	hypothetical transmembrane protein	0	0	0
FD1_0786	penicillin-binding protein 2	11	0	0

FD1_0787	cell division protein FtsW	14	5	0
FD1_0788	type VI secretion system FHA domain protein	8	0	0
FD1_0789**	cell division protein FtsH	56**	5**	0
FD1_0790	tRNA ^{Leu} -lysine synthetase	8	0	0
FD1_0791	primary replicative DNA helicase	7	4	0
FD1_0792	50S ribosomal protein L9	22	13	0
FD1_0793	dHHA1 domain protein	19	0	0
FD1_0794	ribonuclease J	35	0	0
FD1_0795	sodium/alanine symporter family protein	0	0	0
FD1_0796	hypothetical transmembrane protein	13	0	0
FD1_0797	hypothetical transmembrane protein	17	0	12
FD1_0798	AraC family transcriptional regulator	13	20	0
FD1_0799	8-oxoguanine DNA glycosylase	12	5	0
FD1_0800	hypothetical secreted protein	8	0	0
FD1_0801	beta-galactosidase/beta-glucuronidase	39	0	0
FD1_0802	lipid A export permease/ATP-binding protein MsbA	20	0	0
FD1_0803	relA/SpoT domain protein	12	17	0
FD1_0804	hypothetical protein	22	0	0
FD1_0805**	aldo/keto reductase (pseudogene)	52**	7**	0
FD1_0806	aldo/keto reductase (pseudogene)	70	0	0
FD1_0807	flavodoxin	32	10	29
FD1_0808	short-chain dehydrogenase, partial	45	21	0
FD1_0809	CarD family transcriptional regulator	217	72	0
FD1_0810	phage protein Gp37/Gp68	67	21	39
FD1_0811	MmcQ protein	47	0	0
FD1_0812	hypothetical protein	99	0	0
FD1_0813	1-deoxy-D-xylulose-5-phosphate synthase	0	0	0
FD1_0814	flavodoxin	25	0	0
FD1_0815	hypothetical protein	0	0	0
FD1_0816	transcription regulator	18	0	0
FD1_0817	maltose O-acetyltransferase	24	0	0
FD1_0818	flavodoxin	8	15	0
FD1_0819	aldo/keto reductase	22	0	0
FD1_0820	hypothetical protein	12	0	0
FD1_0821	short-chain dehydrogenase	34	0	0
FD1_0822	2,5-diketo-D-gluconic acid reductase (pseudogene)	0	0	0
FD1_0823	2,5-diketo-D-gluconic acid reductase (pseudogene)	0	0	0
FD1_0824	transcriptional regulator	26	7	0
FD1_0825	flavodoxin	0	0	0
FD1_0826	hypothetical protein	0	0	0
FD1_0827	relaxase/mobilization nuclease family protein	0	0	0
FD1_0828	hypothetical protein	0	0	0
FD1_0829	hypothetical protein	0	0	0
FD1_0830	hypothetical protein	0	0	0
FD1_0831	hypothetical protein	0	0	0
FD1_0832	hypothetical protein	0	0	0
FD1_0833	DNA topoisomerase III	0	0	0
FD1_0834	hypothetical protein	0	0	0
FD1_0835	hypothetical protein	0	0	0
FD1_0836	resolvase	0	0	0
FD1_0837	hypothetical transmembrane protein	0	0	0
FD1_0838	hypothetical protein	0	0	0
FD1_0839	hypothetical protein	0	0	0
FD1_0840	hypothetical protein	0	0	0
FD1_0841	hypothetical protein	0	0	0
FD1_0842	glutamate-cysteine ligase	0	0	0
FD1_0843	class II glutamine amidotransferase	0	0	0
FD1_0844***	ferredoxin	120*,**	16**	0*
FD1_0845	lipopolysaccharide transport system permease	9	0	0
FD1_0846	sugar ABC transporter ATP-binding protein	8	0	0
FD1_0847	methionine biosynthesis protein MetW (pseudogene)	7	0	0

FD1_0848	methionine biosynthesis protein MetW (pseudogene)	22	0	0
FD1_0849	glycosyltransferase, group 1 family protein	11	6	0
FD1_0850	hypothetical protein	0	14	0
FD1_0851	transcriptional regulator, y4mF family	5	0	0
FD1_0852	alpha-L-fucosidase	27	5	0
FD1_0853	glycosyl hydrolase family 26	12	7	0
FD1_0854	HAD hydrolase	16	14	0
FD1_0855	sporulation transcriptional activator Spo0A	0	0	0
FD1_0856	flavin reductase	0	0	0
FD1_0857	RNA polymerase sigma-70 factor	7	0	0
FD1_0858	hypothetical protein	23	21	0
FD1_0859	D-Ala-D-Ala carboxypeptidase VanY	16	25	0
FD1_0860	tryptophan synthase subunit beta TrpB	0	24	0
FD1_0861	hypothetical protein	0	11	0
FD1_0862**	RNA polymerase subunit sigma	26**	346**	0
FD1_0863	S-ribosylhomocysteinase	3	0	0
FD1_0864	hypothetical protein	14	0	0
FD1_0865	hypothetical protein	52	0	0
FD1_0866	fructose-2,6-bisphosphatase	9	0	0
FD1_0867***	XRE family transcriptional regulator	99*,**	10**	0*
FD1_0868	peptidase M23B	26	0	8
FD1_0869	hypothetical protein	0	0	0
FD1_0870	hypothetical protein	0	0	0
FD1_0871	hypothetical protein	42	0	0
FD1_0872	hypothetical protein	21	24	0
FD1_0873	hypothetical protein	0	0	0
FD1_0874	hypothetical protein	105	63	0
FD1_0875	GNAT family acetyltransferase	0	0	0
FD1_0876	diguanylate cyclase	17	0	0
FD1_0877	adhesin-like protein	35	0	11
FD1_0878	pyridoxamine 5'-phosphate oxidase	6	12	0
FD1_0879	ATPase (pseudogene)	0	0	0
FD1_0880	ATPase (pseudogene)	9	0	0
FD1_0881	aminoacyl-tRNA synthetase	16	9	0
FD1_0882	hypothetical protein	0	0	0
FD1_0883	hypothetical protein	0	0	0
FD1_0884	hypothetical protein	9	0	0
FD1_0885	cell division protein Fic (pseudogene)	39	0	0
FD1_0886	cell division protein Fic (pseudogene)	0	0	0
FD1_0887	hypothetical protein	0	0	0
FD1_0888	hypothetical transmembrane protein	31	6	0
FD1_0889	resolvase	29	12	0
FD1_0890	hypothetical protein	6	0	0
FD1_0891	hypothetical transmembrane protein	0	0	12
FD1_0892	hypothetical protein	45	6	0
FD1_0893	hypothetical protein	359	0	0
FD1_0894	hypothetical protein	12	0	0
FD1_0895*	ABC transporter	41	771*	0*
FD1_0896	hypothetical protein	0	0	0
FD1_0897	helicase domain protein	31	14	0
FD1_0898	type IV pilin	127	68	0
FD1_0899	prepilin-type cleavage/methylation protein	0	0	0
FD1_0900	hypothetical protein	0	128	0
FD1_0901**	hypothetical protein	22**	576**	24
FD1_0902**	restriction endonuclease-like protein	16**	372**	24
FD1_0903	hypothetical protein	0	0	0
FD1_0904	relaxase/mobilization nuclease family protein	0	0	0
FD1_0905	hypothetical protein	0	0	0
FD1_0906	hypothetical protein	0	0	0
FD1_0907	recombinase	14	5	0
FD1_0908**	twitching motility protein pilT	175**	31**	14

FD1_0909***	type IV-A pilus assembly ATPase PilB	76*,**	9**	0*
FD1_0910***	type II secretory pathway prepilin signal peptidase PulO and related peptidase	1530*,**	260**	21*
FD1_0911***	prepilin-type cleavage/methylation protein	1380*,**	203**	50*
FD1_0912	prepilin-type cleavage/methylation protein	556	135	0
FD1_0913***	adhesin-like protein	541*,**	111**	22*
FD1_0914*	hypothetical protein	1591*	572	20*
FD1_0915***	type IV pilus assembly protein PilM	379*,**	71**	0*
FD1_0916***	type II secretion protein F	383*,**	77**	0*
FD1_0917	von Willebrand factor type A domain protein	0	0	0
FD1_0918*	spore coat protein cotH	52*	21	5*
FD1_0919**	hypothetical protein	59**	5**	22
FD1_0920	hypothetical protein	99	58	0
FD1_0921	glycosyltransferase group 2 family protein	0	0	0
FD1_0922	hypothetical transmembrane protein	10	0	0
FD1_0923	N ⁵ -carboxyaminoimidazole ribonucleotide mutase	11	0	0
FD1_0924	hypothetical protein	38	0	0
FD1_0925	haloacid dehalogenase	38	0	0
FD1_0926	hypothetical protein	3	0	0
FD1_0927	phosphoribosylaminoimidazole-succinocarboxamide synthase	2	0	0
FD1_0928	amidophosphoribosyltransferase	26	5	0
FD1_0929	phosphoribosylformylglycinamide cyclo-ligase	34	0	0
FD1_0930	rare lipoprotein A	13	0	0
FD1_0931	hypothetical protein	0	0	0
FD1_0932	hypothetical protein	31	0	0
FD1_0933	phosphoribosylglycinamide formyltransferase	45	0	0
FD1_0934	hypothetical protein	10	0	0
FD1_0935	hypothetical transmembrane protein	8	0	0
FD1_0936	inosine monophosphate cyclohydrolase	5	0	0
FD1_0937	hypothetical transmembrane protein	3	0	0
FD1_0938	hypothetical protein	0	0	0
FD1_0939	aICAR transformylase/IMP cyclohydrolase PurH	128	0	0
FD1_0940	hypothetical transmembrane protein	50	0	0
FD1_0941	hypothetical transmembrane protein	87	0	0
FD1_0942	laminarinase	7	0	0
FD1_0943	rhomboid family protease GlpG	61	0	0
FD1_0944	hypothetical protein	21	0	0
FD1_0945*	toxic anion resistance protein Tela	41*	9	0*
FD1_0946***	tellurium resistance protein TerD	287*,**	7**	0*
FD1_0947	XRE family transcriptional regulator	5	0	0
FD1_0948	histidine kinase	0	0	0
FD1_0949	multidrug ABC transporter	0	0	0
FD1_0950	hypothetical transmembrane protein	0	0	0
FD1_0951	hypothetical transmembrane protein	0	0	0
FD1_0952	peptidase S41	2	0	0
FD1_0953***	calcium-translocating P-type ATPase	44*,**	3**	0*
FD1_0954	stress protein	73	0	0
FD1_0955	tellurium resistance protein TerD	98	0	0
FD1_0956	ATP/GTP-binding protein	16	0	0
FD1_0957	phosphoribosyltransferase (pseudogene)	2	0	0
FD1_0958	phosphoribosyltransferase (pseudogene)	0	0	0
FD1_0959	carboxylate-amine ligase	8	0	0
FD1_0960	HAD-superfamily hydrolase	24	19	0
FD1_0961	phosphoribosyl transferase	0	0	0
FD1_0962	dihydroorotase	12	0	14
FD1_0963	orotidine 5'-phosphate decarboxylase	3	0	0
FD1_0964	carbamoyl phosphate synthase small subunit	31	12	0
FD1_0965	carbamoyl phosphate synthase large subunit	12	1	0
FD1_0966	hypothetical protein	0	0	0
FD1_0967***	Ig domain protein group 2 domain protein	286*,**	59**	0*
FD1_0968	hypothetical protein	5	0	0

FD1_0969	hypothetical protein	0	20	0
FD1_0970*	serine/threonine protein phosphatase	77*	16	0*
FD1_0971*	hypothetical protein	1082*	451	0*
FD1_0972*	thiazolanyl imide reductase (pseudogene)	436*	247	0*
FD1_0973***	thiazolanyl imide reductase (pseudogene)	890**, **	101**	35*
FD1_0974	ig-like domain-containing protein	48	11	0
FD1_0975**	hypothetical protein	25**	0**	0
FD1_0976	hypothetical protein	30	0	0
FD1_0977	hypothetical protein	0	0	0
FD1_0978	hypothetical protein	10	0	0
FD1_0979	serine recombinase	0	0	0
FD1_0980	recombinase	0	0	0
FD1_0981	recombinase	0	0	0
FD1_0982	hypothetical protein	0	0	0
FD1_0983	hypothetical protein	21	0	0
FD1_0984	glycosyl hydrolase family 25	59	27	16
FD1_0985	holin	86	0	0
FD1_0986*	transposase	150*	46	0*
FD1_0987	aldo/keto reductase family protein	0	0	0
FD1_0988	hypothetical protein	5	0	0
FD1_0989	acetyltransferase	12	21	0
FD1_0990	flavin reductase	0	0	0
FD1_0991	flavodoxin	0	0	0
FD1_0992	hypothetical transmembrane protein	6	0	0
FD1_0993	hypothetical protein	0	0	0
FD1_0994	TetR family transcriptional regulator	29	0	0
FD1_0995	SAM-dependent methyltransferase	0	20	0
FD1_0996	heavy metal translocating P-type ATPase	11	10	0
FD1_0997**	hypothetical protein	198**	4**	12
FD1_0998**	hypothetical protein	61**	10**	0
FD1_0999	pyrimidine-nucleoside phosphorylase	75	13	0
FD1_1000	sigmaK-factor processing regulatory protein BofA	0	0	0
FD1_1001	hypothetical protein	0	0	0
FD1_1002	hypothetical protein	0	0	54
FD1_1003	hypothetical protein	0	0	4
FD1_1004	phosphodiesterase	41	0	0
FD1_1005	hypothetical transmembrane protein	14	0	0
FD1_1006	hypothetical transmembrane protein	17	0	0
FD1_1007	hypothetical transmembrane protein	61	0	0
FD1_1008	pyrroline-5-carboxylate reductase	15	0	0
FD1_1009	hypothetical protein	0	0	0
FD1_1010	Fe-S protein	0	0	0
FD1_1011	RNA polymerase sigma factor	0	0	0
FD1_1012	hypothetical transmembrane protein	12	0	0
FD1_1013	ATP-dependent chaperone protein ClpB	0	0	0
FD1_1014	hypothetical protein	0	0	0
FD1_1015**	TrpR like protein, YecC/YecD	53**	0**	0
FD1_1016***	glycoside hydrolase family 9	129*, **	31**	2*
FD1_1017	hypothetical protein	388	279	0
FD1_1018	Cof-like hydrolase	40	0	0
FD1_1019	cob(I)yrinic acid a,c-diamide adenosyltransferase	10	3	0
FD1_1020	dockerin type I repeat-containing domain protein	0	0	0
FD1_1021***	glycoside hydrolase (pseudogene)	123*, **	27**	0*
FD1_1022	glycoside hydrolase (pseudogene)	37	0	0
FD1_1023***	glycosyl hydrolase family 9	248*, **	39**	13*
FD1_1024	stage II sporulation protein R	2	0	0
FD1_1025**	translation initiation factor IF-3	284**	21**	0
FD1_1026**	50S ribosomal protein L359	319**	1**	0
FD1_1027	50S ribosomal protein L20	198	0	0
FD1_1028	RNA methyltransferase	14	0	0
FD1_1029	DNA protecting protein DprA	12	0	0

FD1_1030	DNA topoisomerase I	41	0	0
FD1_1031	tRNA (uracil-5-)-methyltransferase	9	0	0
FD1_1032	phosphate acyltransferase	4	0	0
FD1_1033	ribonuclease III	11	0	0
FD1_1034	radical SAM protein	33	0	0
FD1_1035	chromosome segregation protein SMC	20	0	4
FD1_1036**	signal recognition particle-docking protein FtsY	36**	2**	0
FD1_1037	non-canonical purine NTP pyrophosphatase	24	12	0
FD1_1038	RNA-binding protein	8	0	0
FD1_1039	flavin reductase	82	0	0
FD1_1040	nicotinate (nicotinamide) nucleotide adenylyltransferase (pseudogene)	6	0	0
FD1_1041	nicotinate (nicotinamide) nucleotide adenylyltransferase (pseudogene)	0	0	0
FD1_1042	hypothetical protein	8	0	0
FD1_1043	cell envelope-related function transcriptional attenuator common domain	22	0	0
FD1_1044	ribosome-associated protein IOJAP	7	0	0
FD1_1045	hypothetical transmembrane protein	34	0	0
FD1_1046	leucine--tRNA ligase	49	0	0
FD1_1047	haloacid dehalogenase	0	0	0
FD1_1048	3-dehydroquinate dehydratase	0	0	0
FD1_1049	peptidase M24	0	0	0
FD1_1050***	elongation factor P	305*,**	65**	0*
FD1_1051**	hypothetical protein	1884**	136**	0
FD1_1052	adhesin-like protein	0	0	0
FD1_1053	adhesin-like protein	11	20	0
FD1_1054	DNA-directed RNA polymerase subunit sigma	0	0	0
FD1_1055	hypothetical protein	0	0	0
FD1_1056	hypothetical transmembrane protein	0	0	0
FD1_1057	hypothetical protein	0	0	0
FD1_1058	hypothetical transmembrane protein	29	16	0
FD1_1059**	biotin/acetyl-CoA-carboxylase ligase	61**	2**	0
FD1_1060	hypothetical transmembrane protein	61	13	25
FD1_1061**	cytochrome b/b6	144**	16**	56
FD1_1062	hypothetical transmembrane protein	62	0	0
FD1_1063	CoA-substrate-specific enzyme activase	24	0	0
FD1_1064	2-hydroxyglutaryl-CoA dehydratase, D-component	54	0	0
FD1_1065***	GerA spore germination protein	80*,**	16**	0*
FD1_1066**	hypothetical transmembrane protein	73**	10**	0
FD1_1067	phosphatidylserine decarboxylase	50	11	0
FD1_1068*	recombinase	50*	14	0*
FD1_1069**	hypothetical protein	61**	7**	0
FD1_1070	RNA polymerase sigma-24 factor	29	0	0
FD1_1071	ABC transporter substrate-binding protein	6	0	0
FD1_1072	D-Ala-D-Ala carboxypeptidase	9	0	0
FD1_1073	AraC family transcriptional regulator	20	0	0
FD1_1074	hypothetical protein	26	0	0
FD1_1075	hypothetical protein	10	0	0
FD1_1076	hypothetical transmembrane protein	26	5	0
FD1_1077	hypothetical protein	19	0	0
FD1_1078	molecular chaperone DnaJ	23	10	0
FD1_1079	chaperone protein DnaK	61	61	0
FD1_1080	co-chaperone GrpE	67	0	0
FD1_1081	heat-inducible transcription repressor HrcA	5	13	0
FD1_1082	peptidase M15	24	0	0
FD1_1083*	hypothetical protein	260*	101	0*
FD1_1084*	hypothetical protein	205*	50	7*
FD1_1085***	large mechanosensitive ion channel protein MscL	427*,**	98**	19*
FD1_1086	proline--tRNA ligase (incomplete, end of contig)	0	0	0
FD1_1087***	gDSL-like Lipase/Acylhydrolase	142*,**	36**	18*
FD1_1088	ATP-dependent Clp protease proteolytic subunit ClpP	0	0	0
FD1_1089	cell division protein FtsK	5	2	0
FD1_1090	GNAT family acetyltransferase	0	0	0

FD1_1091	hypothetical protein	0	0	0
FD1_1092	uncharacterized radical SAM protein	20	0	0
FD1_1093**	FAD-dependent oxidoreductase	80**	4**	0
FD1_1094	hypothetical transmembrane protein	12	0	0
FD1_1095	hypothetical transmembrane protein	22	0	0
FD1_1096	hypothetical transmembrane protein	20	0	0
FD1_1097	hypothetical protein	0	0	76
FD1_1098	cytidylate kinase (pseudogene)	24	0	0
FD1_1099	cytidylate kinase (pseudogene)	0	0	0
FD1_1100***	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	136*,**	24**	0*
FD1_1101***	glycoside hydrolase family 9	268*,**	12**	0*
FD1_1102*	glycoside hydrolase family 9	3117*	909	58*
FD1_1103*	hypothetical protein	61*	12	0*
FD1_1104	50S ribosomal protein L1	0	0	0
FD1_1105	50S ribosomal protein L11	35	0	0
FD1_1106	transcription termination/antitermination factor NusG	22	0	0
FD1_1107	preprotein translocase subunit SecE	0	0	0
FD1_1108	50S ribosomal protein L33	43	0	0
FD1_1109	hypothetical protein	7	7	0
FD1_1110	DNA repair protein RadA	18	0	0
FD1_1111	hypothetical protein	0	0	0
FD1_1112	iron transporter FeoA	0	0	0
FD1_1113	iron transporter FeoA	0	0	0
FD1_1114	cysteine synthase	6	0	0
FD1_1115	phage integrase	69	23	22
FD1_1116	hypothetical protein	48	19	43
FD1_1117	transcriptional regulator	35	54	34
FD1_1118	transcriptional regulator	0	15	0
FD1_1119	DNA-binding protein, excisionase family	0	0	0
FD1_1120	hypothetical protein	13	0	0
FD1_1121	hypothetical protein	7	0	77
FD1_1122	hypothetical protein	0	0	0
FD1_1123	hypothetical protein	0	0	0
FD1_1124	hypothetical protein	0	0	0
FD1_1125	hypothetical protein	25	0	0
FD1_1126	hypothetical protein	6	0	29
FD1_1127	hypothetical protein	0	0	58
FD1_1128	hypothetical protein	6	0	13
FD1_1129	chromosome segregation protein SMC	13	0	0
FD1_1130	phage nucleotide-binding protein	0	0	0
FD1_1131	phage protein	0	0	12
FD1_1132	DEAD/DEAH box helicase	2	2	29
FD1_1133	DNA primase	0	0	0
FD1_1134	endodeoxyribonuclease RusA	0	4	8
FD1_1135	hypothetical protein	0	44	124
FD1_1136	hypothetical protein	0	0	7
FD1_1137	hypothetical protein	0	0	0
FD1_1138	hypothetical protein	0	6	0
FD1_1139	hypothetical protein	0	7	42
FD1_1140	hypothetical protein	0	0	54
FD1_1141	hypothetical protein	0	0	20
FD1_1142	hypothetical protein	0	0	45
FD1_1143	terminase small subunit	0	0	0
FD1_1144	phage terminase, large subunit	0	0	42
FD1_1145	SPP1 Gp6-like phage portal protein	0	0	0
FD1_1146	phage minor capsid protein	11	0	66
FD1_1147	hypothetical protein	13	0	0
FD1_1148	hypothetical protein	0	0	0
FD1_1149	hypothetical protein	10	0	0
FD1_1150	hypothetical protein	7	0	0
FD1_1151	hypothetical protein	23	0	0

FD1_1152	hypothetical protein	18	0	30
FD1_1153	hypothetical protein	0	0	81
FD1_1154	Minor capsid	0	0	0
FD1_1155	hypothetical protein	11	0	0
FD1_1156	hypothetical protein	0	0	0
FD1_1157	hypothetical protein	2	0	0
FD1_1158	hypothetical protein	53	0	0
FD1_1159	bacteriophage Gp15 protein	16	11	0
FD1_1160	hypothetical protein	28	0	131
FD1_1161	phage tail tape measure protein, TP901 family, core region	0	2	20
FD1_1162	Lj928 prophage protein	0	0	0
FD1_1163	phage minor structural protein	2	0	13
FD1_1164	hypothetical protein	0	0	0
FD1_1165	hypothetical protein	0	0	0
FD1_1166	hypothetical protein	0	0	0
FD1_1167	hypothetical protein	0	0	0
FD1_1168	hypothetical protein	0	0	38
FD1_1169	hypothetical protein	0	0	79
FD1_1170	peptidase M15	0	0	0
FD1_1171	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	44	0	2
FD1_1172	prolipoprotein diacylglycerol transferase	55	0	0
FD1_1173	peptidase M16	21	0	37
FD1_1174	peptidase M16	31	0	0
FD1_1175**	glutamate dehydrogenase	82**	3**	0
FD1_1176	alginate <i>O</i> -acetyltransferase	0	0	0
FD1_1177	hypothetical protein	17	3	0
FD1_1178	protein kinase family protein	17	13	0
FD1_1179	hypothetical transmembrane protein	11	0	0
FD1_1180	hypothetical transmembrane protein	86	0	0
FD1_1181**	FolC bifunctional protein	144**	20**	0
FD1_1182	short-chain dehydrogenase	31	0	0
FD1_1183	stress responsive A/B barrel domain protein	14	0	0
FD1_1184	isochorismatase	10	0	0
FD1_1185	valine--tRNA ligase	19	0	0
FD1_1186*	adhesin-like protein	1379	3216*	19*
FD1_1187	pyruvate kinase	1194	1494	25
FD1_1188*	ATP-dependent DNA helicase PcrA	676	1323*	8*
FD1_1189	diguanylate cyclase	165	222	9
FD1_1190	glycoside hydrolase family	1021	1532	2
FD1_1191	regulator (pseudogene)	27	235	0
FD1_1192	regulator (pseudogene)	165	213	0
FD1_1193	hypothetical protein	0	15	0
FD1_1194	spore cortex-lytic enzyme	3	4	0
FD1_1195	spore cortex-lytic enzyme, pre-pro-form	0	0	0
FD1_1196	hypothetical transmembrane protein	4	0	0
FD1_1197	hypothetical transmembrane protein	43	26	0
FD1_1198	RNA polymerase subunit sigma-24	0	14	0
FD1_1199***	hypothetical protein	169*,**	33**	0*
FD1_1200	transcriptional regulator	13	0	0
FD1_1201*	two component sensor kinase	46*	15	0*
FD1_1202**	hypothetical protein	172**	39**	24
FD1_1203	stress protein, partial	9	3	0
FD1_1204	DNA mismatch repair protein MutT	10	0	0
FD1_1205*	hypothetical protein	37*	10	0*
FD1_1206	hypothetical protein	30	28	0
FD1_1207	PadR family transcriptional regulator	7	1	0
FD1_1208	resolvase	26	0	0
FD1_1209	hypothetical protein	0	0	0
FD1_1210	abortive phage infection protein (pseudogene)	14	73	0
FD1_1211	abortive phage infection protein (pseudogene)	4	6	0

FD1_1212	cysteine desulfurase (pseudogene)	0	28	0
FD1_1213	cysteine desulfurase (pseudogene)	15	0	0
FD1_1214	hypothetical protein	0	0	0
FD1_1215	hypothetical protein	0	0	0
FD1_1216	hypothetical protein	0	111	0
FD1_1217	hypothetical protein	0	57	0
FD1_1218	RloB-like protein	6	4	44
FD1_1219	abortive phage infection protein	0	11	0
FD1_1220***	pyruvate phosphate dikinase	438*,**	29**	5*
FD1_1221	hypothetical protein	0	0	0
FD1_1222	<i>N</i> -acetylglucosamine-1-phosphate uridyltransferase	2	0	17
FD1_1223	hypothetical protein	0	0	0
FD1_1224	metallophosphoesterase	53	0	0
FD1_1225	stage V sporulation protein S	474	172	0
FD1_1226***	hypothetical protein	1646*,**	335**	40*
FD1_1227	ATP-dependent DNA helicase RecG	7	9	0
FD1_1228	hypothetical protein	0	0	0
FD1_1229	polysaccharide deacetylase	27	0	0
FD1_1230**	hypothetical protein	40**	0**	0
FD1_1231**	hypothetical protein	109**	0**	0
FD1_1232	SPFH/Band 7/PHB domain protein	8	0	0
FD1_1233	hypothetical protein	40	0	0
FD1_1234	hypothetical protein	28	0	0
FD1_1235	cell-surface transglutaminase	5	0	0
FD1_1236	adhesin-like protein	6	0	0
FD1_1237	cell-surface transglutaminase	8	2	0
FD1_1238	cell-surface transglutaminase	4	2	0
FD1_1239	adhesin-like protein	12	3	0
FD1_1240	hypothetical protein	0	0	0
FD1_1241	chemotaxis protein CheY	0	0	0
FD1_1242	multidrug ABC transporter, ATP-binding subunit	0	0	0
FD1_1243	hypothetical transmembrane protein	0	0	0
FD1_1244	histidine kinase	10	0	0
FD1_1245	peptidoglycan glycosyltransferase	24	0	0
FD1_1246	peptidoglycan glycosyltransferase	76	0	0
FD1_1247	hypothetical transmembrane protein	124	0	0
FD1_1248	endonuclease III	81	0	0
FD1_1249	hypothetical protein	90	0	0
FD1_1250	NAD-dependent deacetylase	43	0	0
FD1_1251	hypothetical protein	26	0	0
FD1_1252	hypothetical transmembrane protein	23	3	0
FD1_1253	GtrA family protein	0	0	0
FD1_1254	flavin containing amine oxidoreductase	15	0	0
FD1_1255*	efflux ABC transporter, permease	36*	11	0*
FD1_1256	peptide ABC transporter ATP-binding protein	38	15	0
FD1_1257	RND transporter	37	13	0
FD1_1258**	galactokinase	118**	7**	0
FD1_1259	beta-lactamase	25	0	0
FD1_1260	glycosylase	18	16	36
FD1_1261	D-alanine--D-alanine ligase	13	0	0
FD1_1262	hypothetical protein	8	0	0
FD1_1263	arginine--tRNA ligase	64	0	0
FD1_1264	CdaR family transcriptional regulator	60	0	0
FD1_1265**	cell division ATP-binding protein FtsE	51**	6**	0
FD1_1266**	protein insertion permease FtsX	63**	1**	0
FD1_1267	peptidase M23 family	38	9	0
FD1_1268	peptidase M23 (pseudogene)	7	0	0
FD1_1269	peptidase M23 (pseudogene)	47	0	0
FD1_1270	peptidase	33	11	0
FD1_1271	hypothetical protein	0	0	0
FD1_1272	ABC transporter ATP-binding protein (pseudogene)	0	0	0

FD1_1273	ABC transporter ATP-binding protein (pseudogene)	18	0	0
FD1_1274	hypothetical protein	4	3	0
FD1_1275	hypothetical protein	0	0	0
FD1_1276	phosphoserine phosphatase/homoserine phosphotransferase bifunctional protein	0	13	0
FD1_1277	hypothetical secreted protein	2	2	0
FD1_1278	hypothetical protein	13	6	0
FD1_1279	AraC family transcriptional regulator	6	5	0
FD1_1280***	polysaccharide lyase	441*,**	58**	12*
FD1_1281	transmembrane DNA binding protein	69	0	0
FD1_1282	glycosyl hydrolases family 11	14	3	0
FD1_1283	efflux ABC transporter permease	2	0	0
FD1_1284	peptide ABC transporter ATP-binding protein	15	0	0
FD1_1285	histidine kinase	0	0	0
FD1_1286	transcriptional regulator (pseudogene)	57	28	0
FD1_1287	transcriptional regulator (pseudogene)	1	0	0
FD1_1288**	acetyl xylan esterase	34**	5**	0
FD1_1289	hypothetical protein	0	0	0
FD1_1290	hypothetical protein	6	0	0
FD1_1291	hypothetical transmembrane protein	12	0	0
FD1_1292***	1,4-beta-xylanase	124*,**	17**	0*
FD1_1293	glycosyl hydrolase family 9	1822	1844	63
FD1_1294**	hypothetical transmembrane protein	79**	5**	0
FD1_1295	RNA methyltransferase RsmE	4	0	0
FD1_1296**	hypothetical transmembrane protein	204**	25**	0
FD1_1297	hypothetical transmembrane protein	9	0	0
FD1_1298	hypothetical transmembrane protein	9	19	0
FD1_1299	hypothetical protein	0	0	0
FD1_1300	GTP-binding protein TypA/BipA	2	2	0
FD1_1301	hypothetical secreted protein	0	0	0
FD1_1302	hypothetical secreted protein	0	0	0
FD1_1303	hypothetical secreted protein	33	9	0
FD1_1304	inosine 5'-monophosphate dehydrogenase	120	0	0
FD1_1305	hypothetical secreted protein	57	0	0
FD1_1306**	amidohydrolase	103**	4**	0
FD1_1307	shikimate kinase	27	21	0
FD1_1308	GNAT family acetyltransferase	61	9	0
FD1_1309	shikimate 5-dehydrogenase	70	0	0
FD1_1310	malonyl CoA-acyl carrier protein transacylase	55	0	0
FD1_1311	3-oxoacyl-ACP synthase	0	0	0
FD1_1312	enoyl-(Acyl-carrier-protein) reductase II	41	0	0
FD1_1313	hypothetical protein	76	46	89
FD1_1314	3-oxoacyl-[acyl-carrier-protein] reductase	40	0	0
FD1_1315	beta-ketoacyl-acyl-carrier-protein synthase II	11	6	0
FD1_1316	acetyl-CoA carboxylase	0	0	0
FD1_1317	3-hydroxyacyl-ACP dehydratase	11	0	0
FD1_1318	acetyl-CoA carboxylase biotin carboxylase subunit	6	4	0
FD1_1319	acetyl-CoA carboxylase subunit beta	7	7	0
FD1_1320	acetyl-CoA carboxylase subunit alpha	48	0	0
FD1_1321	acyl carrier protein	377	104	0
FD1_1322	ATP synthase F0F1 subunit A, partial	0	0	0
FD1_1323	F ₀ F ₁ ATP synthase subunit C	0	0	0
FD1_1324	F ₀ F ₁ ATP synthase subunit C	0	0	0
FD1_1325	ATP synthase F ₀ subunit B	0	0	0
FD1_1326	ATP synthase F ₁ subunit alpha	4	5	0
FD1_1327	F ₀ F ₁ ATP synthase subunit gamma	9	0	0
FD1_1328	cell division protein FtsX	0	0	0
FD1_1329	hypothetical transmembrane protein	6	21	0
FD1_1330	ECF subfamily RNA polymerase sigma-24 factor	0	0	0
FD1_1331	serpin (serine protease inhibitor)	2	9	35
FD1_1332	serpin (serine protease inhibitor)	3	12	0

FD1_1333	transcription elongation factor GreA	18	0	0
FD1_1334	lysine--tRNA ligase	75	0	0
FD1_1335	hypothetical protein	54	5	0
FD1_1336	oxygen-independent coproporphyrinogen III oxidase	8	5	0
FD1_1337	hypothetical transmembrane protein	0	0	0
FD1_1338	hypothetical transmembrane protein	87	0	0
FD1_1339	elongation factor 4	32	0	0
FD1_1340***	hypoxanthine phosphoribosyltransferase	127*,**	25**	0*
FD1_1341*	adenine permease	161*	46	11*
FD1_1342***	hypothetical protein	77*,**	9**	0*
FD1_1343***	tRNA-splicing ligase RtcB	152*,**	26**	0*
FD1_1344	hypothetical protein	1	0	0
FD1_1345	hypothetical protein	13	12	0
FD1_1346	hypothetical protein	29	0	0
FD1_1347*,**	fibronectin (pseudogene)	306*,**	49**	0*
FD1_1348	fibronectin (pseudogene)	116	0	0
FD1_1349	transcriptional regulator	6	0	0
FD1_1350	hypothetical protein	58	0	0
FD1_1351*	cellulase (glycosyl hydrolase family 5)	65*	38	0*
FD1_1352	hypothetical protein	25	0	0
FD1_1353	hypothetical protein	0	0	0
FD1_1354	hypothetical protein	88	0	0
FD1_1355	AraC family transcriptional regulator	8	14	36
FD1_1356***	GDSL family lipase	261*,**	47**	0*
FD1_1357***	hypothetical transmembrane protein	447*,**	32**	0*
FD1_1358	glycoside hydrolase family 16	24	0	0
FD1_1359	multidrug transporter MatE	9	13	0
FD1_1360	CobW/P47K family protein	32	25	0
FD1_1361	glycosyl hydrolase family 3	0	0	0
FD1_1362	NADPH-dependent FMN reductase	38	2	0
FD1_1363	aldo/keto reductase	17	13	0
FD1_1364	exonuclease	83	0	0
FD1_1365**	carbonic anhydrase	304**	23**	0
FD1_1366	hypothetical protein	0	0	0
FD1_1367	signal peptidase	11	0	0
FD1_1368	fibro-slime domain-containing protein	0	0	0
FD1_1369	glycoside hydrolase family protein	0	7	0
FD1_1370	hypothetical transmembrane protein	0	0	0
FD1_1371	fimbrial subunit FimA	0	0	0
FD1_1372	sortase	0	0	0
FD1_1373	oxidoreductase	27	14	0
FD1_1374	exopolysaccharide biosynthesis protein	14	0	0
FD1_1375	LPS biosynthesis protein	5	0	0
FD1_1376	glycerol phosphotransferase	16	0	0
FD1_1377	acyltransferase	0	0	0
FD1_1378	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	16	14	0
FD1_1379	glycosyltransferase	29	0	0
FD1_1380	oligosaccharide repeat unit polymerase	0	0	0
FD1_1381	polysaccharide biosynthesis protein	9	0	0
FD1_1382	acyltransferase	25	0	0
FD1_1383	hypothetical protein	0	0	0
FD1_1384	hypothetical transmembrane protein	0	0	0
FD1_1385	acyltransferase 3	0	7	0
FD1_1386	UDP-galactopyranose mutase	8	0	0
FD1_1387	nucleotide sugar dehydratase	5	0	0
FD1_1388***	hypothetical secreted protein	86*,**	20**	0*
FD1_1389	<i>N</i> -acetylmuramoyl-L-alanine amidase	9	0	0
FD1_1390	phage-shock protein	37	0	0
FD1_1391	hypothetical transmembrane protein	0	0	0
FD1_1392	hypothetical protein	166	0	0
FD1_1393*	metallo-beta-lactamase	119*	88	0*

FD1_1394	isoprenylcysteine carboxyl methyltransferase	50	28	0
FD1_1395	maltose acetyltransferase	80	14	0
FD1_1396	30S ribosomal protein S6	24	16	0
FD1_1397	single-stranded DNA-binding protein	87	37	0
FD1_1398	30S ribosomal protein S18	107	0	0
FD1_1399	hypothetical transmembrane protein	109	0	0
FD1_1400*	nuclease	150*	71	0*
FD1_1401	HPr kinase	18	0	0
FD1_1402	MiaB-like tRNA modifying enzyme (pseudogene)	0	0	0
FD1_1403	MiaB-like tRNA modifying enzyme (pseudogene)	0	0	0
FD1_1404	phosphoribosylformylglycinamide synthase	45	0	5
FD1_1405	ig-like domain-containing surface protein	2	0	0
FD1_1406**	glycogen synthase	71**	4**	0
FD1_1407	hypothetical protein	98	0	0
FD1_1408	HAD family hydrolase	82	0	0
FD1_1409	hypothetical protein	80	0	0
FD1_1410***	DNA-binding protein	958*,**	208**	0*
FD1_1411	hypothetical protein	643	78	0
FD1_1412*	hypothetical protein	130*	83	0*
FD1_1413**	hemolysin activation protein	69**	7**	0
FD1_1414	hypothetical protein	17	0	0
FD1_1415***	cytidylate kinase	510*,**	98**	0*
FD1_1416	hypothetical transmembrane protein	7	0	0
FD1_1417	hypothetical protein	0	0	0
FD1_1418	hypothetical protein	12	11	0
FD1_1419*	plectin	299*	131	0*
FD1_1420*	(4Fe-4S)-binding protein	840*	319	28*
FD1_1421	resolvase	0	0	0
FD1_1422	sigma-70 region 4 type 2	0	0	0
FD1_1423	aldo/keto reductase	31	11	0
FD1_1424	oxidoreductase	47	0	0
FD1_1425	flavodoxin	4	14	0
FD1_1426	hypothetical protein	7	0	0
FD1_1427	resolvase	26	2	0
FD1_1428	hypothetical protein	0	0	0
FD1_1429	hypothetical protein	0	0	0
FD1_1430	hypothetical protein	0	0	0
FD1_1431	bacterial mobilization protein (MobC)	0	0	0
FD1_1432	relaxase	21	0	0
FD1_1433	hypothetical protein	42	0	0
FD1_1434	hypothetical protein	0	0	0
FD1_1435	hypothetical transmembrane protein	0	10	0
FD1_1436	RNA polymerase subunit sigma-24	0	0	0
FD1_1437	hypothetical transmembrane protein	0	7	0
FD1_1438	hypothetical transmembrane protein	4	0	0
FD1_1439	RNA polymerase subunit sigma-24	0	0	0
FD1_1440	carboxymuconolactone decarboxylase	0	0	0
FD1_1441	transcriptional regulator	0	6	0
FD1_1442	DNA-binding protein	0	47	0
FD1_1443	restriction endonuclease EcoRI	0	0	0
FD1_1444	hypothetical protein	50	56	0
FD1_1445	glycoside hydrolase	41	10	0
FD1_1446	AraC family transcriptional regulator	28	9	0
FD1_1447	alpha/beta hydrolase	17	15	0
FD1_1448	hypothetical protein	46	0	0
FD1_1449	acetyltransferase	10	0	88
FD1_1450	hypothetical protein	14	0	0
FD1_1451	GNAT family acetyltransferase	0	0	0
FD1_1452	short-chain dehydrogenase	0	0	0
FD1_1453	hypothetical protein	0	0	0
FD1_1454	hypothetical protein	11	0	0

FD1_1455	CAAX amino protease	0	0	0
FD1_1456	hypothetical transmembrane protein	0	8	0
FD1_1457	hypothetical transmembrane protein	14	0	0
FD1_1458	ABC transporter	9	0	0
FD1_1459	GntR family transcriptional regulator	0	4	0
FD1_1460	flavin oxidoreductase	0	0	0
FD1_1461	hypothetical secreted protein	8	0	0
FD1_1462	hypothetical secreted protein	0	0	0
FD1_1463	hypothetical protein	12	0	0
FD1_1464	hypothetical protein	0	0	0
FD1_1465	hypothetical protein	0	0	0
FD1_1466	UDP pyrophosphate phosphatase	28	6	0
FD1_1467	cyclic nucleotide-binding protein	35	0	0
FD1_1468*	anaerobic ribonucleoside-triphosphate reductase	326*	95	0*
FD1_1469***	rubrerythrin	1562*,**	261**	58*
FD1_1470	diguanylate cyclase	181	160	0
FD1_1471	hypothetical protein	72	43	0
FD1_1472***	hypothetical protein	174*,**	44**	12*
FD1_1473***	sugar ABC transporter substrate-binding protein	146*,**	25**	0*
FD1_1474	hypothetical protein	81	28	0
FD1_1475	pAS domain S-box/diguanylate cyclase (GGDEF) domain protein	61	9	0
FD1_1476	aspartate carbamoyltransferase	36	15	0
FD1_1477	phosphohydrolase	13	0	0
FD1_1478**	asparagine synthase	39**	2**	0
FD1_1479	site-specific recombinase XerD	4	0	0
FD1_1480	NUDIX hydrolase	31	26	0
FD1_1481*	hypothetical protein	228*	52	0*
FD1_1482**	hypothetical protein	396**	21**	73
FD1_1483***	peptidase S1 and S6 chymotrypsin/Hap	182*,**	15**	0*
FD1_1484	ATP synthase subunit D	27	0	0
FD1_1485	ATP synthase subunit B	42	11	0
FD1_1486*	ATP synthase subunit A	36*	18	0*
FD1_1487	ATP synthase subunit F	22	0	0
FD1_1488	ATP synthase subunit C	34	6	0
FD1_1489	V-type proton ATPase subunit E	25	2	0
FD1_1490	ATP synthase subunit C	20	61	0
FD1_1491	H ⁺ -transporting ATPase	27	20	0
FD1_1492	ATP synthase subunit H	62	27	0
FD1_1493	shikimate kinase	7	0	0
FD1_1494	septum site-determining protein MinD	102	0	0
FD1_1495	methylglyoxal synthase	80	0	0
FD1_1496	histidine--tRNA ligase	20	0	0
FD1_1497	aspartyl-tRNA synthetase	46	42	0
FD1_1498	hypothetical protein	49	0	0
FD1_1499	sporulation transcription factor Spo0A	19	0	23
FD1_1500*	alpha-L-arabinofuranosidase	162*	39	0*
FD1_1501	acetyltransferase	11	0	0
FD1_1502	hypothetical protein	64	0	0
FD1_1503	gDSL-like protein	4	0	0
FD1_1504	ribonucleoside triphosphate reductase	104	52	0
FD1_1505	ribonucleoside-triphosphate reductase activating protein	287	70	0
FD1_1506*	orotate phosphoribosyltransferase	115*	35	0*
FD1_1507	helicase domain protein	1	3	0
FD1_1508	hypothetical protein	0	0	0
FD1_1509	protein kinase	4	0	0
FD1_1510	hypothetical protein	7	0	18
FD1_1511	hypothetical protein	0	0	0
FD1_1512	hypothetical protein	0	0	0
FD1_1513	short-chain dehydrogenase (pseudogene)	0	0	0
FD1_1514	short-chain dehydrogenase (pseudogene)	0	0	0
FD1_1515	hypothetical protein	102	39	33

FD1_1516	hypothetical protein	0	0	0
FD1_1517	hypothetical protein	0	0	0
FD1_1518	hypothetical protein	0	0	0
FD1_1519*	hypothetical transmembrane protein	26*	5	0*
FD1_1520	histidine kinase	9	0	0
FD1_1521	transcriptional regulator	12	0	0
FD1_1522	nucleoside-diphosphate sugar epimerase	3	0	0
FD1_1523	short-chain dehydrogenase	0	0	0
FD1_1524	beta-xylosidase	16	18	0
FD1_1525***	glycoside hydrolase (pseudogene)	5**	27*,**	0*
FD1_1526	glycoside hydrolase (pseudogene)	10	0	0
FD1_1527	diguanylate cyclase	704	509	0
FD1_1528	resolvase	64	51	0
FD1_1529	HAD hydrolase (pseudogene)	1460	1559	330
FD1_1530	HAD hydrolase (pseudogene)	1684	1458	292
FD1_1531	Appr-1-p processing protein	9	0	0
FD1_1532	hypothetical protein	22	34	0
FD1_1533	DNA methyltransferase (pseudogene)	0	0	0
FD1_1534	DNA methyltransferase (pseudogene)	5	0	0
FD1_1535	type I restriction modification DNA specificity domain protein	0	0	0
FD1_1536	hypothetical protein	0	0	0
FD1_1537	integrase	9	27	0
FD1_1538	hypothetical protein	0	0	0
FD1_1539***	transposase IS116/IS110/IS902 family protein	937*,**	143**	0*
FD1_1540	hypothetical protein	29	10	0
FD1_1541	hypothetical transmembrane protein	0	0	0
FD1_1542	hypothetical transmembrane protein	38	0	0
FD1_1543	XRE family transcriptional regulator	8	0	0
FD1_1544	hypothetical protein	0	0	0
FD1_1545	asparagine--tRNA ligase	50	0	0
FD1_1546**	aspartate--ammonia ligase	103**	8**	27
FD1_1547***	hypothetical protein	979*,**	49**	0*
FD1_1548**	DNA mismatch repair protein MutT	169**	14**	0
FD1_1549	hypothetical protein	14	21	0
FD1_1550	transcriptional regulators	41	35	0
FD1_1551	hypothetical protein	17	0	0
FD1_1552	hypothetical protein	24	0	0
FD1_1553	polysaccharide biosynthesis protein	14	4	0
FD1_1554	aminotransferase, class I/II	49	34	0
FD1_1555	hypothetical protein	10	13	0
FD1_1556	tryptophanyl-tRNA synthetase	119	41	0
FD1_1557	mazG family protein	57	30	0
FD1_1558**	DNA-binding protein	154**	21**	0
FD1_1559*	RNA-binding protein S4	463*	167	0*
FD1_1560	hypothetical protein	4	9	0
FD1_1561	diguanylate phosphodiesterase	131	40	0
FD1_1562	O-acetylhomoserine aminocarboxypropyltransferase	48	0	0
FD1_1563	hypothetical protein	0	0	0
FD1_1564	dihydroxyacetone kinase	16	0	0
FD1_1565	collagen-binding protein	1089	1341	8
FD1_1566	hypothetical transmembrane protein	22	0	0
FD1_1567	malonyl CoA-ACP transacylase	7	0	0
FD1_1568	acyl carrier protein	22	0	0
FD1_1569	enoyl-CoA hydratase4	25	0	0
FD1_1570	thioesterase	9	0	0
FD1_1571	hypothetical protein	0	0	0
FD1_1572	enoyl-CoA hydratase	10	0	0
FD1_1573	3-hydroxyacyl-CoA dehydrogenase	12	0	0
FD1_1574	3-oxoacyl-ACP synthase	12	4	0
FD1_1575	hypothetical protein	5	0	0
FD1_1576	tRNA modification GTPase	0	0	0

FD1_1577	long-chain acyl-CoA synthetase	11	2	0
FD1_1578	acyl carrier protein	0	0	0
FD1_1579	thioesterase	16	0	0
FD1_1580	hypothetical transmembrane protein	5	0	0
FD1_1581	NUDIX hydrolase	0	0	0
FD1_1582	hypothetical transmembrane protein	13	27	0
FD1_1583	ABC-2 type transporter	8	0	0
FD1_1584	ABC-2 type transporter	5	0	0
FD1_1585	ABC transporter ATP-binding protein	0	0	0
FD1_1586	histidine kinase	0	1	0
FD1_1587	LuxR family transcriptional regulator	4	23	0
FD1_1588	ADP-ribosylglycohydrolase	142	0	34
FD1_1589	hydrolase	76	0	0
FD1_1590	hypothetical protein	0	114	0
FD1_1591	hypothetical protein	8	0	0
FD1_1592	HD domain hydrolase	174	206	0
FD1_1593***	alpha-amylase	108**	265*,**	0*
FD1_1594	hypothetical protein	0	0	0
FD1_1595	hypothetical transmembrane protein	0	0	0
FD1_1596	hypothetical protein	0	0	0
FD1_1597	hypothetical protein	26	0	0
FD1_1598	fibronectin (pseudogene)	138	0	15
FD1_1599	fibronectin (pseudogene)	107	70	0
FD1_1600	fibronectin (pseudogene)	65	0	0
FD1_1601	AraC family transcriptional regulator	25	0	15
FD1_1602	hypothetical secreted protein	515	214	0
FD1_1603	hypothetical protein	381	178	0
FD1_1604	hypothetical protein	240	184	188
FD1_1607	CRISPR-associated endonuclease Cas2	20	0	0
FD1_1608	CRISPR-associated protein Cas1	29	4	42
FD1_1609	CRISPR-associated protein Cas4	30	11	0
FD1_1610	CRISPR-associated protein Cas7/Csd2	52	0	0
FD1_1611**	CRISPR-associated protein Csd1	23**	3**	17
FD1_1612	CRISPR-associated protein Cas5	51	0	0
FD1_1613	CRISPR-associated protein Cas3	40	21	0
FD1_1614*	DEAD/DEAH box helicase	36*	12	0*
FD1_1615	hypothetical protein	37	16	4
FD1_1616	hypothetical protein	0	0	0
FD1_1617	hypothetical protein	0	0	0
FD1_1618	hypothetical protein	5	7	0
FD1_1619*	dockerin type I repeat-containing domain protein	23	44*	0*
FD1_1620	adhesin-like protein	2	0	5
FD1_1621	hypothetical transmembrane protein	3	0	0
FD1_1622	diguanylate cyclase (GGDEF) domain protein	3	3	9
FD1_1623*	ABC transporter permease	42*	11	0*
FD1_1624	ABC transporter ATP-binding protein	99	0	0
FD1_1625	transcriptional regulator	35	29	0
FD1_1626***	histidine kinase	124*,**	21**	0*
FD1_1627	hypothetical protein	284	397	52
FD1_1628	stage V sporulation protein T	0	0	0
FD1_1629**	dinitrogenase iron-molybdenum cofactor biosynthesis protein	149**	16**	0
FD1_1630	C_GCAxxG_C_C family redox protein	153	55	0
FD1_1631**	metallo-beta-lactamase	173**	9**	0
FD1_1632	long-chain-fatty-acid--CoA ligase (pseudogene)	97	0	0
FD1_1633**	long-chain-fatty-acid--CoA ligase (pseudogene)	56**	10**	0
FD1_1634	hypothetical protein	32	0	0
FD1_1635	AMP-binding enzyme	10	0	0
FD1_1636	RNA polymerase subunit sigma-32	15	0	0
FD1_1637	chromate transporter	27	0	0
FD1_1638	chromate transporter	17	0	0
FD1_1639	hypothetical protein	54	0	0

FD1_1640	hypothetical protein	31	6	0
FD1_1641*	transglutaminase/protease	77*	62	5*
FD1_1642	alpha/beta hydrolase	2	12	0
FD1_1643	AAA-ATPase family protein	0	0	0
FD1_1644	hypothetical protein	0	0	0
FD1_1645	<i>N</i> -acetyltransferase	0	7	0
FD1_1646	pyridoxamine 5'-phosphate oxidase	0	0	0
FD1_1647	hypothetical protein	0	0	0
FD1_1648	polyketide biosynthesis methyltransferase	9	0	0
FD1_1649	iron transporter FeoB	0	0	0
FD1_1650	iron transporter FeoA	0	0	0
FD1_1651	hypothetical protein	0	0	0
FD1_1652	transcriptional regulator	7	0	0
FD1_1653	hypothetical protein	176	312	112
FD1_1654	hypothetical protein	2	0	0
FD1_1655	hypothetical protein	5	0	0
FD1_1656	hypothetical protein	9	14	0
FD1_1657	hypothetical protein	31	0	0
FD1_1658	bifunctional aminoglycoside modifying enzyme AacA-AphD	6	10	0
FD1_1659**	GNAT family acetyltransferase	47**	6**	0
FD1_1660	relaxase/mobilization nuclease family protein	0	0	0
FD1_1661	Sir2 silent information regulator family NAD- dependent deacetylase	14	0	0
FD1_1662	hypothetical protein	23	5	0
FD1_1663	(4Fe-4S)-binding protein	11	0	0
FD1_1664	transcriptional regulator	0	0	0
FD1_1665	NADH-flavin reductase	0	0	0
FD1_1666	alpha/beta hydrolase family protein	1	0	60
FD1_1667	efflux ABC transporter permease	7	5	8
FD1_1668	ABC transporter ATP-binding protein	21	9	0
FD1_1669	hypothetical transmembrane protein	7	0	0
FD1_1670	RNA polymerase subunit sigma-24	0	0	0
FD1_1671	hypothetical protein	2	27	0
FD1_1672	hypothetical protein	0	30	0
FD1_1673	hypothetical protein	3	0	0
FD1_1674	hypothetical protein	15	32	0
FD1_1675	sodium:alanine symporter	2	0	0
FD1_1676	hypothetical protein	13	0	0
FD1_1677	cation diffusion facilitator family transporter	24	0	0
FD1_1678	hypothetical transmembrane protein	0	0	0
FD1_1679	amidohydrolase family protein	37	0	0
FD1_1680	arabinogalactan endo-1 4-beta-galactosidase	255	320	9
FD1_1681*	GTPase HflX	90	124*	0*
FD1_1682	cellulase	113	111	0
FD1_1683	hypothetical transmembrane protein	24	47	0
FD1_1684	carbohydrate kinase	106	29	16
FD1_1685	cytidylate kinase	14	0	0
FD1_1686	citrate transporter	5	7	0
FD1_1687	chorismate synthase	29	24	0
FD1_1688	3-deoxy-7-phosphoheptulonate synthase	44	0	0
FD1_1689**	conjugal transfer protein TraX	91**	9**	0
FD1_1690	hypothetical protein	19	16	0
FD1_1691	hypothetical protein	0	1	0
FD1_1692	ATPase	6	5	0
FD1_1693	hypothetical protein	43	13	0
FD1_1694	hypothetical protein	106	0	0
FD1_1695	L,D-transpeptidase catalytic domain protein	34	5	0
FD1_1696	hypothetical protein	12	0	0
FD1_1697	hypothetical protein	45	0	72
FD1_1698	hypothetical secreted protein	44	0	0
FD1_1699	hypothetical transmembrane protein	0	0	0
FD1_1700	phenylalanyl-tRNA synthetase subunit alpha	14	0	0

FD1_1701	hypothetical transmembrane protein	0	0	0
FD1_1702	phenylalanyl-tRNA synthetase subunit beta	12	0	0
FD1_1703	phosphoribosylamine--glycine ligase	19	0	0
FD1_1704	hypothetical protein	43	19	0
FD1_1705**	transcriptional regulator	259**	34**	0
FD1_1706	histidine kinase	24	5	0
FD1_1707	trypsin-like serine proteases	24	0	0
FD1_1708	hypothetical transmembrane protein	96	12	0
FD1_1709	preprotein translocase, YajC subunit	15	0	0
FD1_1710	50S ribosomal protein L17	111	28	0
FD1_1711	DNA-directed RNA polymerase subunit alpha	203	0	0
FD1_1712	30S ribosomal protein S4	63	0	0
FD1_1713	30S ribosomal protein S11	15	0	0
FD1_1714	30S ribosomal protein S13	67	14	0
FD1_1715	translation initiation factor IF-1	13	27	0
FD1_1716	hypothetical protein	69	0	0
FD1_1717	methionine aminopeptidase	55	14	0
FD1_1718	adenylate kinase	44	0	0
FD1_1719**	preprotein translocase subunit SecY	93**	0**	0
FD1_1720	50S ribosomal protein L15	24	16	0
FD1_1721	50S ribosomal protein L30	14	0	0
FD1_1722	30S ribosomal protein S5	49	22	0
FD1_1723	50S ribosomal protein L18	50	0	0
FD1_1724	50S ribosomal protein L6	57	16	0
FD1_1725	30S ribosomal protein S8	51	0	0
FD1_1726	30S ribosomal protein S14	36	0	0
FD1_1727	50S ribosomal protein L5	131	8	0
FD1_1728	50S ribosomal protein L24	1	0	0
FD1_1729	50S ribosomal protein L14	41	0	0
FD1_1730	30S ribosomal protein S17	5	0	0
FD1_1731**	50S ribosomal protein L29	52**	0**	0
FD1_1732	50S ribosomal protein L16	66	15	0
FD1_1733	30S ribosomal protein S3	78	6	0
FD1_1734	50S ribosomal protein L22	28	0	0
FD1_1735	30S ribosomal protein S19	7	0	0
FD1_1736	50S ribosomal protein L2	76	7	0
FD1_1737	50S ribosomal protein L23	0	0	0
FD1_1738	50S ribosomal protein L4	17	0	0
FD1_1739	50S ribosomal protein L3	8	15	0
FD1_1740	30S ribosomal protein S10	57	0	0
FD1_1741	glycerophosphoryl diester phosphodiesterase	35	0	0
FD1_1742	nicotinate-nucleotide pyrophosphorylase	106	0	0
FD1_1743	D-alanyl-D-alanine carboxypeptidase domain containing protein	31	0	0
FD1_1744	nucleotidyltransferase	68	0	0
FD1_1745	hypothetical protein	10	0	0
FD1_1746	fumarate reductase	14	0	0
FD1_1747	hypothetical transmembrane protein	11	7	0
FD1_1748	protein-export membrane protein SecF	14	12	0
FD1_1749	protein-export membrane protein SecD	36	14	0
FD1_1750	ATP synthase epsilon chain 2	0	0	0
FD1_1751	ATP synthase subunit beta	3	0	0
FD1_1752	F ₀ F ₁ ATP synthase subunit gamma	9	0	0
FD1_1753	ATP synthase F ₁ subunit alpha	4	5	0
FD1_1754	ATP synthase F ₀ subunit B	0	0	0
FD1_1755	F ₀ F ₁ ATP synthase subunit C	0	0	0
FD1_1756	F ₀ F ₁ ATP synthase subunit C	0	0	0
FD1_1757	ATP synthase F ₀ F ₁ subunit A	9	0	0
FD1_1758	hypothetical protein	0	0	0
FD1_1759	GDP-D-mannose dehydratase	8	0	0
FD1_1760	glycosyltransferase	1	0	0
FD1_1761	hypothetical protein	0	0	0

FD1_1762	glycosyl transferase family 1	6	0	0
FD1_1763	hypothetical protein	0	0	0
FD1_1764	GDP-mannose 4,6-dehydratase	4	0	0
FD1_1765	mannose-1-phosphate guanylyltransferase	10	0	0
FD1_1766	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	0	0	0
FD1_1767	hypothetical transmembrane protein	0	0	0
FD1_1768	stage IV sporulation protein B	72	35	0
FD1_1769	phosphotransferase System HPr (HPr) Family	203	151	0
FD1_1770	tRNA (guanine-N ₁)-methyltransferase	0	9	0
FD1_1771	hypothetical protein	0	0	0
FD1_1772	hypothetical transmembrane protein	25	0	0
FD1_1773	hypothetical transmembrane protein	20	4	0
FD1_1774	16S rRNA processing protein RimM	11	1	0
FD1_1775	hypothetical transmembrane protein	50	0	0
FD1_1776	hypothetical transmembrane protein	0	0	0
FD1_1777	adenylosuccinate lyase	9	0	0
FD1_1778	alpha,alpha-phosphotrehalase	5	0	24
FD1_1779	alpha-glucan phosphorylase (pseudogene)	11	0	0
FD1_1780**	alpha-glucan phosphorylase (pseudogene)	19**	2**	0
FD1_1781	hypothetical transmembrane protein	86	13	0
FD1_1782	peptidylprolyl isomerase	29	0	0
FD1_1783	hypothetical protein	45	0	0
FD1_1784	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase (pseudogene)	44	11	0
FD1_1785	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase (pseudogene)	0	0	0
FD1_1786	hypothetical protein	148	169	10
FD1_1787	hypothetical protein	113	0	0
FD1_1788	6-pyruvoyl tetrahydropterin synthase	17	0	0
FD1_1789	7-carboxy-7-deazaguanine synthase	18	11	0
FD1_1790	GTP cyclohydrolase	10	0	0
FD1_1791	queuosine biosynthesis protein QueC	0	12	0
FD1_1792	7-cyano-7-deazaguanine reductase	21	14	0
FD1_1793	glycoside hydrolase	89	83	17
FD1_1794	ABC transporter permease	77	34	53
FD1_1795	ABC-type uncharacterized transport system, permease component	35	53	0
FD1_1796	ABC transporter ATP-binding protein	39	25	0
FD1_1797	ZIP zinc transporter	0	13	0
FD1_1798	hypothetical protein	36	0	0
FD1_1799**	glycoside hydrolase family 3	50**	7**	0
FD1_1800	hypothetical protein	18	0	0
FD1_1801*	ricin-type beta-trefoil lectin domain protein	188*	60	0*
FD1_1802	AraC family transcriptional regulator	20	18	0
FD1_1803***	glycoside hydrolase family protein	78*,**	16**	0*
FD1_1804	transcriptional regulator	9	0	0
FD1_1805	hypothetical transmembrane protein	9	0	0
FD1_1806	adhesin-like protein	10	6	0
FD1_1807	aminoglycoside phosphotransferase	0	0	0
FD1_1808	acetaldehyde dehydrogenase (pseudogene)	0	0	0
FD1_1809	acetaldehyde dehydrogenase (pseudogene)	0	0	0
FD1_1810	acetaldehyde dehydrogenase (pseudogene)	0	0	0
FD1_1811	hypothetical protein	329	118	0
FD1_1812	disulfide oxidoreductase	25	47	0
FD1_1813	AcrR family transcriptional regulator	6	0	0
FD1_1814***	hypothetical secreted protein	181*,**	40**	0*
FD1_1815	hypothetical protein	9	19	0
FD1_1816*	hypothetical protein	22	55*	0*
FD1_1817	RNA polymerase sigma-I factor	28	8	0
FD1_1818	hypothetical transmembrane protein	0	8	0
FD1_1819	LytTR family transcriptional regulator	0	7	0
FD1_1820	CAAX prenyl protease domain-containing protein	0	0	0
FD1_1821	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase	42	14	0
FD1_1822	ECF subfamily RNA polymerase sigma factor	0	15	0

FD1_1823	hypothetical transmembrane protein	1	6	0
FD1_1824	hypothetical protein	0	0	0
FD1_1825	sugar fermentation stimulation protein	0	6	0
FD1_1826	deoxyguanosinetriphosphate triphosphohydrolase	16	6	0
FD1_1827	ion transporter	17	36	0
FD1_1828*	hypothetical protein	190*	137	0*
FD1_1829	hypothetical protein	16	0	0
FD1_1830	signal peptidase	16	0	0
FD1_1831***	glycosyl hydrolase family 9	117**	388*,**	4*
FD1_1832***	adhesin-like protein	77**	413*,**	0*
FD1_1833*	sortase	35	168*	0*
FD1_1834*	hypothetical secreted protein	58	121*	0*
FD1_1835***	hypothetical transmembrane protein	4**	50*,**	0*
FD1_1836	ABC-type multidrug transport system ATPase and permease components	12	2	0
FD1_1837	multidrug ABC transporter ATP-binding protein	18	0	0
FD1_1838**	transposase	151**	22**	0
FD1_1839	MerR family transcriptional regulator	22	0	0
FD1_1840	multidrug ABC transporter ATP-binding protein	15	9	0
FD1_1841	sugar ABC transporter ATP-binding protein	13	0	0
FD1_1842**	diguanylate cyclase	59**	6**	10
FD1_1843**	ABC transporter substrate-binding protein	135**	16**	21
FD1_1844**	carbohydrate-binding protein	84**	5**	0
FD1_1845	hypothetical protein	498	324	0
FD1_1846	hypothetical protein	26	0	0
FD1_1847	phosphorylase	23	0	0
FD1_1848	hypothetical transmembrane protein	37	21	0
FD1_1849	hypothetical protein	8	0	0
FD1_1850	iron transporter FeoB (pseudogene)	22	12	0
FD1_1851	iron transporter FeoB (pseudogene)	66	21	0
FD1_1852	LysR family transcriptional regulator	0	0	0
FD1_1853	oxidoreductase	6	0	0
FD1_1854	gamma-carboxymuconolactone decarboxylase	25	13	0
FD1_1855	flavodoxin	0	41	0
FD1_1856	hypothetical transmembrane protein	20	24	0
FD1_1857	ECF subfamily RNA polymerase sigma-24 factor	20	0	0
FD1_1858	transcriptional regulator	6	17	31
FD1_1859	bacitracin ABC transporter ATP-binding protein	17	0	0
FD1_1860	hypothetical transmembrane protein	0	0	0
FD1_1861	histidine kinase	13	0	0
FD1_1862	hypothetical protein	44	0	0
FD1_1863	hypothetical secreted protein	3	1	0
FD1_1864	MATE efflux family protein	12	0	28
FD1_1865	transposase	19	7	0
FD1_1866	integrase family protein	0	0	0
FD1_1867	integrase family protein	5	0	0
FD1_1868	integrase family protein (pseudogene)	16	0	0
FD1_1869	integrase family protein (pseudogene)	39	0	0
FD1_1870	integrase	11	7	0
FD1_1871**	integrase family protein	79**	0**	0
FD1_1872	oxidoreductase	0	7	0
FD1_1873	hypothetical protein	10	0	0
FD1_1874	hypothetical protein	0	0	0
FD1_1875	hypothetical protein	0	0	0
FD1_1876	hypothetical protein	0	0	0
FD1_1877	hypothetical protein	11	0	0
FD1_1878	resolvase	0	11	0
FD1_1879	short-chain dehydrogenase	0	0	0
FD1_1880	nucleoside-diphosphate sugar epimerase	3	0	0
FD1_1881	hypothetical protein	0	0	0
FD1_1882	hypothetical transmembrane protein	18	23	0
FD1_1883*	histidine kinase	38*	8	0*

FD1_1884	transcriptional regulator	24	0	0
FD1_1885	hypothetical protein	0	0	0
FD1_1886	hypothetical protein	8	3	0
FD1_1887	hypothetical protein	0	0	0
FD1_1888	isochorismatase family protein	19	0	0
FD1_1889	transcriptional regulator	2	3	0
FD1_1890	hypothetical transmembrane protein	41	33	0
FD1_1891	unnamed protein product, partial	45	45	0
FD1_1892	EAL domain-containing protein	59	10	0
FD1_1893*	hypothetical secreted protein	294*	111	0*
FD1_1894	<i>N</i> -acetylglucosamine-1-phosphate uridyltransferase	300	102	0
FD1_1895	hypothetical protein	26	30	0
FD1_1896	adhesin-like protein	27	29	0
FD1_1897	cobalt transport protein	1	11	0
FD1_1898	cobalt ABC transporter ATP-binding protein	11	27	0
FD1_1899	metal ion ABC transporter, membrane-spanning subunit	13	0	0
FD1_1900***	1-phosphofructokinase	5**	58*,**	0*
FD1_1901	ArsC family transcriptional regulator	32	0	0
FD1_1902	cysteine synthase	156	185	25
FD1_1903**	Rrf2 family transcriptional regulator	0**	63**	0
FD1_1904	dTDP-glucose 4,6-dehydratase	9	41	0
FD1_1905	hypothetical protein	0	0	0
FD1_1906	hypothetical transmembrane protein	0	0	0
FD1_1907	hypothetical protein	9	0	0
FD1_1908	acetyltransferase	20	33	0
FD1_1909	hypothetical protein	42	6	0
FD1_1910**	hypothetical secreted protein	108**	4**	0
FD1_1911	integrase	54	0	0
FD1_1912	XRE family transcriptional regulator	72	0	0
FD1_1913	hypothetical protein	0	0	0
FD1_1914	hypothetical protein	0	0	0
FD1_1915	hypothetical protein	0	0	0
FD1_1916	hypothetical protein	0	0	0
FD1_1917	hypothetical protein	0	0	0
FD1_1918	hypothetical protein	0	0	0
FD1_1919	resolvase	20	4	0
FD1_1920***	hypothetical protein	1847*,**	330**	63*
FD1_1921	DNA-binding protein	360	80	0
FD1_1922	transposase	0	0	0
FD1_1923	transcriptional regulator	4	0	0
FD1_1924	histidine kinase	18	8	0
FD1_1925	ABC transporter ATP-binding protein	0	0	0
FD1_1926	ABC transporter permease	0	0	0
FD1_1927	hypothetical transmembrane protein	0	0	0
FD1_1928	hypothetical protein	0	0	0
FD1_1929	hypothetical protein	0	0	0
FD1_1930	hypothetical protein	0	0	0
FD1_1931	resolvase	14	8	0
FD1_1932*	hypothetical protein	196*	147	10*
FD1_1933	hypothetical transmembrane protein	24	0	43
FD1_1934	cobalt transporter	0	0	0
FD1_1935	hypothetical transmembrane protein	0	10	0
FD1_1936	hypothetical transmembrane protein	0	0	0
FD1_1937	hypothetical transmembrane protein	8	0	0
FD1_1938	ketopantoate reductase	10	0	0
FD1_1939	hypothetical transmembrane protein	0	0	0
FD1_1940	hypothetical protein	0	0	0
FD1_1941	esterase	0	0	0
FD1_1942	hypothetical transmembrane protein	0	0	0
FD1_1943	copper chaperone	24	0	0
FD1_1944	methyltransferase type 11 (pseudogene)	0	0	0

FD1_1945	methyltransferase type 11 (pseudogene)	0	0	0
FD1_1946	hypothetical transmembrane protein	20	0	0
FD1_1947	protein-S-isoprenylcysteine methyltransferase	0	0	0
FD1_1948	hypothetical transmembrane protein	0	0	0
FD1_1949	hypothetical transmembrane protein	0	0	0
FD1_1950	methyltransferase type 11	0	0	0
FD1_1951	hypothetical transmembrane protein	0	0	0
FD1_1952	methyltransferase	0	0	0
FD1_1953	hypothetical transmembrane protein	0	0	0
FD1_1954	multidrug ABC transporter ATP-binding protein	5	0	13
FD1_1955	multidrug ABC transporter permease	10	0	0
FD1_1956	transcriptional regulator	37	18	0
FD1_1957	recombinase	6	0	0
FD1_1958	DNA-binding protein	0	0	0
FD1_1959	hypothetical protein	0	0	0
FD1_1960	hypothetical protein	0	0	0
FD1_1961	hypothetical protein	0	0	0
FD1_1962	hypothetical protein	0	0	0
FD1_1963	hypothetical protein	11	0	0
FD1_1964**	hypothetical protein	104**	7**	0
FD1_1965***	type I site-specific deoxyribonuclease	333*,**	104**	16*
FD1_1966*	KAP P-loop domain protein	269*	122	0*
FD1_1967*	hypothetical protein	104	172*	0*
FD1_1968	restriction endonuclease subunit S, partial	111	180	0
FD1_1969	type I restriction endonuclease subunit M (pseudogene)	150	112	0
FD1_1970	restriction endonuclease subunit M (pseudogene)	82	165	0
FD1_1971	hypothetical protein	67	135	0
FD1_1972	hypothetical protein	21	54	0
FD1_1973	hypothetical protein	37	36	0
FD1_1974	SMC domain-containing protein	50	65	0
FD1_1975	hypothetical protein	19	0	0
FD1_1976**	excisionase family DNA binding domain-containing protein	1396**	110**	85
FD1_1977	transposase	36	15	0
FD1_1978	hypothetical transmembrane protein	0	0	0
FD1_1979	hypothetical protein	0	0	0
FD1_1980	hypothetical protein	0	0	0
FD1_1981	metal-dependent hydrolase, beta-lactamase superfamily III	0	0	0
FD1_1982	methionine ABC transporter ATP-binding protein	0	0	0
FD1_1983	binding-protein-dependent transport systems inner membrane component	0	0	0
FD1_1984	metal ABC transporter substrate-binding protein	12	0	0
FD1_1985	nitrogenase	7	0	0
FD1_1986	oxidoreductase/nitrogenase component 1	4	0	0
FD1_1987	hypothetical transmembrane protein	0	0	0
FD1_1988	adhesin-like protein	7	0	0
FD1_1989	hypothetical protein	28	88	38
FD1_1990	adhesin-like protein	8	25	0
FD1_1991**	resolvase	587**	135**	95
FD1_1992	hypothetical secreted protein	57	72	15
FD1_1993	NERD nuclease	148	55	0
FD1_1994	hypothetical protein	38	132	45
FD1_1995	hypothetical protein	26	0	0
FD1_1996	hypothetical protein	0	0	0
FD1_1997	hypothetical protein	1	0	0
FD1_1998	hypothetical transmembrane protein	6	11	0
FD1_1999	hypothetical transmembrane protein	0	0	0
FD1_2000	hypothetical transmembrane protein	0	0	0
FD1_2001	hypothetical transmembrane protein	0	0	0
FD1_2002	hypothetical transmembrane protein	0	0	0
FD1_2003	energy-coupling factor transporter ATPase	0	0	0
FD1_2004	cobalt ECF transporter T component CbiQ	5	0	0
FD1_2005	multidrug ABC transporter ATP-binding protein (pseudogene)	0	0	64

FD1_2006	multidrug ABC transporter ATP-binding protein (pseudogene)	7	0	0
FD1_2007	multidrug ABC transporter permease	9	0	17
FD1_2008	AraC family transcriptional regulator	0	0	0
FD1_2009	hypothetical transmembrane protein	0	0	0
FD1_2010	thiol reductant ABC exporter	4	0	0
FD1_2011	lipid A export permease/ATP-binding protein MsbA	4	0	0
FD1_2012	hypothetical protein	0	0	0
FD1_2013	AMP-dependent synthetase	0	0	0
FD1_2014	amino acid adenylation protein	0	0	0
FD1_2015	thioesterase domain protein	0	0	0
FD1_2016	beta-ketoacyl synthase	0	0	0
FD1_2017	3-ketoacyl-ACP reductase	0	0	0
FD1_2018	thioesterase domain protein	6	0	0
FD1_2019	condensation domain protein	3	0	0
FD1_2020	antibiotic ABC transporter ATP-binding protein	0	0	0
FD1_2021	ABC-2 type transporter	0	0	0
FD1_2022	ABC transporter efflux protein	0	0	0
FD1_2023	putative oxidoreductase	0	0	0
FD1_2024	thioesterase	0	0	0
FD1_2025	beta-ketoacyl synthase (pseudogene)	0	0	0
FD1_2026	beta-ketoacyl synthase (pseudogene)	5	0	5
FD1_2027	amino acid adenylation domain protein	2	0	0
FD1_2028	peptide synthetase, siderophore biosynthesis protein	0	0	0
FD1_2029	amino acid adenylation domain protein	4	0	0
FD1_2030	beta-ketoacyl synthase	4	0	9
FD1_2031	amino acid adenylation domain protein	3	0	0
FD1_2032	3-oxoacyl-ACP synthase	0	0	0
FD1_2033	acyl carrier protein	0	0	0
FD1_2034	saccharopine dehydrogenase	0	0	0
FD1_2035	macrolide ABC transporter ATP-binding protein	0	0	0
FD1_2036	peptide ABC transporter permease	1	0	31
FD1_2037	4'-phosphopantetheinyl transferase	0	0	0
FD1_2038	hypothetical transmembrane protein	0	0	0
FD1_2039	FMN-binding protein	0	0	0
FD1_2040	ABC transporter ATP-binding protein	0	0	0
FD1_2041	TetR family transcriptional regulator	7	0	0
FD1_2042	aldo/keto reductase	15	54	0
FD1_2043	enolase	5	23	0
FD1_2044	macrolide ABC transporter ATP-binding protein	0	0	0
FD1_2045	peptide ABC transporter permease	2	0	0
FD1_2046	hypothetical protein	0	0	0
FD1_2047	flavodoxin	0	0	43
FD1_2048	hypothetical protein	0	0	0
FD1_2049	hypothetical transmembrane protein	0	6	0
FD1_2050	transcriptional regulator AraC family	19	7	0
FD1_2051	hypothetical transmembrane protein	116	23	0
FD1_2052	cation transporter	24	19	0
FD1_2053	hypothetical transmembrane protein	0	0	0
FD1_2054	transcriptional regulator TetR family	0	0	0
FD1_2055	diguanylate cyclase	31	44	0
FD1_2056	hypothetical secreted protein	0	0	0
FD1_2057	adhesin-like protein	0	0	0
FD1_2058	type I secretion system ATPase	1	0	0
FD1_2059	type I secretion membrane fusion protein, HlyD family	0	6	0
FD1_2060	hypothetical protein	0	0	0
FD1_2061	RNA polymerase subunit sigma-24	0	0	0
FD1_2062	hypothetical transmembrane protein	6	0	0
FD1_2063	hypothetical protein	0	11	0
FD1_2064	hypothetical protein	0	0	0
FD1_2065	hypothetical transmembrane protein	18	13	0
FD1_2066	ketoacyl reductase	41	0	0

FD1_2067	hypothetical transmembrane protein	9	0	0
FD1_2068	alginate <i>O</i> -acetylation protein	7	0	0
FD1_2069	ribonuclease M5	0	14	0
FD1_2070	DNA polymerase III subunit delta	0	0	0
FD1_2071	competence protein ComEC	25	0	0
FD1_2072	adenine phosphoribosyltransferase	20	10	0
FD1_2073	HIT family hydrolase	81	0	0
FD1_2074	alanyl-tRNA synthetase	11	0	0
FD1_2075**	SPFH/Band 7/PHB domain protein	1937**	549**	0
FD1_2076*	PTS ascorbate transporter subunit IIC	646*	174	0*
FD1_2077	ATPase AAA	3	3	0
FD1_2078	ATPase AAA (pseudogene)	7	0	0
FD1_2079	ATPase AAA (pseudogene)	62	0	0
FD1_2080	hypothetical protein	0	5	0
FD1_2081	hypothetical protein	0	0	0
FD1_2082	hypothetical protein	11	0	0
FD1_2083	hypothetical protein	44	49	0
FD1_2084	cyclic lactone autoinducer peptide family protein	0	91	0
FD1_2085	accessory gene regulator	0	158	0
FD1_2086***	histidine kinase-DNA gyrase B-and HSP90-like ATPase	8*,**	274*,**	81
FD1_2087**	lytTr DNA-binding domain protein	6**	88**	26
FD1_2088**	DNA-binding helix-turn-helix protein	350**	3483**	269
FD1_2089	hypothetical protein	0	0	0
FD1_2090	hypothetical secreted protein	0	0	0
FD1_2091**	hypothetical protein	0**	15**	0
FD1_2092	hypothetical protein	0	3	0
FD1_2093	hypothetical secreted protein	0	11	0
FD1_2094	XRE family transcriptional regulator	39	8	0
FD1_2095	hypothetical protein	47	13	0
FD1_2096	sigma-70, region 4	0	0	0
FD1_2097	hypothetical protein	0	0	0
FD1_2098	hypothetical protein	0	0	0
FD1_2099	hypothetical protein	0	0	0
FD1_2100	recombinase	10	0	15
FD1_2101	protein kinase	39	57	0
FD1_2102	adhesin-like protein	14	23	13
FD1_2103*	hypothetical transmembrane protein	26*	15	0*
FD1_2104	hypothetical transmembrane protein	26	0	0
FD1_2105	iron-dependent transcriptional regulator	35	0	0
FD1_2106	CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase	45	0	0
FD1_2107	ribosomal protein S12 methylthiotransferase	57	4	0
FD1_2108	regulatory protein RecX	8	0	0
FD1_2109	recombinase RecA	22	11	0
FD1_2110	protein-(glutamine-N ⁵) methyltransferase	61	0	0
FD1_2111**	protein-(glutamine-N ⁵) methyltransferase	27**	4**	2
FD1_2112**	histidine kinase	34**	6**	13
FD1_2113	PhoP family transcriptional regulator	44	0	0
FD1_2114	hypothetical transmembrane protein	24	0	0
FD1_2115	citrate synthase	36	4	0
FD1_2116	stage II sporulation protein D	22	0	0
FD1_2117	hypothetical protein	0	0	0
FD1_2118	hypothetical protein	0	0	0
FD1_2119	ABC-type multidrug transport system, ATPase and permease component	0	5	0
FD1_2120	signal peptidase I	0	0	0
FD1_2121	hypothetical protein	0	11	0
FD1_2122	hypothetical protein	0	0	0
FD1_2123	hypothetical protein	0	25	0
FD1_2124	hypothetical protein	0	28	0
FD1_2125	hypothetical protein	3	19	0
FD1_2126	class II glutamine amidotransferase	0	0	0
FD1_2127	LIM zinc-binding protein	0	0	0

FD1_2128	hypothetical protein	11	0	0
FD1_2129	DNA binding domain, excisionase family	0	0	0
FD1_2130	DNA binding domain, excisionase family	0	0	0
FD1_2131*	transposase	278*	206	0*
FD1_2132	transcriptional regulator	0	0	0
FD1_2133	hypothetical protein	0	0	0
FD1_2134	hypothetical protein	0	0	0
FD1_2135	histidine kinase	0	9	0
FD1_2136	DeoR family transcriptional regulator	0	0	0
FD1_2137	SAM-dependent methyltransferase	0	2	0
FD1_2138	hypothetical protein	63	36	20
FD1_2139	LytTr DNA-binding domain-containing protein	19	1	0
FD1_2140	sensor histidine kinase	55	23	0
FD1_2141	hypothetical protein	30	0	0
FD1_2142	hypothetical protein	17	6	0
FD1_2143	hypothetical protein	0	0	0
FD1_2144	hypothetical transmembrane protein	0	0	0
FD1_2145	sortase	43	0	0
FD1_2146	hypothetical protein	0	0	0
FD1_2147**	MIP family channel proteins	281**	22**	0
FD1_2148	GCN5 family acetyltransferase	5	15	0
FD1_2149	peptidase U32	12	0	0
FD1_2150	YceG family protein	12	0	0
FD1_2151	5,10-methenyltetrahydrofolate synthetase	54	0	0
FD1_2152	DJ-1 family protein	20	0	0
FD1_2153**	hypothetical protein	26**	3**	0
FD1_2154	FAD-dependent thymidylate synthase	20	4	0
FD1_2155	hypothetical protein	58	0	0
FD1_2156	DNA replication protein DnaC	28	29	0
FD1_2157	DnaD domain protein	62	38	0
FD1_2158	GTP pyrophosphokinase	7	29	0
FD1_2159	RNA polymerase sigma-K factor	3	0	0
FD1_2160	ribulose-phosphate 3-epimerase	11	8	0
FD1_2161	electron transport complex, RnfABCDGE type, D subunit	14	0	0
FD1_2162	electron transport complex, RnfABCDGE type, E subunit	0	6	0
FD1_2163	electron transport complex, RnfABCDGE type, A subunit	0	3	0
FD1_2164	hypothetical transmembrane protein	33	10	0
FD1_2165	HPr kinase	88	46	0
FD1_2166	UDP-N-acetylenolpyruvoylglucosamine reductase	73	23	0
FD1_2167**	glmZ(sRNA)-inactivating NTPase	84**	12**	0
FD1_2168	DNA-binding protein WhiA	19	0	0
FD1_2169	DNA polymerase III subunit alpha	15	5	7
FD1_2170	6-phosphofructokinase	72	0	0
FD1_2171	RNA-binding protein	55	0	23
FD1_2172	hypothetical protein	12	0	0
FD1_2173	hypothetical protein	12	0	0
FD1_2174	peptide chain release factor 1	5	0	0
FD1_2175	translation factor SUA5	33	8	0
FD1_2176	dephospho-CoA kinase	58	11	0
FD1_2177**	aminopeptidase	73**	3**	0
FD1_2178**	LysR family transcriptional regulator	1194**	373**	0
FD1_2179***	ATP-dependent helicase	654* **	181**	20*
FD1_2180**	biotin carboxylase	575**	171**	0
FD1_2181**	tellurite-resistance protein	491**	108**	0
FD1_2182	RNA polymerase subunit sigma-24	9	0	0
FD1_2183	hypothetical protein	30	3	21
FD1_2184	hypothetical secreted protein	21	34	0
FD1_2185	hypothetical protein	11	10	0
FD1_2186***	transglutaminase domain-containing protein	48* **	7**	0*
FD1_2187*	hypothetical transmembrane protein	63*	30	0*
FD1_2188	ATPase AAA	6	27	0

FD1_2189	hypothetical transmembrane protein	837	427	0
FD1_2190	ArsC family transcriptional regulator	52	0	0
FD1_2191***	hypothetical protein	104**	1829*,**	0*
FD1_2192***	hypothetical protein	225**	942*,**	0*
FD1_2193***	hypothetical protein	76**	1219*,**	0*
FD1_2194***	hypothetical protein	73**	665*,**	0*
FD1_2195**	hypothetical protein	6**	509**	0
FD1_2196***	hypothetical protein	20**	321*,**	0*
FD1_2197***	hypothetical protein	65**	886*,**	0*
FD1_2198	lantibiotic lacticin	0	551	0
FD1_2199	lantibiotic lacticin	0	347	0
FD1_2200**	lantibiotic lacticin	0**	184**	0
FD1_2201**	lantibiotic lacticin	0**	162**	0
FD1_2202***	hypothetical protein	45**	378*,**	0*
FD1_2203**	NHLM bacteriocin system ABC transporter, peptidase/ATP-binding protein	15**	607**	17
FD1_2204***	type 2 lantibiotic biosynthesis protein LanM	19**	1113*,**	6*
FD1_2205***	type 2 lantibiotic biosynthesis protein LanM	26**	1029*,**	6*
FD1_2206**	hypothetical transmembrane protein	43**	1406**	53
FD1_2207**	ABC transporter substrate-binding protein	70**	1218**	0
FD1_2208**	ABC-2 type transport system permease	96**	4958**	102
FD1_2209***	lantibiotic protection ABC transporter, ATP-binding subunit	90**	4482*,**	54*
FD1_2210	metal-dependent hydrolase	0	0	0
FD1_2211*	hypothetical protein	453*	203	0*
FD1_2212*	hypothetical protein	631*	241	35*
FD1_2213	hypothetical protein	4	7	0
FD1_2214	5-methylcytosine-specific restriction protein C	8	0	0
FD1_2215	P-type conjugative transfer ATPase TrbB	11	0	0
FD1_2216	hypothetical protein	8	0	0
FD1_2217	hypothetical protein	0	0	0
FD1_2218	MerR family transcriptional regulator	0	13	0
FD1_2219	hypothetical protein	0	0	0
FD1_2220	plasmid recombination protein	4	11	0
FD1_2221	integrase	22	20	0
FD1_2222**	30S ribosomal protein S9	235**	8**	0
FD1_2223*	50S ribosomal protein L13	167*	62	0*
FD1_2224	hypothetical secreted protein	62	14	0
FD1_2225	integrase	0	8	14
FD1_2226	DNA binding domain protein excisionase family	19	0	0
FD1_2227	phage/plasmid primase P4	15	0	45
FD1_2228	DNA primase	0	0	0
FD1_2229*	hypothetical protein	34*	10	0*
FD1_2230*	hypothetical protein	729*	453	72*
FD1_2231*	molybdopterin-guanine dinucleotide biosynthesis protein MobA	322*	215	6*
FD1_2232	mobilization protein	118	191	0
FD1_2233	hypothetical protein	79	35	0
FD1_2234	hypothetical protein	75	44	0
FD1_2235	type I site-specific deoxyribonuclease, HsdR family	78	76	0
FD1_2236*	ABC transporter substrate-binding protein	88	158*	0*
FD1_2237	type I restriction endonuclease subunit S	29	72	0
FD1_2238	type I restriction-modification system, M subunit	41	59	0
FD1_2239	hypothetical protein	67	75	0
FD1_2240	hypothetical protein	56	184	0
FD1_2241*	hypothetical transmembrane protein	470	1136*	97*
FD1_2242	hypothetical protein	596	1377	375
FD1_2243**	GHH signature containing HNH/Endo VII supernuclease toxin family protein	349**	1236**	85
FD1_2244**	hypothetical protein	339**	833**	41
FD1_2245	hypothetical protein	356	197	0
FD1_2246	XRE family transcriptional regulator	138	134	0
FD1_2247	single-stranded DNA-binding protein	0	0	0
FD1_2248	hypothetical protein	0	0	0

FD1_2249	hypothetical protein	12	0	0
FD1_2250	hypothetical protein	8	0	0
FD1_2251	hypothetical protein	0	0	0
FD1_2252	resolvase	0	0	0
FD1_2253	DNA-binding protein	11	0	0
FD1_2254	DNA-binding helix-turn-helix protein	0	0	0
FD1_2255	hypothetical protein	0	0	0
FD1_2256	hypothetical protein	0	0	0
FD1_2257	hypothetical protein	0	0	0
FD1_2258	ATP:cob(I)alamin adenosyltransferase	6	0	0
FD1_2259	GGGtGRT protein	25	0	0
FD1_2260**	nitrogen-fixing protein NifU	121**	21**	0
FD1_2261	topoisomerase DNA-binding C4 zinc finger domain protein	32	6	0
FD1_2262	hypothetical protein	21	14	0
FD1_2263	ornithine carbamoyltransferase	16	30	0
FD1_2264***	adhesin-like protein	101*,**	17**	0*
FD1_2265**	adhesin-like protein	47**	2**	0
FD1_2266	hypothetical protein	17	0	0
FD1_2267	hypothetical transmembrane protein	22	11	0
FD1_2268	hypothetical transmembrane protein	7	0	0
FD1_2269	hypothetical transmembrane protein	43	0	0
FD1_2270	hypothetical transmembrane protein	51	5	0
FD1_2271	XRE family transcriptional regulator	20	124	0
FD1_2272	hypothetical protein	31	0	0
FD1_2273	proline--tRNA ligase	17	5	0
FD1_2274***	large mechanosensitive ion channel protein MscL	427*,**	98**	19*
FD1_2275*	hypothetical protein	300*	102	2*
FD1_2276	D-Ala-D-Ala carboxypeptidase VanY	24	0	0
FD1_2277	heat-inducible transcription repressor HrcA	5	13	0
FD1_2278	co-chaperone GrpE	67	0	0
FD1_2279	chaperone protein DnaK	61	61	0
FD1_2280	molecular chaperone DnaJ	23	10	0
FD1_2281	hypothetical protein	19	0	0
FD1_2282	hypothetical transmembrane protein	57	22	0
FD1_2283	hypothetical protein	35	0	0
FD1_2284	pectate lyase/Amb allergen	48	50	0
FD1_2285	iron transporter FeoB	18	13	0
FD1_2286	DNA-binding helix-turn-helix protein	0	0	0
FD1_2287	antifreeze protein type I	0	0	0
FD1_2288	hypothetical protein	0	0	0
FD1_2289	hypothetical protein	0	0	0
FD1_2290	hypothetical protein	63	52	0
FD1_2291	urea ABC transporter, permease protein UrtB	40	0	24
FD1_2292**	urea ABC transporter, permease protein UrtC	66**	4**	0
FD1_2293**	D-xylose ABC transporter, ATP-binding protein	41**	3**	9
FD1_2294	D-xylose ABC transporter, D-xylose-binding protein	90	40	15
FD1_2295	GntR family transcriptional regulator	69	27	0
FD1_2296***	phosphotransacetylase	117*,**	12**	0*
FD1_2297	hypothetical transmembrane protein	5	6	0
FD1_2298	RNA polymerase subunit sigma-24	0	0	0
FD1_2299	hypothetical transmembrane protein	52	48	0
FD1_2300	acetyl xylan esterase	10	0	0
FD1_2301*	sugar ABC transporter permease	233	491*	0*
FD1_2302*	ABC transporter permease	130	270*	0*
FD1_2303	ABC transporter substrate-binding protein	985	787	16
FD1_2304	xylose isomerase	173	117	0
FD1_2305	beta-glucosidase	92	81	0
FD1_2306	hypothetical protein	120	141	0
FD1_2307	regulator	19	28	0
FD1_2308**	multidrug transporter MatE	156**	4**	0
FD1_2309	hypothetical transmembrane protein	70	30	46

FD1_2310***	hypothetical protein	323*,**	12**	0*
FD1_2311	hypothetical protein	39	0	0
FD1_2312	von Willebrand factor type A	103	0	0
FD1_2313**	protein kinase	513**	5**	0
FD1_2314	cell wall-binding protein	103	0	0
FD1_2315***	periplasmic binding protein	519*,**	112**	12*
FD1_2316***	diguanylate cyclase	272*,**	31**	0*
FD1_2317	single-stranded DNA-binding protein	58	0	0
FD1_2318	GNAT family acetyltransferase	10	27	0
FD1_2319**	carboxypeptidase	71**	3**	0
FD1_2320	ubiquinone/menaquinone biosynthesis methyltransferase	24	17	0
FD1_2321	methionine aminopeptidase	78	7	0
FD1_2322	DNA-directed DNA polymerase	0	8	0
FD1_2323	recombinase	6	0	0
FD1_2324	hypothetical protein	0	0	0
FD1_2325	hypothetical protein	1	0	0
FD1_2326	hypothetical protein	0	0	0
FD1_2327	hypothetical protein	0	0	0
FD1_2328	hypothetical protein	18	13	0
FD1_2329	hypothetical protein	0	0	0
FD1_2330	hypothetical protein	17	0	0
FD1_2331	recombinase	4	8	0
FD1_2332	hypothetical protein	40	0	0
FD1_2333	hypothetical protein	7	13	0
FD1_2334	hypothetical protein	0	0	0
FD1_2335	glucosamine 6-phosphate synthetase	14	0	0
FD1_2336	hypothetical protein	0	0	0
FD1_2337	LIM zinc-binding protein	0	6	0
FD1_2338	transcriptional regulator	25	0	0
FD1_2339	DNA (cytosine-5-)-methyltransferase	4	6	0
FD1_2340	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	113	28	0
FD1_2341*	Z1 domain-containing protein	35	43*	0*
FD1_2342	hypothetical protein	23	35	0
FD1_2343	hypothetical protein	78	25	0
FD1_2344	recombinase	101	70	0
FD1_2345	prevent-host-death protein	0	73	0
FD1_2346	toxin-antitoxin system, toxin component, PIN family	5	98	0
FD1_2347***	hypothetical protein	2910**	8038*,**	919*
FD1_2348	hypothetical protein	0	0	0
FD1_2349	RNA polymerase subunit sigma-24	0	0	0
FD1_2350	hypothetical transmembrane protein	4	7	0
FD1_2351	hypothetical secreted protein	0	45	0
FD1_2352	hypothetical protein	0	0	0
FD1_2353	hypothetical protein	0	9	0
FD1_2354	hypothetical protein	0	72	0
FD1_2355	adhesin-like protein	0	15	0
FD1_2356	hypothetical protein	6	0	0
FD1_2357	hypothetical protein	0	0	0
FD1_2358	hypothetical transmembrane protein	4	4	0
FD1_2359	phage integrase family	0	0	0
FD1_2360	hypothetical protein	0	0	0
FD1_2361	dockerin type I repeat-containing domain protein	0	0	0
FD1_2362	hypothetical protein	115	0	0
FD1_2363	hypothetical protein	21	23	0
FD1_2364	hypothetical transmembrane protein	24	0	0
FD1_2365**	von Willebrand factor A	31**	2**	0
FD1_2366	hypothetical protein	16	0	0
FD1_2367	acyl-CoA ligase (AMP-forming)	33	0	0
FD1_2368	PP-loop family protein	17	0	0
FD1_2369	DNA gyrase, B subunit	12	0	0
FD1_2370	GNAT family acetyltransferase	20	0	0

FD1_2371	hypothetical transmembrane protein	19	4	0
FD1_2372	topoisomerase IV	41	17	0
FD1_2373	hypothetical protein	14	0	45
FD1_2374	spermidine synthase	9	0	0
FD1_2375	multidrug transporter MatE	2	0	0
FD1_2376	50S ribosomal protein L28	31	0	0
FD1_2377	peptidase M50	0	0	0
FD1_2378	Zn-dependent protease	11	0	0
FD1_2379	chromosome segregation and condensation protein ScpA	0	0	0
FD1_2380	chromosome segregation and condensation protein ScpB	9	0	0
FD1_2381	hypothetical transmembrane protein	3	0	0
FD1_2382	sporulation protein YtfJ	59	16	0
FD1_2383	Serine-type D-Ala-D-Ala carboxypeptidase	5	0	0
FD1_2384	RNA pseudouridine synthase	34	0	0
FD1_2385	hypothetical protein	1	0	0
FD1_2386	homoserine O-succinyltransferase	28	0	0
FD1_2387	hypothetical protein	20	18	0
FD1_2388	hypothetical transmembrane protein	27	0	0
FD1_2389	TspO/MBR family protein	42	0	0
FD1_2390	hypothetical protein	30	0	0
FD1_2391	hypothetical protein	6	0	0
FD1_2392	D-alanyl-D-alanine carboxypeptidase	44	22	0
FD1_2393	NAD-dependent DNA ligase LigA	18	8	0
FD1_2394	peptidoglycan-binding protein	0	0	0
FD1_2395	diaminopimelate dehydrogenase	14	0	0
FD1_2396	glycoside hydrolase family 25	41	0	0
FD1_2397	methionyl-tRNA synthetase	13	2	0
FD1_2398	hypothetical protein	54	11	0
FD1_2399	hypothetical protein	0	0	0
FD1_2400**	hypothetical protein	666**	24**	0
FD1_2401	hypothetical protein	0	0	0
FD1_2402	excinuclease ABC subunit A	9	0	0
FD1_2403	excinuclease ABC subunit B	3	0	23
FD1_2404	amino acid ABC transporter substrate-binding protein	10	0	0
FD1_2405	ATPase components of ABC transporters	3	0	0
FD1_2406	SCIFF radical SAM maturase	45	0	0
FD1_2407	ECF subfamily RNA polymerase sigma-24 factor	13	0	0
FD1_2408	hypothetical protein	33	0	0
FD1_2409**	DNA-directed RNA polymerase subunit beta	48**	3**	0
FD1_2410***	DNA-directed RNA polymerase subunit beta'	69*,**	10**	0*
FD1_2411*	metallo-beta-lactamase	138*	100	0*
FD1_2412	hypothetical protein	21	0	0
FD1_2413	hypothetical protein (pseudogene)	17	0	0
FD1_2414	hypothetical protein (pseudogene)	19	0	0
FD1_2415	transcriptional regulator	0	0	0
FD1_2416	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	18	0	0
FD1_2417	ABC transporter, ATP-binding protein	3	0	0
FD1_2418	ABC transporter permease	4	0	0
FD1_2419	ABC transporter permease	0	0	0
FD1_2420**	hypothetical transmembrane protein	98**	3**	0
FD1_2421	phosphomethylpyrimidine kinase	13	4	0
FD1_2422	hydroxymethylpyrimidine transporter CytX	44	0	0
FD1_2423**	phosphomethylpyrimidine synthase ThiC	55**	4**	0
FD1_2424*	beta-mannosidase	198*	75	0*
FD1_2425*	lysophospholipase L1 and related esterase	95*	40	0*
FD1_2426	hypothetical protein	0	0	0
FD1_2427	asparagine synthase	0	0	0
FD1_2428	anthranilate synthase subunit I	36	7	0
FD1_2429**	anthranilate synthase subunit II	113**	13**	0
FD1_2430*	anthranilate phosphoribosyltransferase	149*	29	0*
FD1_2431	indole-3-glycerol-phosphate synthase	21	21	0

FD1_2432	<i>N</i> -(5'phosphoribosyl)anthranilate isomerase (PRAI)	89	14	0
FD1_2433	SAM-dependent methyltransferase	10	1	0
FD1_2434***	tryptophan synthase subunit beta	80*, **	15**	0*
FD1_2435**	tryptophan synthase subunit alpha	69**	4**	0
FD1_2436*	peptidase S1 and S6 chymotrypsin/Hap	86*	47	0*
FD1_2437	hypothetical protein	17	0	0
FD1_2438	cysteine desulfurase	2	0	0
FD1_2439	hypothetical transmembrane protein	78	33	0
FD1_2440	hypothetical transmembrane protein	71	63	0
FD1_2441	hypothetical transmembrane protein	10	0	0
FD1_2442	CAAX prenyl protease domain-containing protein	49	0	0
FD1_2443	chaperone protein HtpG	11	4	0
FD1_2444	hypothetical protein	23	0	0
FD1_2445	tyrosyl-tRNA synthetase	66	4	0
FD1_2446	type IV pilin	2866	1478	0
FD1_2447***	pyruvate formate lyase-activating protein	924*, **	286**	0*
FD1_2448	tRNA nucleotidyltransferase	57	59	40
FD1_2449	gIY-YIG nuclease superfamily protein	96	61	0
FD1_2450	Tex-like protein	26	23	0
FD1_2451	ferredoxin	205	41	0
FD1_2452	<i>O</i> -Antigen ligase	1	0	0
FD1_2453	hypothetical protein	13	4	0
FD1_2454	ribonuclease	38	0	17
FD1_2455	recombinase	5	0	0
FD1_2456	transposon-encoded protein TnpW	0	0	0
FD1_2457	6- <i>O</i> -methylguanine DNA methyltransferase	0	0	0
FD1_2458	hypothetical protein	0	0	0
FD1_2459	hypothetical secreted protein	0	11	0
FD1_2460	RNA polymerase subunit sigma-24	0	0	0
FD1_2461	hypothetical protein	0	0	0
FD1_2462	molecular chaperone Hsp33	15	0	0
FD1_2463	methyltransferase	21	0	0
FD1_2464	hypothetical transmembrane protein	0	0	0
FD1_2465	preprotein translocase subunit SecA	27	0	7
FD1_2466	dipicolinate synthase subunit A	0	0	0
FD1_2467	dipicolinate synthase	0	0	0
FD1_2468	crystallin	0	0	0
FD1_2469	prolyl-tRNA synthetase	0	0	0
FD1_2470	hypothetical protein	0	0	0
FD1_2471	stage 0 sporulation protein	0	0	0
FD1_2472	DNA polymerase III, delta prime subunit	14	0	0
FD1_2473	arginine/lysine/ornithine decarboxylase	17	0	0
FD1_2474	RNA polymerase sigma factor, sigma-70 family	0	0	0
FD1_2475	hypothetical protein	49	0	0
FD1_2476	HD superfamily hydrolase	0	19	0
FD1_2477	SCP-like extracellular	180	146	0
FD1_2478	hypothetical protein	45	8	0
FD1_2479*	gCN5-related N-acetyltransferase	1103*	524	0*
FD1_2480	16S rRNA pseudouridylylase	11	0	0
FD1_2481**	hypothetical transmembrane protein	144**	1**	0
FD1_2482	NrdR family transcriptional regulator	39	6	0
FD1_2483	sugar phosphate isomerase/epimerase	12	2	0
FD1_2484	(Fe-S)-binding protein	0	11	0
FD1_2485	hydroxylamine reductase	10	0	0
FD1_2486	Sir2 silent information regulator family NAD-dependent deacetylase	20	22	0
FD1_2487	hypothetical protein	0	13	0
FD1_2488	(4Fe-4S)-binding protein	0	0	0
FD1_2489	transcriptional regulator	0	0	0
FD1_2490	dihydrodipicolinate reductase	0	0	0
FD1_2491	hypothetical protein	0	0	0
FD1_2492	hypothetical transmembrane protein	0	0	0

FD1_2493	HIRAN domain-containing protein	11	0	0
FD1_2494	hypothetical protein	3	0	0
FD1_2495	heat shock protein 70	15	0	0
FD1_2496	UvrD/REP helicase	15	0	0
FD1_2497***	helicase domain-containing protein	22*,**	3**	0*
FD1_2498	hypothetical protein	11	0	0
FD1_2499	hypothetical protein	27	0	0
FD1_2500	bacterial mobilization protein	0	0	0
FD1_2501	hypothetical protein	0	0	0
FD1_2502	hypothetical protein	0	0	0
FD1_2503	hypothetical protein	0	0	0
FD1_2504	resolvase	26	0	0
FD1_2505***	phage integrase family protein	326*,**	90**	0*
FD1_2506**	hypothetical protein	95**	8**	0
FD1_2507**	hypothetical protein	124**	6**	0
FD1_2508*	repressor LexA	188*	56	0*
FD1_2509	hypothetical protein	43	17	0
FD1_2510	hypothetical protein	2	4	0
FD1_2511	hypothetical protein	0	0	0
FD1_2512	hypothetical protein	67	0	0
FD1_2513	hypothetical protein	179	0	0
FD1_2514***	hypothetical transmembrane protein	395*,**	67**	0*
FD1_2515	hypothetical protein	39	29	0
FD1_2516	hypothetical protein	25	14	0
FD1_2517	hypothetical secreted protein	91	26	0
FD1_2518	formate/nitrite transporter	27	45	32
FD1_2519*	ChW repeat-/cell adhesion domain-containing transglutaminase-like protease	134	327*	0*
FD1_2520**	aminotransferase	44**	4**	0
FD1_2521	cell envelope-like transcriptional attenuator	51	8	0
FD1_2522***	hypothetical transmembrane protein	31*,**	4**	0*
FD1_2523	RNA methyltransferase	26	0	0
FD1_2524	phosphoesterase	22	0	0
FD1_2525	acyl carrier protein	34	0	0
FD1_2526**	hAD-superfamily phosphatase subfamily IIIC/FkbH-like domain	27**	2*	0
FD1_2527	hypothetical transmembrane protein	11	0	0
FD1_2528	hypothetical transmembrane protein	19	0	0
FD1_2529	MBOAT, membrane-bound <i>O</i> -acyltransferase family protein	69	9	0
FD1_2530*	peptidase (pseudogene)	493*	210	0*
FD1_2531*	peptidase (pseudogene)	398*	123	0*
FD1_2532*	hypothetical protein	509*	206	0*
FD1_2533	LuxR family transcriptional regulator	2	0	0
FD1_2534	histidine kinase	9	0	0
FD1_2535	glutamine synthetase	16	2	0
FD1_2536	hypothetical transmembrane protein	0	0	0
FD1_2537	RNA polymerase sigma 70	0	0	0
FD1_2538	4Fe-4S ferredoxin	5	0	0
FD1_2539	hypothetical protein	0	0	0
FD1_2540	5-nitroimidazole antibiotic resistance protein	11	0	0
FD1_2541	nitroreductase (pseudogene)	0	0	0
FD1_2542	nitroreductase (pseudogene)	0	0	0
FD1_2543	HAD superfamily hydrolase	24	0	0
FD1_2544	hypothetical transmembrane protein	24	16	0
FD1_2545	hypothetical protein	25	10	0
FD1_2546	pyridoxamine 5'-phosphate oxidase family protein	0	0	0
FD1_2547	flavodoxin	98	0	0
FD1_2548	9- <i>O</i> -acetyl- <i>N</i> -acetylneuraminate esterase	27	27	0
FD1_2549***	hypothetical protein	1761*,**	76**	0*
FD1_2550**	formate <i>C</i> -acetyltransferase glycine radical	133**	16**	0
FD1_2551	hypothetical protein	255	0	0
FD1_2552*	formate acetyltransferase	77*	17	0*
FD1_2553	hypothetical transmembrane protein	4	0	0

FD1_2554***	diguanylate cyclase (GGDEF) domain-containing protein	78*,**	11**	0*
FD1_2555	ArsR family transcriptional regulator	73	0	0
FD1_2556	PAS/PAC sensor signal transduction histidine kinase	42	15	0
FD1_2557	hypothetical protein	32	10	0
FD1_2558	hypothetical protein	37	0	0
FD1_2559	elongation factor G	28	0	0
FD1_2560	stage V sporulation protein B	0	0	0
FD1_2561	DNA-binding protein	32	11	0
FD1_2562	CobB/CobQ-like glutamine amidotransferase domain protein	40	0	12
FD1_2563	glutamate ligase	4	0	10
FD1_2564	DNA helicase	13	0	3
FD1_2565	fibro-slime domain-containing protein	0	0	0
FD1_2566	fibro-slime domain-containing protein	0	0	0
FD1_2567	hypothetical protein	0	0	0
FD1_2568	pilin isopeptide linkage domain protein	0	0	0
FD1_2569	sortase	0	0	0
FD1_2570	pilin isopeptide linkage domain protein	5	0	0
FD1_2571	UDP- <i>N</i> -acetylglucosamine pyrophosphorylase	33	0	0
FD1_2572	hypothetical transmembrane protein	19	0	0
FD1_2573	UDP- <i>N</i> -acetylglucosamine 4,6-dehydratase	32	0	0
FD1_2574	exopolysaccharide biosynthesis protein	4	0	0
FD1_2575	capsular exopolysaccharide family	6	2	0
FD1_2576	phosphoribosyl-ATP pyrophosphatase	83	0	0
FD1_2577	phosphoribosyl-AMP cyclohydrolase	19	0	0
FD1_2578	SdpI/YhfL family protein	44	0	0
FD1_2579	ATPase AAA	18	0	0
FD1_2580	cytidine deaminase	0	0	0
FD1_2581	imidazole glycerol phosphate synthase	0	0	0
FD1_2582	hypothetical transmembrane protein	0	0	0
FD1_2583	hypothetical transmembrane protein	0	0	0
FD1_2584	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	0	0	0
FD1_2585	flavodoxin	0	0	0
FD1_2586	protein tyrosine/serine phosphatase	16	0	0
FD1_2587	hypothetical transmembrane protein	0	9	0
FD1_2588	hypothetical transmembrane protein	0	2	0
FD1_2589	imidazole glycerol phosphate synthase	0	0	0
FD1_2590	imidazoleglycerol-phosphate dehydratase	6	0	0
FD1_2591	histidinol-phosphate aminotransferase	12	0	0
FD1_2592	hypothetical transmembrane protein	12	0	0
FD1_2593	histidinol dehydrogenase	11	0	0
FD1_2594	ATP phosphoribosyltransferase	6	0	0
FD1_2595	ATP phosphoribosyltransferase regulatory subunit	21	0	0
FD1_2596	DNA polymerase III subunit alpha	14	0	4
FD1_2597	4-hydroxy-3-methylbut-2- <i>en</i> -1-yl diphosphate synthase	26	0	0
FD1_2598	hypothetical protein	22	0	0
FD1_2599	ribonuclease Z	10	0	0
FD1_2600	RIP metalloprotease RseP	13	0	0
FD1_2601	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0	5	0
FD1_2602	phosphatidate cytidyltransferase	23	0	0
FD1_2603	UDP pyrophosphate synthase	74	0	0
FD1_2604	ribosome recycling factor	56	0	0
FD1_2605	uridylate kinase	32	0	0
FD1_2606	hypothetical protein	0	42	0
FD1_2607	transmembrane transglutaminase	0	12	0
FD1_2608	hypothetical protein	55	0	0
FD1_2609	hypothetical transmembrane protein	14	0	0
FD1_2610	hypothetical protein	0	0	0
FD1_2611	hypothetical protein	0	0	0
FD1_2612	CDP-diacylglycerol--serine <i>O</i> -phosphatidyltransferase	7	6	0
FD1_2613	polyphosphate kinase	25	3	0

FD1_2614	uridine kinase	41	0	0
FD1_2615	RNA-binding protein S1	94	83	0
FD1_2616	septum formation initiator	43	54	0
FD1_2617	spore cortex protein YabQ	8	0	0
FD1_2618	sporulation protein YabP	0	0	0
FD1_2619	hypothetical transmembrane protein	3	2	0
FD1_2620	hypothetical secreted protein	4	0	0
FD1_2621	redox-sensing transcriptional repressor Rex	47	0	0
FD1_2622	dihydropyrimidine dehydrogenase subunit A	55	0	0
FD1_2623**	sulfide dehydrogenase	75**	13**	0
FD1_2624	LysR family transcriptional regulator	31	0	0
FD1_2625	maltose acetyltransferase	15	0	0
FD1_2626	hypothetical transmembrane protein	4	0	0
FD1_2627	D-alanine--D-alanine ligase	4	0	0
FD1_2628	UDP- <i>N</i> -acetylmuramyl pentapeptide synthase	14	15	0
FD1_2629	hydrolase alpha/beta domain protein	8	9	0
FD1_2630**	hypothetical protein	187**	794**	0
FD1_2631**	ankyrin	92**	373**	0
FD1_2632**	TetR family transcriptional regulator	26**	301**	49
FD1_2633	carbamoyl phosphate synthase large subunit	10	17	0
FD1_2634	hypothetical protein	32	0	0
FD1_2635	hypothetical secreted protein	0	0	0
FD1_2636	cell cycle protein	10	0	0
FD1_2637	hypothetical transmembrane protein	23	0	0
FD1_2638	Mg chelatase	12	0	0
FD1_2639	hypothetical transmembrane protein	54	0	0
FD1_2640	hypothetical protein	0	0	0
FD1_2641	sporulation protein YtaF	34	15	0
FD1_2642	metallophosphoesterase	6	0	37
FD1_2643	DNA gyrase subunit A	37	17	0
FD1_2644**	hypothetical protein	45**	1**	0
FD1_2645**	DNA gyrase subunit B	23**	2**	0
FD1_2646	hypothetical protein	0	0	0
FD1_2647	transposase	0	0	0
FD1_2648	DNA replication and repair protein RecF	7	0	0
FD1_2649	S4 domain protein YaaA	0	0	0
FD1_2650	DNA polymerase III subunit beta	11	14	0
FD1_2651**	chromosomal replication initiator protein DnaA	113**	9**	0
FD1_2652	ribonuclease P protein component	20	0	0
FD1_2653	hypothetical protein	11	0	0
FD1_2654	membrane protein insertase	27	0	0
FD1_2655	single-stranded DNA-binding protein	16	5	0
FD1_2656	tRNA modification GTPase TrmE	2	0	23
FD1_2657	tRNA uridine 5-carboxymethylaminomethyl modification protein	0	0	0
FD1_2658	16S rRNA methyltransferase GidB	0	0	0
FD1_2659	chromosome partitioning protein ParB	4	0	1
FD1_2660	chromosome segregation ATPase	33	9	33
FD1_2661	plasmid partitioning protein ParB	92	0	0
FD1_2662	seryl-tRNA synthetase	24	13	0
FD1_2663	hypothetical protein	0	0	0
FD1_2664	GNAT family acetyltransferase	86	0	0
FD1_2665	thioredoxin	89	61	0
FD1_2666	GCN5-related <i>N</i> -acetyltransferase	26	36	0
FD1_2667**	flavodoxin	66**	8**	0
FD1_2668	hypothetical protein	46	15	0
FD1_2669	DNA-directed RNA polymerase specialized sigma subunit	0	0	0
FD1_2670	hypothetical protein	2	0	0
FD1_2671	metallophosphoesterase	40	0	0
FD1_2672	competence protein ComEA	57	80	0
FD1_2673	M42 glutamyl aminopeptidase	8	0	0
FD1_2674	hypothetical transmembrane protein	3	12	0

FD1_2675	glutamyl aminopeptidase	5	0	0
FD1_2676	hypothetical protein	29	0	0
FD1_2677	cystathionine beta-lyase family protein involved in aluminum resistance	16	0	0
FD1_2678	pASTA domain./Protein kinase domain	19	0	0
FD1_2679	ATP-dependent chaperone ClpB	29	7	0
FD1_2680**	hypothetical protein	21**	0**	0
FD1_2681	hypothetical protein	23	12	0
FD1_2682	cell division protein FtsZ	60	49	32
FD1_2683*	molecular chaperone	78*	16	0*
FD1_2684	AraC family transcriptional regulator	10	56	0
FD1_2685***	DNA-3-methyladenine glycosylase II	29**	147*,**	0*
FD1_2686	fibronectin-binding protein	10	44	0
FD1_2687	methyltransferase type 11	4	0	0
FD1_2688	hypothetical protein	20	0	0
FD1_2689	zinc-binding protein	66	24	0
FD1_2690	RNA polymerase factor sigma-70	29	0	0
FD1_2691***	hypothetical protein	424*,**	39**	0*
FD1_2692***	cell division protein FtsZ	231*,**	13**	0*
FD1_2693	cell division septal protein divIB/FtsQ	9	0	0
FD1_2694	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase	11	4	0
FD1_2695	hypothetical protein	20	0	0
FD1_2696	UDP-diphospho-muramoylpentapeptide beta- <i>N</i> -acetylglucosaminyltransferase	4	0	0
FD1_2697**	cell division protein FtsW	20**	3**	0
FD1_2698	phospho- <i>N</i> -acetylmuramoyl-pentapeptide-transferase	17	0	0
FD1_2699	UDP- <i>N</i> -acetylmuramyl peptide synthase	20	0	0
FD1_2700	penicillin-binding protein	36	0	0
FD1_2701	cell division protein FtsL	15	0	36
FD1_2702	16S rRNA methyltransferase	21	0	2
FD1_2703	division/cell wall cluster transcriptional repressor MraZ	125	0	61
FD1_2704	stage II sporulation protein D	17	0	0
FD1_2705	sortase, SrtB family	9	0	0
FD1_2706	sortase, SrtB family	8	16	0
FD1_2707	competence/damage-inducible protein CinA	8	0	0
FD1_2708	thiamine biosynthesis protein ThiI	19	0	0
FD1_2709	hypothetical transmembrane protein	7	0	0
FD1_2710	hypothetical transmembrane protein	0	0	0
FD1_2711	cysteine desulfurase NifS (pseudogene)	17	0	0
FD1_2712	cysteine desulfurase NifS (pseudogene)	0	0	0
FD1_2713	hypothetical transmembrane protein	5	4	0
FD1_2714	nudix-type nucleoside diphosphatase, YffH/AdpP family	150	36	0
FD1_2715**	septation protein spoVG	357**	19**	0
FD1_2716	UDP- <i>N</i> -acetylmuramate--L-alanine ligase	5	0	0
FD1_2717	lexA repressor	10	0	0
FD1_2718	cell division protein ZapA	0	0	0
FD1_2719	peptidase U32	25	4	0
FD1_2720	deoxyuridine 5'-triphosphate nucleotidohydrolase Dut	22	0	0
FD1_2721	hypothetical transmembrane protein	0	0	0
FD1_2722	rod shape-determining protein MreB	0	0	0
FD1_2723	rod shape-determining protein MreC	0	0	0
FD1_2724	rod shape-determining protein MreD	6	0	0
FD1_2725	penicillin-binding protein 2	5	0	0
FD1_2726	peptidase M23B	8	0	0
FD1_2727	glycosyl hydrolase, family 31	11	0	0
FD1_2728	type II restriction m6 adenine DNA methyltransferase	11	0	0
FD1_2729	hypothetical protein	0	0	0
FD1_2730	xylulokinase	29	0	11
FD1_2731	hypothetical protein	35	0	0
FD1_2732	hypothetical transmembrane protein	0	0	0
FD1_2733	VanZ family protein	72	0	0
FD1_2734	NAGC-like transcriptional regulator	635	295	23

FD1_2735	transporter	0	0	0
FD1_2736	hypothetical transmembrane protein	62	13	0
FD1_2737**	hypothetical transmembrane protein	60**	11**	0
FD1_2738	Fe ²⁺ /Zn ²⁺ uptake regulation protein	59	0	0
FD1_2739	hypothetical protein	52	0	0
FD1_2740	phenylacetate--CoA ligase	14	4	0
FD1_2741	indolepyruvate ferredoxin oxidoreductase, beta subunit	0	0	0
FD1_2742	indolepyruvate ferredoxin oxidoreductase, alpha subunit	0	0	11
FD1_2743*	hypothetical secreted protein	106*	54	0*
FD1_2744	thiamine biosynthesis protein ThiS	10	11	0
FD1_2745	thiamine biosynthesis protein ThiF	79	9	0
FD1_2746	thiazole synthase ThiG	94	19	0
FD1_2747	thiamine biosynthesis protein ThiH	35	5	0
FD1_2748	thiamine monophosphate synthase	1	15	0
FD1_2749	thiamine-phosphate diphosphorylase	54	35	0
FD1_2750***	endoglucanase family protein	258*,**	74**	0*
FD1_2751	hypothetical transmembrane protein	138	0	0
FD1_2752	alginate <i>O</i> -acetyltransferase AlgJ	9	2	0
FD1_2753	alginate <i>O</i> -acetylation protein AlgI	14	0	0
FD1_2754	hypothetical secreted protein	14	0	0
FD1_2755	adhesin-like protein	27	0	0
FD1_2756	methyltransferase	0	0	0
FD1_2757**	polyphosphate:nucleotide phosphotransferase	48**	5**	0
FD1_2758	diguanylate cyclase	23	0	0
FD1_2759***	ricin B lectin (pseudogene)	635*,**	115**	12*
FD1_2760***	ricin B lectin (pseudogene)	1107*,**	205**	0*
FD1_2761	transcriptional regulator, tetR family protein	8	25	0
FD1_2762	TetR family transcriptional regulator	62	70	0
FD1_2763**	collagen-binding protein A	148**	16**	17
FD1_2764	stage III sporulation protein D	18	0	0
FD1_2765	adhesin-like protein	13	0	0
FD1_2766	endonuclease V	7	0	0
FD1_2767	PhoB family transcriptional regulator	0	0	0
FD1_2768	phosphate regulon sensor kinase PhoR	17	0	0
FD1_2769	pentapeptide repeat-containing protein	39	0	0
FD1_2770	hypothetical transmembrane protein	8	0	0
FD1_2771	dockerin type I repeat-containing domain protein	0	4	0
FD1_2772	adhesin-like protein	0	1	0
FD1_2773	hypothetical protein	1	0	0
FD1_2774	MerR family transcriptional regulator	4	0	0
FD1_2775	acetyltransferase GNAT family	14	0	0
FD1_2776	DNA-entry nuclease	22	0	0
FD1_2777	hypothetical protein	20	0	0
FD1_2778***	hypothetical protein	464*,**	57**	0*
FD1_2779***	histidinol phosphate phosphatase HisJ family	527*,**	111**	0*
FD1_2780*	hypothetical transmembrane protein	160*	75	0*
FD1_2781	XRE family transcriptional regulator	130	32	35
FD1_2782	peptide ABC transporter ATP-binding protein	70	83	0
FD1_2783***	ABC-type antimicrobial peptide transport system permease component	207*,**	33**	21*
FD1_2784*	transcriptional regulator	529*	269	0*
FD1_2785*	periplasmic sensor signal transduction histidine kinase	697*	299	67*
FD1_2786*	hypothetical protein	727*	235	0*
FD1_2787	hypothetical protein	28	0	0
FD1_2788	Type I restriction-modification system, R subunit	9	7	0
FD1_2789	Type I restriction-modification system, specificity subunit S	7	0	0
FD1_2790	helicase	8	0	0
FD1_2791	hypothetical protein	4	0	0
FD1_2792	hypothetical protein	0	0	0
FD1_2793	RNA polymerase sigma factor, sigma-70 family	0	0	0
FD1_2794	hypothetical protein	25	10	0
FD1_2795	hypothetical protein	0	7	0

FD1_2796	hypothetical protein	14	0	0
FD1_2797	DNA-directed DNA polymerase	0	4	0
FD1_2798	hypothetical protein	0	0	109
FD1_2799	phage/plasmid primase, P4 family domain-containing protein	0	0	0
FD1_2800	nuclease	14	0	0
FD1_2801	DEAD/DEAH box helicase	14	17	0
FD1_2802	hypothetical protein	20	0	0
FD1_2803**	HNH endonuclease	147**	10**	0
FD1_2804	hypothetical protein	34	16	0
FD1_2805	hypothetical protein	0	27	0
FD1_2806	terminase	215	242	0
FD1_2807	adenine methyltransferase	318	346	18
FD1_2808	hypothetical protein	21	0	0
FD1_2809**	virulence-related protein	146**	5**	35
FD1_2810**	hypothetical protein	342**	55**	0
FD1_2811	alpha-L-fucosidase	5	0	0
FD1_2812	gamma-glutamyl cyclotransferase	0	0	0
FD1_2813	hydrogenase maturation protein HypF	0	0	0
FD1_2814	hypothetical protein	0	0	0
FD1_2815	hypothetical protein	0	0	0
FD1_2816	hypothetical protein	0	0	0
FD1_2817	phage Terminase (pseudogene)	12	0	0
FD1_2818*	phage Terminase (pseudogene)	40*	8	0*
FD1_2819	hypothetical protein	11	0	0
FD1_2820	phage portal protein (pseudogene)	11	0	0
FD1_2821	phage portal protein (pseudogene)	0	0	0
FD1_2822	peptidase s14, clpp	26	41	30
FD1_2823**	phage major capsid protein, HK97 family	33**	3**	0
FD1_2824	phage conserved hypothetical protein	50	2	0
FD1_2825	head-tail adaptor	15	85	0
FD1_2826*	prophage pi2 protein 37	229*	60	0*
FD1_2827	phage protein	0	15	0
FD1_2828	phage major tail protein	21	14	0
FD1_2829	hypothetical protein	35	0	0
FD1_2830	hypothetical protein	32	40	20
FD1_2831	hypothetical transmembrane protein	21	49	0
FD1_2832*	phage tail length tape measure protein	87	142*	0*
FD1_2833	hypothetical protein	20	0	0
FD1_2834	hypothetical protein	0	0	0
FD1_2835	phage tail component protein	0	0	0
FD1_2836	siphovirus Requitepy6 Gp37-like protein	5	0	0
FD1_2837	bacterial group 2 Ig-like protein	0	0	0
FD1_2838	hypothetical protein	0	0	0
FD1_2839	hypothetical protein	0	0	0
FD1_2840	holin	0	0	0
FD1_2841	glycosyl hydrolase family 25	0	0	0
FD1_2842	DNA-binding protein	0	0	0
FD1_2843	DNA-binding protein	0	0	80
FD1_2844	DNA-binding protein	0	0	155
FD1_2845	transposase	0	4	0
FD1_2846	hypothetical protein	0	0	0
FD1_2847	phosphotyrosine protein phosphatase	0	0	0
FD1_2848**	hypothetical secreted protein	279**	66**	41
FD1_2849*	hypothetical transmembrane protein	162*	96	9*
FD1_2850	ABC transporter ATP-binding protein	181	141	37
FD1_2851*	histidine kinase	202*	97	10*
FD1_2852	transcriptional regulator	69	84	0
FD1_2853	glycosyl hydrolase family 9	36	27	0
FD1_2854***	hypothetical protein	915*,**	247**	36*
FD1_2855	RNA 2'-phosphotransferase	186	43	0
FD1_2856	hypothetical protein	150	55	0

FD1_2857	hypothetical protein	257	44	0
FD1_2858	glycoside hydrolase family 26	72	15	0
FD1_2859***	1,4-alpha-glucan branching protein	9**	48*,**	0*
FD1_2860	transcriptional regulator, TetR family protein	0	0	15
FD1_2861	adhesin-like protein	14	0	0
FD1_2862	diguanylate cyclase	14	0	0
FD1_2863*	cellulose binding domain./glycosyl hydrolase family 9	137*	47	0*
FD1_2864	hydrolase GDSL	117	137	0
FD1_2865	DNA repair protein RadC	64	18	0
FD1_2866***	DNA repair protein RadC	149*,**	8**	0*
FD1_2867***	hypothetical transmembrane protein	120*,**	12**	0*
FD1_2868	hypothetical protein	37	11	0
FD1_2869***	S-adenosylmethionine synthetase	179*,**	13**	0*
FD1_2870	signal transduction histidine kinase	20	11	0
FD1_2871	transcriptional regulator	6	13	0
FD1_2872	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	51	12	0
FD1_2873	hypothetical protein	36	11	0
FD1_2874***	6-phosphofructokinase	331*,**	52**	0*
FD1_2875**	phosphoglucomutase	69**	3**	0
FD1_2876	hypothetical transmembrane protein	9	0	0
FD1_2877	50S ribosomal protein L31	72	0	0
FD1_2878	hypothetical protein	50	0	0
FD1_2879	hypothetical protein	62	27	0
FD1_2880**	deoxyguanosinetriphosphate triphosphohydrolase	112**	6**	0
FD1_2881**	DNA primase	59**	2**	0
FD1_2882*	RNA polymerase sigma factor RpoD	126*	92	11*
FD1_2883	GNAT family acetyltransferase	33	0	0
FD1_2884	spore coat associated protein JA	82	87	0
FD1_2885	spore-coat protein	101	156	0
FD1_2886	CotJC	175	105	0
FD1_2887	hypothetical protein	213	483	0
FD1_2888***	hypothetical transmembrane protein	147**	535*,**	0*
FD1_2889*	DNA-directed RNA polymerase subunit sigma	106	290*	0*
FD1_2890	hypothetical protein	0	0	0
FD1_2891	aldo/keto reductase	0	0	0
FD1_2892	hypothetical protein	0	0	0
FD1_2893	hypothetical transmembrane protein	5	0	0
FD1_2894	regulatory protein BetI	0	0	0
FD1_2895	hypothetical protein	0	0	0
FD1_2896	hypothetical protein	0	7	0
FD1_2897	hypothetical protein	0	0	0
FD1_2898	DNA invertase Pin	4	0	0
FD1_2899	adhesin-like protein	26	13	0
FD1_2900	signal peptidase (type I)	3	0	0
FD1_2901***	sortase, SrtB family	66*,**	4**	0*
FD1_2902*	hypothetical transmembrane protein	23	66*	0*
FD1_2903	hypothetical protein	1	21	0
FD1_2904	phage/plasmid primase, P4 family domain protein	36	17	0
FD1_2905	hypothetical transmembrane protein	0	0	0
FD1_2906	hypothetical protein	14	0	0
FD1_2907	hypothetical protein	0	0	0
FD1_2908	hypothetical protein	0	0	0
FD1_2909*	hypothetical transmembrane protein	130*	52	0*
FD1_2910	fibro-slime domain-containing protein	39	23	6
FD1_2911	hypothetical transmembrane protein	13	12	0
FD1_2912	signal peptidase I	23	22	0
FD1_2913	sortase, SrtB family	60	18	0
FD1_2914*	hypothetical transmembrane protein	64	121*	0*
FD1_2915***	alternate signal-mediated exported protein	116**	471*,**	19*
FD1_2916*	signal peptidase	135	192*	0*
FD1_2917	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	0	0	0

FD1_2918	dithiobiotin synthetase	0	0	0
FD1_2919	biotin synthase	5	0	0
FD1_2920	biotin biosynthesis protein BioY	3	0	0
FD1_2921	bacterial SH3 domain protein	174	132	0
FD1_2922	multidrug transporter MatE (pseudogene)	8	0	0
FD1_2923	multidrug transporter MatE (pseudogene)	14	0	0
FD1_2924*	dihydroxy-acid dehydratase	40*	8	0*
FD1_2925**	3-isopropylmalate dehydrogenase	33**	5**	0
FD1_2926	ATPase AAA	45	19	0
FD1_2927**	L-threonine ammonia-lyase	94**	16**	22
FD1_2928**	3-isopropylmalate dehydratase large subunit	111**	6**	0
FD1_2929	3-isopropylmalate dehydratase small subunit	119	8	0
FD1_2930**	endoribonuclease L-PSP	142**	0**	0
FD1_2931**	50S rRNA methyltransferase	132**	19**	0
FD1_2932	beta-lactamase	57	0	0
FD1_2933*	cysteinyl-tRNA synthetase	58*	15	0*
FD1_2934	hypothetical protein	51	0	0
FD1_2935	collagenase and related protease	45	0	0
FD1_2936	collagenase and related protease	50	0	46
FD1_2937	biotin synthase	85	14	0
FD1_2938**	quinolinate synthetase	66**	9**	0
FD1_2939	polysaccharide deacetylase	0	0	0
FD1_2940	stage II sporulation protein P	0	0	0
FD1_2941***	hypothetical transmembrane protein	142* **	17**	0*
FD1_2942	hypothetical protein	32	0	0
FD1_2943	RNA polymerase subunit sigma-24	0	0	0
FD1_2944	hypothetical protein	11	7	0
FD1_2945	hypothetical protein	28	0	0
FD1_2946	hypothetical protein	10	9	0
FD1_2947	hypothetical transmembrane protein	14	24	0
FD1_2948	RNA polymerase subunit sigma-24	51	0	0
FD1_2949**	hypothetical secreted protein	0**	16**	0
FD1_2950	hypothetical protein	0	0	0
FD1_2951	GCN5 family acetyltransferase	0	0	0
FD1_2952	hypothetical transmembrane protein	0	0	0
FD1_2953	hypothetical protein	0	0	0
FD1_2954	esterase	0	0	0
FD1_2955	methyltransferase	0	0	0
FD1_2956	methyltransferase type 11	0	0	0
FD1_2957	transcriptional regulator	0	0	0
FD1_2958	ABC transporter ATP-binding protein	8	0	0
FD1_2959	ABC transporter permease (pseudogene)	4	0	0
FD1_2960	ABC transporter permease (pseudogene)	0	4	0
FD1_2961	ABC transporter permease (pseudogene)	0	0	0
FD1_2962	hypothetical transmembrane protein	9	3	11
FD1_2963	hypothetical transmembrane protein	0	35	0
FD1_2964	RNA polymerase subunit sigma-24	0	0	0
FD1_2965	PAS domain S-box protein	17	0	0
FD1_2966	anti-sigma F factor antagonist	15	0	0
FD1_2967	sigma regulatory factor-histidine kinase	8	0	0
FD1_2968	histidine kinase	14	0	0
FD1_2969	diguanylate cyclase	4	0	0
FD1_2970	diguanylate cyclase	0	0	0
FD1_2971***	collagen-binding protein A	511**	1759*,**	9*
FD1_2972	magnesium transporter	23	14	0
FD1_2973***	RNA polymerase, sigma-24 subunit, ECF subfamily protein	288**	1278*,**	0*
FD1_2974*	hypothetical transmembrane protein	167	562*	0*
FD1_2975*	hypothetical transmembrane protein	126	298*	0*
FD1_2976	hypothetical protein	413	296	176
FD1_2977*	molecular chaperone GroEL	17	48*	0*
FD1_2978	co-chaperonin GroES	0	0	0

FD1_2979*	phosphoenolpyruvate carboxykinase	193*	65	28*
FD1_2980	hypothetical transmembrane protein	213	80	0
FD1_2981***	XRE family transcriptional regulator	335*,**	57**	0*
FD1_2982	hypothetical protein	50	44	0
FD1_2983	polysaccharide synthesis protein GtrA	0	13	0
FD1_2984	TIM-barrel protein, nifR3 family	1	7	0
FD1_2985	capsule biosynthesis protein	10	21	0
FD1_2986***	scaffoldin C	2374*,**	288**	32*
FD1_2987***	hypothetical protein	1252*,**	325**	15*
FD1_2988*	cohesin	932*	289	59*
FD1_2989**	cohesin-dockerin -x Domain Complex, Chain B	996**	16**	0
FD1_2990**	cohesin-dockerin -x Domain Complex, Chain A	1599**	66**	44
FD1_2991	PP-loop family protein	0	0	0
FD1_2992*	hypothetical protein	4260*	2933	218*
FD1_2993	uracil-DNA glycosylase	112	67	62
FD1_2994**	5,10-methylenetetrahydrofolate reductase	55**	7**	0
FD1_2995	vitamin B12 dependent methionine synthase activation domain	64	10	0
FD1_2996	sugar ABC transporter substrate-binding protein	129	88	0
FD1_2997*	UDP-glucose 4-epimerase	253*	112	0*
FD1_2998	ATPase AAA	18	0	0
FD1_2999	hypothetical protein	13	0	0
FD1_3000	hypothetical protein	49	0	0
FD1_3001	hypothetical protein	0	0	0
FD1_3002	hypothetical transmembrane protein	0	0	0
FD1_3003	hypothetical protein	0	5	0
FD1_3004	hypothetical secreted protein	0	0	0
FD1_3005	hypothetical transmembrane protein	18	0	26
FD1_3006	acetyltransferase	12	0	0
FD1_3007	nitroreductase	41	0	0
FD1_3008	hypothetical transmembrane protein	0	0	0
FD1_3009	glucan biosynthesis protein (pseudogene)	32	0	0
FD1_3010	glucan biosynthesis protein (pseudogene)	5	0	0
FD1_3011	hypothetical protein	0	0	0
FD1_3012	ATPase AAA	3	0	0
FD1_3013	hypothetical protein	0	0	0
FD1_3014	hypothetical protein	0	12	0
FD1_3015	heavy metal transporter	152	0	0
FD1_3016	zinc ABC transporter ATPase	58	60	23
FD1_3017	hypothetical protein	439	565	122
FD1_3018	ATP/GTP-binding protein	7	9	0
FD1_3019	restriction endonuclease	10	13	0
FD1_3020	hypothetical protein	0	0	0
FD1_3021	hypothetical protein	28	0	0
FD1_3022	hypothetical protein	0	0	0
FD1_3023	mobilization protein	356	111	8
FD1_3024	relaxase/mobilization nuclease family protein	66	15	13
FD1_3025	hypothetical protein	0	3	6
FD1_3026	DNA primase	0	0	0
FD1_3027	hypothetical protein	0	0	0
FD1_3028	phage integrase family protein	6	0	0
FD1_3029	Na ⁺ -driven multidrug efflux pump	0	0	0
FD1_3030*	mobilization protein	536*	289	0*
FD1_3031***	hypothetical protein	982*,**	159**	0*
FD1_3032	phage/plasmid primase, P4 family	323	192	242
FD1_3033*	integrase	338*	175	0*
FD1_3034**	DNA-binding protein	276**	33**	0
FD1_3035	hypothetical protein	25	0	0
FD1_3036	iron-containing alcohol dehydrogenase	23	10	0
FD1_3037***	ECF subfamily RNA polymerase sigma-24 factor	26**	201*,**	0*
FD1_3038***	hypothetical protein	19**	222*,**	0*
FD1_3039	hypothetical protein	0	45	0

FD1_3040	hypothetical protein	9	4	0
FD1_3041	integrase	11	16	36
FD1_3042	glucosamine 6-phosphate synthetase	0	4	48
FD1_3043	hypothetical protein	0	35	0
FD1_3044	LIM zinc-binding protein	0	0	0
FD1_3045	hypothetical protein	0	0	0
FD1_3046***	hypothetical protein	166*,**	20**	0*
FD1_3047	transcriptional regulator	2	10	0
FD1_3048**	hypothetical protein	839**	10**	0
FD1_3049***	hypothetical transmembrane protein	701*,**	64**	19*
FD1_3050***	transposase	432*,**	96**	0*
FD1_3051	helicase	0	0	0
FD1_3052	hypothetical protein	6	0	0
FD1_3053	hypothetical protein	9	11	0
FD1_3054	type I deoxyribonuclease HsdR	15	0	0
FD1_3055	hypothetical protein	0	0	0
FD1_3056	type I restriction endonuclease subunit S	4	0	0
FD1_3057***	transposase, IS116/IS110/IS902 family	848*,**	137**	20*
FD1_3058	stage V sporulation protein AEB	0	0	0
FD1_3059	stage V sporulation protein AD	0	0	0
FD1_3060	ATPase	0	0	0
FD1_3061	growth inhibitor PemK	0	0	0
FD1_3062	adhesin-like protein	0	0	0
FD1_3063	XRE family transcriptional regulator	0	0	0
FD1_3064	hypothetical transmembrane protein	44	0	0
FD1_3065	ATP-binding protein	24	2	0
FD1_3066	hypothetical transmembrane protein	11	0	0
FD1_3067	malate dehydrogenase	5	0	0
FD1_3068	lactate dehydrogenase	0	0	0
FD1_3069**	argininosuccinate synthase	177**	11**	0
FD1_3070	acetyltransferase	14	0	0
FD1_3071	argininosuccinate lyase	26	15	0
FD1_3072	hypothetical transmembrane protein	7	0	0
FD1_3073	<i>N</i> -acetyl-gamma-glutamyl-phosphate reductase	8	7	0
FD1_3074	hypothetical protein	0	0	0
FD1_3075	glutamate <i>N</i> -acetyltransferase/amino-acid acetyltransferase	44	0	0
FD1_3076	hypothetical transmembrane protein	0	0	0
FD1_3077	acetylglutamate kinase	31	0	0
FD1_3078	acetylornithine aminotransferase	50	13	0
FD1_3079	hypothetical protein	6	0	0
FD1_3080	ornithine carbamoyltransferase	43	14	0
FD1_3081	transcriptional regulator	249	0	0
FD1_3082	hypothetical transmembrane protein	17	0	0
FD1_3083	hypothetical transmembrane protein	13	33	0
FD1_3084	hypothetical protein	60	0	0
FD1_3085*	hydrolase GDSL	213*	98	5*
FD1_3086***	diguanylate cyclase	134*,**	5**	0*
FD1_3087	hypothetical protein	72	0	0
FD1_3088**	DNA mismatch repair protein	158**	2**	0
FD1_3089	hypothetical secreted protein	14	0	0
FD1_3090	hypothetical transmembrane protein	12	7	0
FD1_3091	ECF subfamily RNA polymerase sigma factor	6	12	0
FD1_3092***	LacI family transcriptional regulator	141*,**	17**	0*
FD1_3093***	sodium:proton antiporter	273*,**	36**	14*
FD1_3094	hypothetical transmembrane protein	30	63	0
FD1_3095	adhesin-like protein	4	25	0
FD1_3096	hypothetical protein	158	42	0
FD1_3097**	hypothetical protein	31**	5**	0
FD1_3098	resolvase	6	0	12
FD1_3099	hypothetical protein	25	0	0
FD1_3100	recombinase	0	0	0

FD1_3101	resolvase	3	0	0
FD1_3102	hypothetical protein	28	0	0
FD1_3103	hypothetical protein	315	0	0
FD1_3104**	helicase c2	55**	1**	0
FD1_3105	PemK family DNA-binding protein	11	0	0
FD1_3106***	hypothetical protein	57408*,**	993**	97*
FD1_3107	RNA polymerase subunit sigma-24	20	0	0
FD1_3108	hypothetical protein	0	0	0
FD1_3109	NAD synthetase	0	0	0
FD1_3110	GCN5-related <i>N</i> -acetyltransferase	19	0	0
FD1_3111	phosphoenolpyruvate synthase	35	0	0
FD1_3112	Cof-like hydrolase	15	0	0
FD1_3113	citrate synthase	16	5	0
FD1_3114	isocitrate dehydrogenase	28	0	0
FD1_3115	UDP- <i>N</i> -acetylmuramate dehydrogenase	45	0	0
FD1_3116	hypothetical protein	70	0	0
FD1_3117	transglutaminase domain-containing protein	83	0	0
FD1_3118	succinylglutamate desuccinylase	58	0	0
FD1_3119	succinylglutamate desuccinylase	96	27	0
FD1_3120**	hypothetical protein	82**	0**	0
FD1_3121	guanosine polyphosphate pyrophosphohydrolase	70	0	0
FD1_3122	urease subunit alpha	9	0	0
FD1_3123	amidotransferase	0	0	0
FD1_3124	hypothetical protein	0	0	0
FD1_3125	asparagine synthase	2	0	0
FD1_3126*	ammonium transporter	370*	192	15*
FD1_3127*	glutamine synthetase	979*	312	43*
FD1_3128**	hypothetical protein	67**	12**	0
FD1_3129***	hypothetical protein	3298*,**	805**	17*
FD1_3130**	hypothetical protein	13546**	2452**	0
FD1_3131***	hypothetical protein	16922*,**	3179**	114*
FD1_3132***	DNA-binding helix-turn-helix protein	290*,**	53**	0*
FD1_3133***	hypothetical protein	548* **	80**	0*
FD1_3134**	DNA repair protein (pseudogene)	880**	168**	0
FD1_3135	DNA repair protein (pseudogene)	597	181	0
FD1_3136**	amidotransferase	216**	11**	0
FD1_3137**	transcriptional regulator, LuxR family protein	256**	10**	0
FD1_3138***	urea carboxylase-associated protein 2	419*,**	48**	0*
FD1_3139***	urea carboxylase-associated protein 1	350*,**	75**	0*
FD1_3140**	urea carboxylase	370**	22**	19
FD1_3141	recombinase	28	0	0
FD1_3142	hypothetical protein	18	0	0
FD1_3143	resolvase	30	0	0
FD1_3144	hypothetical protein	0	0	0
FD1_3145	hypothetical protein	0	0	0
FD1_3146**	hypothetical protein	81**	9**	0
FD1_3147	conjugal transfer protein	151	0	0
FD1_3148**	hypothetical protein	146**	20**	0
FD1_3149***	restriction-modification system control element BclI	481**	1737*,**	140*
FD1_3150***	type II restriction endonuclease ScaI	361**	1089*,**	135*
FD1_3151**	hypothetical protein	455**	1049**	35
FD1_3152	hypothetical protein	451	771	0
FD1_3153	Cro/C1 family transcriptional regulator	80	332	0
FD1_3154**	hypothetical protein	140**	11**	0
FD1_3155	hypothetical protein	116	0	0
FD1_3156	myosin-cross-reactive antigen	142	0	0
FD1_3157	regulatory protein TetR	198	0	35
FD1_3158	hypothetical protein	78	0	0
FD1_3159	citrate synthase	151	0	0
FD1_3160**	hypothetical protein	70**	0**	0
FD1_3161	hypothetical transmembrane protein	155	0	0

FD1_3162**	urea carboxylase	537**	19**	0
FD1_3163**	allophanate hydrolase	456**	11**	0
FD1_3164**	nitrogen regulatory protein PII	308**	14**	0
FD1_3165**	amino acid transporter	271**	6**	0
FD1_3166	hypothetical protein	0	0	0
FD1_3167	hypothetical protein	204	0	0
FD1_3168	methylase	12	0	0
FD1_3169	hypothetical protein	8	0	0
FD1_3170	hypothetical protein	38	0	0
FD1_3171***	RNA polymerase subunit sigma-24	637*,**	160**	0*
FD1_3172***	hypothetical transmembrane protein	584*,**	49**	0*
FD1_3173***	hypothetical transmembrane protein	376*,**	51**	11*
FD1_3174	hypothetical protein	12	0	0
FD1_3175	hypothetical transmembrane protein	27	58	17
FD1_3176	hypothetical protein	0	0	0
FD1_3177	hypothetical protein	0	0	0
FD1_3178	cytosine methyltransferase	33	0	0
FD1_3179	hypothetical protein	0	0	0
FD1_3180	hypothetical protein	28	0	0
FD1_3181	hypothetical protein	14	0	0
FD1_3182	CopG family transcriptional regulator	0	0	0
FD1_3183	hypothetical protein	4	5	0
FD1_3184	hypothetical protein	25	0	0
FD1_3185	transcriptional regulator	342	0	0
FD1_3186	lipid kinase	0	0	0
FD1_3187	hypothetical protein	7	0	0
FD1_3188	sporulation integral membrane protein YlbJ	14	15	0
FD1_3189	sporulation protein YqfC	0	0	0
FD1_3190	sporulation protein YqfD	0	0	0
FD1_3191**	methyltransferase	94**	6**	6
FD1_3192	hypothetical protein	66	0	0
FD1_3193	cytidine deaminase	34	0	0
FD1_3194	rRNA methyltransferase	22	23	0
FD1_3195	transcriptional regulator, AraC family protein	23	44	0
FD1_3196*	FeS assembly ATPase SufC	120*	77	0*
FD1_3197	FeS assembly protein SufD	75	97	0
FD1_3198	hypothetical transmembrane protein	96	59	47
FD1_3199	RNA polymerase subunit sigma-24	57	24	0
FD1_3200***	hypothetical transmembrane protein	15**	295*,**	0*
FD1_3201	integral membrane sensor signal transduction histidine kinase	28	4	0
FD1_3202	transcriptional regulator	62	8	0
FD1_3203	hypothetical protein	15	0	0
FD1_3204	lipoprotein releasing system, ATP-binding protein	22	22	0
FD1_3205	lipoprotein releasing system, transmembrane protein, LolC/E family	11	8	0
FD1_3206*	O-glycosyl hydrolase	99*	36	10*
FD1_3207	M6 family metalloprotease domain-containing protein	72	97	0
FD1_3208*	ABC transporter substrate-binding protein	72	90*	0*
FD1_3209*	diguanylate cyclase	34*	15	0*
FD1_3210***	phospho-2-dehydro-3-deoxyheptonate aldolase	66*,**	9**	0*
FD1_3211	glutamine synthetase type III (pseudogene)	50	38	0
FD1_3212**	glutamine synthetase type III (pseudogene)	7**	65**	0
FD1_3213	CTP synthase	21	27	0
FD1_3214	ammonium transporter	5	17	0
FD1_3215	glutamate synthase	4	4	0
FD1_3216	glutamate synthase, NADH/NADPH, small subunit	10	0	0
FD1_3217	glutamine synthetase	6	2	0
FD1_3218	transcription antitermination regulator	22	7	0
FD1_3219	amidophosphoribosyltransferase	0	0	0
FD1_3220	aminoethylphosphonate catabolism associated LysR family transcriptional regulator	0	0	0
FD1_3221*	transposase	150*	46	0*

FD1_3222	aminoacyl-tRNA synthetase	35	27	0
FD1_3223	signal transduction histidine kinase	28	0	0
FD1_3224	PhoB family transcriptional regulator	3	0	0
FD1_3225	FMN-binding protein	1	0	0
FD1_3226	ApbE family protein	0	0	0
FD1_3227	hypothetical secreted protein	0	0	0
FD1_3228	amidohydrolase domain containing protein	0	0	0
FD1_3229	hypothetical protein	0	10	0
FD1_3230	toxin Fic	152	93	0
FD1_3231	DeoR family transcriptional regulator	16	0	0
FD1_3232**	1-phosphofructokinase	114**	5**	0
FD1_3233*	PTS fructose transporter subunit IIC	41*	11	0*
FD1_3234	PTS glucose transporter subunit IIABC	23	0	0
FD1_3235	phosphoenolpyruvate-protein phosphotransferase	11	0	0
FD1_3236	LysR family transcriptional regulator 4	0	0	0
FD1_3237	hypothetical protein	0	0	0
FD1_3238	alpha/beta hydrolase	6	11	0
FD1_3239	hypothetical protein	22	0	0
FD1_3240	aldo/keto reductase	13	0	0
FD1_3241	FMN reductase	0	14	0
FD1_3242	resolvase	10	24	0
FD1_3243	glucosamine 6-phosphate synthetase	4	0	0
FD1_3244	hypothetical protein	0	0	0
FD1_3245	LIM zinc-binding protein (pseudogene)	11	0	0
FD1_3246	LIM zinc-binding protein (pseudogene)	0	0	0
FD1_3247	LIM zinc-binding protein (pseudogene)	0	0	0
FD1_3248	hypothetical protein	0	0	0
FD1_3249	hypothetical protein	20	0	0
FD1_3250	hypothetical protein	25	0	0
FD1_3251	hypothetical protein	20	9	0
FD1_3252	hypothetical protein	83	3	0
FD1_3253	pentapeptide repeat-containing protein	47	0	0
FD1_3254*	pentapeptide repeat-containing protein	95*	40	0*
FD1_3255***	L,D-transpeptidase catalytic domain protein	86**	357*,**	0*
FD1_3256*	hypothetical transmembrane protein	43	102*	0*
FD1_3257	hypothetical transmembrane protein	33	84	0
FD1_3258	hypothetical protein	147	58	0
FD1_3259	superfamily II DNA/RNA helicases, SNF2 family	17	1	0
FD1_3260	hypothetical protein	15	0	0
FD1_3261	KAP P-loop domain-containing protein	8	0	0
FD1_3262	DNA (cytosine-5-)-methyltransferase	29	19	0
FD1_3263	hypothetical transmembrane protein	4	0	0
FD1_3264	type III restriction endonuclease subunit R	20	0	0
FD1_3265	glycoside hydrolase family 3 domain protein	12	0	0
FD1_3266	GDSL-like Lipase/Acylhydrolase	17	3	26
FD1_3267	hypothetical protein	244	125	67
FD1_3268	hypothetical protein	235	45	137
FD1_3269	transposase	0	0	0
FD1_3270	hypothetical protein	5	9	0
FD1_3271	leucine rich repeats containing protein	14	9	0
FD1_3272	RNA polymerase subunit sigma-24	0	11	0
FD1_3273	hypothetical transmembrane protein	8	39	0
FD1_3274	hypothetical transmembrane protein	14	32	0
FD1_3275	transketolase	0	0	0
FD1_3276	sporulation factor SpoIIIGA	6	0	46
FD1_3277	sporulation sigma factor SigE	5	0	0
FD1_3278	radical SAM protein	3	7	0
FD1_3279	single-stranded-DNA-specific exonuclease RecJ	22	0	0
FD1_3280**	(p)ppGpp synthetase	37**	3**	0
FD1_3281	metallo-beta-lactamase family protein	21	0	0
FD1_3282	coproporphyrinogen dehydrogenase HemZ	6	0	0

FD1_3283	23S rRNA methyltransferase	28	0	0
FD1_3284	hypothetical protein	0	0	0
FD1_3285	hypothetical protein	0	0	0
FD1_3286	GNAT family acetyltransferase	0	0	0
FD1_3287	hypothetical protein	0	0	0
FD1_3288	restriction system-associated AAA family ATPase	24	63	7
FD1_3289	hypothetical protein	0	66	0
FD1_3290	hypothetical protein	383	414	26
FD1_3291	phage portal protein, HK97 family	0	17	0
FD1_3292	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP	0	22	0
FD1_3293	hypothetical transmembrane protein	0	0	0
FD1_3294	hypothetical transmembrane protein	18	0	0
FD1_3295	hypothetical transmembrane protein	0	0	0
FD1_3296	hypothetical protein	0	8	0
FD1_3297	chloramphenicol acetyltransferase	30	0	0
FD1_3298	phage tail length tape measure protein	5	0	0
FD1_3299	VanZ family protein	0	0	0
FD1_3300	phage tail component protein	0	0	0
FD1_3301	siphovirus Reqiumpy6 Gp37-like protein	0	0	0
FD1_3302	leucine rich repeat containing protein	2	0	0
FD1_3303	hypothetical protein	0	0	0
FD1_3304	hypothetical protein	0	6	0
FD1_3305	9- <i>O</i> -acetyl- <i>N</i> -acetylneuraminate esterase	13	10	14
FD1_3306	transposase, IS4 family protein	44	33	0
FD1_3307*	mannan endo-1,4-beta-mannosidase	29*	6	0*
FD1_3308	alpha-glucosidase	68	13	0
FD1_3309	glycoside hydrolase 97	23	4	10
FD1_3310	AraC family transcriptional regulator	9	5	0
FD1_3311	ricin-type beta-trefoil lectin domain protein	17	0	0
FD1_3312***	endo-arabinase	80*,**	8**	0*
FD1_3313	hypothetical protein	28	0	0
FD1_3314	hypothetical secreted protein	0	0	0
FD1_3315	glycoside hydrolase	0	0	0
FD1_3316	hypothetical protein	0	0	0
FD1_3317	hypothetical protein	0	0	0
FD1_3318	hypothetical protein	0	0	0
FD1_3319	hypothetical protein	0	0	0
FD1_3320	group II intron reverse transcriptase/maturase	0	0	0
FD1_3321	glycoside hydrolase family 73 protein	0	0	0
FD1_3322**	transposase	151**	22**	0
FD1_3323	sodium ion-translocating decarboxylase subunit beta	13	0	0
FD1_3324	oxaloacetate decarboxylase alpha subunit	0	0	0
FD1_3325	oxaloacetate decarboxylase gamma chain	0	4	0
FD1_3326	oxaloacetate decarboxylase	15	4	0
FD1_3327	translation elongation factor G	18	0	0
FD1_3328*	hypothetical protein	20	67*	0*
FD1_3329	sporulation protein YunB	0	49	0
FD1_3330***	hypothetical protein	31**	242*,**	0*
FD1_3331	glyoxalase	0	0	0
FD1_3332**	glutamine-fructose-6-phosphate transaminase (isomerizing)	37**	1**	0
FD1_3333	hypothetical protein	0	11	0
FD1_3334	hypothetical transmembrane protein	3	0	0
FD1_3335	SPFH domain-band 7 family protein	86	0	0
FD1_3336	GntR family transcriptional regulator	0	0	0
FD1_3337	ABC transporter	11	0	0
FD1_3338	ABC-2 transporter family protein	8	0	0
FD1_3339	methyltransferase FkbM	12	6	0
FD1_3340	hypothetical protein	20	19	0
FD1_3341*	30S ribosomal protein S15	98	159*	0*
FD1_3342	polyribonucleotide nucleotidyltransferase	198	246	0
FD1_3343***	hypothetical protein	1949*,**	541**	0*

FD1_3344	hypothetical protein	56	0	0
FD1_3345	hypothetical transmembrane protein	23	76	0
FD1_3346	hypothetical protein	0	48	0
FD1_3347	hypothetical protein	44	8	0
FD1_3348**	serine hydroxymethyltransferase	95**	5**	0
FD1_3349	cupin	2	0	0
FD1_3350	GCN5-related N-acetyltransferase	0	0	0
FD1_3351	AAA ATPase central domain protein	7	6	0
FD1_3352	amino acid-binding protein	69	29	0
FD1_3353	homoserine dehydrogenase	45	16	0
FD1_3354	hypothetical transmembrane protein	0	0	13
FD1_3355	ArsR family transcriptional regulator	20	0	0
FD1_3356	hypothetical transmembrane protein	30	24	0
FD1_3357	hypothetical transmembrane protein	0	0	0
FD1_3358	hypothetical protein	9	0	0
FD1_3359	hypothetical protein	19	0	0
FD1_3360	alpha/beta fold family hydrolase	0	8	0
FD1_3361**	permease	97**	9**	0
FD1_3362**	fumarate reductase	329**	15**	0
FD1_3363	4Fe-4S ferredoxin	118	0	0
FD1_3364	sulfite reductase, subunit B	99	0	0
FD1_3365**	sulfite reductase, subunit A	103**	8**	0
FD1_3366	4Fe-4S ferredoxin	68	0	0
FD1_3367	methyl-viologen-reducing hydrogenase delta subunit	99	0	0
FD1_3368**	heterodisulfide reductase subunit A	68**	4**	0
FD1_3369**	heterodisulfide reductase subunit C-like protein	84**	10**	0
FD1_3370	CoB--CoM heterodisulfide reductase, subunit B	49	27	0
FD1_3371	fumarate hydratase	37	17	0
FD1_3372	REX family transcriptional regulator	91	0	0
FD1_3373**	isocitrate dehydrogenase	155**	16**	0
FD1_3374	hypothetical transmembrane protein	65	15	0
FD1_3375	hypothetical transmembrane protein	201	0	0
FD1_3376	hypothetical protein	66	0	0
FD1_3377**	aconitate hydratase	73**	3**	0
FD1_3378*	diaminopimelate decarboxylase	235*	75	0*
FD1_3379**	ribosome biogenesis GTP-binding protein YsxC	229**	13**	55
FD1_3380	endopeptidase La	48	34	0
FD1_3381**	Clp protease ATP-binding protein	219**	11**	12
FD1_3382	ATP-dependent Clp protease proteolytic subunit	88	0	0
FD1_3383	trigger factor	79	0	18
FD1_3384	ser/threonine protein phosphatase	37	0	0
FD1_3385	threonine synthase	22	0	0
FD1_3386	hypothetical protein	61	0	0
FD1_3387	ribonuclease HII	8	0	0
FD1_3388	ribosome biogenesis GTPase A	32	0	0
FD1_3389	signal peptidase I	32	0	0
FD1_3390	50S ribosomal protein L19	112	0	0
FD1_3391	radical SAM-linked protein	0	0	0
FD1_3392	Fe-S oxidoreductase	19	3	0
FD1_3393	hypothetical protein	89	22	0
FD1_3394**	GNAT family acetyltransferase	42**	3**	0
FD1_3395	cytidine deaminase	61	16	0
FD1_3396	hypothetical protein	7	5	0
FD1_3397	3-ketoacyl-ACP reductase	61	0	0
FD1_3398	hypothetical protein	12	0	0
FD1_3399	hypothetical protein	15	0	0
FD1_3400**	phosphoglycerol transferase	75**	15**	0
FD1_3401	dihydrolipoamide acyltransferase	81	0	0
FD1_3402	GNAT family acetyltransferase	78	0	0
FD1_3403	hypothetical protein	0	0	0
FD1_3404	sortase B	0	0	0

FD1_3405	hypothetical transmembrane protein	0	0	0
FD1_3406***	adhesin-like protein	238*,**	60**	4*
FD1_3407*	sortase	319*	94	0*
FD1_3408***	signal peptidase I	577*,**	149**	0*
FD1_3409	response regulator receiver and SARP domain protein	9	10	0
FD1_3410	signal transduction histidine kinase	3	4	0
FD1_3411	signal transduction histidine kinase	8	8	0
FD1_3412	stage II sporulation protein E	6	4	0
FD1_3413	acyl-coenzyme A synthetase/AMP-(Fatty) acid ligase	15	0	0
FD1_3414	hypothetical protein	0	0	0
FD1_3415***	ATPase AAA	17**	72*,**	0*
FD1_3416	hypothetical protein	625	1134	38
FD1_3417	hypothetical protein	0	34	0
FD1_3418	glucosamine 6-phosphate synthetase	0	4	0
FD1_3419	hypothetical protein	0	0	0
FD1_3420	LIM zinc-binding protein	13	0	0
FD1_3421	hypothetical protein	16	0	0
FD1_3422	hypothetical transmembrane protein	0	0	0
FD1_3423	lytTr DNA-binding domain protein	0	0	0
FD1_3424	metal-dependent hydrolase	0	0	0
FD1_3425	hypothetical transmembrane protein	1	2	0
FD1_3426	hypothetical protein	6	0	0
FD1_3427	transposase	8	0	0
FD1_3428	transposase IS66	4	0	23
FD1_3429	glycoside hydrolase family 9	0	11	0
FD1_3430	adhesin-like protein	0	0	0
FD1_3431	hypothetical protein	0	0	0
FD1_3432	ABC-type multidrug transport system ATPase and permease component	7	0	0
FD1_3433	methylase involved in ubiquinone/menaquinone biosynthesis	0	0	0
FD1_3434	hypothetical protein	0	0	0
FD1_3435	coenzyme PQQ synthesis protein D	0	0	0
FD1_3436	hypothetical protein	7	0	0
FD1_3437	hypothetical protein	0	0	0
FD1_3438	adhesin-like protein	3	4	0
FD1_3439	site-specific recombinase, phage integrase family	0	0	0
FD1_3440	lipoprotein releasing system, transmembrane protein	7	2	23
FD1_3441	lipoprotein releasing system, ATP-binding protein	0	0	0
FD1_3442	signal transduction histidine kinase	24	0	0
FD1_3443	sensory transduction protein RegX3	0	0	0
FD1_3444	alpha/beta hydrolase	1	0	0
FD1_3445	transposase (pseudogene)	0	0	0
FD1_3446	transposase (pseudogene)	0	0	0
FD1_3447	cytoplasmic protein	0	17	0
FD1_3448	hypothetical protein	0	0	0
FD1_3449	GCN5 family acetyltransferase	13	0	0
FD1_3450	acetyltransferase	0	0	0
FD1_3451*	hypothetical protein	588*	197	0*
FD1_3452**	hypothetical protein	17**	131**	21
FD1_3453*	type-IV secretion system protein TraC	787	1329*	41*
FD1_3454	hypothetical protein	0	0	0
FD1_3455	hypothetical protein	35	0	0
FD1_3456	hypothetical protein	3	0	0
FD1_3457	hypothetical protein	0	0	0
FD1_3458	crystallin	5	17	0
FD1_3459	hypothetical protein	21	0	0
FD1_3460	hypothetical protein	0	0	0
FD1_3461	chromosomal replication initiator protein DnaA	21	0	0
FD1_3462	hypothetical protein	15	7	0
FD1_3463	hypothetical protein	0	0	0
FD1_3464	hypothetical protein	0	7	0
FD1_3465	sortase family protein	0	0	36

FD1_3466	hypothetical transmembrane protein	0	0	0
FD1_3467	DNA-binding protein	0	0	0
FD1_3468	hypothetical protein	4	0	0
FD1_3469	VanZ-like protein	0	0	0
FD1_3470	aminotransferase DegT	8	12	0
FD1_3471	VanZ-like protein	0	0	0
FD1_3472	PglB	5	0	0
FD1_3473	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	23	0	0
FD1_3474	polysaccharide pyruvyl transferase	35	0	0
FD1_3475	tungsten cofactor oxidoreducace radical SAM maturase	0	13	0
FD1_3476	glycosyl transferase family protein	8	10	0
FD1_3477	glycosyl transferase group 1	15	8	0
FD1_3478	EpsG protein	33	11	0
FD1_3479	glycosyl transferase, group 2	110	49	0
FD1_3480	Polysaccharide pyruvyl transferase	71	34	0
FD1_3481	polysaccharide biosynthesis protein	54	61	0
FD1_3482	glycosyl transferase family 2	18	47	0
FD1_3483	UDP-galactose-4-epimerase	54	0	0
FD1_3484	glutamine--fructose-6-phosphate aminotransferase (pseudogene)	0	0	0
FD1_3485***	glutamine--fructose-6-phosphate aminotransferase (pseudogene)	43*,**	6**	0*
FD1_3486	cobyrinic acid a,c-diamide synthase	20	45	0
FD1_3487	hypothetical protein	30	0	0
FD1_3488	hypothetical protein	0	0	0
FD1_3489***	integrase	131*,**	25**	0*
FD1_3490	IstB domain protein ATP-binding protein	111	96	0
FD1_3491	ABC transporter	155	0	0
FD1_3492	adhesin-like protein	0	3	0
FD1_3493	resolvase	0	0	0
FD1_3494	hypothetical protein	4	0	0
FD1_3495	hypothetical protein	30	86	0
FD1_3496	ribonuclease 3	16	14	0
FD1_3497	phospholipase	0	0	0
FD1_3498*	hypothetical protein	146*	42	0*
FD1_3499	hypothetical protein	121	57	0
FD1_3500	radical SAM domain-containing protein	80	30	13
FD1_3501	hypothetical protein	143	0	0
FD1_3502	glycosyl transferase	204	94	0
FD1_3503	PfkB family kinase	112	35	0
FD1_3504***	radical SAM peptide maturase, CXXX-repeat target family	178*,**	17**	0*
FD1_3505	hypothetical protein	5	0	0
FD1_3506	hypothetical transmembrane protein	10	0	0
FD1_3507	hypothetical transmembrane protein	0	0	0
FD1_3508	stage V sporulation protein T	7	2	0
FD1_3509	hypothetical protein	0	0	0
FD1_3510	phage head-tail adapter protein	20	0	33
FD1_3511	hypothetical protein	42	31	0
FD1_3512	serine recombinase	42	47	0
FD1_3513	hypothetical protein	31	0	17
FD1_3514	peptidase M23	0	0	0
FD1_3515*	LIM zinc-binding protein	463*	150	0*
FD1_3516	hypothetical protein	44	10	0
FD1_3517	polysaccharide deacetylase	14	10	0
FD1_3518*	conjugative coupling factor TraD, SXT/TOL subfamily	25	82*	0*
FD1_3519**	hypothetical protein	22**	2**	0
FD1_3520	DNA-binding protein	31	14	0
FD1_3521	hypothetical protein	53	6	0
FD1_3522	DNA-binding protein	0	0	0
FD1_3523	phage integrase family site specific recombinase	36	7	0
FD1_3524	hypothetical protein	0	0	0
FD1_3525	DNA-binding protein	222	0	0
FD1_3526	DNA binding domain, excisionase family	113	0	0

FD1_3527	hypothetical protein	0	0	0
FD1_3528	hypothetical protein	0	0	0
FD1_3529	glycoside hydrolase family protein	0	0	0
FD1_3530	DNA binding domain, excisionase family	0	38	0
FD1_3531	DNA binding domain, excisionase family	187	94	140
FD1_3532	hypothetical protein	0	0	0
FD1_3533	transcriptional regulator	0	0	0
FD1_3534	Cro/C1 family transcriptional regulator	0	0	0
FD1_3535	hypothetical protein	0	0	0
FD1_3536	tyrosine recombinase XerC	0	0	0
FD1_3537**	VanZ-like protein	28**	0**	0
FD1_3538	aminotransferase DegT	18	11	0
FD1_3539	UDP-galactose phosphate transferase	17	6	0
FD1_3540	hexapeptide transferase	45	3	0
FD1_3541	family 2 glycosyl transferase	95	0	21
FD1_3542	glycosyl transferase family 1	25	14	0
FD1_3543	hypothetical transmembrane protein	20	19	0
FD1_3544	polysaccharide transport protein	26	15	0
FD1_3545	hypothetical protein	49	20	0
FD1_3546**	LICD family protein	60**	5**	0
FD1_3547	glycerol-3-phosphate cytidylyltransferase	42	0	0
FD1_3548	UDP- <i>N</i> -acetylglucosamine 2-epimerase	24	0	0
FD1_3549	mannose-1-phosphate guanylyltransferase	59	1	0
FD1_3550	mannose-6-phosphate isomerase	42	16	0
FD1_3551	glycosyl transferase	67	20	0
FD1_3552**	UDP- <i>N</i> -acetylglucosamine 2-epimerase	30**	0**	0
FD1_3553	capsular biosynthesis protein	47	0	0
FD1_3554	UDP-glucose dehydrogenase	40	0	0
FD1_3555	UDP- <i>N</i> -acetylglucosamine 4,6-dehydratase	40	9	0
FD1_3556	hypothetical protein	27	0	0
FD1_3557	hypothetical protein	16	0	0
FD1_3558**	helicase	85**	19**	9
FD1_3559	hypothetical protein	2	41	0
FD1_3560	saccharopine dehydrogenase	92	0	0
FD1_3561	hypothetical protein	18	0	0
FD1_3562	hypothetical protein	20	0	0
FD1_3563	transcriptional regulator	0	0	0
FD1_3564	pectinacetylesterase	8	19	0
FD1_3565	permease	0	0	0
FD1_3566	C_GCAxxG_C_C family protein	0	0	0
FD1_3567	ArsR family transcriptional regulator	0	0	0
FD1_3568	sulfurtransferase	10	0	0
FD1_3569	thiazole biosynthesis adenylyltransferase ThiF	72	25	0
FD1_3570	metallo-beta-lactamase domain protein	6	0	0
FD1_3571	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	17	0	0
FD1_3572	transcriptional regulator	0	0	0
FD1_3573	beta-lactamase	1	0	0
FD1_3574	efflux ABC transporter, permease	0	2	0
FD1_3575	ABC transporter ATP-binding protein	0	0	0
FD1_3576	glycoside hydrolase family 43	15	8	0
FD1_3577	hypothetical transmembrane protein	0	0	0
FD1_3578	helicase, RecD/TraA family	8	0	0
FD1_3579	rod shape-determining protein MreB	7	0	0
FD1_3580	major cell surface glycoprotein	0	0	0
FD1_3581	PASTA domain protein	13	0	0
FD1_3582	cell division ATPase MinD	5	7	0
FD1_3583	hypothetical protein	129	13	0
FD1_3584	hypothetical protein	0	0	0
FD1_3585	riboflavin biosynthesis protein RibD	16	0	0
FD1_3586	riboflavin synthase subunit alpha	21	0	0

FD1_3587	cytidine/deoxycytidylate deaminase/nudix/methyltransferase domains protein	0	0	0
FD1_3588	cytidine/deoxycytidylate deaminase/nudix/methyltransferase domains protein	13	0	0
FD1_3589	GTP cyclohydrolase	8	0	0
FD1_3590	hypothetical transmembrane protein	14	0	0
FD1_3591	hypothetical transmembrane protein	0	0	0
FD1_3592	6,7-dimethyl-8-ribityllumazine synthase	3	46	0
FD1_3593	haloacid dehalogenase-like hydrolase	17	20	0
FD1_3594	hypothetical secreted protein	0	3	0
FD1_3595	hypothetical secreted protein	0	17	0
FD1_3596	hypothetical transmembrane protein	3	0	0
FD1_3597	ECF subfamily RNA polymerase sigma-24 factor	0	0	0
FD1_3598	hypothetical protein	0	0	0
FD1_3599	transposon-encoded protein TnpW	0	0	0
FD1_3600	recombinase	3	0	0
FD1_3601	ABC transporter	22	0	0
FD1_3602*	hypothetical protein	420*	100	0*
FD1_3603	ribose-phosphate pyrophosphokinase	27	12	0
FD1_3604	inorganic pyrophosphatase	5	0	0
FD1_3605	arabinogalactan endo-1 4-beta-galactosidase	19	0	0
FD1_3606	disulfide oxidoreductase	0	0	0
FD1_3607	nitrogenase iron protein subunit NifH	0	0	0
FD1_3608	nitrogenase cofactor biosynthesis protein NifB	0	0	0
FD1_3609	dinitrogenase iron-molybdenum cofactor biosynthesis protein	0	0	0
FD1_3610	acetyltransferase	0	0	0
FD1_3611	hypothetical protein	0	0	0
FD1_3612	glutamylcysteine synthetase	0	0	0
FD1_3613	thiamine biosynthesis protein ThiF	3	0	0
FD1_3614**	LysR family transcriptional regulator	112**	9**	24
FD1_3615**	hypothetical transmembrane protein	105**	7**	0
FD1_3616	peptide chain release factor 2	21	10	0
FD1_3617	vacuolar-type H ⁺ -ATPase subunit H	47	13	0
FD1_3618	phosphopantetheine adenylyltransferase	57	0	0
FD1_3619	16S rRNA (guanine(966)-N ²)-methyltransferase RsmD	12	0	0
FD1_3620*	hypothetical protein	65*	43	0*
FD1_3621	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	39	35	0
FD1_3622**	hypothetical protein	3**	58**	0
FD1_3623***	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	10**	116*,**	0*
FD1_3624	XRE family transcriptional regulator	0	0	0
FD1_3625	hypothetical protein	0	10	0
FD1_3626	hypothetical protein	0	80	0
FD1_3627	hypothetical protein	0	9	0
FD1_3628	hypothetical protein	8	34	0
FD1_3629	hypothetical protein	14	16	0
FD1_3630	hypothetical protein	0	65	0
FD1_3631	hypothetical transmembrane protein	0	74	0
FD1_3632**	hypothetical transmembrane protein	291**	5968**	289
FD1_3633**	hypothetical secreted protein	109**	4690**	322
FD1_3634**	serine/threonine protein kinase	200**	3846**	270
FD1_3635***	antitoxin HicB	287**	2317*,**	124*
FD1_3636***	toxin HicA	186**	1863*,**	0*
FD1_3637	hypothetical protein	0	0	0
FD1_3638	resolvase	0	0	0
FD1_3639	hypothetical protein	16	1	0
FD1_3640	hypothetical protein	0	0	0
FD1_3641	hypothetical protein	0	0	0
FD1_3642	hypothetical protein	0	0	0
FD1_3643	hypothetical protein	0	0	0
FD1_3644	hypothetical protein	0	30	0
FD1_3645**	hypothetical protein	0**	92**	0
FD1_3646	hypothetical protein	0	632	43

FD1_3647**	hypothetical protein	5**	1375**	97
FD1_3648**	hypothetical protein	3**	827**	63
FD1_3649**	hypothetical protein	8**	465**	7
FD1_3650	DNA topoisomerase III (pseudogene)	0	7	0
FD1_3651	DNA topoisomerase III (pseudogene)	0	0	0
FD1_3652	transcriptional regulator	0	0	0
FD1_3653	hypothetical protein	0	0	0
FD1_3654	hypothetical protein	8	0	0
FD1_3655	type IV secretion/conjugal transfer ATPase	3	6	0
FD1_3656	hypothetical transmembrane protein	40	0	0
FD1_3657	hypothetical transmembrane protein	16	14	0
FD1_3658	hypothetical secreted protein	0	0	0
FD1_3659	hypothetical transmembrane protein	0	0	0
FD1_3660	Ti-type conjugative transfer system protein TraG	2	3	0
FD1_3661	hypothetical transmembrane protein	0	8	0
FD1_3662	hypothetical transmembrane protein	0	0	0
FD1_3663	single-strand binding protein	0	0	0
FD1_3664	hypothetical protein	0	0	0
FD1_3665	hypothetical transmembrane protein	0	0	0
FD1_3666	hypothetical protein	0	0	0
FD1_3667	hypothetical protein	0	0	0
FD1_3668	hypothetical protein	0	0	0
FD1_3669	hypothetical protein	0	0	0
FD1_3670	hypothetical transmembrane protein	0	0	0
FD1_3671	hypothetical transmembrane protein	0	0	0
FD1_3672	ParB protein	0	0	0
FD1_3673	ParA family ATPase	0	0	0
FD1_3674	recombinase	20	0	17
FD1_3675***	adhesin-like protein	99*,**	21**	0*
FD1_3676**	branched-chain amino acid aminotransferase	436**	5**	0
FD1_3677	hypothetical transmembrane protein	20	0	0
FD1_3678	radical SAM protein	8	24	0
FD1_3679	alanine racemase	48	0	0
FD1_3680***	hypothetical protein	454*,**	41**	0*
FD1_3681	cell envelope-related transcriptional attenuator	9	0	0
FD1_3682	hydrolase TatD	0	0	0
FD1_3683	protein phosphatase 2C	0	0	0
FD1_3684	Cof-like hydrolase	16	0	0
FD1_3685	indolepyruvate ferredoxin oxidoreductase, alpha subunit	30	5	0
FD1_3686	hypothetical protein	0	0	0
FD1_3687	hypothetical protein	13	0	0
FD1_3688	hypothetical transmembrane protein	34	0	0
FD1_3689	indolepyruvate ferredoxin oxidoreductase, beta subunit	35	0	0
FD1_3690	phenylacetate-CoA ligase	124	0	0
FD1_3691	hypothetical protein	0	26	0
FD1_3692**	acetolactate synthase, small subunit	98**	5**	0
FD1_3693	hypothetical protein	0	0	0
FD1_3694	hypothetical protein	294	47	0
FD1_3695	triacylglycerol lipase	39	16	0
FD1_3696***	hypothetical transmembrane protein	520*,**	61**	0*
FD1_3697	4-alpha-glucanotransferase	20	0	0
FD1_3698	glycogen/starch/alpha-glucan phosphorylases	34	5	0
FD1_3699	hypothetical protein	20	74	0
FD1_3700	hypothetical transmembrane protein	21	27	0
FD1_3701*	ubiquinone/menaquinone biosynthesis methyltransferase	35	83*	0*
FD1_3702***	glycosyltransferase family 36	77*,**	13**	0*
FD1_3703	galactose mutarotase	34	0	0
FD1_3704**	citrate synthase	100**	6**	0
FD1_3705	CAAX prenyl protease domain-containing protein	25	0	0
FD1_3706	hypothetical transmembrane protein	6	0	0
FD1_3707	adenosine deaminase	0	0	0

FD1_3708	hypothetical transmembrane protein	0	5	0
FD1_3709	ATP-dependent DNA helicase RecQ	0	0	0
FD1_3710**	beta-1 4-xylanase	2128**	416**	0
FD1_3711	sporulation transcription factor Spo0A	0	0	0
FD1_3712	phosphoserine aminotransferase	40	13	0
FD1_3713	3-phosphoglycerate dehydrogenase	73	0	0
FD1_3714	hypothetical transmembrane protein	0	0	0
FD1_3715	peptidase family M50	0	0	0
FD1_3716	NAD-dependent epimerase/dehydratase	53	15	0
FD1_3717**	NADH-dependent butanol dehydrogenase	189**	8**	0
FD1_3718	hypothetical protein	353	0	0
FD1_3719	phenylacetic acid degradation protein	84	0	0
FD1_3720	acetyltransferase	11	2	0
FD1_3721	hypothetical protein	87	0	0
FD1_3722	hypothetical protein	45	0	0
FD1_3723	phosphohydrolase	47	0	0
FD1_3724	dihydrodipicolinate reductase	20	10	0
FD1_3725	dihydrodipicolinate synthase (pseudogene)	0	0	0
FD1_3726	dihydrodipicolinate synthase (pseudogene)	0	0	0
FD1_3727	four helix bundle protein	429	285	0
FD1_3728	aspartate-semialdehyde dehydrogenase	31	0	0
FD1_3729**	hypothetical protein	378**	18**	0
FD1_3730	S-adenosylmethionine tRNA ribosyltransferase	2	0	0
FD1_3731	hypothetical protein	20	0	0
FD1_3732	hypothetical protein	1	0	0
FD1_3733	queuine tRNA-ribosyltransferase	0	11	0
FD1_3734	phosphoglycolate phosphatase	7	0	0
FD1_3735**	glutathione peroxidase	0**	66**	0
FD1_3736	hypothetical protein	29	0	0
FD1_3737	hypothetical protein	13	0	0
FD1_3738	hypothetical protein	0	0	0
FD1_3739	hypothetical protein	24	0	0
FD1_3740**	hypothetical transmembrane protein	39**	4**	0
FD1_3741	DNA-binding helix-turn-helix protein	0	0	0
FD1_3742	hypothetical secreted protein	16	0	0
FD1_3743	polysaccharide deacetylase family sporulation protein PdaB	9	5	4
FD1_3744**	cotH protein	37**	1**	0
FD1_3745	Nitroreductase	17	9	0
FD1_3746*	pseudouridine synthase	251*	66	0*
FD1_3747**	NADPH-dependent FMN reductase	240**	12**	0
FD1_3748***	sodium transporter	290*,**	42**	0*
FD1_3749	hypothetical protein	12	18	0
FD1_3750	von Willebrand factor A	13	0	0
FD1_3751	hypothetical protein	7	2	0
FD1_3752	ATPase	0	4	0
FD1_3753	hypothetical protein	30	0	0
FD1_3754	hypothetical protein	4	0	0
FD1_3755	hypothetical protein	0	0	0
FD1_3756	SWIM zinc finger domain protein	20	0	0
FD1_3757	adhesin-like protein	35	36	0
FD1_3758	nicotinate phosphoribosyltransferase	24	10	0
FD1_3759	hypothetical protein	10	8	0
FD1_3760	beta-lactamase	1	0	0
FD1_3761	ABC transporter permease	0	0	0
FD1_3762	hypothetical transmembrane protein	0	0	0
FD1_3763	ABC transporter ATP-binding protein	0	0	0
FD1_3764	GntR family transcriptional regulator	0	0	0
FD1_3765	pyrimidine utilization regulatory protein R	19	0	0
FD1_3766	alpha/beta hydrolase	0	0	0
FD1_3767	hypothetical transmembrane protein	12	23	0
FD1_3768	gliding-associated putative ABC transporter substrate-binding component	14	0	0

FD1_3769	gliding motility-associated ABC transporter permease protein GldF	0	0	0
FD1_3770	gliding motility-associated ABC transporter ATP- binding subunit GldA	13	0	0
FD1_3771*	glycoside hydrolase 48 family protein0	4143*	2079	67*
FD1_3772	TIGR00255 family protein	34	0	0
FD1_3773	hypothetical protein	158	0	0
FD1_3774	guanylate kinase	47	0	0
FD1_3775	DNA-directed RNA polymerase subunit omega	42	0	0
FD1_3776***	primosomal protein N'	35*,**	6**	0*
FD1_3777	peptide deformylase	19	2	0
FD1_3778	methionyl-tRNA formyltransferase	9	0	0
FD1_3779	zinc metalloproteinase	20	0	0
FD1_3780	ribosomal RNA small subunit methyltransferase RsmB	27	0	0
FD1_3781	ribosomal RNA large subunit methyltransferase N	45	8	0
FD1_3782	serine/threonine phosphatase stp	30	0	0
FD1_3783***	serine/threonine protein kinase	65*,**	4**	0*
FD1_3784	ribosome small subunit-dependent GTPase A	9	3	0
FD1_3785	thiamin pyrophosphokinase	9	5	0
FD1_3786	tRNA-i ⁶ A37 thiotransferase enzyme MiaB	7	0	0
FD1_3787	hypothetical protein	0	0	0
FD1_3788	DNA mismatch repair protein MutS	8	3	0
FD1_3789	hypothetical protein	5	0	0
FD1_3790	DNA mismatch repair protein MutL	4	2	0
FD1_3791	hypothetical transmembrane protein	0	0	0
FD1_3792	hypothetical transmembrane protein	0	0	0
FD1_3793	tRNA dimethylallyltransferase	0	0	0
FD1_3794	RNA-binding protein Hfq	22	57	0
FD1_3795	secretion protein HlyD	19	1	0
FD1_3796	pyridoxal phosphate biosynthesis protein	8	0	0
FD1_3797	cell division protein SepF	12	0	0
FD1_3798	RNA-binding S4	102	0	0
FD1_3799	cell division initiation protein	0	0	0
FD1_3800*	isoleucyl-tRNA synthetase	31*	13	0*
FD1_3801	signal peptidase II	12	30	0
FD1_3802	pseudouridine synthase	12	26	0
FD1_3803	Cof-like hydrolase	45	9	0
FD1_3804	tellurium resistance protein	61	36	0
FD1_3805	transketolase	10	8	0
FD1_3806	transketolase	57	25	0
FD1_3807	hypothetical protein	0	0	0
FD1_3808	hypothetical protein	0	0	0
FD1_3809*	DNA methylase	37	49*	0*
FD1_3810	ACT domain protein	10	0	0
FD1_3811	hypothetical protein	36	0	48
FD1_3812	aminoglycoside phosphotransferase	6	0	0
FD1_3813	dockerin type 1	12	2	0
FD1_3814	hypothetical protein	74	0	0
FD1_3815**	dockerin	42**	3**	0
FD1_3816	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	21	8	0
FD1_3817	aromatic amino acid aminotransferase	7	0	0
FD1_3818	AsnC family transcriptional regulator	69	0	0
FD1_3819	histidinol phosphate phosphatase HisJ family	28	0	0
FD1_3820	glycoside hydrolase	984	1107	5
FD1_3821	glycoside hydrolase	141	182	2
FD1_3822	glycoside hydrolase	402	351	0
FD1_3823	adhesin-like protein	6	0	0
FD1_3824	lipid A export permease/ATP-binding protein MsbA	4	0	0
FD1_3825	ABC transporter ATP-binding protein	0	0	0
FD1_3826**	hypothetical secreted protein	48**	5**	0
FD1_3827	hypothetical protein	17	0	22
FD1_3828**	quinolinate synthetase	66**	9**	0
FD1_3829	iron-only hydrogenase maturation rSAM protein HydE	85	14	0

FD1_3830	collagenase and related protease	50	0	46
FD1_3831	collagenase and related protease	45	0	0
FD1_3832	collagenase and related protease	51	0	0
FD1_3833*	cysteinyl-tRNA synthetase	58*	15	0*
FD1_3834	beta-lactamase	57	0	0
FD1_3835**	rRNA large subunit m3Psi methyltransferase RlmH	132**	19**	0
FD1_3836**	endoribonuclease L-PSP	142**	0**	0
FD1_3837	3-isopropylmalate dehydratase small subunit	119	8	0
FD1_3838**	3-isopropylmalate dehydratase large subunit	111**	6**	0
FD1_3839**	threonine ammonia-lyase	94**	16**	22
FD1_3840	ATPase AAA	45	19	0
FD1_3841**	3-isopropylmalate dehydrogenase	33**	5**	0
FD1_3842*	dihydroxy-acid dehydratase	40*	8	0*
FD1_3843	hypothetical transmembrane protein	16	23	0
FD1_3844	hypothetical transmembrane protein	0	0	0
FD1_3845	ketol-acid reductoisomerase	94	0	0
FD1_3846	acetolactate synthase, small subunit	10	0	0
FD1_3847	acetolactate synthase, large subunit, biosynthetic type	33	0	0
FD1_3848	hypothetical transmembrane protein	0	0	0
FD1_3849	hypothetical protein	0	0	0
FD1_3850	hypothetical protein	21	0	0
FD1_3851	2-isopropylmalate synthase	7	0	0
FD1_3852	hypothetical protein	0	0	0
FD1_3853	alpha-glucosidase	0	0	0
FD1_3854	transcriptional regulator	12	45	0
FD1_3855	transcriptional regulator	6	47	0
FD1_3856	glycoside hydrolase, family 10	0	0	0
FD1_3857	transcriptional regulator	10	0	0
FD1_3858	hydroxyneurosporene synthase	0	5	0
FD1_3859	ATPase AAA	22	9	0
FD1_3860	nitrogenase	0	0	0
FD1_3861	hydrogenase	4	0	0
FD1_3862	hypothetical transmembrane protein	0	0	0
FD1_3863	hypothetical transmembrane protein	0	0	0
FD1_3864	carbon-monoxide dehydrogenase	0	0	0
FD1_3865	nitrate ABC transporter ATP-binding protein	0	0	0
FD1_3866	nitrate ABC transporter, permease protein	0	0	0
FD1_3867	metal ABC transporter substrate-binding protein	0	0	0
FD1_3868***	hypothetical protein	358***	67**	0*
FD1_3869	sugar ABC transporter permease	4	0	38
FD1_3870	sugar ABC transporter permease	0	0	0
FD1_3871	RND family efflux transporter MFP subunit	5	0	0
FD1_3872	ABC-type antimicrobial peptide transport system, permease component	6	7	0
FD1_3873	carbohydrate ABC transporter, <i>N</i> - acetylglucosamine/diacetylchitobiose-binding protein	2	3	0
FD1_3874	ABC transporter substrate-binding protein	10	7	0
FD1_3875	hypothetical transmembrane protein	0	0	0
FD1_3876	ABC transporter permease	9	0	0
FD1_3877	ABC transporter permease	8	0	0
FD1_3878	tetratricopeptide repeat protein	6	3	0
FD1_3879	Yip1 domain protein	0	0	0
FD1_3880	hypothetical protein	20	11	0
FD1_3881	ABC transporter permease	9	0	0
FD1_3882	ABC transporter permease	14	7	0
FD1_3883	purine nucleoside phosphorylase	61	0	0
FD1_3884	capsular exopolysaccharide biosynthesis protein (Wzx)	15	0	0
FD1_3885	hypothetical protein	11	8	0
FD1_3886	sulfatase family protein	4	0	0
FD1_3887	hypothetical transmembrane protein	0	0	0
FD1_3888	inner membrane protein YhaI	32	15	0
FD1_3889	KH domain protein	30	28	0

FD1_3890**	30S ribosomal protein S16	32**	0**	0
FD1_3891	signal recognition particle protein	37	0	0
FD1_3892	DNA-binding protein	0	0	0
FD1_3893	serine acetyltransferase	11	8	0
FD1_3894	diguanylate cyclase (pseudogene)	52	9	0
FD1_3895	diguanylate cyclase (pseudogene)	103	0	0
FD1_3896	DNA binding domain, excisionase family	109	0	0
FD1_3897	hypothetical transmembrane protein	0	0	0
FD1_3898	hypothetical protein	0	0	0
FD1_3899	RNA polymerase sigma-70 factor, bacteroides expansion family 1	0	0	0
FD1_3900	XRE family transcriptional regulator	33	50	0
FD1_3901**	adhesin-like protein	78**	345**	0
FD1_3902	hypothetical secreted protein	11	0	0
FD1_3903	hypothetical transmembrane protein	29	0	0
FD1_3904	RNA polymerase subunit sigma-24	2	0	0
FD1_3905	cell wall binding repeat-containing protein	0	0	0
FD1_3906	hypothetical secreted protein	0	0	0
FD1_3907	RNA polymerase subunit sigma-24	0	0	0
FD1_3908	hypothetical transmembrane protein	0	0	0
FD1_3909	adhesin-like protein	26	31	0
FD1_3910	RNA polymerase subunit sigma-24	0	11	0
FD1_3911	hypothetical transmembrane protein	0	14	36
FD1_3912	hypothetical protein	0	0	0
FD1_3913	hRNA polymerase sigma-70 factor, bacteroides expansion family 1	0	0	0
FD1_3914	hypothetical protein	9	13	0
FD1_3915	XRE family transcriptional regulator	39	8	0
FD1_3916	hypothetical transmembrane protein	0	0	0
FD1_3917	transposase	0	5	0
FD1_3918	pilus formation protein	0	15	0
FD1_3919	hypothetical transmembrane protein	0	5	0
FD1_3920	RNA polymerase subunit sigma-24	4	10	0
FD1_3921**	adhesin-like protein	6**	112**	53
FD1_3922**	ISPsy14, transposase family protein	119**	880**	0
FD1_3923***	ATPase AAA	144**	794***	0*
FD1_3924***	ABC transporter	198**	1435***	0*
FD1_3925	hypothetical transmembrane protein	0	0	0
FD1_3926	hypothetical secreted protein	1	4	0
FD1_3927	hypothetical protein	0	0	0
FD1_3928	hypothetical transmembrane protein	0	0	0
FD1_3929	transglutaminase domain protein	1	4	0
FD1_3930	hypothetical protein	0	0	0
FD1_3931	hypothetical protein	0	0	0
FD1_3932	hypothetical protein	0	0	0
FD1_3933	hypothetical protein	7	0	0
FD1_3934	integrase	66	17	24
FD1_3935	IstB-like ATP binding protein	59	42	57
FD1_3936	ABC transporter	24	15	0
FD1_3937**	hypothetical protein	66**	5**	0
FD1_3938**	RNA polymerase sigma factor, sigma-70 family	354**	49**	62
FD1_3939	RNA polymerase sigma factor, sigma-70 family	9	0	0
FD1_3940	hypothetical protein	87	36	0
FD1_3941***	XRE family transcriptional regulator	515**	1555***	13*
FD1_3942***	adhesin-like protein	302**	1571***	53*
FD1_3943***	hypothetical protein	180**	750***	73*
FD1_3944	stage 0 sporulation protein A	76	198	82
FD1_3945*	adhesin-like protein	86	118*	0*
FD1_3946*	adhesin-like protein	543*	301	0*
FD1_3947*	hypothetical protein	459*	96	0*
FD1_3948***	accessory gene regulator	70***	10**	0*
FD1_3949	signal transduction histidine kinase regulating citrate/malate metabolism	15	4	0
FD1_3950	DNA-binding response regulator	5	0	0

FD1_3951	phage integrase family site specific recombinase	0	20	69
FD1_3952	Sell repeat protein	58	49	0
FD1_3953	hypothetical protein	11	0	0
FD1_3954	hypothetical protein	0	0	0
FD1_3955	hypothetical protein	0	4	0
FD1_3956	antirestriction protein (ArdA)	0	0	0
FD1_3957	hypothetical transmembrane protein	0	0	0
FD1_3958	type VI secretion protein	0	0	0
FD1_3959	hypothetical protein	0	0	0
FD1_3960	hypothetical transmembrane protein	0	0	0
FD1_3961	hypothetical transmembrane protein	0	0	0
FD1_3962	transcriptional regulator	0	0	0
FD1_3963	Ti-type conjugative transfer system protein TraG	3	0	0
FD1_3964	CDGSH-type zinc finger protein	0	0	0
FD1_3965	hypothetical transmembrane protein	0	0	0
FD1_3966	sortase B	4	0	0
FD1_3967	Cna protein B-type domain protein	7	5	0
FD1_3968	hypothetical protein	0	10	0
FD1_3969	hypothetical protein	0	0	0
FD1_3970	hypothetical protein	0	0	0
FD1_3971	hypothetical protein	0	0	0
FD1_3972	DNA methyltransferase	0	0	0
FD1_3973	hypothetical protein	0	0	0
FD1_3974	hypothetical protein	0	0	0
FD1_3975***	ATPase AAA	6**	57***	0*
FD1_3976	hypothetical protein	13	0	0
FD1_3977	hypothetical protein	0	0	0
FD1_3978	hypothetical protein	0	0	0
FD1_3979	hypothetical protein	0	0	0
FD1_3980	ATPase AAA	0	0	0
FD1_3981	integrase	4	4	0
FD1_3982	endo-1,4-beta-glucanase	30	23	8
FD1_3983	hypothetical transmembrane protein	14	0	0
FD1_3984	ABC transporter permease	10	0	0
FD1_3985	hypothetical transmembrane protein	0	0	0
FD1_3986	ABC transporter	0	0	0
FD1_3987	GntR family transcriptional regulator	25	0	0
FD1_3988	hypothetical protein	43	0	0
FD1_3989	hypothetical protein	46	0	0
FD1_3990	transglutaminase0	12	0	0
FD1_3991	hypothetical protein	8	0	0
FD1_3992	hypothetical protein	0	114	0
FD1_3993	hypothetical protein	99	21	0
FD1_3994	alpha-galactosidase	23	11	0
FD1_3995	sugar (glycoside-pentoside-hexuronide) transporter	18	0	0
FD1_3996	transcriptional regulator	33	0	0
FD1_3997	hypothetical protein	11	0	0
FD1_3998	endo-xylanase	116	0	0
FD1_3999	electron transporter RnfC	20	9	0
FD1_4000	electron transport complex, RnfABCDGE type, D subunit	71	19	0
FD1_4001	electron transport complex, RnfABCDGE type, G subunit	114	32	102
FD1_4002	electron transport complex, RnfABCDGE type, E subunit	43	0	0
FD1_4003	electron transport complex, RnfABCDGE type, A subunit	82	36	0
FD1_4004***	electron transport complex, RnfABCDGE type, B subunit	153***	15**	0*
FD1_4005	hypothetical protein	39	16	0
FD1_4006	von Willebrand factor type A	689	542	0
FD1_4007***	transcriptional regulator, AraC family	241***	51**	0*
FD1_4008	sugar transferase involved in lipopolysaccharide synthesis	62	0	33
FD1_4009	thymidylate kinase	73	0	0
FD1_4010	UDP-N-acetylglucosamine pyrophosphorylase	17	0	0
FD1_4011	peptidoglycan-binding LysM domain protein (pseudogene)	31	31	0

FD1_4012	peptidoglycan-binding LysM domain protein (pseudogene)	13	4	0
FD1_4013	stage IV sporulation protein A	44	12	0
FD1_4014	phage replication protein O	0	0	0
FD1_4015**	sulfate permease	61**	12**	0
FD1_4016	site-specific recombinase XerD	7	5	0
FD1_4017	DNA binding domain excisionase family	0	0	0
FD1_4018	phage antirepressor protein	0	0	0
FD1_4019	RNA polymerase sigma factor, sigma-70 family	49	0	0
FD1_4020	helix-turn-helix protein	0	0	0
FD1_4021	exonuclease	34	0	0
FD1_4022	MFS transporter	0	13	0
FD1_4023	hydroxylamine reductase	3	2	0
FD1_4024	(Fe-S)-binding protein	0	7	0
FD1_4025	cAMP-binding protein	0	0	0
FD1_4026	hypothetical protein	13	0	0
FD1_4027	hypothetical protein	0	0	0
FD1_4028	transcriptional regulator	9	0	0
FD1_4029	bacterial mobilization protein (MobC)	0	0	0
FD1_4030	relaxase	71	10	0
FD1_4031	hypothetical protein	12	0	0
FD1_4032	hypothetical protein	6	0	0
FD1_4033	single-stranded DNA-binding protein	0	0	0
FD1_4034	cobyrinic acid a,c-diamide synthase	0	0	0
FD1_4035	hypothetical protein	0	0	91
FD1_4036	hypothetical protein	0	0	0
FD1_4037	ParB-like protein	0	21	0
FD1_4038	hypothetical transmembrane protein	0	14	0
FD1_4039	hypothetical protein	0	0	0
FD1_4040	hypothetical protein	0	22	0
FD1_4041	ribosomal-protein-alanine acetyltransferase	10	0	0
FD1_4042	hypothetical protein	18	0	0
FD1_4043	hypothetical protein	29	8	0
FD1_4044	hypothetical protein	17	29	0
FD1_4045***	hypothetical transmembrane protein	199***	22**	0*
FD1_4046	hypothetical protein	0	0	0
FD1_4047	hypothetical protein	0	0	0
FD1_4048	hypothetical protein	17	0	0
FD1_4049	restriction system-associated AAA family ATPase	0	0	0
FD1_4050	DNA methylase	7	4	0
FD1_4051	hypothetical transmembrane protein	0	0	0
FD1_4052	acetyltransferase	0	0	0
FD1_4053	hypothetical protein	17	0	0
FD1_4054	hypothetical transmembrane protein	6	0	0
FD1_4055	hypothetical protein	9	8	0
FD1_4056	hypothetical protein	2	0	0
FD1_4057	XRE family transcriptional regulator	0	14	0
FD1_4058	restriction endonuclease subunit M	12	0	0
FD1_4059	restriction endonuclease subunit S	0	0	0
FD1_4060	restriction endonuclease subunit R	0	0	0
FD1_4061	integrase	0	0	0
FD1_4062	hypothetical protein	7	0	0
FD1_4063	hypothetical protein	0	0	0
FD1_4064	hypothetical protein	0	0	0
FD1_4065	XRE family transcriptional regulator	0	0	0
FD1_4066	OmpR family, sensor histidine kinase KdpD	0	0	0
FD1_4067	hypothetical protein	0	0	0
FD1_4068	potassium transporter TrkA	0	0	0
FD1_4069	potassium transporter TrkH	0	0	0
FD1_4070	resolvase	0	0	0
FD1_4071	acetyltransferase	0	0	0
FD1_4072	relaxase	0	0	0

FD1_4073	hypothetical protein	0	0	0
FD1_4074	beta-lactamase class C and other penicillin binding proteins	0	0	0
FD1_4075	hypothetical protein	0	0	0
FD1_4076	hypothetical protein	0	0	0
FD1_4077	hypothetical protein	0	0	0
FD1_4078	hypothetical protein	2	0	0
FD1_4079**	resolvase	72**	2**	0
FD1_4080**	helicase SNF2	98**	27**	0
FD1_4081	hypothetical protein	0	0	0
FD1_4082	hypothetical protein	0	0	0
FD1_4083	hypothetical protein	0	0	0
FD1_4084	DNA topoisomerase III	0	0	0
FD1_4085	hypothetical protein	0	0	0
FD1_4086	hypothetical protein	0	0	0
FD1_4087	hypothetical protein	0	0	0
FD1_4088	phosphoadenosine phosphosulfate reductase	0	0	0
FD1_4089	DNA-cytosine methyltransferase	0	0	0
FD1_4090	hypothetical transmembrane protein	0	0	0
FD1_4091	hypothetical transmembrane protein	0	0	0
FD1_4092	hypothetical protein	0	0	0
FD1_4093**	hypothetical transmembrane protein	362*	83*	0
FD1_4094**	type-IV secretion system protein TraC	499*	89*	0
FD1_4095**	conjugal transfer protein	396*	29*	0
FD1_4096***	conjugal transfer protein TrbL	326***	33**	0*
FD1_4097**	tRNA (adenine- <i>N</i> ⁶)-methyltransferase	288*	13*	0
FD1_4098	hypothetical protein	0	0	0
FD1_4099	DNA (cytosine-5-)-methyltransferase	0	0	0
FD1_4100	type II R-M system restriction endonuclease	7	0	0
FD1_4101	hypothetical protein	58	0	0
FD1_4102	resolvase	0	0	0
FD1_4103	conjugal transfer protein	0	0	0
FD1_4104	AT hook motif	0	0	0
FD1_4105	hypothetical protein	6	0	0
FD1_4106	hypothetical protein	0	0	0
FD1_4107	recombinase	10	0	0
FD1_4108	hypothetical transmembrane protein	143	0	0
FD1_4109***	type IV conjugative transfer system coupling protein TraD	229***	15**	0*
FD1_4110*	hypothetical protein	160	41	0
FD1_4111	hypothetical protein	57	0	0
FD1_4112	flagellar hook-length control protein	299	0	0
FD1_4113***	transcriptional regulator	111***	10**	0*
FD1_4114**	hypothetical protein	151**	14**	0
FD1_4115	glycoside hydrolase family 25	5	7	0
FD1_4116*	transposase	132*	44	0*
FD1_4117	hypothetical secreted protein	29	0	0
FD1_4118	rubrerythrin	55	4	0
FD1_4119	thiamine biosynthesis protein ThiF	30	0	0
FD1_4120	hypothetical protein	16	0	0
FD1_4121	septum formation protein Maf	0	0	0
FD1_4122	hypothetical transmembrane protein	0	0	0
FD1_4123**	glyceraldehyde-3-phosphate dehydrogenase	3968**	46**	0
FD1_4124	hypothetical protein	67	44	0
FD1_4125	hypothetical protein	42	0	0
FD1_4126	phosphate starvation protein PhoH	67	0	0
FD1_4127	16S rRNA maturation RNase YbeY	66	16	72
FD1_4128***	GTPase Era	219***	14**	0*
FD1_4129	DNA replication and repair protein RecO	13	0	0
FD1_4130	MutS2 protein	7	2	0
FD1_4131***	diguanylate cyclase (GGDEF) domain (pseudogene)	129***	20**	0*
FD1_4132	diguanylate cyclase (GGDEF) domain (pseudogene)	88	0	0
FD1_4133	hydrolase, alpha/beta domain protein	56	18	0

FD1_4134	S-adenosylmethionine decarboxylase	15	0	0
FD1_4135	arginine decarboxylase	8	0	0
FD1_4136	signal peptidase II	12	0	0
FD1_4137	hypothetical transmembrane protein	15	0	0
FD1_4138	hypothetical protein	23	0	0
FD1_4139	spermidine synthase	41	9	0
FD1_4140	agmatinase	91	0	0
FD1_4141	hypothetical transmembrane protein	15	0	0
FD1_4142	hypothetical transmembrane protein	22	0	41
FD1_4143	hypothetical transmembrane protein	0	0	0
FD1_4144	hypothetical transmembrane protein	0	0	0
FD1_4145	hypothetical protein	126	0	0
FD1_4146	hypothetical protein	1	0	0
FD1_4147	hypothetical protein	46	24	0
FD1_4148	hypothetical transmembrane protein	21	0	0
FD1_4149	saccharopine dehydrogenase	92	0	0
FD1_4150	hypothetical protein	18	0	0
FD1_4151	hypothetical protein	62	0	0
FD1_4152	hypothetical protein	26	0	0
FD1_4153	peptidylprolyl isomerase	44	0	0
FD1_4154	carboxynorspermidine decarboxylase	10	0	0
FD1_4155	hypothetical transmembrane protein	31	0	0
FD1_4156	competence protein	28	0	0
FD1_4157	DNA recombination protein RmuC	11	0	0
FD1_4158	RNA methyltransferase	16	0	18
FD1_4159	1A family penicillin-binding protein	16	6	0
FD1_4160	hypothetical transmembrane protein	74	0	0
FD1_4161	flavin reductase	0	0	0
FD1_4162	anti-sigma-factor antagonist domain-containing protein	1	0	0
FD1_4163	anti-sigma F factor	0	0	0
FD1_4164	RNA polymerase sigma-F factor	9	0	0
FD1_4165	hypothetical transmembrane protein	2	0	0
FD1_4166***	cellulose 1,4-beta-cellobiosidase	191***	21**	0*
FD1_4167	2-hydroxyglutaryl-CoA dehydratase	10	0	0
FD1_4168	2-hydroxyglutaryl-CoA dehydratase	19	0	0

Trt2: ISO4-H5 enrichment culture +FD1 with high H₂ on methanol. Trt3: ISO4-H5 enrichment culture +FD1 with low H₂ on methanol. Trt4: ISO4-H5 enrichment culture +FD1 with low H₂ on monomethylamine. *: Genes that are above two fold differentially expressed with q<0.05 for both Krusgal-Wallis test and Benjamini-Hochberg test. **: Genes that are above two fold differentially expressed between Trt2 and Trt3, with q<0.05 for both Krusgal-Wallis test and Benjamini-Hochberg test excluding Trt4.

Table A.5.06 Genes with 2-fold expression difference in Trt2 and Trt3

Locus tag	Predicted gene product	Expression	
Genes with higher expression in Trt2		Trt2	Trt3
Carbohydrate Utilisation			
FD1_0599	sugar ABC transporter permease	270	46
FD1_0600	sugar ABC transporter permease	171	25
FD1_0621	beta-galactosidase	239	24
FD1_0641	sugar ABC transporter substrate-binding protein	181	2
FD1_0650	sugar ABC transporter permease	66	7
FD1_0651	carbohydrate ABC transporter substrate-binding protein	163	35
FD1_0743	glycoside hydrolase family 43	134	38
FD1_0746	beta-galactosidase	50	11
FD1_0748	alpha-N-arabinofuranosidase	67	4
FD1_0753	xylanase	186	16
FD1_0754	glycerate kinase	243	11
FD1_1016	glycoside hydrolase family 9	129	31
FD1_1021	glycoside hydrolase (pseudogene)	123	27
FD1_1023	glycosyl hydrolase family 9	248	39
FD1_1101	glycoside hydrolase family 9	268	12
FD1_1258	galactokinase	118	7
FD1_1280	polysaccharide lyase	441	58
FD1_1288	acetyl xylan esterase	34	5

FD1_1292	1,4-beta-xylanase	124	17
FD1_1473	sugar ABC transporter substrate-binding protein	146	25
FD1_1799	glycoside hydrolase family 3	50	7
FD1_1803	glycoside hydrolase family protein	78	16
FD1_1844	carbohydrate-binding protein	84	5
FD1_2293	D-xylose ABC transporter, ATP-binding protein	41	3
FD1_3702	glycosyltransferase family 36	77	13
FD1_3710	beta-1 4-xylanase	2128	416
FD1_4166	cellulose 1,4-beta-cellobiosidase	191	21
Cellulosome			
FD1_2986	scaffoldin C	2374	288
FD1_2987	hypothetical protein	1252	325
FD1_2989	cohesin-dockerin -x Domain Complex, Chain B	996	16
FD1_2990	cohesin-dockerin -x Domain Complex, Chain A	1599	66
Carbon metabolism			
FD1_0408	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductase beta subunit	82	7
FD1_0409	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductase gamma subunit	162	15
FD1_0431	carbohydrate binding module (family 6)/glycoside hydrolase 97	240	21
FD1_0635	1-phosphofructokinase	131	7
FD1_0693	acetate kinase	283	42
FD1_1181	FolC bifunctional protein	144	20
FD1_1365	carbonic anhydrase	304	23
FD1_1406	glycogen synthase	71	4
FD1_2447	pyruvate formate lyase-activating protein	924	286
FD1_2874	6-phosphofructokinase	331	52
FD1_2875	phosphoglucomutase	69	3
FD1_3069	argininosuccinate synthase	177	11
FD1_3362	fumarate reductase	329	15
FD1_3373	isocitrate dehydrogenase	155	16
FD1_3377	aconitate hydratase	73	3
FD1_3704	citrate synthase	100	6
FD1_3717	NADH-dependent butanol dehydrogenase	189	8
FD1_4123	glyceraldehyde-3-phosphate dehydrogenase	3968	46
Nitrogen metabolism			
FD1_1175	glutamate dehydrogenase	82	3
FD1_2260	nitrogen-fixing protein NifU	121	21
FD1_2292	urea ABC transporter, permease protein UrtC	66	4
FD1_3138	urea carboxylase-associated protein 2	419	48
FD1_3139	urea carboxylase-associated protein 1	350	75
FD1_3140	urea carboxylase	370	22
FD1_3162	urea carboxylase	537	19
FD1_3163	allophanate hydrolase	456	11
FD1_3164	nitrogen regulatory protein PII	308	14
FD1_3165	amino acid transporter	271	6
Electron transfer			
FD1_0455	Fe-S oxidoreductase	241	51
FD1_0586	flavodoxin	284	22
FD1_0844	ferredoxin	120	16
FD1_1061	cytochrome b/b6	144	16
FD1_1469	rubrerythrin	1562	261
FD1_2667	flavodoxin	66	8
FD1_4004	electron transport complex, RnfABCDGE type, B subunit	153	15
Transporters			
FD1_0436	multidrug transporter	328	5
FD1_0744	citrate transporter	331	19
FD1_1085	large mechanosensitive ion channel protein MscL	427	98
FD1_1266	protein insertion permease FtsX	63	1
FD1_2147	MIP family channel proteins	281	22
FD1_2274	large mechanosensitive ion channel protein MscL	427	98
FD1_3093	sodium:proton antiporter	273	36
FD1_3361	permease	97	9
FD1_3748	sodium transporter	290	42
FD1_4015	sulfate permease	61	12
Cell surface protein			
FD1_0908	twitching motility protein pilT	175	31
FD1_0909	type IV-A pilus assembly ATPase PilB	76	9
FD1_0910	type II secretory pathway prepilin signal peptidase PulO and related peptidase	1530	260
FD1_0911	prepilin-type cleavage/methylation protein	1380	203
FD1_0913	adhesin-like protein	541	111
FD1_0915	type IV pilus assembly protein PilM	379	71
FD1_0916	type II secretion protein F	383	77
FD1_0946	tellurium resistance protein TerD	287	7
FD1_0953	calcium-translocating P-type ATPase	44	3

FD1_0967	Ig domain protein group 2 domain protein	286	59
FD1_1689	conjugal transfer protein TraX	91	9
FD1_2181	tellurite-resistance protein	491	108
FD1_2264	adhesin-like protein	101	17
FD1_2265	adhesin-like protein	47	2
FD1_2315	periplasmic binding protein	519	112
FD1_2316	diguanylate cyclase	272	31
FD1_2763	collagen-binding protein A	148	16
FD1_3406	adhesin-like protein	238	60
FD1_3675	adhesin-like protein	99	21
FD1_3815	dockerin	42	3
FD1_4094	type-IV secretion system protein TraC	499	89
FD1_4095	conjugal transfer protein	396	29
FD1_4096	conjugal transfer protein TrbL	326	33
FD1_4109	type IV conjugative transfer system coupling protein TraD	229	15
Secretion system			
FD1_1036	signal recognition particle-docking protein FtsY	36	2
FD1_1719	preprotein translocase subunit SecY	93	0
FD1_2901	sortase, SrtB family	66	4
FD1_3408	signal peptidase I	577	149
FD1_3901	signal recognition particle protein	37	0
Cell replication and house-keeping genes			
FD1_0619	DNA repair protein RecN	107	13
FD1_0628	DNA mismatch repair protein MutS	44	3
FD1_0683	elongation factor Tu	2692	227
FD1_0742	RNA polymerase sigma factor, sigma-70 family protein	265	12
FD1_0789	cell division protein FtsH	56	5
FD1_1025	translation initiation factor IF-3	284	21
FD1_1026	50S ribosomal protein L359	319	1
FD1_1050	elongation factor P	305	65
FD1_1265	cell division ATP-binding protein FtsE	51	6
FD1_1343	tRNA-splicing ligase RtcB	152	26
FD1_1548	DNA mismatch repair protein MutT	169	14
FD1_1731	50S ribosomal protein L29	52	0
FD1_2179	ATP-dependent helicase	654	181
FD1_2222	30S ribosomal protein S9	235	8
FD1_2409	DNA-directed RNA polymerase subunit beta	48	3
FD1_2410	DNA-directed RNA polymerase subunit beta'	69	10
FD1_2645	DNA gyrase subunit B	23	2
FD1_2651	chromosomal replication initiator protein DnaA	113	9
FD1_2692	cell division protein FtsZ	231	13
FD1_2697	cell division protein FtsW	20	3
FD1_2715	septation protein spoVG	357	19
FD1_2881	DNA primase	59	2
FD1_2931	50S rRNA methyltransferase	132	19
FD1_3104	helicase c2	55	1
FD1_3171	RNA polymerase subunit sigma-24	637	160
FD1_3379	ribosome biogenesis GTP-binding protein YsxC	229	13
FD1_3558	helicase	85	19
FD1_3835	rRNA large subunit m3Psi methyltransferase RlmH	132	19
FD1_3890	30S ribosomal protein S16	32	0
FD1_3938	RNA polymerase sigma factor, sigma-70 family	354	49
FD1_4079	resolvase	72	2
FD1_4080	helicase SNF2	98	27
Cofactor biosynthesis			
FD1_0292	cobalt-precorrin-6A synthase (pseudogene)	22	0
FD1_0537	phosphoglucosamine mutase	41	4
FD1_0617	NAD ⁺ kinase	102	7
FD1_1629	dinitrogenase iron-molybdenum cofactor biosynthesis protein	149	16
FD1_2869	S-adenosylmethionine synthetase	179	13
FD1_2938	quinolinate synthetase	66	9
FD1_2994	5,10-methylenetetrahydrofolate reductase	55	7
FD1_3828	quinolinate synthetase	66	9
Amino acid biosynthesis			
FD1_1546	aspartate--ammonia ligase	103	8
FD1_2429	anthranilate synthase subunit II	113	13
FD1_2434	tryptophan synthase subunit beta	80	15
FD1_2435	tryptophan synthase subunit alpha	69	4
FD1_2779	histidinol phosphate phosphatase HisJ family	527	111
FD1_2925	3-isopropylmalate dehydrogenase	33	5
FD1_2928	3-isopropylmalate dehydratase large subunit	111	6
FD1_3348	serine hydroxymethyltransferase	95	5
FD1_3676	branched-chain amino acid aminotransferase	436	5
FD1_3692	acetolactate synthase, small subunit	98	5
FD1_3838	3-isopropylmalate dehydratase large subunit	111	6

FD1_3841	3-isopropylmalate dehydrogenase	33	5
Genes with higher expression in Trt3			
Carbohydrate Utilisation		Trt2	Trt3
FD1_1525	glycoside hydrolase (pseudogene)	5	27
FD1_1593	alpha-amylase	108	265
FD1_1831	glycosyl hydrolase family 9	117	388
Lantibiotic island			
FD1_2191	hypothetical protein	104	1829
FD1_2192	hypothetical protein	225	942
FD1_2193	hypothetical protein	76	1219
FD1_2194	hypothetical protein	73	665
FD1_2195	hypothetical protein	6	509
FD1_2196	hypothetical protein	20	321
FD1_2197	hypothetical protein	65	886
FD1_2200	lantibiotic lacticin	0	184
FD1_2201	lantibiotic lacticin	0	162
FD1_2202	hypothetical protein	45	378
FD1_2203	NHLM bacteriocin system ABC transporter, peptidase/ATP-binding protein	15	607
FD1_2204	type 2 lantibiotic biosynthesis protein LanM	19	1113
FD1_2205	type 2 lantibiotic biosynthesis protein LanM	26	1029
FD1_2206	hypothetical transmembrane protein	43	1406
FD1_2207	ABC transporter substrate-binding protein	70	1218
FD1_2208	ABC-2 type transport system permease	96	4958
FD1_2209	lantibiotic protection ABC transporter, ATP-binding subunit	90	4482
Cell surface proteins			
FD1_1832	adhesin-like protein	77	413
FD1_2971	collagen-binding protein A	511	1759
FD1_3632	hypothetical transmembrane protein	291	5968
FD1_3921	adhesin-like protein	6	112
FD1_3942	adhesin-like protein	302	1571
Toxin/antitoxin system			
FD1_3635	antitoxin HicB	287	2317
FD1_3636	toxin HicA	186	1863
Transporter			
FD1_3924	ABC transporter	198	1435
Secreted proteins			
FD1_2915	alternate signal-mediated exported protein	116	471
FD1_3633	hypothetical secreted protein	109	4690
DNA modification			
FD1_0902	restriction endonuclease-like protein	16	372
FD1_3149	restriction-modification system control element BclI	481	1737
FD1_3150	type II restriction endonuclease ScaI	361	1089
RNA polymerase			
FD1_0273	RNA polymerase sigma-70 factor	0	48
FD1_0692	DNA-directed RNA polymerase subunit sigma	153	2049
FD1_0862	RNA polymerase subunit sigma	26	346
FD1_2973	RNA polymerase, sigma-24 subunit, ECF subfamily protein	288	1278
FD1_3037	ECF subfamily RNA polymerase sigma-24 factor	26	201

Trt2: ISO4-H5 enrichment culture +FD1 with high H₂ on methanol. Trt3: ISO4-H5 enrichment culture +FD1 with low H₂ on methanol. Genes that are above two fold differentially expressed between Trt2 and Trt3, with q<0.05 for both Kruskal-Wallis test and Benjamini-Hochberg test excluding Trt4.

Table A.6.01 Manual functional annotation of the *Methanobrevibacter* sp. D5 predicted open reading frames. Table excludes hypothetical proteins.

AMINO ACID METABOLISM

Alanine	
D5_0658	alanine aminotransferase
Arginine	
D5_1847	acetylglutamate kinase ArgB
D5_2420	acetylornithine aminotransferase ArgD
D5_1643	argininosuccinate lyase ArgH
D5_0217	argininosuccinate synthase ArgG
D5_1862	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein ArgJ
D5_0549	<i>N</i> -acetyl-gamma-glutamyl-phosphate reductase ArgC
D5_0054	ornithine carbamoyltransferase ArgF
Aspartate/asparagine	
D5_1577	asparagine synthase (glutamine-hydrolyzing) AsnB
Chorismate	
D5_1672	3-dehydroquinate dehydratase type I AroD
D5_1468	3-dehydroquinate synthase AroB
D5_1705	3-phosphoshikimate 1-carboxyvinyltransferase AroA
D5_0787	chorismate synthase AroC
D5_0101	shikimate 5-dehydrogenase AroE
D5_0604	shikimate kinase AroK
Cysteine	
D5_1336	cysteine synthase CysKM1
D5_1703	cysteine synthase CysKM2
D5_1702	serine <i>O</i> -acetyltransferase CysE
General	
D5_0852	aspartate aminotransferase
Glutamate/glutamine	
D5_0429	glutamate dehydrogenase GdhA
D5_1876	glutamate synthase domain containing protein
D5_0780	glutamine amidotransferase
D5_2271	glutamine amidotransferase
D5_2378	glutamine synthetase GlnA
D5_2379	transcriptional repressor of nif and glnA operons NrpR
Glycine	
D5_2464	serine hydroxymethyltransferase GlyA
Histidine	
D5_0004	ATP phosphoribosyltransferase HisG1
D5_0992	ATP phosphoribosyltransferase HisG2
D5_0078	bifunctional imidazoleglycerol-phosphate dehydratase HisB
D5_1014	hisA/hisF family protein HisAF
D5_0040	histidinol dehydrogenase HisD
D5_2254	histidinol-phosphate aminotransferase HisC
D5_0143	imidazole glycerol phosphate synthase glutamine amidotransferase subunit HisH
D5_2425	imidazoleglycerol-phosphate synthase cyclase subunit HisF
D5_0099	phosphoribosyl-AMP cyclohydrolase HisI
D5_0201	phosphoribosyl-ATP pyrophosphohydrolase HisE
D5_0551	phosphoribosylformimino-5- aminoimidazole carboxamide ribotide isomerase HisA
Homoserine	
D5_1574	allosteric regulator of homoserine dehydrogenase
D5_1573	homoserine dehydrogenase Hom
Lysine	
D5_0440	aspartate kinase Ask
D5_0608	aspartate kinase Ask

D5_0609	dihydrodipicolinate synthase DapA
D5_0610	dihydrodipicolinate reductase DapB
D5_0611	aspartate-semialdehyde dehydrogenase Asd
D5_0757	diaminopimelate aminotransferase DapL
D5_2417	diaminopimelate decarboxylase LysA
D5_2416	diaminopimelate epimerase DapF
Methionine	
D5_1070	cystathionine beta-lyase
D5_1588	homoserine <i>O</i> -acetyltransferase MetX1
D5_1798	homoserine <i>O</i> -acetyltransferase MetX2
D5_2016	homoserine <i>O</i> -acetyltransferase MetX3
D5_2017	homoserine <i>O</i> -acetyltransferase MetX4
D5_2019	homoserine <i>O</i> -acetyltransferase MetX5
D5_1522	methionine synthase MetE
D5_1635	<i>O</i> -acetylhomoserine/ <i>O</i> -acetylserine sulfhydrylase MetZ/CysK1
D5_1699	<i>O</i> -acetylhomoserine/ <i>O</i> -acetylserine sulfhydrylase MetZ/CysK2
Phenylalanine/tyrosine	
D5_0606	chorismate mutase AroH
D5_0250	prephenate dehydratase PheA
D5_0938	prephenate dehydrogenase TyrA1
D5_2241	prephenate dehydrogenase TyrA2
Polyamines	
D5_0524	arginase/agmatinase family protein
D5_2023	<i>N</i> -carbamoyl-D-amino acid amidohydrolase AguB
D5_0522	pyruvoyl-dependent arginine decarboxylase PdaD
Proline	
Serine	
D5_2285	aminotransferase class V family
D5_1964	phosphoglycerate dehydrogenase SerA
D5_2363	phosphoserine phosphatase SerB
Threonine	
D5_1657	threonine synthase ThrC
Tryptophan	
D5_0159	anthranilate phosphoribosyltransferase TrpD
D5_0157	anthranilate synthase component I TrpE
D5_0158	anthranilate synthase component II TrpG
D5_0160	indole-3-glycerol phosphate synthase TrpC
D5_0161	phosphoribosylanthranilate isomerase TrpF
D5_0163	tryptophan synthase alpha subunit TrpA
D5_0162	tryptophan synthase beta subunit TrpB
D5_0030	tryptophan synthase beta subunit TrpB1
D5_2234	tryptophan-binding repressor TrpY
Valine/leucine/isoleucine	
D5_0026	2-isopropylmalate synthase LeuA
D5_2494	3-isopropylmalate dehydratase large subunit LeuC
D5_2493	3-isopropylmalate dehydratase small subunit LeuD
D5_2492	3-isopropylmalate dehydrogenase LeuB
D5_0057	acetolactate synthase large subunit IlvB1
D5_2290	acetolactate synthase large subunit IlvB2
D5_0058	acetolactate synthase small subunit IlvN
D5_0080	branched-chain-amino-acid aminotransferase IlvE
D5_1814	citramalate synthase CimA
D5_0039	dihydroxy-acid dehydratase IlvD
D5_0061	ketol-acid reductoisomerase IlvC
Salvage- general	
D5_1890	indolepyruvate ferredoxin oxidoreductase alpha subunit IorA
D5_1889	indolepyruvate ferredoxin oxidoreductase beta subunit IorB
D5_1795	ketoisovalerate ferredoxin oxidoreductase alpha subunit VorA
D5_1794	ketoisovalerate ferredoxin oxidoreductase beta subunit VorB
D5_1793	ketoisovalerate ferredoxin oxidoreductase gamma subunit VorC
Salvage- methionine	
D5_2274	methylthioadenosine phosphorylase MtnP
D5_2375	<i>S</i> -adenosyl-L-homocysteine hydrolase AhcY
D5_1338	<i>S</i> -adenosylmethionine synthetase MetK

CELL CYCLE

Cell division

- D5_0031 cell division ATPase MinD
- D5_2242 cell division control protein Cdc48
- D5_2227 cell division protein FtsZ
- D5_2239 cell division protein pelota PelA

Chromosome replication

- D5_2246 ATP-dependent DNA ligase DnII
- D5_0001 cdc6 family replication initiation protein Cdc6-1
- D5_2279 cdc6 family replication initiation protein Cdc6-2
- D5_0261 DNA polymerase family B PolB1
- D5_0803 DNA polymerase family B PolB2
- D5_2404 DNA polymerase large subunit DP2 PolD2
- D5_0164 DNA polymerase sliding clamp subunit PCNA family Pcn
- D5_2507 DNA polymerase small subunit DP1 PolD1
- D5_1934 DNA primase DnaG
- D5_1490 DNA primase large subunit PriB
- D5_1495 DNA primase small subunit PriA
- D5_1959 DNA-binding protein
- D5_2373 flap endonuclease Fen
- D5_0515 HIRAN domain-containing protein
- D5_2250 OB fold nucleic acid binding domain-containing protein
- D5_2470 replication factor A
- D5_0103 replication factor C large subunit RfcL
- D5_0104 replication factor C small subunit RfcS
- D5_2033 replicative DNA helicase Mcm
- D5_0320 ribonuclease HII RnhB
- D5_1611 ribonuclease HI

Genome segregation

- D5_1415 chromosome partitioning ParA/MinD-like ATPase
- D5_2361 DNA topoisomerase I TopA
- D5_0347 DNA topoisomerase VI subunit A
- D5_0348 DNA topoisomerase VI subunit B
- D5_1538 DNA double-strand break repair protein Rad50

CELL ENVELOPE

Cell surface proteins

- D5_0014 adhesin-like protein
- D5_0015 adhesin-like protein
- D5_0016 adhesin-like protein
- D5_0036 adhesin-like protein
- D5_0038 adhesin-like protein
- D5_0051 adhesin-like protein
- D5_0111 adhesin-like protein
- D5_0112 adhesin-like protein
- D5_0127 adhesin-like protein
- D5_0173 adhesin-like protein
- D5_0188 adhesin-like protein
- D5_0189 adhesin-like protein
- D5_0218 adhesin-like protein
- D5_0219 adhesin-like protein
- D5_0252 adhesin-like protein
- D5_0262 adhesin-like protein
- D5_0452 adhesin-like protein
- D5_0453 adhesin-like protein
- D5_0458 adhesin-like protein
- D5_0459 adhesin-like protein
- D5_0478 adhesin-like protein
- D5_0640 adhesin-like protein
- D5_0660 adhesin-like protein
- D5_0715 adhesin-like protein
- D5_0821 adhesin-like protein
- D5_0825 adhesin-like protein
- D5_0867 adhesin-like protein

- D5_0965 adhesin-like protein
- D5_0970 adhesin-like protein
- D5_0971 adhesin-like protein
- D5_0973 adhesin-like protein
- D5_0974 adhesin-like protein
- D5_0976 adhesin-like protein
- D5_0978 adhesin-like protein
- D5_0979 adhesin-like protein
- D5_1071 adhesin-like protein
- D5_1092 adhesin-like protein
- D5_1152 adhesin-like protein
- D5_1322 adhesin-like protein
- D5_1393 adhesin-like protein
- D5_1400 adhesin-like protein
- D5_1406 adhesin-like protein
- D5_1411 adhesin-like protein
- D5_1412 adhesin-like protein
- D5_1413 adhesin-like protein
- D5_1423 adhesin-like protein
- D5_1424 adhesin-like protein
- D5_1473 adhesin-like protein
- D5_1476 adhesin-like protein
- D5_1494 adhesin-like protein
- D5_1610 adhesin-like protein
- D5_1618 adhesin-like protein
- D5_1619 adhesin-like protein
- D5_1715 adhesin-like protein
- D5_1716 adhesin-like protein
- D5_1746 adhesin-like protein
- D5_1758 adhesin-like protein
- D5_1764 adhesin-like protein
- D5_1896 adhesin-like protein
- D5_1912 adhesin-like protein
- D5_1921 adhesin-like protein
- D5_2120 adhesin-like protein
- D5_2160 adhesin-like protein
- D5_2173 adhesin-like protein
- D5_2175 adhesin-like protein
- D5_2176 adhesin-like protein
- D5_2261 adhesin-like protein
- D5_2264 adhesin-like protein
- D5_2265 adhesin-like protein
- D5_2266 adhesin-like protein
- D5_2335 adhesin-like protein
- D5_2337 adhesin-like protein
- D5_2354 adhesin-like protein
- D5_2356 adhesin-like protein
- D5_2357 adhesin-like protein
- D5_2407 adhesin-like protein

Expolysaccharide synthesis

- D5_0041 acetyltransferase
- D5_0199 polysaccharide/polyol phosphate ABC transporter ATP-binding protein
- D5_0200 polysaccharide/polyol phosphate ABC transporter permease protein
- D5_0223 glycosyl transferase GT2 family
- D5_0447 glycosyl transferase GT2 family
- D5_0448 polysaccharide deacetylase domain-containing protein
- D5_0462 glycosyl transferase GT2 family
- D5_0463 glycosyl transferase
- D5_0465 glycosyl transferase
- D5_0467 glycosyl transferase GT2 family
- D5_0474 polysaccharide/polyol phosphate ABC transporter permease protein
- D5_0475 polysaccharide/polyol phosphate ABC transporter ATP-binding protein
- D5_0484 glycosyl transferase GT2 family
- D5_0485 glycosyl transferase GT2 family
- D5_0488 glycosyl transferase GT2 family
- D5_0493 glycosyl transferase GT2 family
- D5_0498 UDP-glucose pyrophosphorylase GalU
- D5_0501 glycosyl transferase GT2 family
- D5_0504 glycosyl transferase

D5_0542	UDP-glucose/GDP-mannose dehydrogenase
D5_0583	UDP- <i>N</i> -acetylglucosamine 2-epimerase
D5_0603	glycosyl transferase GT4 family
D5_0612	glycosyl transferase
D5_0762	glycosyl transferase GT2 family with response regulator receiver domain
D5_0817	UDP-galactopyranose mutase Glf
D5_0818	glycosyl transferase GT2 family
D5_0836	UDP-galactopyranose mutase Glf
D5_0840	glycosyl transferase
D5_0842	UDP- <i>N</i> -acetylglucosamine 2-epimerase
D5_0848	polysaccharide biosynthesis protein
D5_0849	glycosyl transferase
D5_0884	polysaccharide biosynthesis protein
D5_0986	UDP-glucose pyrophosphorylase GalU
D5_1003	glycosyl transferase GT2 family
D5_1286	glycosyl transferase GT2 family
D5_1287	glycosyl transferase GT2 family
D5_1288	glycosyl transferase GT2 family
D5_1289	glycosyl transferase GT2 family
D5_1290	glycosyl transferase GT2 family
D5_1291	glycosyl transferase GT2 family
D5_1292	UDP-glucose 6-dehydrogenase
D5_1293	glycosyl transferase GT2 family
D5_1305	glycosyl transferase GT2 family
D5_1307	glycosyl transferase GT2 family
D5_1609	response regulator/glycosyl transferase GT2 family protein
D5_1756	dolichol kinase
D5_1929	glycosyl transferase GT2 family
D5_2471	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase
D5_2472	glycosyl transferase GT2 family
D5_2473	glycosyl transferase GT2 family
D5_2474	glycosyl transferase GT2 family
D5_2475	CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase
D5_2478	dTDP-glucose 4,6-dehydratase RfbB
D5_2479	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC
D5_2480	glucose-1-phosphate thymidyltransferase RfbA
D5_2483	dTDP-4-dehydrorhamnose reductase RfbD
D5_2484	UDP- <i>N</i> -acetyl-D-mannosaminuronate dehydrogenase

Pseudomurein biosynthesis

D5_0075	polysaccharide biosynthesis protein
D5_0081	undecaprenyl-diphosphatase UppP
D5_0091	cell wall biosynthesis protein Mur ligase family
D5_0092	cell wall biosynthesis protein Mur ligase family
D5_0520	cell wall biosynthesis protein Mur ligase family
D5_0534	phosphosugar isomerase
D5_0838	polysaccharide biosynthesis protein
D5_0854	lipopolysaccharide cholinephosphotransferase
D5_0866	glucosamine-fructose-6-phosphate aminotransferase GlmS
D5_0908	glucosamine-fructose-6-phosphate aminotransferase GlmS
D5_0948	cell wall biosynthesis protein Mur ligase family
D5_1033	UDP-glucose 4-epimerase GalE
D5_1120	glucosamine-fructose-6-phosphate aminotransferase GlmS
D5_1126	diacylglycerol kinase DagK
D5_1483	cell wall biosynthesis protein phospho-N-acetylmuramoyl-pentapeptide-transferase family
D5_1512	undecaprenyl pyrophosphate synthetase UppS
D5_1536	cell wall biosynthesis protein Mur ligase family
D5_1788	NAD-dependent epimerase/dehydratase
D5_1822	cell wall biosynthesis protein Mur ligase family
D5_1823	cell wall biosynthesis protein phospho-N-acetylmuramoyl-pentapeptide-transferase family
D5_2172	PeiW-related protein
D5_2237	cell wall biosynthesis protein UDP-glycosyltransferase family
D5_2238	cell wall biosynthesis protein
D5_2251	phosphoglucosamine mutase GlmM1
D5_2256	UDP- <i>N</i> -acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU
D5_2258	phosphoglucosamine mutase GlmM2
D5_2488	cell wall biosynthesis glycosyl transferase GT2 family

Sialic acid biosynthesis

D5_0365	pseudaminic acid CMP-transferase PseF
D5_0366	<i>N</i> -acetyl neuramic acid synthetase NeuB
D5_0841	sialic acid synthase

Teichoic acid biosynthesis

D5_0197	glycosyl transferase GT2 family/CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase
D5_0446	cell wall teichoic acid glycosylation protein
D5_0550	glycerol-3-phosphate cytidyltransferase
D5_0853	glycerol-3-phosphate cytidyltransferase
D5_1302	alcohol dehydrogenase
D5_1303	LPS biosynthesis protein
D5_1857	alcohol dehydrogenase
D5_1858	2- <i>C</i> -methyl-D-erythritol 4-phosphate cytidyltransferase IspD

CELLULAR PROCESSES

Oxidative stress response

D5_0115	NADH oxidase Nox
D5_0599	thioredoxin
D5_1807	thioredoxin-disulfide reductase TrxS
D5_1416	NADH oxidase Nox
D5_1478	F ₄₂₀ H ₂ oxidase FprA
D5_1600	rubredoxin Rub1
D5_1601	rubredoxin Rub2
D5_1622	rubrerythrin Rbr1
D5_1623	rubrerythrin Rbr2
D5_1624	rubrerythrin Rbr3
D5_1696	desulfoferrodoxin Dfx
D5_2257	rubredoxin Rub
D5_2452	F ₄₂₀ H ₂ oxidase FprA
D5_2453	rubrerythrin Rbr4

Stress response

D5_1620	bile salt hydrolase
D5_1030	universal stress protein UspA
D5_1283	universal stress protein UspA
D5_2005	UspA domain-containing protein

CENTRAL CARBON METABOLISM

Acetate

D5_0784	ADP-dependent acetyl-CoA synthetase Acs
D5_1792	acetyl-CoA synthetase Acs
D5_1883	cation/acetate symporter, actP
D5_2122	pyruvate ferredoxin oxidoreductase gamma subunit PorC
D5_2123	pyruvate ferredoxin oxidoreductase delta subunit PorD
D5_2124	pyruvate ferredoxin oxidoreductase alpha subunit PorA
D5_2125	pyruvate ferredoxin oxidoreductase beta subunit PorB
D5_2126	pyruvate ferredoxin oxidoreductase-associated PorE
D5_2127	pyruvate ferredoxin oxidoreductase-associated PorF

Aromatic compounds

D5_1516	carboxymuconolactone decarboxylase family protein PcaC1
D5_1732	carboxymuconolactone decarboxylase family protein PcaC2
D5_1877	carboxymuconolactone decarboxylase family protein PcaC3
D5_2292	4-oxalocrotonate tautomerase family enzyme DmpI1
D5_2321	4-oxalocrotonate tautomerase family enzyme DmpI2

Bicarbonate

D5_0059	carbonic anhydrase Cab
D5_1726	bicarbonate ABC transporter ATP-binding protein BtcA
D5_1727	bicarbonate ABC transporter permease protein BtcB
D5_0782	bicarbonate ABC transporter substrate-binding protein BtcC

Formate

D5_0837	pyruvate formate-lyase-activating enzyme PflA
D5_0839	pyruvate-formate lyase
D5_2253	pyruvate formate-lyase-activating enzyme PflA

Gluconeogenesis

D5_0312	phosphoenolpyruvate synthase PpsA
D5_0339	glyceraldehyde-3-phosphate dehydrogenase Gap
D5_0405	triose-phosphate isomerase TpiA
D5_0406	phosphoglycerate kinase Pgk
D5_0655	2-phosphoglycerate kinase Pgk
D5_0728	phosphopyruvate hydratase Eno
D5_1509	cyclic 2,3-diphosphoglycerate-synthetase CpgS
D5_1572	2,3-bisphosphoglycerate-independent phosphoglycerate mutase ApgM
D5_1909	2-phosphoglycerate kinase Pgk2A
D5_2214	pyruvate kinase PykA
D5_2218	fructose 1,6-bisphosphatase Fbp
D5_2259	2,3-bisphosphoglycerate-independent phosphoglycerate mutase ApgM
D5_1469	phospho-2-dehydro-3-deoxyheptonate aldolase/fructose-bisphosphate aldolase

Glycolate salvage pathway

D5_0363	phosphoglycolate phosphatase Gph
D5_1053	phosphoglycolate phosphatase Gph

Inositol biosynthesis

D5_0521	bifunctional inositol-1 monophosphatase/fructose-1,6-bisphosphatase/ATP-NAD kinase
D5_0878	inositol-phosphate phosphatase domain containing protein
D5_0370	myo-inositol-1-phosphate synthase

Propanoate

D5_1954	2-methylcitrate dehydratase PrpD
D5_1951	2-methylcitrate synthase/citrate synthase II PrpC/CitZ

PRPP synthesis

D5_0954	ribose-phosphate diphosphokinase Prs
D5_1719	ribose 5-phosphate isomerase A RpiA

Ribulose monophosphate pathway

D5_0070	bifunctional formaldehyde-activating enzyme/3- hexulose-6-phosphate synthase Fae/Hps
D5_1128	3-hexulose-6-phosphate isomerase Phi1
D5_2395	3-hexulose-6-phosphate isomerase Phi1

Tricarboxylic cycle

D5_0007	succinate dehydrogenase/fumarate reductase flavoprotein subunit SdhA
D5_0372	pyruvate carboxylase subunit B PycB
D5_0396	fumarate hydratase FumA
D5_0397	2-oxoglutarate ferredoxin oxidoreductase subunit delta KorD
D5_0398	2-oxoglutarate ferredoxin oxidoreductase subunit alpha KorA
D5_0399	2-oxoglutarate ferredoxin oxidoreductase subunit beta KorB
D5_0400	2-oxoglutarate ferredoxin oxidoreductase subunit gamma KorC
D5_0401	succinyl-CoA synthetase beta subunit SucC
D5_0674	fumarate hydratase FumA
D5_0678	pyruvate carboxylase subunit A PycA
D5_1041	succinate dehydrogenase/fumarate reductase flavoprotein subunit SdhA
D5_1042	succinate dehydrogenase/fumarate reductase iron-sulfur protein SdhB
D5_1372	malate dehydrogenase Mdh
D5_1670	succinate-CoA ligase alpha subunit SucD
D5_1899	succinate dehydrogenase/fumarate reductase iron-sulfur protein SdhB
D5_1952	fumarate hydratase FumA
D5_2128	fumarate hydratase FumA

Other

D5_0594	deoxyribose-phosphate aldolase DeoC
---------	-------------------------------------

ENERGY METABOLISM

Electron transfer

D5_0436	4Fe-4S ferredoxin binding domain-containing protein
---------	---

D5_0525	4Fe-4S ferredoxin binding domain-containing protein
D5_0576	4Fe-4S ferredoxin binding domain-containing protein
D5_0663	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein
D5_1060	4Fe-4S binding domain-containing protein
D5_1006	iron-sulfur cluster-binding protein
D5_1382	4Fe-4S ferredoxin binding domain-containing protein
D5_1556	4Fe-4S binding domain-containing protein
D5_1639	4Fe-4S binding domain-containing protein
D5_1767	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein
D5_1848	4Fe-4S ferredoxin binding domain-containing protein
D5_1901	4Fe-4S binding domain-containing protein
D5_2139	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein
D5_2206	4Fe-4S ferredoxin iron-sulfur binding domain protein
D5_0003	flavodoxin domain-containing protein
D5_0077	ferredoxin
D5_0183	flavodoxin
D5_0548	flavodoxin
D5_0662	ferredoxin
D5_0729	ferredoxin
D5_0823	flavodoxin
D5_1031	ferredoxin
D5_1137	flavodoxin
D5_1477	flavodoxin
D5_2010	flavodoxin
D5_0641	thioreduxon TrxA
D5_0642	cytochrome C-type biogenesis protein DsbD
D5_0074	NADPH-dependent FMN reductase
D5_0824	NADPH-dependent FMN reductase
D5_1064	NADPH-dependent FMN reductase
D5_1065	NADPH-dependent FMN reductase
D5_1326	NADPH-dependent FMN reductase
D5_1359	NADPH-dependent FMN reductase
D5_1385	NADPH-dependent FMN reductase
D5_1472	NADPH-dependent FMN reductase
D5_1571	NADPH-dependent FMN reductase
D5_1834	NADPH-dependent FMN reductase
D5_1835	NADPH-dependent FMN reductase
D5_2273	NADPH-dependent FMN reductase
D5_1938	A ₁ A ₀ archaeal ATP synthase subunit D AhaD
D5_1939	A ₁ A ₀ archaeal ATP synthase subunit B AhaB
D5_1940	A ₁ A ₀ archaeal ATP synthase subunit A AhaA
D5_1941	A ₁ A ₀ archaeal ATP synthase subunit F AhaF
D5_1942	A ₁ A ₀ archaeal ATP synthase subunit C AhaC
D5_1943	A ₁ A ₀ archaeal ATP synthase subunit E AhaE
D5_1944	A ₁ A ₀ archaeal ATP synthase subunit K AhaK
D5_1945	A ₁ A ₀ archaeal ATP synthase subunit I AhaI
D5_1946	A ₁ A ₀ archaeal ATP synthase subunit H AhaH

Alcohol metabolism

D5_1461	NADPH-dependent F ₄₂₀ reductase NpdG
---------	---

Formate metabolism

D5_0738	formate dehydrogenase alpha subunit FdhA1
D5_0739	formate dehydrogenase beta subunit FdhB1
D5_0772	formate dehydrogenase accessory protein FdhD
D5_2391	formate dehydrogenase beta subunit FdhB2
D5_2392	formate dehydrogenase alpha subunit FdhA2
D5_2393	formate/nitrite transporter FdhC
D5_2394	formate dehydrogenase accessory protein FdhD

H₂ metabolism

D5_0174	coenzyme F ₄₂₀ hydrogenase alpha subunit FrhA
D5_0175	coenzyme F ₄₂₀ hydrogenase delta subunit FrhD
D5_0176	coenzyme F ₄₂₀ hydrogenase gamma subunit FrhG
D5_0177	coenzyme F ₄₂₀ hydrogenase beta subunit FrhB
D5_0225	energy-converting hydrogenase B subunit A EhbA
D5_0226	energy-converting hydrogenase B subunit B EhbB
D5_0227	energy-converting hydrogenase B subunit C EhbC
D5_0228	energy-converting hydrogenase B subunit D EhbD
D5_0229	energy-converting hydrogenase B subunit E EhbE
D5_0230	energy-converting hydrogenase B subunit F EhbF
D5_0231	energy-converting hydrogenase B subunit G EhbG

D5_0232	energy-converting hydrogenase B subunit H EhbH
D5_0233	energy-converting hydrogenase B subunit I EhbI
D5_0234	energy-converting hydrogenase B subunit J EhbJ
D5_0235	energy-converting hydrogenase B subunit K EhbK
D5_0236	energy-converting hydrogenase B subunit L EhbL
D5_0237	energy-converting hydrogenase B subunit M EhbM
D5_0238	energy-converting hydrogenase B subunit N EhbN
D5_0239	energy-converting hydrogenase B, subunit O, EhbO
D5_0240	energy-converting hydrogenase B subunit P EhbP
D5_0241	energy-converting hydrogenase B subunit Q EhbQ
D5_0302	methyl viologen-reducing hydrogenase delta subunit MvhD
D5_0303	methyl viologen-reducing hydrogenase gamma subunit MvhG
D5_0304	methyl viologen-reducing hydrogenase alpha subunit MvhA
D5_0305	methyl viologen-reducing hydrogenase beta subunit MvhB
D5_0740	methyl viologen-reducing hydrogenase delta subunit MvhD
D5_1770	energy-converting hydrogenase A subunit R EhaR
D5_1771	energy-converting hydrogenase A subunit Q EhaQ
D5_1772	energy-converting hydrogenase A subunit P EhaP
D5_1773	energy-converting hydrogenase A subunit O EhaO
D5_1774	energy-converting hydrogenase A subunit N EhaN
D5_1775	energy-converting hydrogenase A subunit M EhaM
D5_1776	energy-converting hydrogenase A subunit L EhaL
D5_1777	energy-converting hydrogenase A subunit K EhaK
D5_1778	energy-converting hydrogenase A subunit J EhaJ
D5_1779	energy-converting hydrogenase A subunit I EhaI
D5_1780	energy-converting hydrogenase A subunit H EhaH
D5_1781	energy-converting hydrogenase A subunit G EhaG
D5_1782	energy-converting hydrogenase A subunit F EhaF
D5_1783	energy-converting hydrogenase A subunit E EhaE
D5_1784	energy-converting hydrogenase A subunit D EhaD
D5_1785	energy-converting hydrogenase A subunit C EhaC
D5_1786	energy-converting hydrogenase A subunit B EhaB
D5_1787	energy-converting hydrogenase A subunit A EhaA
D5_0144	hydrogenase expression/formation protein, HypE
D5_0194	hydrogenase maturation factor HypF
D5_0364	hydrogenase expression/formation protein HypD
D5_0807	hydrogenase expression/formation protein HypE
D5_1527	hydrogenase accessory protein HypB
D5_1528	hydrogenase nickel insertion protein HypA
D5_1825	hydrogenase maturation protease HycI
D5_2235	hydrogenase assembly chaperone HypC
Methanogenesis pathway	
D5_2110	5,10-methylenetetrahydromethanopterin reductase Mer
D5_0649	CoB--CoM heterodisulfide reductase subunit C HdrC
D5_0650	CoB--CoM heterodisulfide reductase subunit B HdrB
D5_1005	CoB--CoM heterodisulfide reductase subunit B HdrB2
D5_1502	CoB--CoM heterodisulfide reductase subunit A HdrA1
D5_1503	CoB--CoM heterodisulfide reductase subunit B HdrB3
D5_1504	CoB--CoM heterodisulfide reductase subunit C HdrC2
D5_2467	CoB--CoM heterodisulfide reductase subunit A HdrA2
D5_1879	coenzyme F ₄₂₀ -dependent N^5,N^{10} -methenyltetrahydromethanopterin reductase Hmd (pseudo)
D5_2132	coenzyme F ₄₂₀ -dependent N^5,N^{10} -methenyltetrahydromethanopterin reductase Hmd
D5_0079	F ₄₂₀ -dependent methylenetetrahydromethanopterin dehydrogenase Mtd
D5_0741	F ₄₂₀ -dependent methylenetetrahydromethanopterin dehydrogenase Mtd
D5_0210	formylmethanofuran-tetrahydromethanopterin formyltransferase Ftr
D5_1769	formylmethanofuran-tetrahydromethanopterin formyltransferase Ftr2
D5_0284	methyl-coenzyme M reductase beta subunit McrB
D5_0285	methyl-coenzyme M reductase D subunit McrD
D5_0286	methyl-coenzyme M reductase C subunit McrC
D5_0287	methyl-coenzyme M reductase gamma subunit McrG
D5_0288	methyl-coenzyme M reductase alpha subunit McrA
D5_0328	methyl-coenzyme M reductase component A2 AtwA
D5_0742	methyl-coenzyme M reductase II beta subunit MrtB
D5_0743	methyl-coenzyme M reductase II D subunit MrtD
D5_0744	methyl-coenzyme M reductase II gamma subunit MrtG
D5_0745	methyl-coenzyme M reductase II alpha subunit MrtA
D5_0289	tetrahydromethanopterin S-methyltransferase subunit E MtrE
D5_0290	tetrahydromethanopterin S-methyltransferase subunit D MtrD

D5_0291	tetrahydromethanopterin S-methyltransferase subunit C MtrC
D5_0292	tetrahydromethanopterin S-methyltransferase subunit B MtrB
D5_0293	tetrahydromethanopterin S-methyltransferase subunit A MtrA
D5_0294	tetrahydromethanopterin S-methyltransferase subunit F MtrF
D5_0295	tetrahydromethanopterin S-methyltransferase subunit G MtrG
D5_0296	tetrahydromethanopterin S-methyltransferase subunit H MtrH
D5_0350	tetrahydromethanopterin S-methyltransferase subunit H MtrH2
D5_0510	tetrahydromethanopterin S-methyltransferase subunit A MtrA
D5_1751	tungsten formylmethanofuran dehydrogenase subunit E FwdE
D5_2382	tungsten formylmethanofuran dehydrogenase subunit C FwdC
D5_2383	tungsten formylmethanofuran dehydrogenase subunit A FwdA
D5_2384	tungsten formylmethanofuran dehydrogenase subunit B FwdB
D5_2385	tungsten formylmethanofuran dehydrogenase subunit D FwdD
D5_2386	tungsten formylmethanofuran dehydrogenase subunit G FwdG
D5_2387	tungsten formylmethanofuran dehydrogenase subunit F FwdF
D5_2388	tungsten formylmethanofuran dehydrogenase subunit H FwdH
D5_1626	methenyltetrahydromethanopterin cyclohydrolase Mch
D5_0737	FlpE-related protein

LIPID METABOLISM

Biosynthesis bacterial

D5_1077	3-oxoacyl-(acyl-carrier-protein) reductase FabG
D5_1126	diacylglycerol kinase DagK

Biosynthesis general

D5_1032	geranylgeranyl reductase family protein
---------	---

Lipid backbone

D5_1721	NAD(P)-dependent glycerol-1-phosphate dehydrogenase EgsA
---------	--

Phospholipid biosynthesis

D5_0317	phosphatidylserine synthase PssA
D5_0369	geranylgeranylglyceryl phosphate synthase
D5_0799	membrane-associated phospholipid phosphatase
D5_1038	phosphatidylglycerophosphate synthase PgsA
D5_1542	digeranylgeranylglyceryl phosphate synthase
D5_2212	phosphatidylglycerophosphate synthase PgsA

Mevalonate pathway

D5_0732	mevalonate kinase Mvk
D5_0733	isopentenyl diphosphate kinase
D5_0734	isopentenyl diphosphate delta-isomerase Fni
D5_0872	hydroxymethylglutaryl-CoA synthase
D5_0873	acetyl-CoA acetyltransferase
D5_1669	hydroxymethylglutaryl-CoA reductase (NADPH) HmgA
D5_0731	phosphomevalonate decarboxylase

Elongation of isoprenoid side chains

D5_0736	bifunctional short chain isoprenyl diphosphate synthase IdsA
---------	--

MOBILE ELEMENTS

CRISPR-associated genes

D5_0883	CRISPR-associated protein Cas1
D5_0882	CRISPR-associated protein Cas2
D5_0811	CRISPR-associated protein Cas4
D5_1211	CRISPR-associated protein Cas6
D5_1924	CRISPR-associated protein TIGR02710 family

Transposase

D5_0019	transposase
D5_0441	transposase
D5_0443	transposase
D5_0444	transposase
D5_0497	transposase
D5_0508	transposase
D5_0892	transposase
D5_0935	transposase
D5_1076	transposase

D5_1096	transposase
D5_1170	transposase
D5_1214	transposase
D5_1234	transposase
D5_1395	transposase
D5_1396	transposase
D5_1474	transposase
D5_1475	transposase
D5_1499	transposase
D5_1615	transposase
D5_1717	transposase
D5_1718	transposase
D5_1760	transposase
D5_1922	transposase
D5_1989	transposase
D5_2336	transposase
D5_2465	transposase
D5_0469	transposase IS4 family
D5_1997	transposase IS4 family protein
D5_0509	transposase IS605 OrfB family
D5_1021	transposase IS605 OrfB family
D5_1323	transposase IS605 OrfB family
D5_1324	transposase IS605 OrfB family
D5_2267	transposase IS605 OrfB family
D5_0830	transposase IS605 OrfB family, partial
D5_0832	transposase IS605 OrfB family, partial
D5_0712	transposase, partial
D5_0713	transposase, partial
D5_0714	transposase, partial

NITROGEN METABOLISM

Fixation

D5_1039	4Fe-4S iron sulfur cluster binding protein NifH/frxC family
D5_1379	NifU-like FeS cluster assembly scaffold protein
D5_1697	NifU-like FeS cluster assembly scaffold protein
D5_1698	cysteine desulfurase NifS

General

D5_0048	nitroreductase family protein
D5_0505	nitroreductase family protein
D5_0797	nitroreductase family protein
D5_0798	nitroreductase family protein
D5_1069	nitroreductase family protein
D5_1117	nitroreductase family protein
D5_1744	nitroreductase family protein
D5_1915	nitroreductase family protein
D5_1950	nitroreductase family protein

Other

D5_1162	ADP-ribosylglycohydrolase family protein
D5_1163	ADP-ribosylglycohydrolase family protein
D5_0749	hydroxylamine reductase Hcp

Regulation

D5_0958	nitrogen regulatory protein P-II GlnK
D5_1674	nitrogen regulatory protein P-II GlnK

Transport

D5_0957	ammonium transporter Amt
D5_1675	ammonium transporter Amt

NUCLEIC ACID METABOLISM

DNA-binding proteins

D5_0005	archaeal histone
D5_0593	archaeal histone
D5_0027	DNA-binding protein Alba
D5_2345	DNA-binding protein
D5_0595	histone acetyltransferase ELP3 family

D5_0215	NAD-dependent deacetylase Sir2 family
---------	---------------------------------------

Helicase

D5_0216	DNA helicase
D5_0220	DNA helicase
D5_0592	DEAD/DEAH box helicase domain-containing protein
D5_0813	DEAD/DEAH box helicase domain-containing protein
D5_0966	DEAD/DEAH box helicase domain-containing protein
D5_1025	helicase
D5_1225	ATP-dependent DNA helicase PcrA
D5_1239	ATP-dependent DNA helicase UvrD/REP family
D5_1246	ATP-dependent DNA helicase UvrD/REP family
D5_1255	ATP-dependent DNA helicase UvrD/REP family
D5_1261	ATP-dependent DNA helicase
D5_1530	DEAD/DEAH box helicase domain-containing protein
D5_1531	ATP-dependent DNA helicase UvrD/REP family
D5_2011	helicase SNF2 family
D5_2026	DEAD/DEAH box helicase domain-containing protein
D5_2298	helicase
D5_2438	ATP-dependent DNA helicase

Recombination and repair

D5_0087	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase
D5_0089	ssDNA exonuclease RecJ
D5_0096	Hef nuclease
D5_0205	archaeal Holliday junction resolvase Hjc
D5_0338	endonuclease IV
D5_0616	exodeoxyribonuclease VII small subunit XseB
D5_0617	exodeoxyribonuclease VII large subunit XseA
D5_0618	exodeoxyribonuclease VII large subunit XseA
D5_0630	staphylococcal nuclease domain-containing protein
D5_0769	excinuclease ABC A subunit UvrA
D5_0801	exodeoxyribonuclease III Xth
D5_0810	nuclease
D5_0815	Single strand DNA binding protein
D5_0956	excinuclease ABC B subunit UvrB
D5_0959	excinuclease ABC A subunit UvrA
D5_1026	excinuclease ABC C subunit UvrC
D5_1043	6-O-methylguanine DNA methyltransferase Ogt
D5_1072	NADH pyrophosphatase NudC
D5_1198	exodeoxyribonuclease III Xth
D5_1199	endonuclease III-related protein
D5_1221	DNA mismatch endonuclease Vsr
D5_1233	exodeoxyribonuclease VII large subunit XseA
D5_1236	exodeoxyribonuclease VII small subunit XseB
D5_1349	DNA mismatch repair ATPase MutS family
D5_1364	uracil-DNA glycosylase Ung
D5_1538	DNA double-strand break repair protein Rad50
D5_1539	DNA double-strand break repair protein Mre11
D5_1558	exonuclease
D5_1694	archaea-specific RecJ-like exonuclease
D5_1704	endonuclease III Nth
D5_1870	DNA-3-methyladenine glycosylase I Tag
D5_2041	DNA mismatch repair ATPase MutS family
D5_2083	DNA repair photolyase
D5_2093	GIY-YIG catalytic domain-containing endonuclease
D5_2094	GIY-YIG catalytic domain-containing endonuclease
D5_2208	DNA repair and recombination protein RadB
D5_2243	exonuclease
D5_2299	DNA mismatch repair protein MutT
D5_2424	8-oxoguanine DNA-glycosylase Ogg
D5_2469	DNA repair and recombination protein RadA

Restriction and modification

D5_0066	type II restriction endonuclease
D5_0404	DNA methylase
D5_0512	type I restriction-modification enzyme S subunit HsdS2
D5_0513	type I restriction-modification system M subunit HsdM2
D5_1219	DNA-cytosine methyltransferase Dcm
D5_1220	DNA-cytosine methyltransferase Dcm
D5_2082	restriction endonuclease
D5_2084	type I site-specific deoxyribonuclease HsdR family
D5_2085	type I restriction endonuclease subunit S
D5_2086	type I restriction endonuclease subunit M

D5_2165 type III restriction endonuclease res subunit
D5_2166 type III restriction endonuclease methylation subunit
D5_2307 DNA phosphorothioation system restriction enzyme

PROTEIN FATE

Protein degradation

D5_0086 glycoprotease M22 family
D5_0105 peptidase M48 family
D5_0178 methionine aminopeptidase Map
D5_0221 succinylglutamate desuccinylase/aspartoacylase
D5_0362 peptidase U62 family
D5_0379 peptidase M48 family
D5_0545 peptidase U62 family
D5_0947 ATP-dependent protease S16 family
D5_1037 peptidase U32
D5_1555 glutamyl aminopeptidase PepA
D5_1998 Xaa-Pro aminopeptidase
D5_1999 peptidase M50 family
D5_2039 peptidase U32 family
D5_2040 peptidase U32 family
D5_2049 transglutaminase domain-containing protein
D5_2454 peptidase M50 family
D5_0266 proteasome beta subunit
D5_1686 proteasome alpha subunit PsmA
D5_1817 proteasome-activating nucleotidase
D5_2399 proteasome-activating nucleotidase

Protein folding

D5_0190 molecular chaperone DnaJ
D5_0191 chaperone protein DnaK
D5_0192 molecular chaperone GrpE
D5_0395 peptidyl-prolyl cis-trans isomerase FKBP-type
D5_0535 heat shock protein Hsp20/alpha crystallin family
D5_0614 thermosome subunit
D5_1012 prefoldin beta subunit PfdB
D5_1428 chaperone protein DnaJ
D5_1663 thermosome subunit
D5_1867 nascent polypeptide-associated complex protein
D5_2339 prefoldin alpha subunit PfdA
D5_2421 peptidyl-prolyl cis-trans isomerase

Protein secretion

D5_0046 signal peptidase I
D5_0315 sortase family protein
D5_0704 preprotein translocase subunit SecY
D5_0816 signal recognition particle SRP19 protein
D5_1565 type IV leader peptidase family protein
D5_1673 signal peptidase I
D5_1979 type II secretion system protein F GspF
D5_2197 type II secretion system protein E GspE
D5_2198 type II secretion system protein F GspF
D5_2226 preprotein translocase subunit SecE
D5_2338 signal recognition particle receptor FtsY
D5_2360 oligosaccharyl transferase
D5_2426 preprotein translocase subunit SecG
D5_2429 signal recognition particle SRP54 protein

PROTEIN SYNTHESIS

Other

D5_0134 translation-associated GTPase
D5_0265 RNA-metabolising metallo-beta-lactamase
D5_0349 RNA-binding protein
D5_0735 RNA-metabolising metallo-beta-lactamase
D5_1596 RNA-binding protein
D5_1815 RNA methylase
D5_1826 RNA methylase
D5_2201 RNA-binding protein
D5_2204 ATPase RIL

D5_2211 Sua5/YciO/YrdC/YwIc family translation factor
D5_2232 RNA-binding protein
D5_2344 tRNA methyltransferase subunit
D5_2347 RNA-binding protein
D5_2412 RNA-binding protein
D5_2428 pseudouridylate synthase
D5_2481 ribonuclease inhibitor
D5_2482 ribonuclease

Ribosomal proteins

D5_0088 ribosomal protein S15P Rps15p
D5_0166 ribosomal protein L44e Rpl44e
D5_0167 ribosomal protein S27e Rps27e
D5_0311 ribosomal protein L10e Rpl10e
D5_0414 ribosomal protein L30e Rpl30e
D5_0416 ribosomal protein S12P Rps12p
D5_0417 ribosomal protein S7P Rps7p
D5_0420 ribosomal protein S10P Rps10p
D5_0539 ribosomal protein L40e Rpl40e
D5_0607 ribosomal protein S17e Rps17e
D5_0681 ribosomal protein L3P Rpl3p
D5_0682 ribosomal protein L4p Rpl4p
D5_0683 ribosomal protein L23P Rpl23p
D5_0684 ribosomal protein L2P Rpl2p
D5_0685 ribosomal protein S19P Rps19p
D5_0686 ribosomal protein L22P Rpl22p
D5_0687 ribosomal protein S3P Rps3p
D5_0688 ribosomal protein L29P Rpl29p
D5_0691 ribosomal protein S18P Rpl3p
D5_0692 ribosomal protein L14P Rpl14p
D5_0693 ribosomal protein L24P Rpl24p
D5_0694 ribosomal protein S4e Rps4e
D5_0695 ribosomal protein L5P Rpl5p
D5_0696 ribosomal protein S8P Rps8p
D5_0697 ribosomal protein L6P Rpl6p
D5_0698 ribosomal protein L32e Rpl32e
D5_0699 ribosomal protein L19e Rpl19e
D5_0700 ribosomal protein L18P Rpl18p
D5_0701 ribosomal protein S5P Rps5p
D5_0702 ribosomal protein L30P Rpl30p
D5_0703 ribosomal protein L15P Rpl15p
D5_0707 ribosomal protein L34e Rpl34e
D5_0709 ribosomal protein L14e Rpl14e
D5_0719 ribosomal protein S13P Rps13p
D5_0720 ribosomal protein S4P Rps4p
D5_0721 ribosomal protein S11P Rps11p
D5_0723 ribosomal protein L18e Rpl18e
D5_0724 ribosomal protein L13P Rpl13p
D5_0725 ribosomal protein S9P Rps9p
D5_0730 ribosomal protein S2P Rps2p
D5_0806 ribosomal protein S8e Rps8e
D5_1009 ribosomal protein L37Ae Rpl37ae
D5_1543 ribosomal protein L40e Rpl40e
D5_1593 ribosomal protein L37e Rpl37e
D5_1644 ribosomal protein S27ae Rps27ae
D5_1645 ribosomal protein S24e Rps24e
D5_1651 ribosomal protein S6e Rps6e
D5_1654 ribosomal protein L24e Rpl24e
D5_1655 ribosomal protein S28e Rps28e
D5_1656 ribosomal protein L7Ae Rpl7ae
D5_1755 ribosomal protein L15e Rpl15e
D5_2221 ribosomal protein L12P Rpl12p
D5_2222 acidic ribosomal protein P0 RplPO
D5_2223 ribosomal protein L1P Rpl1p
D5_2224 ribosomal protein L11P Rpl11p
D5_2225 ribosomal protein L24 family
D5_2269 ribosomal protein S3Ae Rps3ae
D5_2340 ribosomal protein LX RplX
D5_2342 ribosomal protein L31e Rpl31e
D5_2343 ribosomal protein L39e Rpl39e
D5_2346 ribosomal protein S19e Rps19e
D5_2410 ribosomal protein L21e Rpl21e

RNA processing

D5_0106 tRNA(1-methyladenosine) methyltransferase

D5_0146	tRNA pseudouridine synthase D TruD
D5_0169	H/ACA RNA-protein complex component Nop10p
D5_0185	tRNA-dihydrouridine synthase DusA1
D5_0246	queuosine biosynthesis protein QueD
D5_0247	7-cyano-7-deazaguanosine biosynthesis protein QueE
D5_0255	fibrillarin FlpA
D5_0256	pre-mRNA splicing ribonucleoprotein PRP31
D5_0272	<i>N</i> ² , <i>N</i> ² -dimethylguanosine tRNA methyltransferase Trm1
D5_0327	tRNA-dihydrouridine synthase
D5_0382	queuosine biosynthesis protein QueC
D5_0425	ribosomal-protein-alanine acetyltransferase RimI
D5_0581	tRNA pseudouridine synthase A TruA
D5_0591	MiaB-like tRNA modifying enzyme
D5_0648	archaeosine tRNA-ribosyltransferase TgtA
D5_0679	ribosomal protein L11 methyltransferase PrmA
D5_0710	H/ACA RNA-protein complex component Cbf5p
D5_0870	archaeosine tRNA-ribosyltransferase TgtA
D5_0920	RNA-splicingI igase RtcB
D5_1466	tRNA nucleotidyltransferase Cca
D5_1467	2'-5' RNA ligase LigT
D5_1660	tRNA intron endonuclease EndA
D5_1682	exosome complex RNA-binding protein Rrp42
D5_1683	exosome complex exonuclease Rrp41
D5_1684	exosome complex RNA-binding protein Rrp4
D5_1685	exosome subunit
D5_0690	ribonuclease P subunit P29
D5_1687	ribonuclease P subunit P14
D5_1688	ribonuclease P subunit P30
D5_2348	ribonuclease P subunit RPR2
D5_1748	exosome subunit
D5_1900	RNA methyltransferase TrmH family
D5_1932	H/ACA RNA-protein complex component GarI
D5_1966	tRNA(His) guanylyltransferase ThgL
D5_2013	ribonuclease Z Rnz
D5_2031	ribosomal RNA large subunit methyltransferase J RrmJ
D5_2035	NMD3 family protein
D5_2413	dimethyladenosine transferase KsgA
D5_2432	exosome complex RNA-binding protein Csl4
Translation factors	
D5_0168	translation initiation factor aIF-2 alpha subunit
D5_0358	translation initiation factor aIF-1A
D5_0418	translation elongation factor aEF-2
D5_0419	translation elongation factor aEF-1 alpha
D5_0428	peptide chain release factor aRF1
D5_0523	translation initiation factor aIF-5A
D5_0639	translation initiation factor aIF-2B alpha subunit
D5_0644	diphthine synthase DphB
D5_0689	translation initiation factor aSUII
D5_0911	translation elongation factor aEF-2
D5_0994	deoxyhypusine synthase Dys
D5_1650	translation initiation factor aIF-2 gamma subunit
D5_1652	translation initiation factor IF-2
D5_2034	translation initiation factor aIF-2 beta subunit
D5_2200	translation elongation factor aEF-1 beta
D5_2203	peptidyl-tRNA hydrolase
D5_2341	translation initiation factor aIF-6
D5_2431	diphthamide biosynthesis protein
tRNA aminoacylation	
D5_0013	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit A GatA
D5_0042	aspartyl-tRNA synthetase AspS
D5_0047	arginyl-tRNA synthetase ArgS
D5_0069	threonyl-tRNA synthetase ThrS
D5_0100	histidyl-tRNA synthetase HisS
D5_0107	leucyl-tRNA synthetase LeuS
D5_0203	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit B GatB
D5_0754	glutamyl-tRNA synthetase GltX
D5_0800	phenylalanyl-tRNA synthetase alpha subunit PheS
D5_1062	seryl-tRNA synthetase SerS
D5_1370	D-tyrosyl-tRNA ^{Tyr} deacylase Dtd
D5_1489	methionyl-tRNA synthetase MetG
D5_1575	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit C GatC
D5_1659	tryptophanyl-tRNA synthetase TrpS
D5_1700	cysteinyl-tRNA synthetase CysS

D5_1708	valyl-tRNA synthetase ValS
D5_1713	phenylalanyl-tRNA synthetase subunit beta PheT
D5_1722	prolyl-tRNA synthetase ProS
D5_1796	glutamyl-tRNA ^{Gln} amidotransferase subunit D GatD
D5_1797	glutamyl-tRNA ^{Gln} amidotransferase subunit E GatE
D5_1903	glycyl-tRNA synthetase GlyS
D5_1969	tRNA binding domain-containing protein
D5_2036	tyrosyl-tRNA synthetase TyrS
D5_2220	alanyl-tRNA synthetase AlaS
D5_2400	lysyl-tRNA synthetase LysS
D5_2457	isoleucyl-tRNA synthetase IleS

PURINES AND PYRIMIDINES

Purine biosynthesis	
D5_0052	phosphoribosylamine--glycine ligase, purD
D5_0153	adenylosuccinate lyase PurB
D5_0195	phosphoribosylaminoimidazole carboxylase catalytic subunit PurE
D5_0264	phosphoribosylformylglycinamide cyclo-ligase PurM
D5_0323	IMP cyclohydrolase PurO
D5_0862	phosphoribosylaminoimidazole-succinocarboxamide synthase PurC
D5_0863	phosphoribosylformylglycinamide (FGAM) synthase PurS
D5_0864	phosphoribosylformylglycinamide (FGAM) synthase PurQ
D5_1036	amidophosphoribosyltransferase PurF
D5_2029	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-monophosphate-formate ligase PurP
D5_2430	adenine phosphoribosyltransferase Apt
D5_2456	phosphoribosylformylglycinamide (FGAM) synthase II PurL
D5_2486	<i>N</i> ⁵ -carboxyaminoimidazole ribonucleotide synthetase purK

Purine interconversion	
D5_0532	adenine deaminase Ade
D5_0705	adenylate kinase Adk
D5_2367	adenylate cyclase CyaA
D5_0766	adenylosuccinate synthetase PurA

Pyrimidine biosynthesis	
D5_0002	aspartate carbamoyltransferase
D5_0258	dihydroorotate dehydrogenase PyrD
D5_0259	dihydroorotate dehydrogenase electron transfer subunit PyrK
D5_0307	dihydroorotase PyrC
D5_0517	orotate phosphoribosyltransferase PyrE
D5_0547	aspartate carbamoyltransferase regulatory subunit PyrI
D5_0620	orotate phosphoribosyltransferase PyrE
D5_0997	orotidine 5'-phosphate decarboxylase PyrF
D5_2008	carbamoyl-phosphate synthase large subunit CarB
D5_2009	carbamoyl-phosphate synthase small subunit CarA

Pyrimidine interconversion	
D5_0708	cytidylate kinase Cmk
D5_1176	CMP/dCMP deaminase
D5_1497	thymidylate kinase Tmk
D5_1566	CTP synthase PyrG
D5_1617	thymidylate synthase ThyA
D5_1902	deoxycytidine triphosphate deaminase Dcd
D5_1916	uridylate kinase PyrH
D5_2038	thymidylate kinase Tmk
D5_2291	dUTP diphosphatase Dut
D5_2402	CMP/dCMP deaminase

Interconversion	
D5_0065	5'-nucleotidase SurE
D5_1008	inosine-5'-monophosphate dehydrogenase GuaB
D5_1333	5'-nucleotidase SurE
D5_1653	nucleoside diphosphate kinase Ndk
D5_1808	GMP synthase subunit A GuaA
D5_1810	GMP synthase subunit B GuaAb
D5_2405	anaerobic ribonucleoside-triphosphate reductase NrdD

Salvage	
D5_1762	uracil phosphoribosyltransferase Upp

Transport

D5_1315 xanthine/uracil permease
D5_1763 xanthine/uracil permease

REGULATION

Protein interaction

D5_0025 serine/threonine protein kinase related protein
D5_0357 serine/threonine protein kinase RIO1 family
D5_0753 TPR repeat-containing protein
D5_0904 WD40 repeat-containing protein
D5_1022 TPR repeat-containing protein
D5_1123 TPR repeat-containing protein
D5_1130 Hsp70 family protein with protein kinase domain
D5_1153 TPR repeat-containing protein
D5_1154 WD40 repeat-containing protein
D5_1240 TPR domain-containing protein
D5_1268 TPR repeat-containing protein
D5_1554 WD40 repeat-containing protein
D5_1664 TPR repeat-containing protein
D5_1884 TPR repeat-containing protein
D5_1992 anti-sigma factor antagonist
D5_1993 anti-sigma regulatory factor serine/threonine protein kinase
D5_1994 serine phosphatase
D5_1995 4'-phosphopantetheinyl transferase family protein
D5_2079 TPR repeat-containing protein
D5_2129 phosphate uptake regulator PhoU
D5_2252 TPR repeat-containing protein
D5_2444 TPR repeat-containing protein

Transcriptional regulator

D5_0022 transcriptional regulator PadR-like family
D5_0049 transcriptional regulator MarR family
D5_0113 transcriptional regulator
D5_0114 transcriptional regulator
D5_0129 transcriptional regulator HxlR family
D5_0154 HTH domain-containing protein
D5_0193 transcriptional regulator ArsR family
D5_0271 transcriptional regulator AsnC family
D5_0308 nucleotidyl transferase
D5_0352 transcriptional regulator
D5_0360 transcriptional regulator
D5_0380 transcriptional regulator
D5_0386 transcriptional regulator HxlR family
D5_0434 transcriptional regulator
D5_0552 transcriptional regulator AraC family
D5_0563 transcriptional regulator ArsR family
D5_0622 transcriptional regulator ArsR family
D5_0623 transcriptional regulator
D5_0624 transcriptional regulator ArsR family
D5_0748 transcriptional regulator TrmB family
D5_0796 transcriptional regulator HxlR family
D5_0814 transcriptional regulator MarR family
D5_0828 rOK family protein
D5_0942 transcriptional regulator HxlR family
D5_0993 transcriptional regulator
D5_1051 transcriptional regulator MarR family
D5_1055 transcriptional regulator AraC family
D5_1056 transcriptional regulator HxlR family
D5_1061 transcriptional regulator HxlR family
D5_1140 transcriptional regulator HxlR family
D5_1141 transcriptional regulator TetR family
D5_1155 transcriptional regulator
D5_1178 transcription regulator
D5_1184 transcriptional regulator MarR family
D5_1267 transcriptional regulator MarR family
D5_1269 transcription regulator
D5_1310 transcriptional regulator MarR family
D5_1342 transcriptional regulator MarR family
D5_1353 transcriptional regulator MarR family
D5_1361 transcriptional regulator
D5_1392 transcriptional regulator MarR family

D5_1510 transcriptional regulator
D5_1585 transcriptional regulator
D5_1661 iron-dependent repressor
D5_1690 transcription regulator
D5_1753 transcriptional regulator LytR family
D5_1791 HTH and cupin domain-containing protein
D5_1803 transcriptional regulator
D5_1804 transcriptional regulator
D5_1805 transcriptional regulator MarR family
D5_1818 HTH domain-containing protein
D5_1827 nickel responsive transcriptional regulator NikR
D5_1840 transcriptional regulator HxlR family
D5_1842 transcriptional regulator MarR family
D5_1904 transcriptional regulator
D5_1960 HTH domain-containing protein
D5_2191 transcriptional regulator MarR family
D5_2320 transcriptional regulator HxlR family
D5_2396 transcriptional regulator LysR family
D5_2440 transcriptional regulator ArsR family

Other

D5_0214 sugar fermentation stimulation protein SfsA
D5_1142 sugar fermentation stimulation protein SfsA

SECONDARY METABOLITES

NRPS

D5_0482 non-ribosomal surfactin synthase
D5_1740 non-ribosomal peptide synthetase

Other

D5_1741 anti-sigma factor antagonist
D5_1739 MatE efflux family protein

TRANSCRIPTION

RNA polymerase

D5_0409 DNA-directed RNA polymerase subunit H RpoH
D5_0410 DNA-directed RNA polymerase subunit B" RpoB2
D5_0411 DNA-directed RNA polymerase subunit B' RpoB1
D5_0412 DNA-directed RNA polymerase subunit A' RpoA1
D5_0413 DNA-directed RNA polymerase subunit A" RpoA2
D5_0722 DNA-directed RNA polymerase subunit D RpoD
D5_0726 DNA-directed RNA polymerase subunit N RpoN
D5_0727 DNA-directed RNA polymerase subunit K RpoK
D5_1647 DNA-directed RNA polymerase subunit E" RpoE2
D5_1648 DNA-directed RNA polymerase subunit E' RpoE1
D5_2411 DNA-directed RNA polymerase subunit F RpoF
D5_2433 DNA-directed RNA polymerase subunit L RpoL

Transcription factors

D5_0415 transcription elongation factor NusA-like protein
D5_1088 transcription factor S Tfs
D5_1931 transcription initiation factor TFIIB Tfb
D5_2109 transcription initiation factor TFIIB Tfb
D5_2230 transcription initiation factor TFIIE alpha subunit Tfe
D5_2364 TATA-box binding protein Tbp
D5_2436 transcription factor S Tfs

Other

D5_0063 LSM domain-containing protein
D5_0668 RNA-binding protein
D5_1589 ribonuclease III Rnc
D5_1594 LSM domain-containing protein
D5_2487 RNA-binding S1 domain-containing protein

TRANSPORTERS

Amino acids	
D5_1090	amino acid carrier protein AGCS family
D5_1586	branched-chain amino acid transport protein AzlD
D5_1587	branched-chain amino acid transport protein AzlC
Anions	
D5_0126	anion-transporting ATPase
D5_1116	voltage-gated chloride channel protein
Cations	
D5_0151	heavy metal translocating P-type ATPase
D5_0207	potassium uptake protein TrkA family
D5_0208	potassium uptake protein TrkH family
D5_0212	potassium channel protein
D5_0276	K ⁺ -dependent Na ⁺ /Ca ⁺ exchanger
D5_0341	copper ion binding protein
D5_0342	heavy metal translocating P-type ATPase
D5_0422	cation-transporting P-type ATPase
D5_0516	transporter Na ⁺ /H ⁺ antiporter family
D5_0564	heavy metal-translocating P-type ATPase
D5_0567	nickel ABC transporter substrate-binding protein NikA
D5_0568	nickel ABC transporter permease protein NikB
D5_0569	nickel ABC transporter permease protein NikC
D5_0570	nickel ABC transporter ATP-binding protein NikD
D5_0571	nickel ABC transporter ATP-binding protein NikE
D5_0573	nickel ABC transporter ATP-binding protein NikE
D5_0574	nickel ABC transporter ATP-binding protein NikD
D5_0577	nickel ABC transporter substrate-binding protein NikA
D5_0578	nickel ABC transporter permease protein NikB
D5_0579	nickel ABC transporter permease protein NikC
D5_0657	transporter CDF family
D5_0990	heavy metal translocating P-type ATPase
D5_1018	heavy metal efflux pump CzcD family
D5_1195	ion transport protein
D5_1201	ion transport protein (pseudo)
D5_1279	transporter CDF family
D5_1328	SPFH domain, Band 7 family protein
D5_1397	transporter Na ⁺ /H ⁺ antiporter family (pseudo)
D5_1728	heavy metal translocating P-type ATPase
D5_1743	transporter Na ⁺ /H ⁺ antiporter family
D5_1799	ferrous iron transport protein B FeoB
D5_1980	potassium uptake protein TrkH family
D5_2147	ferrous iron transport protein A FeoA
D5_2148	ferrous iron transport protein B FeoB
D5_2313	potassium channel protein (pseudo)
D5_2503	divalent cation transporter mgtE family
D5_2504	TrkA domain-containing protein
Other	
D5_0023	ABC transporter ATP-binding protein
D5_0024	ABC transporter permease protein
D5_0050	MATE efflux family protein, matE
D5_0137	transporter
D5_0139	MatE efflux family protein
D5_0224	permease
D5_0243	Na ⁺ dependent transporter SNF family
D5_0319	cell shape determining protein, MreB/Mrl family
D5_0321	transporter MotA/TolQ/ExbB proton channel family
D5_0322	transporter ExbD/TolR family
D5_0351	Na ⁺ dependent transporter SBF family
D5_0385	MFS transporter
D5_0537	MFS transporter
D5_0553	ABC transporter ATP-binding/permease protein
D5_0554	ABC transporter ATP-binding/permease protein
D5_0555	ABC transporter ATP-binding protein
D5_0556	ABC transporter permease protein
D5_0557	ABC transporter permease protein
D5_0559	ABC transporter permease protein
D5_0572	MatE efflux family protein
D5_0779	ABC transporter substrate-binding protein
D5_0793	MatE efflux family protein
D5_0856	Na ⁺ -dependent transporter SNF family
D5_0935	MFS transporter
D5_0937	ABC transporter ATP-binding/permease protein
D5_0934	MFS transporter

D5_0941	transporter SDF family
D5_0961	transporter MIP family
D5_0980	ABC transporter permease protein
D5_1029	ABC transporter ATP-binding protein
D5_1045	MFS transporter
D5_1050	MFS transporter
D5_1085	MotA/TolQ/ExbB proton channel family protein
D5_1097	MatE efflux family protein
D5_1100	MatE efflux family protein
D5_1145	MatE efflux family protein
D5_1149	MotA/TolQ/ExbB proton channel family protein
D5_1294	amino acid ABC transporter substrate-binding protein
D5_1295	amino acid ABC transporter permease protein
D5_1296	amino acid ABC transporter ATP-binding protein
D5_1311	MatE efflux family protein
D5_1354	MFS transporter
D5_1355	MFS transporter
D5_1371	transporter SDF family
D5_1570	MatE efflux family protein
D5_1576	MatE efflux family protein
D5_1580	ABC transporter permease protein
D5_1581	ABC transporter ATP-binding protein
D5_1613	ABC transporter ATP-binding/permease protein
D5_1614	ABC transporter ATP-binding/permease protein
D5_1759	MFS transporter
D5_1914	transporter MIP family
D5_2014	mechanosensitive ion channel protein
D5_2319	MFS transporter
D5_2333	Na ⁺ -dependent transporter SNF family
D5_2409	MatE efflux family protein
D5_2422	MatE efflux family protein
D5_2423	MFS transporter
D5_2466	MFS transporter
D5_2468	transporter

UNKNOWN FUNCTION

Methanogenesis marker proteins

D5_0062	methanogenesis marker protein 12
D5_0142	methanogenesis marker protein 13
D5_0150	methanogenesis marker protein 16
D5_0171	methanogenesis marker protein 5
D5_0282	methanogenesis marker protein 7
D5_0283	methanogenesis marker protein 10
D5_0297	methanogenesis marker protein 14
D5_0332	methanogenesis marker protein 9
D5_0627	methanogenesis marker protein 2
D5_0631	methanogenesis marker protein 3
D5_0632	methanogenesis marker protein 6
D5_0633	methanogenesis marker protein 5
D5_0634	methanogenesis marker protein 15
D5_0635	methanogenesis marker protein 17
D5_1505	methanogenesis marker protein 16
D5_1511	methanogenesis marker protein 4
D5_2000	methanogenesis marker protein 1
D5_2244	methanogenesis marker protein 8
D5_2489	methanogenesis marker protein 11

Others

D5_0006	amidohydrolase
D5_0017	hydrolase HAD superfamily
D5_0021	xylose isomerase-like TIM barrel domain-containing protein
D5_0028	PHP domain-containing protein
D5_0032	ATPase AAA
D5_0033	radical SAM domain-containing protein
D5_0041	acetyltransferase
D5_0090	aconitase
D5_0093	pyridoxamine-phosphate oxidase (pseudo)
D5_0097	xylose isomerase-like TIM barrel domain-containing protein
D5_0098	PIN domain-containing protein
D5_0102	ATPase
D5_0119	phage antirepressor
D5_0130	macro domain-containing protein

D5_0133 calcineurin-like phosphoesterase
D5_0140 radical SAM domain-containing protein
D5_0141 C_GCAxxG_C_C family protein
D5_0149 amidohydrolase
D5_0155 CAAX amino terminal protease family protein
D5_0184 ainc dependent oxidoreductase
D5_0196 acetyltransferase GNAT family
D5_0202 CBS domain-containing protein
D5_0204 radical SAM domain-containing protein
D5_0206 metallo-beta-lactamase superfamily protein
D5_0213 carbohydrate kinase
D5_0248 CBS domain-containing protein
D5_0249 CBS domain-containing protein
D5_0267 Met-10 like-protein
D5_0273 aminotransferase DegT/DnrJ/EryC1/StrS family
D5_0275 PP-loop family protein
D5_0277 CBS domain-containing protein
D5_0279 TraB family protein
D5_0299 PRC-barrel domain-containing protein
D5_0335 ATPase
D5_0336 calcineurin-like phosphoesterase
D5_0340 hydrolase alpha/beta fold family
D5_0344 aldo/keto reductase family protein
D5_0345 aldo/keto reductase family protein
D5_0346 aldo/keto reductase family protein
D5_0373 NADH-dependent flavin oxidoreductase
D5_0377 acetyltransferase GNAT family
D5_0381 von Willebrand factor type A domain-containing protein
D5_0402 radical SAM domain-containing protein
D5_0424 maltose *O*-acetyltransferase
D5_0435 thioesterase family protein
D5_0439 cupin domain-containing protein
D5_0461 SAM-dependent methyltransferase
D5_0464 methyltransferase FkbM family
D5_0466 GtrA-like protein
D5_0470 acetyltransferase
D5_0471 SAM-dependent methyltransferase
D5_0479 SAM-dependent methyltransferase
D5_0499 acetyltransferase
D5_0507 phosphatase PAP2 family
D5_0518 oxidoreductase GFO/IDH/MOCA family
D5_0543 GTP-binding protein
D5_0544 AMMECR1 domain-containing protein
D5_0546 GMC oxidoreductase family protein
D5_0575 acetyltransferase GNAT family
D5_0580 acetyltransferase GNAT family
D5_0619 PRC-barrel domain-containing protein
D5_0637 phosphodiesterase MJ0936 family
D5_0638 manganese-dependent inorganic pyrophosphatase PpaC
D5_0643 Met-10 like-protein
D5_0653 calcineurin-like phosphoesterase
D5_0656 CBS domain-containing protein
D5_0659 radical SAM domain-containing protein
D5_0667 metallo-beta-lactamase superfamily protein
D5_0676 pyridoxal phosphate enzyme
D5_0718 LemA family protein
D5_0746 SAM-dependent methyltransferase
D5_0750 cupin 2 domain-containing protein
D5_0751 SAM-dependent methyltransferase
D5_0752 oxidoreductase aldo/keto reductase family
D5_0756 ATPase
D5_0767 acetyltransferase GNAT family
D5_0769 NADH-dependent flavin oxidoreductase
D5_0772 PP-loop family protein
D5_0776 GMC oxidoreductase family protein
D5_0778 SAM-dependent methyltransferase
D5_0786 metallo-beta-lactamase superfamily protein
D5_0792 DGC domain-containing protein
D5_0794 radical SAM domain-containing protein
D5_0795 radical SAM domain-containing protein
D5_0802 hydrolase HAD superfamily
D5_0812 radical SAM domain-containing protein
D5_0829 Fic family protein
D5_0833 ATPase
D5_0843 oxidoreductase domain-containing protein

D5_0844 oxidoreductase GFO/IDH/MOCA family
D5_0845 cytidyltransferase-related domain-containing protein
D5_0847 aminotransferase DegT/DnrJ/EryC1/StrS family
D5_0851 SAM-dependent methyltransferase
D5_0868 SAM-dependent methyltransferase
D5_0871 SAM-dependent methyltransferase
D5_0875 ATPase
D5_0877 von Willebrand factor type A domain-containing protein
D5_0929 ATPase
D5_0930 ATPase
D5_0931 acetyltransferase GNAT family (pseudo)
D5_0943 oxidoreductase aldo/keto reductase family
D5_0944 SAM-dependent methyltransferase
D5_0945 oxidoreductase aldo/keto reductase family
D5_0951 acetyltransferase GNAT family
D5_0987 oxidoreductase aldo/keto reductase family
D5_0989 radical SAM domain-containing protein
D5_1015 CAAX amino terminal protease family protein
D5_1019 carbohydrate kinase PfkB family
D5_1047 oxidoreductase aldo/keto reductase family
D5_1048 short-chain dehydrogenase family protein
D5_1049 short-chain dehydrogenase family protein
D5_1058 radical SAM domain-containing protein
D5_1078 ACT domain-containing protein
D5_1115 ATPase
D5_1129 FHA domain-containing protein
D5_1131 metallophosphoesterase
D5_1138 metallo-beta-lactamase superfamily protein
D5_1139 DSBA oxidoreductase
D5_1144 NADH-dependent flavin oxidoreductase
D5_1156 acyl-CoA synthetase
D5_1164 MazG domain-containing protein
D5_1172 thioesterase family protein
D5_1208 ATPase AAA family
D5_1209 MazG domain-containing protein
D5_1217 ATPase
D5_1265 ATPase AAA family
D5_1275 acetyltransferase GNAT family
D5_1299 nucleotidyltransferase
D5_1300 phosphoenolpyruvate phosphomutase AepX
D5_1301 phosphoenolpyruvate decarboxylase AepY
D5_1313 NADH-dependent flavin oxidoreductase
D5_1318 NADH-dependent flavin oxidoreductase
D5_1337 CAAX amino terminal protease family protein
D5_1339 flavin reductase domain-containing protein
D5_1340 metallo-beta-lactamase superfamily protein
D5_1343 ACT domain-containing protein
D5_1345 radical SAM domain-containing protein
D5_1348 C_GCAxxG_C_C family protein
D5_1357 pyridoxamine 5'-phosphate oxidase family protein
D5_1358 acetyltransferase GNAT family
D5_1360 acetyltransferase
D5_1367 toxic anion resistance protein
D5_1374 amidohydrolase
D5_1375 prophage antirepressor, partial
D5_1376 prophage antirepressor, partial
D5_1377 NUDIX domain-containing protein
D5_1383 hydrolase alpha/beta fold family
D5_1387 *O*-methyltransferase domain containing protein
D5_1389 SAM-dependent methyltransferase
D5_1409 peptide methionine sulfoxide reductase Msr
D5_1417 chloramphenicol *O*-acetyltransferase
D5_1470 SAM-dependent methyltransferase
D5_1479 PHP domain-containing protein
D5_1484 CAAX amino terminal protease family protein
D5_1485 CAAX amino terminal protease family protein
D5_1486 CAAX amino terminal protease family protein
D5_1513 hydrolase TatD family
D5_1529 oxidoreductase aldo/keto reductase family
D5_1534 MobA-related protein
D5_1540 ATPase
D5_1541 NurA domain-containing protein
D5_1557 HEAT repeat-containing protein
D5_1562 ATP-binding protein
D5_1568 acetyltransferase

D5_1569 acetyltransferase GNAT family
D5_1569 acetyltransferase
D5_1602 acetyltransferase
D5_1616 acetyltransferase
D5_1641 ATPase
D5_1677 HD domain-containing protein
D5_1706 acetyltransferase
D5_1710 CAAX amino terminal protease family protein
D5_1725 DGC domain-containing protein
D5_1731 CAAX amino terminal protease family protein
D5_1766 CBS domain-containing protein
D5_1768 carbohydrate kinase PfkB family
D5_1789 CAAX amino terminal protease family protein
D5_1824 D-alanine--D-alanine ligase
D5_1836 radical SAM domain-containing protein
D5_1843 HEAT repeat-containing protein
D5_1845 AMP-binding enzyme
D5_1846 acetyltransferase GNAT family
D5_1859 SAM-dependent methyltransferase
D5_1860 SAM-dependent methyltransferase
D5_1866 calcineurin-like phosphoesterase
D5_1868 oxidoreductase aldo/keto reductase family
D5_1875 pyridoxamine 5'-phosphate oxidase family protein
D5_1878 short chain dehydrogenase
D5_1886 ACT domain-containing protein
D5_1891 YhgE/Pip-like protein
D5_1905 hydrolase TatD family
D5_1910 ZPR1 zinc-finger domain-containing protein
D5_1917 hydrolase TatD family
D5_1933 demethylmenaquinone methyltransferase
D5_1937 ATP-grasp domain-containing protein
D5_1986 acyltransferase
D5_1987 hydrolase alpha/beta fold family
D5_2001 TfuA-like protein
D5_2002 PP-loop family protein
D5_2004 CBS domain-containing protein
D5_2006 amidohydrolase
D5_2024 HEAT repeat-containing protein
D5_2025 short chain dehydrogenase
D5_2030 phosphodiesterase MJ0936 family
D5_2045 PAP2 family protein
D5_2048 metallophosphoesterase
D5_2051 ATPase AAA family
D5_2073 collagen triple helix repeat domain-containing protein
D5_2076 collagen triple helix repeat domain-containing protein
D5_2111 radical SAM domain-containing protein
D5_2113 cytidyltransferase-related domain-containing protein
D5_2117 PP-loop family protein
D5_2118 von Willebrand factor type A domain-containing protein
D5_2119 ATPase
D5_2158 collagen triple helix repeat domain-containing protein
D5_2195 SAM-dependent methyltransferase
D5_2205 DGC domain-containing protein
D5_2231 HD domain-containing protein
D5_2234 tryptophan-binding regulator TrpY
D5_2240 NADH-dependent flavin oxidoreductase
D5_2242 cell division control protein Cdc48
D5_2248 metallo-beta-lactamase superfamily protein
D5_2255 acetyltransferase
D5_2349 PIN domain-containing protein
D5_2352 GTP-binding protein
D5_2376 oxidoreductase aldo/keto reductase family
D5_2397 carbohydrate kinase PfkB family
D5_2398 thiamine biosynthesis protein ThiC
D5_2401 acetyltransferase GNAT family
D5_2413 acyltransferase
D5_2414 SAM-dependent methyltransferase HemK-related
D5_2418 NUDIX domain-containing protein
D5_2434 NUDIX domain-containing protein
D5_2441 hydrolase TatD family
D5_2443 HEAT repeat-containing protein
D5_2447 ATPase
D5_2449 ATPase
D5_2458 DSBA oxidoreductase
D5_2459 DSBA oxidoreductase

VITAMINS AND COFACTORS

Biotin

D5_2496 glycyl-radical enzyme activating protein
D5_0677 biotin-acetyl-CoA-carboxylase ligase BirA
D5_1332 biotin synthase BioB
D5_2133 biotin synthase BioB

Cobalamin

D5_0012 cobyrinic acid a,c-diamide synthase CbiA
D5_0044 precorrin-8X methylmutase CbiC
D5_0045 glutamate-1-semialdehyde-2,1-aminomutase HemL
D5_0068 cobyrinic acid a,c-diamide synthase CbiA
D5_0084 nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase CobT
D5_0128 precorrin-6Y C5,15-methyltransferase (decarboxylating) CbiE
D5_0187 cobaltochelataase CobN
D5_0298 GTP:adenosylcobinamide-phosphate guanylyltransferase CobY
D5_0333 siroheme synthase CysG
D5_0334 glutamyl-tRNA reductase HemA
D5_0384 alpha-ribazole phosphatase CobZ
D5_0389 cobalamin 5'-phosphate synthase CobS
D5_0421 precorrin-6X reductase CbiJ
D5_0519 porphobilinogen deaminase HemC
D5_0600 cobalamin biosynthesis protein CbiD
D5_0615 adenosylcobinamide amidohydrolase CbiZ
D5_0789 delta-aminolevulinic acid dehydratase HemB
D5_0819 uroporphyrinogen III synthase HemD
D5_0865 uroporphyrin-III C-methyltransferase CorA
D5_0946 cobyric acid synthase CbiP
D5_0998 cobalamin biosynthesis protein CbiM
D5_0999 cobalt transport protein CbiN
D5_1000 cobalt ABC transporter permease protein CbiQ
D5_1001 cobalt ABC transporter ATP-binding protein CbiO
D5_1082 cobalamin biosynthesis protein CbiM
D5_1146 cobaltochelataase CobN
D5_1519 precorrin-4 C11-methyltransferase CbiF
D5_1679 precorrin-6Y C5,15- methyltransferase (decarboxylating) CbiT
D5_2142 cobalamin biosynthesis protein CbiM
D5_2143 cobalt transport protein CbiN
D5_2144 cobalt ABC transporter permease protein CbiQ
D5_2145 cobalt ABC transporter ATP-binding protein CbiO
D5_2439 precorrin-2 C20-methyltransferase CbiL
D5_2498 cobalamin biosynthesis protein CbiX
D5_2499 cobalamin biosynthesis protein CbiX
D5_2505 precorrin-3B C17-methyltransferase CbiH
D5_2511 cobalamin biosynthesis protein CbiG
D5_2512 cobalamin biosynthesis protein CbiB

Coenzyme B

D5_0588 homoaconitase small subunit AksE
D5_1844 isohomocitrate dehydrogenase AksF
D5_2368 homocitrate synthase AksA
D5_2369 homoaconitase large subunit AksD

Coenzyme F₄₂₀

D5_0268 FO synthase subunit 1 CofG
D5_0324 F₄₂₀-0:gamma-glutamyl ligase CofE
D5_0325 LPPG:FO 2-phospho-L-lactate transferase CofD
D5_0503 F₄₂₀-0:gamma-glutamyl ligase CofE
D5_1079 coenzyme F₃₉₀ synthetase FtsA
D5_1498 FO synthase subunit 2 CofH
D5_1723 2-phospho-L-lactate guanylyltransferase CofC
D5_1885 coenzyme F₃₉₀ synthetase FtsA
D5_1974 lactaldehyde dehydrogenase CofA
D5_2229 F₄₂₀-0:gamma-glutamyl ligase CofE
D5_2508 fuculose 1-phosphate aldolase FucA

Coenzyme M

D5_0263 L-sulfolactate dehydrogenase ComC
D5_0280 2-phosphosulfolactate phosphatase ComB
D5_1500 sulfofurylate decarboxylase subunit alpha ComD

D5_1501	sulfofpyruvate decarboxylase subunit beta ComE
D5_1506	phosphosulfolactate synthase ComA
Glutathione	
D5_0781	gamma-glutamylcysteine synthetase GshA
D5_1281	glutathione peroxidase GpxA
D5_1347	glutathione-disulfide reductase Gor
D5_1806	glutathione peroxidase GpxA
D5_2236	glutathione-disulfide reductase Gor
D5_2270	bifunctional glutamate-cysteine ligase/glutathione synthetase GshF
Metal-binding pterin	
D5_0076	molybdate transport system regulatory protein ModE
D5_0359	molybdopterin biosynthesis protein MoeA
D5_0621	molybdenum cofactor biosynthesis protein B MoaB
D5_0774	molybdopterin biosynthesis protein MoeB
D5_1550	molybdenum cofactor biosynthesis protein MoaE
D5_1551	molybdenum-pterin binding protein Mop1
D5_1552	molybdenum-pterin binding protein Mop2
D5_1681	molybdopterin-guanine dinucleotide biosynthesis protein A MobA
D5_1871	molybdate ABC transporter ATP-binding protein ModC
D5_1872	molybdate ABC transporter ATP-binding protein ModC
D5_1873	molybdate ABC transporter permease protein ModB
D5_1874	molybdate ABC transporter substrate-binding protein ModA
D5_2377	molybdopterin biosynthesis protein MoeB
D5_2389	molybdopterin-guanine dinucleotide biosynthesis protein B MobB
D5_2390	molybdopterin cofactor biosynthesis protein A MobA
D5_2427	molybdenum cofactor biosynthesis protein C MoaC
D5_2455	molybdopterin biosynthesis protein MoeA
Methanofuran	
D5_0313	L-tyrosine decarboxylase MfnA
D5_1007	2-furaldehyde phosphate synthase MfnB
D5_0584	tyramine—L-glutamate ligase MfnD
D5_2202	[5-(aminomethyl)furan-3-yl]methyl phosphate kinase MfnE
D5_0585	(4-{4-[2-(γ-L-glutamylamino)ethyl]phenoxy)methyl}furan-2-yl)methanamine synthase MfnF
Methanopterin	
D5_0270	GTP cyclohydrolase ArfA
D5_0314	dihydronepterin aldolase MtnD
D5_0587	7,8-dihydro-6-hydroxymethylpterin dimethyltransferase
D5_0790	ATP:dephospho-CoA triphosphoribosyl transferase CitG
D5_1075	beta-ribofuranosylaminobenzene 5'-phosphate synthase MptG
D5_1597	creatinine amidohydrolase ArfB
D5_2280	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase MptE
D5_2463	dihydromethanopterin reductase (acceptor) DmrX
Nicotinate	
D5_0108	NAD synthetase NadE
D5_1381	ATP-NAD kinase NadK
D5_1549	nicotinamide-nucleotide adenyllyltransferase NadD
D5_1621	nicotinate phosphoribosyltransferase
D5_1967	L-aspartate dehydrogenase AspDH
D5_2012	nicotinate-nucleotide pyrophosphorylase NadC
D5_2025	quinolinate synthetase A protein NadA
Others	
D5_0300	FeS assembly ATPase SufC
D5_0301	FeS assembly protein SufBD
D5_0636	nitrogenase cofactor biosynthesis protein NifB
D5_2121	dihydropteroate synthase-related protein
D5_2272	dinitrogenase iron-molybdenum cofactor biosynthesis protein
Pantothenate and coenzyme A	
D5_0253	phosphopantothenoylcysteine decarboxylase CoaC
D5_0254	phosphopantothenate-cysteine ligase CoaB
D5_0661	phosphopantetheine adenyllyltransferase CoaD
D5_1402	2-dehydropantoate 2-reductase PanE
D5_1471	pantothenate kinase CoaA
D5_1560	pantothenate synthase PanC
D5_1561	dephospho-CoA kinase CoaE

Riboflavin	
D5_0008	riboflavin kinase RibK
D5_0010	3,4-dihydroxy-2-butanone 4-phosphate synthase RibB
D5_0326	GTP cyclohydrolase III ArfA
D5_1002	riboflavin synthase RibC
D5_1482	diaminohydroxyphosphoribosylaminopyrimidine reductase RibD
D5_2490	6,7-dimethyl-8-ribityllumazine synthase RibH
Thiamine	
D5_0407	thiamine monophosphate synthase ThiE
D5_0408	hydroxyethylthiazole kinase ThiM
D5_0777	thiamine biosynthesis protein ThiS
D5_1334	hydroxymethylpyrimidine transporter CytX
D5_1335	phosphomethylpyrimidine kinase ThiD
D5_1724	phosphomethylpyrimidine kinase ThiD
D5_2116	thiamine biosynthesis protein ThiS
D5_2219	thiamine biosynthesis ATP pyrophosphatase ThiI
D5_2245	thiamine biosynthesis protein ThiC
D5_2398	thiamine biosynthesis protein ThiC
D5_2497	thiamine-monophosphate kinase ThiL
D5_1327	thiazole biosynthesis enzyme
D5_2137	ThiF family protein
D5_2442	ThiF family protein
Ubiquinone	
D5_1678	3-polyprenyl-4-hydroxybenzoate decarboxylase UbiX
D5_1893	2-polyprenylphenol 6- hydroxylase UbiB
D5_1897	2-polyprenylphenol 6- hydroxylase UbiB2
D5_2042	2-polyprenylphenol 6- hydroxylase UbiB
D5_2485	UbiD family decarboxylase

Table A.6.02 Percentage codon usage in *Methanobrevibacter* genomes

Amino acid	Codon	D5	YE31 5	ZA- 10 ^T	SM9	HO ^T	PS ^T	JMR0 1	M1 ^T	KM1H5 -1P ^T	YLM 1	SH ^T	AbM4	JH1 ^T	RFM -1 ^T	RFM -2 ^T	RFM -3 ^T	ANOR 1	ATM ^T
Ser (S)	UCA	3.6 [34.1]	2.0 [32.4]	3.7 [35.4]	3.4 [34.2]	2.1 [31.8]	2 [28.5]	2.2 [28.9]	2.7 [25.3]	1.7 [23.1]	1.7 [22.7]	1.9 [28.2]	1.9 [29.6]	2.0 [29.3]	1.7 [23.7]	1.9 [25.5]	1.8 [24.8]	1.9 [24.7]	1.5 [23.5]
	UCC	1.4 [13]	1.0 [15.4]	1.9 [17.7]	1.2 [11.8]	0.6 [8.6]	0.7 [10.2]	0.4 [4.8]	1.7 [16.1]	0.4 [5.2]	0.4 [5.1]	0.2 [2.7]	0.8 [13.9]	0.9 [13.8]	0.4 [5.4]	0.4 [5]	0.3 [4.7]	0.3 [3.6]	0.4 [5.5]
	UCG	0.2 [1.4]	0.1 [1.6]	0.3 [2.4]	0.1 [1.5]	0.1 [1.8]	0 [0.7]	0.1 [1.9]	0 [0.6]	0 [0.6]	0 [0.6]	0 [0.2]	0.04 [0.6]	0 [0.5]	0.1 [1.4]	0.1 [1.1]	0.1 [1.2]	0.1 [1.4]	0 [0.3]
	UCU	2.3 [21.7]	1.3 [20.6]	1.5 [14.4]	2.4 [24]	1.9 [28.9]	2.0 [28.7]	2.6 [33.9]	2.5 [24]	2.8 [38.9]	2.9 [38.6]	2.5 [37.9]	1.7 [25.6]	1.8 [25.9]	2.5 [34.9]	2.5 [34.7]	2.3 [30.8]	3.0 [39.7]	2 [31.6]
	AGC	1.1 [10.2]	0.8 [12.6]	1.8 [17.3]	0.9 [9.5]	0.4 [6.0]	0.6 [9]	0.3 [4.6]	2.2 [20.7]	0.5 [6.6]	0.5 [6.6]	0.1 [2.1]	0.4 [5.5]	0.4 [5.5]	0.5 [6.4]	0.5 [6.8]	0.4 [5.8]	0.4 [4.9]	0.2 [3.6]
	AGU	2.1 [19.6]	1.1 [17.5]	1.4 [12.8]	1.9 [18.9]	1.5 [22.9]	1.6 [22.9]	2.0 [25.9]	1.4 [13.3]	1.9 [25.6]	2.0 [26.5]	1.9 [28.9]	1.6 [24.9]	1.7 [25.1]	2 [28.1]	2 [26.9]	2.4 [32.6]	1.9 [25.8]	2.3 [35.5]
Phe (F)	UUC	2.7 [37.4]	1.8 [40.6]	3.3 [46]	2.2 [32.2]	1.2 [26.8]	1.2 [25.2]	0.8 [16.4]	2.7 [40.3]	1 [21.6]	1.0 [21.9]	0.8 [18.2]	1.2 [28.3]	1.2 [27.7]	1 [24.6]	0.7 [14.8]	1 [22.8]	0.8 [17]	1.1 [26.7]
	UUU	4.5 [62.6]	2.6 [59.4]	3.9 [54]	4.6 [67.8]	3.2 [73.2]	3.5 [74.8]	4.2 [83.6]	3.9 [59.7]	3.6 [78.4]	3.7 [78.1]	3.5 [81.8]	2.96 [71.7]	3.1 [72.3]	3.2 [75.4]	3.8 [85.2]	3.2 [77.2]	3.9 [83]	3 [73.3]
Thr (T)	ACA	3.8 [40.9]	2.1 [38.9]	2.7 [30.4]	3.3 [39.5]	2.0 [38.7]	2.2 [38.1]	2.3 [40.8]	3.0 [37.0]	1.6 [31.5]	1.7 [31.5]	2.0 [38.8]	1.9 [38.1]	2.1 [37.9]	2.1 [35.7]	2.1 [38.1]	2.4 [38.7]	1.9 [35.8]	2.2 [40.6]
	ACC	1.6 [17.1]	1.1 [20.3]	2.4 [27]	1.1 [13.9]	0.5 [10.2]	0.7 [12.6]	0.4 [7.5]	1.8 [22.9]	0.5 [9.3]	0.5 [9.4]	0.2 [4.6]	1.1 [21.1]	1.1 [20.6]	0.5 [9.3]	0.4 [8.1]	0.5 [7.5]	0.3 [6]	0.4 [8.1]
	ACG	0.2 [1.7]	0.1 [1.8]	1.1 [11.9]	0.3 [3.7]	0.1 [1.8]	0.1 [1.3]	0.1 [2.4]	0 [0.8]	0 [0.9]	0.1 [1]	0 [0.6]	0.1 [2.6]	0.1 [2.6]	0.1 [2.1]	0.1 [1.3]	0.1 [1.9]	0.1 [1.7]	0 [0.8]
	ACU	3.8 [40.3]	2.1 [39.0]	2.7 [30.7]	3.5 [42.9]	2.5 [49.3]	2.8 [48]	2.8 [49.3]	3.0 [38.4]	3 [58.3]	3.1 [58.1]	2.9 [56]	2.0 [38.2]	2.1 [38.9]	3.1 [52.9]	2.9 [52.4]	3.2 [51.9]	3 [56.6]	2.7 [50.4]
Asn (N)	AAC	3.6 [32.6]	2.0 [32.6]	4.7 [41.6]	2.8 [26.7]	1.3 [20.1]	1.8 [23.9]	1.3 [15.9]	3.3 [33.4]	1.1 [16.5]	1.2 [16.6]	0.9 [11.4]	1.6 [24.5]	1.7 [23.8]	1.7 [20.4]	1.7 [18.9]	1.7 [18.2]	1.2 [14.2]	1.2 [16.8]
	AAU	7.6 [67.4]	4.2 [67.4]	6.5 [58.4]	7.7 [73.3]	5.2 [79.9]	5.7 [76.1]	7 [84.1]	6.7 [66.6]	5.8 [83.5]	6.0 [83.4]	6.7 [88.6]	5.1 [75.5]	5.5 [76.2]	6.8 [79.6]	7.1 [81.1]	7.7 [81.8]	7 [85.8]	5.9 [83.2]
Lys (K)	AAA	9.8 [79.6]	5.4 [77.4]	7.4 [66.7]	9 [80.8]	7.0 [88.4]	7.7 [88.1]	8.5 [88.8]	6.0 [54.7]	7.4 [84.6]	7.6 [84]	8.2 [92.7]	6.1 [77]	6.4 [77]	7.1 [84.8]	7.8 [86.6]	6.9 [84.7]	7.8 [84.6]	7.5 [89.4]
	AAG	2.5 [20.4]	1.6 [22.6]	3.7 [33.3]	2.1 [19.2]	0.9 [11.6]	1.0 [11.9]	1.1 [11.2]	5.0 [45.3]	1.4 [15.4]	1.5 [16]	0.6 [7.3]	1.8 [23]	1.9 [23]	1.3 [15.2]	1.2 [13.4]	1.3 [15.3]	1.4 [15.4]	0.9 [10.6]
Glu (E)	GAA	9.6 [82.8]	6.1 [83.2]	9.3 [79.9]	8.7 [85.4]	6.2 [86.9]	6.8 [88.3]	6.6 [87]	8.1 [72]	6.9 [85]	7.1 [84.8]	6.3 [90.8]	5.1 [71.9]	5.3 [71.9]	5.6 [85.2]	5.5 [84.5]	5.3 [84.3]	6.4 [85.2]	6.4 [90.8]
	GAG	2.0 [17.2]	1.2 [16.8]	2.3 [20.1]	1.5 [14.6]	0.9 [13.1]	0.9 [11.7]	1 [13]	3.2 [28]	1.2 [15]	1.3 [15.6]	0.6 [9.2]	2.0 [28.1]	2.1 [28.1]	1 [14.8]	1 [15.5]	1 [15.7]	1.1 [14.8]	0.6 [9.2]
Tyr (Y)	UAC	2.0 [30.1]	1.2 [29.2]	2.6 [38]	1.5 [23.4]	0.8 [21.6]	1.1 [24.9]	0.8 [17.1]	1.7 [26.6]	0.8 [18.5]	0.8 [18.4]	0.5 [12.1]	0.8 [18.3]	0.8 [18]	0.7 [18.5]	0.9 [22.7]	0.9 [22.7]	0.4 [12]	0.8 [20.3]
	UAU	4.7 [69.9]	2.8 [70.8]	4.3 [62]	4.9 [76.6]	3.1 [78.4]	3.3 [75.1]	3.8 [82.9]	4.6 [73.4]	3.4 [81.5]	3.7 [81.6]	3.8 [87.9]	3.4 [81.7]	3.6 [82]	3.1 [81.5]	3.1 [77.3]	3 [77.3]	3.5 [88]	3.1 [79.7]
Val (V)	GUA	3.4 [30.1]	2.0 [28.8]	2.9 [27.3]	3 [30.3]	2.0 [31.3]	2.6 [35]	2.3 [32.4]	3.1 [32.9]	2.6 [40.4]	2.7 [40]	2.6 [41.8]	2.5 [38.1]	2.6 [37.8]	1.8 [29.6]	1.6 [25.8]	1.8 [27.5]	1.9 [28.9]	2.3 [37.6]

His (H)	CAC	0.8 [32]	0.5 [30.5]	1 [40.5]	0.6 [26.3]	0.4 [22.5]	0.4 [24.9]	0.3 [18.1]	0.6 [28.4]	0.3 [20]	0.3 [19.6]	0.2 [11.4]	0.3 [19.3]	0.3 [18.6]	0.2 [16.9]	0.3 [19.5]	0.3 [20.2]	0.2 [13.2]	0.3 [17.9]
	CAU	1.7 [68]	1.1 [69.5]	1.5 [59.5]	1.7 [73.7]	1.3 [77.5]	1.3 [75.1]	1.4 [81.9]	1.6 [71.6]	1.3 [80]	1.3 [80.4]	1.4 [88.6]	1.3 [80.7]	1.4 [81.4]	1.2 [83.1]	1.2 [80.5]	1.2 [79.8]	1.4 [86.8]	1.4 [82.1]
Asp (D)	GAC	3.2 [29.3]	1.9 [28.0]	4.3 [39.2]	2.3 [23.3]	1.0 [15.9]	1.6 [22.9]	0.8 [12.2]	3.7 [35.2]	0.9 [13]	0.9 [13]	0.5 [7.7]	1.3 [18.6]	1.3 [18.4]	0.7 [12.6]	0.9 [16.9]	0.8 [14.5]	0.6 [9.6]	0.7 [10.8]
	GAU	7.7 [70.7]	4.9 [72.0]	6.6 [60.8]	7.6 [76.7]	5.4 [84.1]	5.5 [77.1]	6.1 [87.8]	6.8 [64.8]	6 [87]	6.2 [87]	6 [92.3]	5.6 [81.4]	5.9 [81.6]	5 [87.4]	4.6 [83.1]	4.7 [85.5]	5.8 [90.4]	5.4 [89.2]
Arg (R)	CGA	0.2 [4.4]	0.1 [2.8]	0.2 [3.8]	0.2 [4.7]	0.1 [3.0]	0.1 [2.4]	0.2 [5]	0.2 [3.5]	0 [2]	0.1 [2.1]	0 [1.8]	0.0 [2.1]	0 [2.1]	0.2 [7.9]	0.2 [6.2]	0.2 [8.4]	0.2 [5]	0.3 [8.6]
	CGC	0.2 [3.6]	0.1 [4.5]	0.3 [6.1]	0.2 [3.6]	0.1 [2.2]	0.1 [2.4]	0 [1.8]	0.2 [3.9]	0 [1.7]	0.1 [1.6]	0 [0.5]	0.0 [1.1]	0 [1.2]	0 [1.6]	0.1 [2.1]	0.1 [2]	0 [1]	0 [1.2]
	CGG	0.1 [1.7]	0.0 [1.1]	0.1 [1.9]	0.1 [1.6]	0 [1.1]	0 [0.9]	0 [1]	0 [0.9]	0 [0.4]	0 [0.5]	0 [0.4]	0.0 [0.8]	0 [0.8]	0 [1.3]	0 [0.9]	0 [1.7]	0 [1]	0.1 [2.3]
	CGU	0.8 [15.6]	0.5 [14.8]	0.7 [13.6]	0.8 [16.6]	0.5 [16.5]	0.5 [15.3]	0.5 [15.8]	0.5 [10.9]	0.5 [13.4]	0.5 [13.8]	0.6 [18.5]	0.5 [15.4]	0.6 [15.9]	0.3 [11.2]	0.4 [13.2]	0.3 [12.2]	0.4 [11.8]	0.7 [24]
	AGA	2.7 [54.6]	1.7 [54.0]	2.3 [46.6]	2.6 [56.5]	2.0 [62.2]	2.0 [61.6]	2.1 [62.9]	2.7 [55.9]	2.4 [69]	2.4 [68.1]	2.1 [67.5]	2.0 [58.1]	2.0 [57.7]	1.8 [64.1]	1.8 [65.7]	1.7 [62.1]	2.1 [65.8]	1.7 [58.4]
	AGG	1.0 [20.1]	0.7 [22.8]	1.4 [28]	0.8 [16.9]	0.5 [15.0]	0.6 [17.4]	0.4 [13.4]	1.2 [24.8]	0.5 [13.5]	0.5 [13.8]	0.3 [11.2]	0.8 [22.5]	0.8 [22.4]	0.4 [14]	0.3 [12]	0.4 [13.6]	0.5 [15.4]	0.2 [5.6]
	AUA	4 [26.8]	2.4 [25.2]	3.9 [26.6]	4 [28.4]	2.3 [24.3]	3 [29.4]	3.2 [28.1]	4.3 [31.5]	2.9 [27.8]	3 [28.1]	3.0 [29.6]	2.8 [29.9]	2.9 [29.7]	4 [39.4]	3.4 [33.5]	3.8 [38.2]	4.2 [37.7]	3.7 [38.7]
	AUC	2.9 [19.5]	2.1 [22.3]	3.9 [26.5]	2.3 [16.2]	1.2 [12.5]	1.3 [12.6]	1 [8.5]	3.3 [24.1]	1.2 [11.4]	1.2 [11.5]	0.6 [6.2]	1.4 [14.9]	1.5 [14.8]	1.2 [11.5]	0.8 [7.6]	0.9 [9.2]	0.9 [7.8]	0.8 [8.6]
Gly (G)	AUU	8 [53.6]	4.9 [52.4]	7 [47]	7.8 [55.4]	6.1 [63.2]	6 [58]	7.3 [63.4]	6.0 [44.4]	6.3 [60.8]	6.4 [60.4]	6.5 [64.2]	5.2 [55.2]	5.4 [55.5]	5 [49]	5.9 [58.9]	5.2 [52.6]	1.4 [54.4]	5.1 [52.7]
	GGA	4.5 [42]	2.7 [40.4]	4.6 [43.1]	4.0 [41.7]	2.7 [42.1]	3.4 [46.3]	3.1 [44]	4.9 [49.4]	2.8 [41.5]	2.9 [40.9]	2.6 [40.8]	2.5 [38.9]	2.6 [38.8]	3.1 [45.7]	2.9 [45.6]	2.9 [43.5]	3.2 [46]	2.8 [44.4]
	GGC	1.2 [11.2]	1.0 [14.7]	2.3 [21.3]	1.0 [10.2]	0.5 [7.5]	0.6 [8.1]	0.4 [5.4]	1.7 [17.6]	0.5 [7.7]	0.5 [7.6]	0.1 [1.9]	0.4 [5.9]	0.4 [5.9]	0.4 [6.1]	0.4 [6.4]	0.3 [4.7]	0.3 [4.5]	0.2 [3]
	GGG	0.6 [5.9]	6.3 [0.4]	0.5 [5]	0.5 [5.1]	0.5 [7.5]	0.4 [5.7]	0.4 [5.7]	0.6 [6.5]	0.4 [6.1]	0.4 [6.2]	0.2 [3.1]	0.3 [5.1]	0.4 [5.2]	0.6 [8.7]	0.5 [7.1]	0.5 [8]	0.6 [8.5]	0.5 [7.9]
	GGU	4.4 [40.9]	2.6 [38.6]	3.2 [30.6]	4.1 [43.1]	2.8 [43.2]	2.9 [39.9]	3.1 [43.5]	2.6 [26.6]	3.1 [44.8]	3.2 [45.3]	3.5 [54.2]	3.2 [50.1]	3.4 [50.1]	2.7 [39.5]	2.6 [40.8]	2.9 [43.8]	2.9 [41]	2.9 [44.8]
Stop codons																			
<i>ochre</i>	UAA	59	58.1	57.5	62.1	62.1	64.9	64.4	61.5	74.1	73.9	74.9	68.2	68.4	64.9	72.9	66.8	68.2	86.9
<i>amber</i>	UAG	23.6	25.4	24	18.1	19.5	19.7	21.3	23.9	17.3	17	17.3	23.1	22.1	17.5	14.6	17.3	18.4	5.5
<i>opal</i>	UGA	17.4	16.5	18.5	19.8	18.4	15.4	14.3	14.6	8.6	9.1	7.8	8.7	9.5	17.7	12.5	15.9	13.4	7.6
Translation initiator																			
M	AUG	90.9	89.5	89.8	90.6	89.6	91.5	85.8	91.0	90.1	91.7	90.9	92.0	90.7	99.5	99.4	98.7	83.9	99.6
L	GUG	6.1	5	5.7	5.6	5.5	5.5	9.6	6.4	5.8	6.1	6.1	5.7	5.8	0.3	0.2	0.9	12.4	0
V	UUG	2.9	2.5	2.9	3.7	3.4	3.1	3.9	2.6	2.7	2.2	3	2.3	2.8	0.2	0.4	0.4	3.7	0

#the number outside square bracket indicates percentage of codon in genome, number in square bracket indicates percentage of codon used for each amino acid.

Table A.6.03 CRISPR associated genes in *Mbb.* spp.

[illegible]

<i>csx1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	MJ1666
<i>csx15</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TTE2665
<i>csf1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	AFE_1038
<i>csf2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	AFE_1039
<i>csf3</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	AFE_1040
<i>csf4</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	AFE_1037

Prediction cutoff: E-04. +Represents the gene is predicted in the particular genome. –indicates the absence of gene in the particular genome. *Reference protein is displayed in either locus tag or gene name within the NCBI protein database

Table A.6.04 Domains of predicted secretome

Pfam/TIGRfam	D5	YE315	ZA-10 ^T	SM9	HO _T	P _{S^T}	JMR01	M1 _T	KM1H5-1P ^T	YLM1	SH _T	AbM4	JH1 _T	RFM-1 ^T	RFM-2 ^T	RFM-3 ^T	AT _{M^T}	ANOR1
Repeat domains (containing PF13306: Leucine rich repeats (6 copies), PF13754: Bacterial Ig-like domain (group 3) , PF02369: Bacterial Ig-like domain (group 1), PF09479: Listeria-Bacteroides repeat domain, PF05345: Putative Ig domain, PF02368: Bacterial Ig-like domain (group 2), PF09373: Pseudomurein-binding repeat, TIGR02167: bacterial surface protein 26-residue repeat)	27	19	22	26	5	11	7	37	9	10	3	2	3	12	3	9	2	6
LPxTG motif containing proteins																		
PF01345: DUF11	-	-	1	2	-	2	-	1	1	1	-	1	1	-	-	-	-	-
PF13229: Right handed beta helix region	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
Lipo-box containing protein																		
PF00112: peptidase_C1	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
PF00288: GHMP kinases N terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF00384: Molybdopter in oxidoreductase	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	1	1	-
PF00497: Bacterial extracellular solute-binding proteins, family 3	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF00756: Esterase	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01058: NADH ubiquinone oxidoreductase, 20 Kd subunit	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-
PF01345: DUF11	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01497: Periplasmic binding protein	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-	2	-	-
PF01841: Transglutaminase-like superfamily	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02655: ATP-grasp domain	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF02663: FmdE, Molybdenum formylmethanofuran dehydrogenase operon	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF03063: Prismane/CO dehydrogenase family	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF03275: UDP-galactopyranose mutase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-
PF03577: Peptidase family C69	-	-	-	2	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF03412: Peptidase C39 family	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF05048: Periplasmic copper-binding protein (NosD)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-

PF07705: CARDB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1
PF09394: Chagasin family peptidase inhibitor I42	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF09972: DUF2207	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
PF11824: DUF3344	-	-	-	-	-	-	1	-	1	1	-	-	-	-	-	-	-	-	-
PF13197: DUF4013	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
PF12695: Alpha/beta hydrolase family	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13190: PDGLE domain	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	1	-	1	-
PF13200: Putative glycosyl hydrolase domain (DUF4015)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-
PF13229: Right handed beta helix region	1	-	1	1	1	-	-	1	-	-	1	1	1	1	1	1	1	-	-
PF13290: Chitobiase/beta-hexosaminidase C-terminal domain	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF13360: PQQ-like domain	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13391: HNH endonuclease	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF13425: O-antigen ligase like membrane protein	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13459: 4Fe-4S single cluster domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-
PF13531: Bacterial extracellular solute-binding protein	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13620: Carboxypeptidase regulatory-like domain	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF14347: DUF4399	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
Integral membrane protein (3 or more TMH)																			
PF00112: peptidase_C1	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF00534: Glycosyl transferase family 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF00535: Glycosyl transferase family 2	1	1	1	1	1	-	-	1	1	1	-	-	-	1	-	-	1	1	-
PF00892: EamA-like transporter family	-	-	1	-	-	-	-	-	1	1	1	1	1	-	-	-	-	-	-
PF00893: Small Multidrug Resistance protein	-	1	-	-	-	-	-	2	-	-	-	-	-	-	-	1	-	-	-
PF01345: DUF11	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF01569: PAP2 superfamily	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01595: DUF21	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
PF01699: Sodium/calcium exchanger protein	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
PF01891: Cobalt uptake substrate-specific transmembrane region CbiM	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-
PF02163: Peptidase family M50	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02386: Cation transport protein	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
PF02516: Oligosaccharyl transferase STT3 subunit	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-	1	1
PF02554: Carbon starvation protein CstA	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02588: DUF161	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02659: Putative manganese efflux pump (DUF204)	1	1	1	1	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-
PF02687: FtsX-like permease family	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
PF03186: CobD/Cbib protein	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF03553: Na ⁺ /H ⁺ antiporter family	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF04018: DUF368	-	-	1	1	1	-	-	-	1	-	-	-	-	1	1	-	-	-	1

PF04020: Mycobacterial 4 TMS phage holin, superfamily IV	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF04203: Sortase family	-	-	-	-	-	-	-	-	-	-	1	1	1	1	-	-	-	-
PF04206: Tetrahydromethanopterin S-methyltransferase, subunit E	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PF04207: Tetrahydromethanopterin S-methyltransferase, subunit D	-	-	-	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-
PF07690: Major Facilitator Superfamily	1	1	-	-	2	1	1	-	-	1	-	-	-	-	-	-	1	-
PF09376: NurA domain	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
PF09972: DUF2207	1	1	1	1	1	1	1	3	1	1	1	1	1	-	1	-	1	1
PF13197: DUF4013	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-
PF13229: Right handed beta helix	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-
PF13439: Glycosyltransferase Family 4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
Dual membrane anchored																		
PF00005: ABC transporter	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
PF00112: peptidase_C1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF00375: Sodium:dicarboxylate symporter family	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF00482: Type II secretion system (T2SS), protein F	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF00565: Staphylococcal nuclease homologue	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
PF01345: DUF11	5	-	1	5	-	-	-	-	1	3	1	-	1	-	1	3	-	3
PF02514: CobN/Magnesium Chelatase	-	-	-	-	1	1	-	1	-	1	1	-	-	1	1	-	-	1
PF02553: Cobalt transport protein component CbiN	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	1	-	-
PF02663: FmdE, Molybdenum formylmethanofuran dehydrogenase operon	1	-	1	-	2	1	-	-	-	-	-	-	1	-	-	-	-	1
PF02805: Metal binding domain of Ada	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
PF03412: Peptidase C39 family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF04304: DUF454	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF05048: Periplasmic copper-binding protein (NosD)	1	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-
PF07705: CARDB	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF09880: DUF2107	1	-	1	-	-	-	-	1	1	1	-	-	-	-	-	-	-	-
PF05399: Ectropic viral integration site 2A protein (EVI2A)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF13190: PDGLE domain	1	-	1	1	-	-	-	-	-	-	-	1	1	-	-	1	-	-
PF13229: Right handed beta helix	4	4	1	1	1	3	2	2	1	2	1	2	1	6	-	2	-	1
PF13360: PQQ-like domain	-	-	-	1	1	1	-	-	-	-	1	1	1	1	1	-	-	-
PF13620: Carboxypeptidase regulatory-like domain	3	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-
C-terminal anchored																		
PF01345: DUF11	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	1	-	-
PF02514: CobN/Magnesium Chelatase	-	-	-	1	-	-	-	-	-	-	-	1	1	-	-	-	-	-
PF02663: FmdE, Molybdenum formylmethanofuran dehydrogenase operon	-	-	1	1	-	1	-	-	1	1	-	-	-	-	-	-	-	-
PF05048: Periplasmic copper-binding protein (NosD)	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-

PF05048: Periplasmic copper-binding protein (NosD)	2	-	-	-	-	-	1	-	-	-	-	-	1	2	3	-	-	-
PF05738: Cna protein B-type domain	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF06009: Laminin Domain II	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF06207: DUF1002	2	1	1	1	2	-	1	1	1	-	-	-	-	-	-	-	-	-
PF07602: DUF1565	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	1
PF07685: CobB/CobQ-like glutamine amidotransferase domain	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
PF07705: CARDB	1	-	-	-	-	-	-	-	-	-	-	-	-	4	2	3	-	2
PF07790: DUF1628	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
PF08308: PEGA domain	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF09084: NMT1/THI5 like	1	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF09394: Chagasin family peptidase inhibitor I42	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF09587: Bacterial capsule synthesis protein PGA_cap	-	-	-	1	1	1	-	-	-	-	-	-	-	-	-	-	-	-
PF09752: DUF2048	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
PF09972: DUF2207	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF10670: DUF4198	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF11824: DUF3344	1	-	3	2	-	1	-	2	1	1	-	-	-	-	-	-	-	-
PF11959: DUF3473	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF12682: Flavodoxin_4	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF12804: MobA-like NTP transferase domain	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF12849: PBP superfamily domain	-	-	1	-	-	-	-	-	-	-	1	1	-	1	1	1	-	-
PF13098: Thioredoxin-like domain	-	1	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF13200: Putative glycosyl hydrolase domain (DUF4015)	1	-	-	1	-	-	1	-	-	-	1	-	-	-	-	-	-	-
PF13229: Right handed beta helix	3	5	10	5	7	5	9	12	6	6	2	1	4	27	15	6	3	7
PF13360: PQQ-like domain	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF13499: EF-hand domain pair	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
PF13531: Bacterial extracellular solute-binding protein	-	2	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13570: PQQ-like domain	1	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF13620: Carboxypeptidase regulatory-like domain	12	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	1	-
PF14347: DUF4399	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF14947: Winged helix-turn-helix	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13379: NMT1-like family	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2	1	-	-
Secreted																		
PF00112: peptidase_C1	-	-	6	3	-	-	-	2	-	-	-	-	-	-	-	-	-	-
PF00188: Cysteine-rich secretory protein family	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF00215: Orotidine 5'-phosphate decarboxylase / HUMPS family	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF00534: Glycosyl transferases group 1	-	-	-	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-
PF00590: Tetrapyrrole (Corrin/Porphyrin) Methylases	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF00682: HMGL-like	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-

PF00984: UDP-glucose/GDP-mannose dehydrogenase family	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-
PF01058: NADH ubiquinone oxidoreductase, 20 Kd subunit	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	1
PF01157: Ribosomal protein L21e	1	-	-	1	-	-	-	-	-	-	-	-	1	1	1	1	-
PF01180: Dihydroorotate dehydrogenase	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-	-	-
PF01379: Porphobilinogen deaminase, dipyromethane cofactor binding domain	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF01345: DUF11	-	-	-	-	1	-	-	-	-	-	-	-	1	-	4	-	-
PF01370: NAD dependent epimerase/dehydratase family	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
PF01451: Low molecular weight phosphotyrosine protein phosphatase	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF01471: Putative peptidoglycan binding domain	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF01497: Periplasmic binding protein	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
PF01554: MatE	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01641: SelR domain	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01841: Transglutaminase-like superfamily	2	-	2	-	-	1	-	1	3	3	1	1	2	3	3	-	2
PF01850: PIN domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1
PF01872: RibD C-terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF01888: CbiD	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
PF01890: Cobalamin synthesis G C-terminus	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF01909: Nucleotidyltransferase domain	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF02254: TrkA-N domain	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02514: CobN/Magnesium Chelatase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-
PF02558: Ketopantoate reductase PanE/ApbA	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF02805: Metal binding domain of Ada	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-
PF03412: Peptidase C39 family	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-
PF03900: Porphobilinogen deaminase, C-terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF04427: Brix domain	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF04466: Phage terminase large subunit	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF04851: Type III restriction enzyme, res subunit	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF04919: DUF655	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF04952: Succinylglutamate desuccinylase	1	-	-	-	1	-	-	-	-	-	-	-	1	-	1	1	-
PF05048: Periplasmic copper-binding protein (NosD)	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-
PF06207: DUF1002	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
PF07602: DUF1565	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF07705: CARDB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1
PF08011: PD-(D/E)XK nuclease superfamily	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF08245: Mur ligase middle domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF08353: DUF1727	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
PF08502: LeuA allosteric (dimerisation) domain	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-
PF08859: DGC domain	1	1	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-
PF09820: Predicted AAA-ATPase	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-

PF09869: DUF2096	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-
PF11760: Cobalamin synthesis G N-terminal	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
PF11797: DUF3324	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13200: Putative glycosyl hydrolase domain (DUF4015)	-	-	1	1	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-
PF13229: Right handed beta helix	1	1	2	3	-	-	1	1	-	-	-	-	-	-	3	-	-	-	-
PF13290: Chitinase/beta-hexosaminidase C-terminal domain	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13307: Helicase C-terminal domain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
PF13360: PQQ-like domain	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PF13379: NMT1-like family	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
PF13620: Carboxypeptidase regulatory-like domain	3	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
PF17147: Pyruvate:ferredoxin oxidoreductase core domain II	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-

Prediction cutoff: E-05. Pfam conserved between rumen members of Methanomassiliicoccales are highlighted, Pfam of interest are underlined. Predicted transmembrane extracellular proteins with two or more TMH or C-terminal anchor are highlighted in blue, predicted transmembrane extracellular proteins with N-terminal anchor are highlighted in purple, secreted extracellular proteins are highlighted in yellow. *Signal peptides are potentially false positive. ** Including PF13306: Leucine rich repeats (6 copies), PF13754: Bacterial Ig-like domain (group 3), PF09479: Listeria-Bacteroides repeat domain, PF05345: Putative Ig domain, PF02368: Bacterial Ig-like domain (group 2), TIGR02167: bacterial surface protein 26-residue repeat.

Table A.6.05 Predicted *Methanobrevibacter* sp. D5 genes within the *Methanobrevibacter* core genome

Locus tag	Predicted gene product	COG category
D5_0001	cell division control protein Cdc6	[L]
D5_0004	ATP phosphoribosyltransferase HisG	[E]
D5_0005	archaeal histone HmfB	[B]
D5_0006	amidohydrolase	[F]
D5_0007	succinate dehydrogenase/fumarate reductase flavoprotein subunit SdhA	[C]
D5_0013	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit A GatA	[J]
D5_0021	xylose isomerase-like TIM barrel domain-containing protein	[G]
D5_0028	PHP domain-containing protein	[R]
D5_0033	radical SAM domain-containing protein	[R]
D5_0039	dihydroxy-acid dehydratase	[E]
D5_0040	histidinol dehydrogenase	[E]
D5_0042	aspartyl-tRNA synthetase AspS	[J]
D5_0045	glutamate-1-semialdehyde-2,1-aminomutase HemL	[H]
D5_0046	signal peptidase I	[U]
D5_0047	arginyl-tRNA synthetase ArgS	[J]
D5_0050	MATE efflux family protein, matE	[V]
D5_0052	phosphoribosylamine--glycine ligase, PurD	[F]
D5_0054	ornithine carbamoyltransferase ArgF	[E]
D5_0057	acetolactate synthase large subunit IlvB	[E]
D5_0058	acetolactate synthase small subunit IlvN	[E]
D5_0059	carbonic anhydrase Cab	[E]
D5_0061	ketol-acid reductoisomerase IlvC	[E]
D5_0062	methanogenesis marker protein 12	[S]
D5_0063	LSM domain-containing protein	[K]
D5_0065	5'-nucleotidase SurE	[R]
D5_0067	conserved hypothetical transmembrane protein	[S]
D5_0069	threonyl-tRNA synthetase ThrS	[J]
D5_0070	bifunctional formaldehyde-activating enzyme /3- hexulose-6-phosphate synthase Fae/Hps	[G]
D5_0074	NADPH-dependent FMN reductase	[R]
D5_0075	polysaccharide biosynthesis protein	[R]
D5_0076	molybdate transport system regulatory protein ModE	[R]
D5_0078	imidazoleglycerol-phosphate dehydratase HisB	[E]
D5_0080	branched-chain-amino-acid aminotransferase IlvE	[E]
D5_0081	undecaprenyl-diphosphatase	[V]
D5_0084	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase CobT	[H]
D5_0086	glycoprotease M22 family	[O]
D5_0087	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	[F]
D5_0088	ribosomal protein S15P Rps15p	[J]
D5_0090	aconitase	[S]
D5_0096	Hef nuclease	[L]
D5_0097	xylose isomerase-like TIM barrel domain-containing protein	[G]
D5_0098	PIN domain-containing protein	[R]
D5_0099	phosphoribosyl-AMP cyclohydrolase HisI	[E]
D5_0100	histidyl-tRNA synthetase HisS	[J]
D5_0101	shikimate 5-dehydrogenase AroE	[E]
D5_0103	replication factor C large subunit RfcL	[K]
D5_0104	replication factor C small subunit RfcS	[L]
D5_0105	peptidase M48 family	[O]
D5_0106	tRNA(1-methyladenosine) methyltransferase	[J]
D5_0107	leucyl-tRNA synthetase LeuS	[J]
D5_0126	Anion-transporting ATPase	[P]
D5_0134	translation-associated GTPase	[J]
D5_0142	methanogenesis marker 13	[C]
D5_0143	imidazole glycerol phosphate synthase	[E]
D5_0144	hydrogenase expression/formation protein, HypE	[O]
D5_0148	hypothetical protein	[S]
D5_0149	amidohydrolase	[Q]

D5_0153	adenylosuccinate lyase PurB	[F]
D5_0154	HTH domain-containing protein	[K]
D5_0164	DNA polymerase sliding clamp subunit PCNA family Pcn	[S]
D5_0167	ribosomal protein S27e Rps27e	[J]
D5_0168	translation initiation factor aIF-2 alpha subunit	[J]
D5_0169	H/ACA RNA-protein complex component Nop10p	[R]
D5_0170	conserved hypothetical protein	[S]
D5_0174	coenzyme F ₄₂₀ hydrogenase alpha subunit FrhA	[C]
D5_0175	coenzyme F ₄₂₀ hydrogenase delta subunit FrhD	[C]
D5_0176	coenzyme F ₄₂₀ hydrogenase gamma subunit FrhG	[C]
D5_0177	coenzyme F ₄₂₀ hydrogenase beta subunit FrhB	[C]
D5_0178	methionine aminopeptidase Map	[J]
D5_0179	conserved hypothetical secreted protein	[Unclassified]
D5_0190	molecular chaperone DnaJ	[O]
D5_0191	chaperone protein DnaK	[O]
D5_0192	chaperone protein DnaK	[O]
D5_0193	transcriptional regulator ArsR family	[K]
D5_0194	hydrogenase maturation factor HypF	[O]
D5_0199	polysaccharide/polyol phosphate ABC transporter ATP-binding protein	[G]
D5_0200	polysaccharide/polyol phosphate ABC transporter permease protein	[G]
D5_0201	phosphoribosyl-ATP pyrophosphohydrolase HisE	[E]
D5_0202	CBS domain-containing protein	[K]
D5_0203	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit B GatB	[J]
D5_0204	radical SAM domain-containing protein	[H]
D5_0205	archaeal Holliday junction resolvase Hjc	[L]
D5_0206	metallo-beta-lactamase superfamily protein	[R]
D5_0207	potassium uptake protein TrkA family	[P]
D5_0208	potassium uptake protein TrkH family	[P]
D5_0210	formylmethanofuran-tetrahydromethanopterin formyltransferase Ftr	[C]
D5_0213	carbohydrate kinase	[G]
D5_0214	sugar fermentation stimulation protein SfsA	[R]
D5_0217	argininosuccinate synthase ArgG	[E]
D5_0221	succinylglutamate desuccinylase /aspartoacylase	[R]
D5_0225	energy-converting hydrogenase B subunit A EhbA	[P]
D5_0226	energy-converting hydrogenase B subunit B EhbB	[P]
D5_0229	energy-converting hydrogenase B subunit E EhbE	[P]
D5_0230	energy-converting hydrogenase B subunit F EhbF	[C]
D5_0232	energy-converting hydrogenase B subunit H EhbH	[P]
D5_0233	energy-converting hydrogenase B subunit I EhbI	[P]
D5_0235	energy-converting hydrogenase B subunit K EhbK	Not in COGs
D5_0236	energy-converting hydrogenase B subunit L EhbL	[C]
D5_0237	energy-converting hydrogenase B subunit M EhbM	[C]
D5_0238	energy-converting hydrogenase B subunit N EhbN	[C]
D5_0239	energy-converting hydrogenase B, subunit O, EhbO	[C]
D5_0240	energy-converting hydrogenase B subunit P EhbP	Not in COGs
D5_0241	energy-converting hydrogenase B subunit Q EhbQ	[R]
D5_0244	conserved hypothetical protein	[S]
D5_0248	CBS domain-containing protein	[R]
D5_0249	CBS domain-containing protein	[R]

D5_0250	prephenate dehydratase PheA	[E]	D5_0325	LPPG:FO 2-phospho-L-lactate transferase	
D5_0254	phosphopantothenate-cysteine ligase CoaB	[H]		CofD	[S]
D5_0255	fibrillarin FlpA	[J]	D5_0326	GTP cyclohydrolase III ArfA	[S]
D5_0256	pre-mRNA splicing ribonucleoprotein PRP31	[J]	D5_0327	tRNA-dihydrouridine synthase	[J]
D5_0258	dihydroorotate dehydrogenase PyrD	[F]	D5_0328	methyl-coenzyme M reductase component A2	
D5_0259	dihydroorotate dehydrogenase electron transfer subunit PyrK	[H]		AtwA	[R]
D5_0260	conserved hypothetical transmembrane protein	[R]	D5_0332	methanogenesis marker domain 9	[K]
D5_0261	DNA polymerase family B PolB	[L]	D5_0333	siroheme synthase CysG	[H]
D5_0263	L-sulfolactate dehydrogenase ComC	[C]	D5_0334	glutamyl-tRNA reductase HemA	[H]
D5_0264	phosphoribosylformylglycinamide cyclo-ligase PurM	[F]	D5_0335	ATPase	[R]
D5_0265	RNA-metabolising metallo-beta-lactamase	[R]	D5_0339	glyceraldehyde-3-phosphate dehydrogenase	
D5_0266	proteasome beta subunit	[O]		Gap	[G]
D5_0267	Met-10 like-protein	[R]	D5_0347	DNA topoisomerase VI subunit A	[L]
D5_0268	FO synthase subunit 1 CofG	[H]	D5_0348	DNA topoisomerase VI subunit B	[L]
D5_0270	GTP cyclohydrolase MptA	[S]	D5_0349	RNA-binding protein	[R]
D5_0271	transcriptional regulator AsnC family	[K]	D5_0350	tetrahydromethanopterin S-methyltransferase	
D5_0272	N ² ,N ² -dimethylguanosine tRNA methyltransferase TrmI	[J]		subunit H MtrH2	[H]
D5_0273	aminotransferase DegT/DnrJ/EryC1/StrS family	[M]	D5_0357	serine/threonine protein kinase RIO1 family	[T]
D5_0275	PP-loop family protein	[D]	D5_0358	translation initiation factor aIF-1A	[J]
D5_0277	CBS domain-containing protein	[R]	D5_0359	molybdopterin biosynthesis protein MoeA	[H]
D5_0278	conserved hypothetical protein	[Unclassified]	D5_0360	transcriptional regulator	[K]
D5_0279	TraB family protein	[S]	D5_0362	peptidase U62 family	[R]
D5_0280	2-phosphosulfolactate phosphatase ComB	[H]	D5_0364	hydrogenase expression/formation protein	
D5_0282	methanogenesis marker protein 7	[R]		HypD	[O]
D5_0283	methanogenesis marker protein 10	[C]	D5_0369	digeranylgeranylglyceryl phosphate synthase	
D5_0284	methyl-coenzyme M reductase beta subunit McrB	[H]		DGGGPS	[H]
D5_0285	methyl-coenzyme M reductase D subunit McrD	[H]	D5_0370	myo-inositol-1-phosphate synthase	[I]
D5_0286	methyl-coenzyme M reductase C subunit McrC	[H]	D5_0372	pyruvate carboxylase subunit B PycB	[C]
D5_0288	methyl-coenzyme M reductase alpha subunit McrA	[H]	D5_0390	conserved hypothetical protein	[S]
D5_0289	tetrahydromethanopterin S-methyltransferase subunit E MtrE	[H]	D5_0396	fumarate hydratase FumA	[C]
D5_0290	tetrahydromethanopterin S-methyltransferase subunit D MtrD	[H]	D5_0398	2-oxoglutarate ferredoxin oxidoreductase	
D5_0291	tetrahydromethanopterin S-methyltransferase subunit C MtrC	[H]		subunit alpha KorA	[C]
D5_0292	tetrahydromethanopterin S-methyltransferase subunit B MtrB	[H]	D5_0399	2-oxoglutarate ferredoxin oxidoreductase	
D5_0294	tetrahydromethanopterin S-methyltransferase subunit F MtrF	[H]		subunit beta KorB	[C]
D5_0295	tetrahydromethanopterin S-methyltransferase subunit G MtrG	[H]	D5_0400	2-oxoglutarate ferredoxin oxidoreductase	
D5_0297	methanogenesis marker protein 14	[S]		subunit gamma KorC	[C]
D5_0299	PRC-barrel domain-containing protein	[S]	D5_0401	succinyl-CoA synthetase beta subunit SucC	[C]
D5_0302	methyl viologen-reducing hydrogenase delta subunit MvhD	[C]	D5_0402	radical SAM domain-containing protein	Not in COGs
D5_0303	methyl viologen-reducing hydrogenase gamma subunit MvhG	[C]	D5_0405	triose-phosphate isomerase TpiA	[G]
D5_0304	methyl viologen-reducing hydrogenase alpha subunit MvhA	[C]	D5_0406	phosphoglycerate kinase Pgc	[G]
D5_0305	methyl viologen-reducing hydrogenase beta subunit MvhB	[C]	D5_0408	hydroxyethylthiazole kinase	[H]
D5_0308	nucleotidyl transferase	[R]	D5_0409	DNA-directed RNA polymerase subunit H	
D5_0310	hypothetical protein	Not in COGs		RpoH	[K]
D5_0311	ribosomal protein L10e Rpl10e	[J]	D5_0411	DNA-directed RNA polymerase subunit B'	
D5_0312	phosphoenolpyruvate synthase PpsA	[G]		RpoB1	[K]
D5_0313	L-tyrosine decarboxylase MfnA	[E]	D5_0412	DNA-directed RNA polymerase subunit A'	
D5_0314	dihydronepterin aldolase MtnD	[S]		RpoA1	[K]
D5_0315	sortase family protein	[M]	D5_0413	DNA-directed RNA polymerase subunit A''	
D5_0317	phosphoenolpyruvate synthase PpsA	[G]		RpoA2	[K]
D5_0319	cell shape determining protein, MreB/Mrl family	[D]	D5_0414	ribosomal protein L30e Rpl30e	[J]
D5_0320	ribonuclease HIII RnhB	[L]	D5_0415	transcription elongation factor NusA-like protein	[K]
D5_0322	transporter ExbD/TolR family	[Unclassified]	D5_0416	ribosomal protein S12P Rps12p	[J]
D5_0323	IMP cyclohydrolase PurO	[F]	D5_0419	translation elongation factor aEF-1 alpha	[J]
D5_0324	F ₄₂₀ -0:gamma-glutamyl ligase CofE	[S]	D5_0420	ribosomal protein S10P Rps10p	[J]
			D5_0423	conserved hypothetical protein	[S]
			D5_0425	ribosomal-protein-alanine acetyltransferase	
				RimI	[R]
			D5_0428	peptide chain release factor aRF1	[J]
			D5_0429	glutamate dehydrogenase GdhA	[E]
			D5_0498	UDP-glucose pyrophosphorylase GalU	[M]
			D5_0510	tetrahydromethanopterin S-methyltransferase	
				subunit A MtrA	[H]
			D5_0517	orotate phosphoribosyltransferase PyrE	[F]
			D5_0518	oxidoreductase GFO/IDH/MOCA family	[R]
			D5_0519	porphobilinogen deaminase HemC	[H]
			D5_0521	bifunctional inositol-1 monophosphatase/	
				fructose-1,6-bisphosphatase/ATP-NAD	
				kinase	[G]
			D5_0522	pyruvoyl-dependent arginine decarboxylase	
				PdaD	[S]
			D5_0523	translation initiation factor aIF-5A	[J]
			D5_0524	arginase/agmatinase family protein	[E]
			D5_0531	conserved hypothetical protein	[S]
			D5_0532	adenine deaminase Ade	[F]

D5_0534	phosphosugar isomerase	[M]
D5_0543	GTP-binding protein	[R]
D5_0544	AMMECR1 domain-containing protein	[S]
D5_0545	peptidase U62 family	[R]
D5_0546	GMC oxidoreductase family protein	[E]
D5_0547	aspartate carbamoyltransferase regulatory subunit PyrI	[F]
D5_0549	<i>N</i> -acetyl-gamma-glutamyl-phosphate reductase ArgC	[E]
D5_0550	glycerol-3-phosphate cytidyltransferase	[M]
D5_0551	phosphoribosylformimino-5- aminoimidazole carboxamide ribotide isomerase, hisA	[E]
D5_0560	conserved hypothetical transmembrane protein	[Unclassified]
D5_0581	tRNA pseudouridine synthase A TruA	[J]
D5_0583	UDP-N-acetylglucosamine 2-epimerase	[R]
D5_0585	(4-{4-[2-(γ -L-glutamylamino)ethyl]phenoxy)methyl}furan-2-yl)methanamine synthase MfnF	[I]
D5_0586	conserved hypothetical transmembrane protein	[R]
D5_0587	7,8-dihydro-6-hydroxymethylpterin dimethyltransferase	[E]
D5_0589	hypothetical protein	[R]
D5_0592	MiaB-like tRNA modifying enzyme	[J]
D5_0595	histone acetyltransferase ELP3 family	[K]
D5_0598	DEAD/DEAH box helicase domain-containing protein	[R]
D5_0599	thioredoxin	[O]
D5_0603	glycosyl transferase GT4 family	[M]
D5_0604	shikimate kinase AroK	[E]
D5_0606	chorismate mutase, aroH	[E]
D5_0608	aspartate kinase Ask	[E]
D5_0609	dihydrodipicolinate synthase DapA	[E]
D5_0610	dihydrodipicolinate reductase DapB	[E]
D5_0611	aspartate-semialdehyde dehydrogenase Asd	[E]
D5_0614	thermosome subunit	[O]
D5_0619	PRC-barrel domain-containing protein	[S]
D5_0620	orotate phosphoribosyltransferase PyrE	[F]
D5_0621	molybdenum cofactor biosynthesis protein B MoaB	[H]
D5_0625	hypothetical protein	[R]
D5_0627	methanogenesis marker protein 2	[R]
D5_0631	methanogenesis marker protein 3	[O]
D5_0632	methanogenesis marker protein 6	[S]
D5_0633	methanogenesis marker protein 5	[S]
D5_0634	methanogenesis marker protein 15	[I]
D5_0635	methanogenesis marker protein 17	[S]
D5_0636	nitrogenase cofactor biosynthesis protein NifB	[R]
D5_0639	translation initiation factor aIF-2B alpha subunit	[J]
D5_0643	Met-10 like-protein	[R]
D5_0644	diphthine synthase DphB	[J]
D5_0648	archaeosine tRNA-ribosyltransferase TgtA	[J]
D5_0649	CoB--CoM heterodisulfide reductase subunit C HdrC	[C]
D5_0650	CoB--CoM heterodisulfide reductase subunit B HdrB	[C]
D5_0651	conserved hypothetical protein	[S]
D5_0652	conserved hypothetical protein	[S]
D5_0653	calcineurin-like phosphoesterase	[R]
D5_0655	2-phosphoglycerate kinase Pgk	[G]
D5_0656	CBS domain-containing protein	[R]
D5_0657	transporter CDF family	[P]
D5_0658	alanine aminotransferase	[E]
D5_0659	radical SAM domain-containing protein	[C]
D5_0661	phosphopantetheine adenyltransferase CoaD	[E]
D5_0667	metallo-beta-lactamase superfamily protein	[Unclassified]
D5_0670	conserved hypothetical protein	[S]
D5_0674	fumarate hydratase FumA	[L]
D5_0675	conserved hypothetical protein	[C]
D5_0676	pyridoxal phosphate enzyme	[Unclassified]
D5_0677	biotin-acetyl-CoA-carboxylase ligase BirA	[E]
D5_0678	pyruvate carboxylase subunit A PycA	[H]

D5_0680	conserved hypothetical protein	[J]
D5_0681	ribosomal protein L3P Rpl3p	[S]
D5_0682	ribosomal protein L4p Rpl4p	[J]
D5_0683	ribosomal protein L23P Rpl23p	[J]
D5_0685	ribosomal protein S19P Rps19p	[J]
D5_0686	ribosomal protein L22P Rpl22p	[J]
D5_0687	ribosomal protein S3P Rps3p	[J]
D5_0688	ribosomal protein L29P Rpl29p	[J]
D5_0689	translation initiation factor aSUI1	[J]
D5_0692	ribosomal protein L14P Rpl14p	[J]
D5_0693	ribosomal protein L24P Rpl24p	[J]
D5_0694	ribosomal protein S4e Rps4e	[J]
D5_0695	ribosomal protein L5P Rpl5p	[J]
D5_0696	ribosomal protein S8P Rps8p	[J]
D5_0697	ribosomal protein L6P Rpl6p	[J]
D5_0698	ribosomal protein L32e Rpl32e	[J]
D5_0699	ribosomal protein L19e Rpl19e	[J]
D5_0700	ribosomal protein L18P Rpl18p	[J]
D5_0701	ribosomal protein S5P Rps5p	[J]
D5_0702	ribosomal protein L30P Rpl30p	[J]
D5_0703	ribosomal protein L15P Rpl15p	[J]
D5_0704	preprotein translocase subunit SecY	[U]
D5_0705	adenylate kinase Adk	[F]
D5_0706	conserved hypothetical transmembrane protein	[S]
D5_0708	cytidylate kinase Cmk	[S]
D5_0709	ribosomal protein L14e Rpl14e	[J]
D5_0710	H/ACA RNA-protein complex component Cbf5p	[J]
D5_0719	ribosomal protein S13P Rps13p	[J]
D5_0720	ribosomal protein S4P Rps4p	[J]
D5_0721	ribosomal protein S11P Rps11p	[J]
D5_0722	DNA-directed RNA polymerase subunit D RpoD	[C]
D5_0723	ribosomal protein L18e Rpl18e	[J]
D5_0724	ribosomal protein L13P Rpl13p	[J]
D5_0725	ribosomal protein S9P Rps9p	[J]
D5_0726	DNA-directed RNA polymerase subunit N RpoN	[K]
D5_0727	DNA-directed RNA polymerase subunit K RpoK	[K]
D5_0728	phosphopyruvate hydratase Eno	[G]
D5_0730	ribosomal protein S2P Rps2p	[J]
D5_0731	conserved hypothetical protein	[R]
D5_0732	mevalonate kinase Mvk	[I]
D5_0733	isopentenyl diphosphate kinase	[R]
D5_0734	isopentenyl diphosphate delta-isomerase Fni	[C]
D5_0735	RNA-metabolising metallo-beta-lactamase	[R]
D5_0736	bifunctional short chain isoprenyl diphosphate synthase IdsA	[H]
D5_0741	F ₄₂₀ -dependent methylenetetrahydromethanopterin dehydrogenase Mtd	[C]
D5_0744	methyl-coenzyme M reductase II gamma subunit MrtG	[H]
D5_0745	methyl-coenzyme M reductase II alpha subunit MrtA	[H]
D5_0748	transcriptional regulator TrmB family	[K]
D5_0749	hydroxylamine reductase Hcp	[C]
D5_0750	cupin 2 domain-containing protein	[S]
D5_0751	SAM-dependent methyltransferase	[Q]
D5_0754	glutamyl-tRNA synthetase GltX	[J]
D5_0757	diaminopimelate aminotransferase DapL	[E]
D5_0766	adenylosuccinate synthetase PurA	[F]
D5_0785	conserved hypothetical protein	[S]
D5_0786	metallo-beta-lactamase superfamily protein	[R]
D5_0787	chorismate synthase AroC	[E]
D5_0790	ATP:dephospho-CoA triphosphoribosyl transferase CitG	[H]
D5_0800	phenylalanyl-tRNA synthetase alpha subunit PheS	[J]
D5_0801	exodeoxyribonuclease III Xth	[L]
D5_0802	hydrolase HAD superfamily	[R]
D5_0806	ribosomal protein S8e Rps8e	[J]
D5_0807	hydrogenase expression/formation protein HypE	[O]

D5_0808	hypothetical transmembrane protein	[Unclassified]	D5_1469	phospho-2-dehydro-3-deoxyheptonate aldolase/fructose-bisphosphate aldolase	[G]
D5_0811	CRISPR-associated protein Cas4	[Unclassified]	D5_1470	SAM-dependent methyltransferase	[R]
D5_0814	transcriptional regulator MarR family	[K]	D5_1479	PHP domain-containing protein	[E]
D5_0815	ssDNA exonuclease RecJ	[L]	D5_1482	diaminohydroxyphosphoribosylaminopyrimidine reductase RibD	[H]
D5_0816	signal recognition particle SRP19 protein	[U]	D5_1483	cell wall biosynthesis protein phospho- <i>N</i> -acetylmuramoyl-pentapeptide-transferase family	[M]
D5_0819	uroporphyrinogen III synthase HemD	[H]	D5_1488	conserved hypothetical protein	[S]
D5_0855	hypothetical transmembrane protein	[S]	D5_1489	methionyl-tRNA synthetase MetG	[J]
D5_0862	phosphoribosylaminoimidazole-succinocarboxamide synthase PurC	[F]	D5_1490	DNA primase large subunit PriB	[L]
D5_0863	phosphoribosylformylglycinamide (FGAM) synthase PurS	[F]	D5_1495	DNA primase small subunit PriA	[L]
D5_0864	phosphoribosylformylglycinamide (FGAM) synthase PurQ	[F]	D5_1498	FO synthase subunit 2 CofH	[H]
D5_0865	uroporphyrin-III C-methyltransferase CobA	[H]	D5_1507	conserved hypothetical protein	[R]
D5_0868	SAM-dependent methyltransferase	[S]	D5_1509	cyclic 2,3-diphosphoglycerate-synthetase CpgS	[R]
D5_0870	archaeosine tRNA-ribosyltransferase TgtA	[J]	D5_1512	undecaprenyl pyrophosphate synthetase UppS	[I]
D5_0872	hydroxymethylglutaryl-CoA synthase	[I]	D5_1513	hydrolase TatD family	[L]
D5_0873	acetyl-CoA acetyltransferase	[I]	D5_1523	conserved hypothetical protein	[S]
D5_0908	glucosamine-fructose-6-phosphate aminotransferase GlmS	[M]	D5_1524	conserved hypothetical protein	[S]
D5_0911	translation elongation factor aEF-2	[J]	D5_1525	conserved hypothetical transmembrane protein	Not in COGs
D5_0946	cobyric acid synthase CbiP	[H]	D5_1526	conserved hypothetical protein	[S]
D5_0947	ATP-dependent protease S16 family	[O]	D5_1528	hydrogenase nickel insertion protein HypA	[R]
D5_0954	ribose-phosphate diphosphokinase Prs	[F]	D5_1531	ATP-dependent DNA helicase UvrD/REP family	[L]
D5_0956	excinuclease ABC B subunit UvrB	[L]	D5_1533	conserved hypothetical protein	[S]
D5_0957	ammonium transporter Amt	[P]	D5_1537	hypothetical protein	[Unclassified]
D5_0958	nitrogen regulatory protein P-II GlnK	[E]	D5_1540	ATPase	[R]
D5_0959	excinuclease ABC A subunit UvrA	[L]	D5_1542	geranylgeranyl glyceryl phosphate synthase	[R]
D5_0961	transporter MIP family	[G]	D5_1543	ribosomal protein L40e Rpl40e	[J]
D5_0964	conserved hypothetical transmembrane protein	[S]	D5_1546	conserved hypothetical protein	[S]
D5_0967	hypothetical protein	[S]	D5_1549	nicotinamide-nucleotide adenyllyltransferase	[H]
D5_0988	hypothetical protein	[Unclassified]	D5_1553	conserved hypothetical protein	[S]
D5_0989	radical SAM domain-containing protein	[R]	D5_1555	glutamyl aminopeptidase PepA	[G]
D5_0993	transcriptional regulator	[K]	D5_1558	exonuclease	[L]
D5_0995	conserved hypothetical transmembrane protein	[Unclassified]	D5_1560	pantothenate synthase PanC	[S]
D5_0997	orotidine 5'-phosphate decarboxylase PyrF	[F]	D5_1561	dephospho-CoA kinase CoaE	[H]
D5_0998	cobalamin biosynthesis protein CbiM	[P]	D5_1562	ATP-binding protein	[R]
D5_0999	cobalt transport protein CbiN	[P]	D5_1566	CTP synthase PyrG	[F]
D5_1000	cobalt ABC transporter permease protein CbiQ	[P]	D5_1572	2,3-bisphosphoglycerate-independent phosphoglycerate mutase ApgM	[G]
D5_1001	cobalt ABC transporter ATP-binding protein CbiO	[P]	D5_1575	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase subunit C GatC	Not in COGs
D5_1002	riboflavin synthase RibC	[H]	D5_1588	homoserine <i>O</i> -acetyltransferase MetX	[E]
D5_1003	glycosyl transferase GT2 family	[M]	D5_1589	ribonuclease III Rnc	[K]
D5_1005	CoB--CoM heterodisulfide reductase subunit B HdrB	[C]	D5_1590	conserved hypothetical protein	Not in COGs
D5_1006	iron-sulfur cluster-binding protein	[C]	D5_1596	RNA-binding protein	[J]
D5_1007	2-furaldehyde phosphate synthase MfnB	[S]	D5_1597	creatinine amidohydrolase ArfB	[R]
D5_1008	inosine-5'-monophosphate dehydrogenase GuaB	[F]	D5_1599	conserved hypothetical protein	[S]
D5_1009	ribosomal protein L37Ae Rpl37ae	[J]	D5_1626	methenyltetrahydromethanopterin cyclohydrolase Mch	[H]
D5_1012	prefoldin beta subunit PfdB	[O]	D5_1635	<i>O</i> -acetylhomoserine/ <i>O</i> -acetylserine sulfhydrylase MetZ/CysK2	[E]
D5_1014	hisA/hisF family protein HisAF	[R]	D5_1641	ATPase	[R]
D5_1025	helicase	[L]	D5_1643	argininosuccinate lyase ArgH	[J]
D5_1026	excinuclease ABC C subunit UvrC	[L]	D5_1644	ribosomal protein S27ae Rps27ae	[J]
D5_1029	ABC transporter ATP-binding protein	[R]	D5_1645	ribosomal protein S24e Rps24e	[S]
D5_1031	ferredoxin	[C]	D5_1647	DNA-directed RNA polymerase subunit E" RpoE2	[K]
D5_1032	geranylgeranyl reductase family protein	[C]	D5_1648	DNA-directed RNA polymerase subunit E' RpoE1	[R]
D5_1033	UDP-glucose 4-epimerase GalE	[M]	D5_1649	conserved hypothetical protein	[J]
D5_1036	amidophosphoribosyltransferase PurF	[F]	D5_1651	ribosomal protein S6e Rps6e	[J]
D5_1037	peptidase U32	[O]	D5_1652	translation initiation factor IF-2	[F]
D5_1039	4Fe-4S iron sulfur cluster binding protein NifH/FrxC family	[P]	D5_1653	nucleoside diphosphate kinase Ndk	[J]
D5_1075	beta-ribofuranosylaminobenzene 5'-phosphate synthase MptG	[R]	D5_1654	ribosomal protein L24e Rpl24e	[J]
D5_1079	coenzyme F ₃₉₀ synthetase FtsA	[H]	D5_1655	ribosomal protein S28e Rps28e	[J]
D5_1084	hypothetical transmembrane protein	[R]	D5_1656	ribosomal protein L7Ae Rpl7ae	[E]
D5_1283	universal stress protein, UspA	[T]	D5_1657	threonine synthase ThrC	[S]
D5_1311	MatE efflux family protein	[V]	D5_1659	tryptophanyl-tRNA synthetase TrpS	[J]
D5_1316	hypothetical transmembrane protein	[S]	D5_1660	tRNA intron endonuclease EndA	[K]
D5_1461	NADPH-dependent F ₄₂₀ reductase NpdG	[R]	D5_1661	iron-dependent repressor	[Unclassified]
D5_1466	tRNA nucleotidyltransferase Cca	[J]			
D5_1468	3-dehydroquinate synthase AroB	[E]			

D5_1666	conserved hypothetical protein	[S]
D5_1667	conserved hypothetical transmembrane protein	Not in COGs
D5_1669	hydroxymethylglutaryl-CoA reductase (NADPH) HmgA	[I]
D5_1670	succinate-CoA ligase alpha subunit SucD	[C]
D5_1671	conserved hypothetical protein	[S]
D5_1672	3-dehydroquinate dehydratase type I AroD	[E]
D5_1677	HD domain-containing protein	[R]
D5_1678	3-polyprenyl-4-hydroxybenzoate decarboxylase UbiX	[H]
D5_1682	exosome complex RNA-binding protein Rrp42	[J]
D5_1683	exosome complex exonuclease Rrp41	[J]
D5_1684	exosome complex RNA-binding protein Rrp4	[J]
D5_1685	exosome subunit	[J]
D5_1686	proteasome alpha subunit PsmA	[O]
D5_1687	ribonuclease P subunit P14	[J]
D5_1694	archaea-specific RecJ-like exonuclease	[L]
D5_1697	NifU-like FeS cluster assembly scaffold protein	[C]
D5_1698	cysteine desulfurase NifS	[C]
D5_1700	cysteinyl-tRNA synthetase CysS	[E]
D5_1701	conserved hypothetical protein	[J]
D5_1702	serine <i>O</i> -acetyltransferase CysE	[R]
D5_1703	cysteine synthase CysKM1	[E]
D5_1704	endonuclease III Nth	[E]
D5_1705	3-phosphoshikimate 1-carboxyvinyltransferase AroA	[L]
D5_1708	valyl-tRNA synthetase ValS	[J]
D5_1712	conserved hypothetical transmembrane protein	Not in COGs
D5_1713	phenylalanyl-tRNA synthetase subunit beta PheT	[J]
D5_1714	conserved hypothetical protein	[S]
D5_1719	ribose 5-phosphate isomerase A RpiA	[G]
D5_1720	hypothetical protein	[S]
D5_1721	NAD(P)-dependent glycerol-1-phosphate dehydrogenase EgsA	[C]
D5_1722	prolyl-tRNA synthetase ProS	[J]
D5_1723	2-phospho-L-lactate guanylyltransferase CofC	[S]
D5_1724	phosphomethylpyrimidine kinase ThiD	[H]
D5_1732	carboxymuconolactone decarboxylase family protein	[S]
D5_1748	exosome subunit	[J]
D5_1749	ribosomal protein L15e Rpl15e	[J]
D5_1751	tungsten formylmethanofuran dehydrogenase subunit E FwdE	[C]
D5_1766	CBS domain-containing protein	[R]
D5_1768	carbohydrate kinase PfkB family	[G]
D5_1769	formylmethanofuran-tetrahydromethanopterin formyltransferase Ftr1	[C]
D5_1771	energy-converting hydrogenase A subunit Q EhaQ	[C]
D5_1772	energy-converting hydrogenase A subunit P EhaP	[C]
D5_1773	energy-converting hydrogenase A subunit O EhaO	[C]
D5_1774	energy-converting hydrogenase A subunit N EhaN	[C]
D5_1778	energy-converting hydrogenase A subunit J EhaJ	[C]
D5_1779	energy-converting hydrogenase A subunit I EhaI	[Unclassified]
D5_1780	energy-converting hydrogenase A subunit H EhaH	[S]
D5_1781	energy-converting hydrogenase A subunit G EhaG	[S]
D5_1782	energy-converting hydrogenase A subunit F EhaF	[S]
D5_1783	energy-converting hydrogenase A subunit E EhaE	[S]

D5_1784	energy-converting hydrogenase A subunit D EhaD	[S]
D5_1785	energy-converting hydrogenase A subunit C EhaC	[S]
D5_1786	energy-converting hydrogenase A subunit B EhaB	[S]
D5_1787	energy-converting hydrogenase A subunit A EhaA	[S]
D5_1791	HTH and cupin domain-containing protein	[K]
D5_1792	acetyl-CoA synthetase AcsA	[I]
D5_1796	glutamyl-tRNA ^{Gln} amidotransferase subunit D GatD	[E]
D5_1797	glutamyl-tRNA ^{Gln} amidotransferase subunit E GatE	[J]
D5_1799	ferrous iron transport protein B FeoB	[P]
D5_1809	hypothetical protein	Not in COGs
D5_1810	GMP synthase subunit B GuaAb	[F]
D5_1811	conserved hypothetical protein	[S]
D5_1812	conserved hypothetical protein	[M]
D5_1813	conserved hypothetical protein	[S]
D5_1815	RNA methylase	[L]
D5_1818	HTH domain-containing protein	[K]
D5_1819	conserved hypothetical protein	[S]
D5_1820	conserved hypothetical transmembrane protein	Not in COGs
D5_1821	conserved hypothetical transmembrane protein	Not in COGs
D5_1822	cell wall biosynthesis protein Mur ligase family	[M]
D5_1823	cell wall biosynthesis protein phospho- <i>N</i> -acetylmuramoyl-pentapeptide-transferase family	[M]
D5_1824	D-alanine--D-alanine ligase	[F]
D5_1827	nickel responsive transcriptional regulator NikR	[K]
D5_1828	conserved hypothetical protein	[Unclassified]
D5_1843	HEAT repeat-containing protein	[C]
D5_1844	isohomocitrate dehydrogenase AksF	[C]
D5_1847	acetylglutamate kinase ArgB	[E]
D5_1862	bifunctional ornithine acetyltransferase/ <i>N</i> -acetylglutamate synthase protein ArgJ	[E]
D5_1864	conserved hypothetical transmembrane protein	Not in COGs
D5_1865	conserved hypothetical protein	Not in COGs
D5_1867	nascent polypeptide-associated complex protein	[K]
D5_1883	cation/acetate symporter, actP	[E]
D5_1886	ACT domain-containing protein	[R]
D5_1888	hypothetical protein	Not in COGs
D5_1889	indolepyruvate ferredoxin oxidoreductase beta subunit IorB	[C]
D5_1890	indolepyruvate ferredoxin oxidoreductase alpha subunit IorA	[C]
D5_1899	succinate dehydrogenase/fumarate reductase iron-sulfur protein, sdhB	[C]
D5_1900	RNA methyltransferase TrmH family	[J]
D5_1902	deoxycytidine triphosphate deaminase Dcd	[F]
D5_1903	glycyl-tRNA synthetase GlyS	[J]
D5_1905	hydrolase TatD family	[R]
D5_1907	conserved hypothetical protein	[S]
D5_1908	conserved hypothetical transmembrane protein	[S]
D5_1910	ZPR1 zinc-finger domain-containing protein	[R]
D5_1916	uridylate kinase PyrH	[F]
D5_1918	hypothetical transmembrane protein	[S]
D5_1929	glycosyl transferase GT2 family	[M]
D5_1934	DNA primase DnaG	[L]
D5_1938	A ₁ A ₀ archaeal ATP synthase subunit D AhaD	[C]
D5_1939	A ₁ A ₀ archaeal ATP synthase subunit B AhaB	[C]
D5_1940	A ₁ A ₀ archaeal ATP synthase subunit A AhaA	[C]
D5_1941	A ₁ A ₀ archaeal ATP synthase subunit F AhaF	[C]

D5_1942	A ₁ A ₀ archaeal ATP synthase subunit C AhaC	[C]
D5_1943	A ₁ A ₀ archaeal ATP synthase subunit E AhaE	[C]
D5_1944	A ₁ A ₀ archaeal ATP synthase subunit K AhaK	[C]
D5_1945	A ₁ A ₀ archaeal ATP synthase subunit I AhaI	[C]
D5_1946	A1A0 archaeal ATP synthase subunit H AhaH	[C]
D5_1951	2-methylcitrate synthase/citrate synthase II PrpC/CitZ	[C]
D5_1952	fumarate hydratase FumA	[C]
D5_1953	conserved hypothetical protein	[Unclassified]
D5_1959	DNA-binding protein	[R]
D5_1960	HTH domain-containing protein	[K]
D5_1962	conserved hypothetical protein	Not in COGs
D5_1964	phosphoglycerate dehydrogenase SerA	[H]
D5_1965	conserved hypothetical protein	[R]
D5_1966	tRNA ^{His} guanylyltransferase ThgL	[S]
D5_1967	L-aspartate dehydrogenase	[R]
D5_1969	tRNA binding domain-containing protein	[R]
D5_1974	lactaldehyde dehydrogenase CofA	[C]
D5_1998	Xaa-Pro aminopeptidase	[E]
D5_1999	peptidase M50 family	[R]
D5_2000	methanogenesis marker protein 1	[S]
D5_2001	TfuA-like protein	[S]
D5_2004	CBS domain-containing protein	[R]
D5_2006	amidohydrolase	[F]
D5_2008	carbamoyl-phosphate synthase large subunit CarB	[E]
D5_2009	carbamoyl-phosphate synthase small subunit CarA	[E]
D5_2012	nicotinate-nucleotide pyrophosphorylase NadC	[H]
D5_2013	ribonuclease Z Rnz	[R]
D5_2015	quinolinate synthetase A protein NadA	[H]
D5_2019	homoserine O-acetyltransferase MetX3	[E]
D5_2020	conserved hypothetical protein	[L]
D5_2024	HEAT repeat-containing protein	[C]
D5_2026	DEAD/DEAH box helicase domain-containing protein	[R]
D5_2029	5-formaminoimidazole-4-carboxamide-1-β-D-ribofuranosyl 5'-monophosphate-formate ligase PurP	[R]
D5_2030	phosphodiesterase MJ0936 family	[R]
D5_2031	ribosomal RNA large subunit methyltransferase J, rrmJ	[J]
D5_2033	MCM family protein	[L]
D5_2034	translation initiation factor aIF-2 beta subunit	[J]
D5_2035	NMD3 family protein	[J]
D5_2036	tyrosyl-tRNA synthetase TyrS	[J]
D5_2038	thymidylate kinase Tmk	[F]
D5_2041	DNA mismatch repair ATPase MutS family	[L]
D5_2109	transcription initiation factor TFIIB Tfb	[K]
D5_2110	5,10-methylenetetrahydromethanopterin reductase Mer	[C]
D5_2111	radical SAM domain-containing protein	[R]
D5_2112	conserved hypothetical transmembrane protein	[Unclassified]
D5_2116	thiamine biosynthesis protein ThiS	[H]
D5_2117	PP-loop family protein	[D]
D5_2121	dihydropteroate synthase-related protein	[H]
D5_2122	pyruvate ferredoxin oxidoreductase gamma subunit PorC	[C]
D5_2123	pyruvate ferredoxin oxidoreductase delta subunit PorD	[C]
D5_2124	pyruvate ferredoxin oxidoreductase alpha subunit PorA	[C]
D5_2125	pyruvate ferredoxin oxidoreductase beta subunit PorB	[C]
D5_2126	pyruvate ferredoxin oxidoreductase-associated PorE	[C]
D5_2128	fumarate hydratase FumA	[C]

D5_2141	conserved hypothetical transmembrane protein	[S]
D5_2142	cobalamin biosynthesis protein CbiM	[P]
D5_2145	cobalt ABC transporter ATP-binding protein CbiO	[P]
D5_2146	hypothetical protein	[Unclassified]
D5_2147	ferrous iron transport protein A FeoA	[P]
D5_2200	translation elongation factor aEF-1 beta	[J]
D5_2202	delta 1-pyrroline-5-carboxylate synthetase	[R]
D5_2203	peptidyl-tRNA hydrolase	[S]
D5_2204	ATPase RIL	[R]
D5_2207	aspartate aminotransferase	[E]
D5_2208	DNA repair and recombination protein RadB	[L]
D5_2211	Sua5/YciO/YrdC/YwlC family translation factor	[J]
D5_2212	phosphatidylglycerophosphate synthase PgsA	[I]
D5_2213	conserved hypothetical protein	[S]
D5_2218	fructose 1,6-bisphosphatase Fbp	[G]
D5_2219	thiamine biosynthesis ATP pyrophosphatase ThiI	[H]
D5_2220	alanyl-tRNA synthetase AlaS	[J]
D5_2221	ribosomal protein L12P Rpl12p	[J]
D5_2222	acidic ribosomal protein P0 RplPO	[J]
D5_2223	ribosomal protein L1P Rpl1p	[J]
D5_2224	ribosomal protein L11P Rpl11p	[J]
D5_2225	ribosomal protein L24 family	[K]
D5_2226	preprotein translocase subunit SecE	[U]
D5_2227	cell division protein FtsZ	[D]
D5_2229	F ₄₂₀ -O:gamma-glutamyl ligase CofE	[S]
D5_2231	HD domain-containing protein	[R]
D5_2232	RNA-binding protein	[J]
D5_2233	conserved hypothetical protein	[R]
D5_2234	tryptophan-binding regulator TrpY	[R]
D5_2235	hydrogenase assembly chaperone HypC	[O]
D5_2236	glutathione-disulfide reductase Gor	[C]
D5_2237	cell wall biosynthesis protein UDP-glycosyltransferase family	[Unclassified]
D5_2241	prephenate dehydrogenase TyrA	[J]
D5_2242	cell division control protein Cdc48	[O]
D5_2244	methanogenesis marker protein 8 [S]	[S]
D5_2246	ATP-dependent DNA ligase DnII	[L]
D5_2251	phosphoglucosamine mutase GlmM	[G]
D5_2252	TPR repeat-containing protein	[R]
D5_2253	pyruvate formate-lyase-activating enzyme PflA	[O]
D5_2254	histidinol-phosphate aminotransferase HisC	[E]
D5_2255	acetyltransferase	[R]
D5_2256	UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	[M]
D5_2257	rubredoxin	[C]
D5_2258	phosphoglucosamine mutase GlmM	[G]
D5_2259	2,3-bisphosphoglycerate-independent phosphoglycerate mutase ApgM	[G]
D5_2260	conserved hypothetical transmembrane protein	[S]
D5_2269	ribosomal protein S3Ae Rps3ae	[J]
D5_2272	dinitrogenase iron-molybdenum cofactor biosynthesis protein	[Unclassified]
D5_2274	methylthioadenosine phosphorylase MtnP	[F]
D5_2275	conserved hypothetical protein	[S]
D5_2277	conserved hypothetical protein	[S]
D5_2279	cdc6 family replication initiation protein Cdc6-2	[L]
D5_2280	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase MptE	[R]
D5_2285	aminotransferase class V family	[E]
D5_2338	signal recognition particle receptor FtsY	[U]
D5_2339	prefoldin alpha subunit PfdA	[O]
D5_2340	ribosomal protein LX RplX	[J]
D5_2341	translation initiation factor aIF-6	[J]
D5_2342	ribosomal protein L31e Rpl31e	[J]
D5_2343	ribosomal protein L39e Rpl39e	[J]

D5_2345	DNA-binding protein	[R]
D5_2348	ribonuclease P subunit RPR2	[J]
D5_2352	GTP-binding protein	[R]
D5_2361	DNA topoisomerase I TopA	[L]
D5_2363	phosphoserine phosphatase SerB	[S]
D5_2364	TATA-box binding protein Tbp	[K]
D5_2367	adenylate cyclase CyaA	[F]
D5_2368	homocitrate synthase AksA	[E]
D5_2372	conserved hypothetical protein	[H]
D5_2373	flap endonuclease Fen	[L]
D5_2375	S-adenosyl-L-homocysteine hydrolase AhcY	[H]
D5_2378	glutamine synthetase GlnA	[E]
D5_2379	conserved hypothetical protein	[S]
D5_2381	conserved hypothetical protein	[S]
D5_2382	tungsten formylmethanofuran dehydrogenase subunit C FwdC	[C]
D5_2383	tungsten formylmethanofuran dehydrogenase subunit A FwdA	[C]
D5_2384	tungsten formylmethanofuran dehydrogenase subunit B FwdB	[C]
D5_2385	tungsten formylmethanofuran dehydrogenase subunit D FwdD	[C]
D5_2386	tungsten formylmethanofuran dehydrogenase subunit G FwdG	[C]
D5_2387	tungsten formylmethanofuran dehydrogenase subunit F FwdF	[C]
D5_2388	tungsten formylmethanofuran dehydrogenase subunit H FwdH	[Unclassified]
D5_2389	molybdopterin-guanine dinucleotide biosynthesis protein B MobB	[H]
D5_2391	formate dehydrogenase beta subunit FdhB	[C]
D5_2393	formate/nitrite transporter FdhC	[P]
D5_2394	formate dehydrogenase accessory protein, FdhD	[C]
D5_2395	3-hexulose-6-phosphate isomerase Phi1	[M]
D5_2396	transcriptional regulator LysR family	[K]
D5_2397	carbohydrate kinase PfkB family	[G]
D5_2398	thiamine biosynthesis protein ThiC	[H]
D5_2399	proteasome-activating nucleotidase	[O]
D5_2400	lysyl-tRNA synthetase LysS	[J]
D5_2402	CMP/dCMP deaminase	[F]
D5_2404	DNA polymerase large subunit DP2 PolD	[L]
D5_2405	anaerobic ribonucleoside-triphosphate reductase NrdD	[F]
D5_2410	ribosomal protein L21e Rpl21e	[J]
D5_2411	DNA-directed RNA polymerase subunit F RpoF	[S]
D5_2412	RNA-binding protein	[J]
D5_2414	SAM-dependent methyltransferase HemK-related	[J]
D5_2416	diaminopimelate epimerase DapF	[E]
D5_2417	diaminopimelate decarboxylase LysA	[E]
D5_2420	acetylornithine aminotransferase ArgD	[E]
D5_2421	peptidyl-prolyl cis-trans isomerase	[O]
D5_2423	MFS transporter	[G]
D5_2424	8-oxoguanine DNA-glycosylase Ogg	[L]
D5_2425	imidazoleglycerol-phosphate synthase cyclase subunit HisF	[E]
D5_2426	preprotein translocase subunit SecE	[U]
D5_2427	molybdenum cofactor biosynthesis protein C MoaC	[H]
D5_2428	pseudouridylylase synthase	[J]
D5_2429	signal recognition particle SRP54 protein	[U]
D5_2430	adenine phosphoribosyltransferase Apt	[F]
D5_2431	diphthamide biosynthesis protein	[J]
D5_2432	exosome complex RNA-binding protein Csl4	[J]
D5_2433	DNA-directed RNA polymerase subunit L RpoL	[K]
D5_2435	transcription factor S Tfs	[K]
D5_2452	F ₄₂₀ H ₂ oxidase FprA	[C]
D5_2454	peptidase M50 family	[M]
D5_2455	molybdopterin biosynthesis protein MoeA	[H]
D5_2456	phosphoribosylformylglycinamide (FGAM) synthase II PurL	[F]

D5_2457	isoleucyl-tRNA synthetase IleS	[J]
D5_2463	dihydromethanopterin reductase (acceptor) DmrX	[C]
D5_2464	serine hydroxymethyltransferase GlyA	[E]
D5_2467	CoB--CoM heterodisulfide reductase subunit A HdrA	[C]
D5_2469	DNA repair and recombination protein RadA	[L]
D5_2470	replication factor A	[L]
D5_2471	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	[M]
D5_2472	glycosyl transferase GT2 family	[R]
D5_2473	glycosyl transferase GT2 family	[R]
D5_2478	dTDP-glucose 4,6-dehydratase RfbB	[M]
D5_2479	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC	[M]
D5_2480	glucose-1-phosphate thymidyltransferase RfbA	[M]
D5_2483	dTDP-4-dehydrorhamnose reductase RfbD	[M]
D5_2484	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	[M]
D5_2485	UbiD family decarboxylase	[H]
D5_2486	phosphoribosylaminoimidazole carboxylase PurE	[F]
D5_2488	cell wall biosynthesis glycosyl transferase GT2 family	[M]
D5_2489	methanogenesis marker protein 11	[R]
D5_2490	6,7-dimethyl-8-ribityllumazine synthase, RibH	[H]
D5_2494	3-isopropylmalate dehydratase large subunit LeuC	[E]
D5_2498	cobalamin biosynthesis protein CbiX	[S]
D5_2500	conserved hypothetical protein	[R]
D5_2503	divalent cation transporter mgtE family	[P]
D5_2504	TrkA domain-containing protein	[S]
D5_2506	conserved hypothetical protein	[Unclassified]
D5_2507	DNA polymerase small subunit DP1 PolD1	[L]
D5_2508	fucose 1-phosphate aldolase FucA	[G]
D5_2510	conserved hypothetical protein	[S]

*only one gene from D5 for each gene family is represented

Table A.6.06 Predicted *Methanobrevibacter ruminantium* M1 genes conserved within the *Methanobrevibacter ruminantium* clade

Locus_tag	Predicted gene product	COG category
MRU_RS00630	hypothetical protein	[S]
MRU_RS00655	hypothetical protein	Not in COGs
MRU_RS00920	protein disulfide isomerase	[C]
MRU_RS00945	4Fe-4S ferredoxin-binding domain- containing protein	[C]
MRU_RS00980	hypothetical protein	Not in COGs
MRU_RS01255	hypothetical protein	[unclassified]
MRU_RS01265	hypothetical protein	Not in COGs
MRU_RS01270	hypothetical protein	[R]
MRU_RS01300	hypothetical protein	[unclassified]
MRU_RS01360	adhesin-like protein	[P]
MRU_RS01675	adhesin-like protein	Not in COGs
MRU_RS01680	adhesin-like protein	Not in COGs
MRU_RS01685	hypothetical protein	Not in COGs
MRU_RS01725	hypothetical protein	Not in COGs
MRU_RS01780	hypothetical protein	[S]
MRU_RS02075	Na ⁺ -dependent transporter SNF family	[R]
MRU_RS02080	hypothetical protein	Not in COGs
MRU_RS02090	hypothetical protein	Not in COGs
MRU_RS02095	hypothetical protein	Not in COGs
MRU_RS02180	hypothetical protein	Not in COGs
MRU_RS02220	7-cyano-7-deazaguanine synthase	[R]

MRU_RS02225	queuosine biosynthesis protein QueD	[H]	MRU_RS05650	hypothetical protein	Not in COGs
MRU_RS02230	7-cyano-7- deazaguanosine biosynthesis protein QueE	[O]	MRU_RS05695	restriction endonuclease	[V]
MRU_RS02545	hypothetical protein	Not in COGs	MRU_RS05700	hypothetical protein	Not in COGs
MRU_RS02685	hypothetical protein	[S]	MRU_RS05740	hypothetical protein	[S]
MRU_RS02750	hypothetical protein	[unclassified]	MRU_RS05800	hypothetical protein	Not in COGs
MRU_RS02770	hypothetical protein	[unclassified]	MRU_RS05900	CRISPR-associated protein	
MRU_RS02875	hypothetical protein	[I]		TIGR02710 family	[unclassified]
MRU_RS02990	peptidase U32	[O]	MRU_RS05955	hypothetical protein	Not in COGs
MRU_RS03050	hypothetical protein	Not in COGs	MRU_RS05965	hypothetical protein	[S]
MRU_RS03090	hypothetical protein	Not in COGs	MRU_RS06085	hypothetical protein	Not in COGs
MRU_RS03095	hypothetical protein	Not in COGs	MRU_RS06095	adenosylcobinamide	
MRU_RS03150	mechanosensitive ion channel protein	[M]		amidohydrolase CbiZ	[S]
MRU_RS03165	hypothetical protein	Not in COGs	MRU_RS06100	hypothetical protein	[unclassified]
MRU_RS03300	transcriptional regulator	[K]	MRU_RS06110	cobalt ABC transporter permease	Not in COGs
MRU_RS03385	PP-loop family protein	[R]	MRU_RS06140	hypothetical protein	Not in COGs
MRU_RS03490	2-methylcitrate dehydratase	[R]	MRU_RS06155	hypothetical protein	Not in COGs
MRU_RS03520	hypothetical protein	Not in COGs	MRU_RS06165	hypothetical protein	[unclassified]
MRU_RS03600	ATP-grasp domain-containing protein	[R]	MRU_RS06170	hypothetical protein	[unclassified]
MRU_RS03635	hypothetical protein	[unclassified]	MRU_RS06185	hypothetical protein	[unclassified]
MRU_RS03645	hypothetical protein	[unclassified]	MRU_RS06220	hypothetical protein	[unclassified]
MRU_RS03695	RNA-binding protein	[J]	MRU_RS06390	molybdopterin-guanine dinucleotide biosynthesis protein A MobA2	[H]
MRU_RS03700	hypothetical protein	Not in COGs	MRU_RS06590	hypothetical protein	Not in COGs
MRU_RS03705	hypothetical protein	Not in COGs	MRU_RS06735	hypothetical protein	[unclassified]
MRU_RS03710	hypothetical protein	Not in COGs	MRU_RS06790	adhesin-like protein	[unclassified]
MRU_RS03715	hypothetical protein	Not in COGs	MRU_RS06925	hypothetical protein	Not in COGs
MRU_RS03735	hypothetical protein	Not in COGs	MRU_RS07080	adhesin-like protein	[unclassified]
MRU_RS03740	hypothetical protein	Not in COGs	MRU_RS07145	NAD synthetase	[H]
MRU_RS03980	hypothetical protein	[unclassified]	MRU_RS07295	hypothetical protein	[unclassified]
MRU_RS03985	ion transporter	[P]	MRU_RS07345	hypothetical protein	[R]
MRU_RS04070	hypothetical protein	Not in COGs	MRU_RS07465	hypothetical protein	[S]
MRU_RS04075	hypothetical protein	Not in COGs	MRU_RS07495	hypothetical protein	[E]
MRU_RS04080	hypothetical protein	Not in COGs	MRU_RS07515	hypothetical protein	Not in COGs
MRU_RS04110	MarR family transcriptional regulator	[K]	MRU_RS07540	hydrolase alpha/beta fold family	[R]
MRU_RS04470	precorrin-2 C20-methyltransferase CbiL	[H]	MRU_RS07545	pyrroline-5-carboxylate reductase ProC	[E]
MRU_RS04475	cobalamin biosynthesis protein CbiD	[H]	MRU_RS07675	hypothetical protein	Not in COGs
MRU_RS04485	cobalamin biosynthesis protein CbiG	[H]	MRU_RS07715	hypothetical protein	[M]
MRU_RS04490	precorrin-3B C17-methyltransferase	[H]	MRU_RS07815	hypothetical protein	[unclassified]
MRU_RS04495	precorrin-6X reductase CbiJ	[H]	MRU_RS07890	6-O-methylguanine DNA methyltransferase Ogt	[L]
MRU_RS04500	precorrin-6Y C5,15-methyltransferase (decarboxylating) CbiET	[H]		hypothetical protein	Not in COGs
MRU_RS04505	cobyrinic acid a,c-diamide synthase	[H]	MRU_RS07965	hypothetical protein	Not in COGs
MRU_RS04510	precorrin-8X methylmutase	[H]	MRU_RS07990	hypothetical protein	Not in COGs
MRU_RS04515	sirohydrochlorin cobaltochelata[H]		MRU_RS08030	adhesin-like protein with transglutaminase domain	[E]
MRU_RS04540	hypothetical protein	Not in COGs		hypothetical protein	[unclassified]
MRU_RS04555	hypothetical protein	[R]	MRU_RS08035	hypothetical protein	[unclassified]
MRU_RS04705	SAM-dependent methyltransferase	[R]	MRU_RS08285	hypothetical protein	[unclassified]
MRU_RS04720	hypothetical protein	Not in COGs	MRU_RS08385	peptidase S49	[O]
MRU_RS04760	hypothetical protein	Not in COGs	MRU_RS08410	hypothetical protein	[S]
MRU_RS04875	hypothetical protein	[unclassified]	MRU_RS08490	hypothetical protein	[R]
MRU_RS04900	hypothetical protein	Not in COGs	MRU_RS08530	NADH pyrophosphatase NudC	[L]
MRU_RS04910	hypothetical protein	Not in COGs	MRU_RS08655	heat-shock protein Hsp20/alpha crystallin family	[O]
MRU_RS05140	hypothetical protein	Not in COGs	MRU_RS08725	cell wall biosynthesis protein Mur ligase family	[M]
MRU_RS05165	hypothetical protein	Not in COGs	MRU_RS08760	hypothetical protein	Not in COGs
MRU_RS05220	RNA methylase	[R]	MRU_RS08810	ArsR family transcriptional regulator	[K]
MRU_RS05245	hypothetical protein	Not in COGs		hypothetical protein	Not in COGs
MRU_RS05460	hypothetical protein	Not in COGs	MRU_RS08815	hypothetical protein	Not in COGs
MRU_RS05465	hypothetical protein	[R]	MRU_RS08970	hypothetical protein	Not in COGs
MRU_RS05520	hypothetical protein	Not in COGs	MRU_RS08975	hypothetical protein	Not in COGs
MRU_RS05540	hypothetical protein	[S]	MRU_RS08985	hypothetical protein	Not in COGs
MRU_RS05555	DNA double-strand break repair protein Rad50	[L]	MRU_RS09185	hypothetical protein	[unclassified]
MRU_RS05570	hypothetical protein	[L]	MRU_RS09225	hypothetical protein	Not in COGs
MRU_RS05630	hypothetical protein	Not in COGs	MRU_RS09370	hypothetical protein	Not in COGs
			MRU_RS09420	hypothetical protein	[unclassified]
			MRU_RS09430	hypothetical protein	[unclassified]
			MRU_RS09455	hypothetical protein	Not in COGs
			MRU_RS09510	hypothetical protein	[unclassified]
			MRU_RS09740	hypothetical protein	Not in COGs
			MRU_RS09875	hypothetical protein	[S]
			MRU_RS09920	hypothetical protein	Not in COGs
			MRU_RS09965	hypothetical protein	[unclassified]
			MRU_RS10040	energy-converting hydrogenase B subunit J EhbJ	[unclassified]

MRU_RS10055	energy-converting hydrogenase B subunit G EhbG	[unclassified]
MRU_RS10090	hypothetical protein	[R]
MRU_RS10115	hypothetical protein	[P]
MRU_RS10255	6-carboxyhexanoate--CoA ligase	[H]
MRU_RS10260	8-amino-7-oxononanoate synthase	[H]
MRU_RS10315	adhesin-like protein	Not in COGs
MRU_RS10380	hypothetical protein	Not in COGs
MRU_RS10410	hypothetical protein	[S]
MRU_RS10425	formate dehydrogenase alpha chain FdhA2	[C]
MRU_RS10475	adenosylmethionine--8-amino-7-oxononanoate aminotransferase BioA	[H]
MRU_RS10485	dithiobiotin synthetase	[H]
MRU_RS10635	hypothetical protein	Not in COGs
MRU_RS10645	hypothetical protein	[R]
MRU_RS10730	hypothetical protein	Not in COGs
MRU_RS10875	NADH oxidase	[C]
MRU_RS11055	hypothetical protein	[unclassified]
MRU_RS11060	hypothetical protein	[unclassified]
MRU_RS11095	hypothetical protein	[H]
MRU_RS11185	hypothetical protein	[unclassified]
MRU_RS11200	asparagine synthase (glutamine-hydrolyzing) AsnB	[E]
MRU_RS11210	hypothetical protein	Not in COGs
MRU_RS11245	hypothetical protein	[L]
MRU_RS11250	hypothetical protein	[R]
MRU_RS11260	type II restriction endonuclease	[unclassified]

*only one gene from M1 for each gene family is represented

Table A.6.07 Predicted *Methanobrevibacter* sp. AbM4 genes conserved within the *Methanobrevibacter wolinii* clade

Locus tag	Predicted gene product	COG category
2540853212	flavodoxin domain-containing protein	[C]
2540853237	PQQ repeat-containing cell surface protein	[S]
2540853282	Protein of unknown function (DUF4013)	[unclassified]
2540853310	ABC transporter permease protein	[V]
2540853362	hypothetical protein	[T]
2540853369	glutamine amidotransferase class II	[R]
2540853371	hypothetical protein	[unclassified]
2540853438	OB fold nucleic acid binding domain-containing protein	[R]
2540853473	NADPH-dependent FMN reductase	[R]
2540853489	transposase	Not in COGs
2540853495	hypothetical protein	Not in COGs
2540853502	adhesin-like protein	[unclassified]
2540853507	hypothetical protein	[unclassified]
2540853509	dolichyl-phosphate-mannose-protein mannosyltransferase	[unclassified]
2540853511	dolichyl-phosphate-mannose-protein mannosyltransferase	[unclassified]
2540853512	hypothetical protein	Not in COGs
2540853516	hexapeptide repeat-containing acetyltransferase	[R]
2540853526	methanogenesis marker protein 5	[S]
2540853571	aspartate racemase Asp	[M]
2540853577	hypothetical protein	Not in COGs
2540853578	hypothetical protein	[D]
2540853579	hypothetical protein	Not in COGs

2540853582	adhesin-like protein	Not in COGs
2540853597	hypothetical protein	Not in COGs
2540853602	hypothetical protein	[unclassified]
2540853610	MFS transporter	[P]
2540853623	prpD 2-methylcitrate dehydratase PrpD	[R]
2540853628	hypothetical protein	Not in COGs
2540853629	hypothetical protein	Not in COGs
2540853639	hypothetical protein	Not in COGs
2540853642	hypothetical protein	Not in COGs
2540853646	uncharacterized conserved protein	[S]
2540853654	hypothetical protein	[unclassified]
2540853661	putative heavy-metal-binding transporter	[M]
2540853686	heat shock protein Hsp20	[R]
2540853689	heat shock protein Hsp20	[O]
2540853693	hypothetical protein	[unclassified]
2540853707	predicted ATP-utilizing enzyme (ATP-grasp superfamily)	[R]
2540853721	hsdS2 type I restriction-modification system S subunit HsdS2	[V]
2540853723	hsdS3 type I restriction-modification system S subunit HsdS3	[V]
2540853731	deoxyribose-phosphate aldolase DeoC	[F]
2540853735	Short repeat of unknown function (DUF308)	[unclassified]
2540853741	hypothetical protein	Not in COGs
2540853753	hypothetical protein	[unclassified]
2540853769	transcriptional regulator, TetR family	[K]
2540853772	two-component system histidine kinase	[T]
2540853777	adhesin-like protein	[R]
2540853780	adhesin-like protein with PMBR domains	[unclassified]
2540853781	zinc-ribbon domain	[S]
2540853784	uncharacterized protein conserved in bacteria	Not in COGs
2540853787	hypothetical protein	Not in COGs
2540853793	adhesin-like protein	[unclassified]
2540853810	hypothetical protein	Not in COGs
2540853818	hypothetical protein	[unclassified]
2540853827	hypothetical protein	Not in COGs
2540853833	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	[C]
2540853834	hypothetical protein	Not in COGs
2540853835	TauE family transporter	[R]
2540853841	SAM-dependent methyltransferase	[R]
2540853853	adhesin-like protein	[unclassified]
2540853854	adhesin-like protein	Not in COGs
2540853855	adhesin-like protein	[unclassified]
2540853868	ATPase	[R]
2540853871	TPR domain-containing protein	[R]
2540853873	TPR domain-containing protein	[R]
2540853874	TPR domain-containing protein	[R]
2540853875	TPR domain-containing protein	[R]
2540853876	TPR domain-containing protein	[R]
2540853882	hypothetical protein	Not in COGs
2540853885	flavoprotein HI0933 family	[R]
2540853891	pyrroline-5-carboxylate reductase ProC	[E]
2540853898	acetyl esterase	[R]
2540853942	hypothetical protein	Not in COGs
2540853945	hypothetical protein	Not in COGs
2540853947	hypothetical protein	Not in COGs
2540853956	adenosylcobinamide amidohydrolase CbiZ	[H]
2540853959	uncharacterized conserved protein	[S]
2540853966	hypothetical protein	[unclassified]

2540853992	hypothetical protein	[S]
2540854005	double zinc ribbon	[S]
2540854007	asnB asparagine synthase	[E]
2540854015	oxidoreductase aldo/keto reductase family	[R]
2540854017	adhesin-like protein	[unclassified]
2540854030	ogt 6- <i>O</i> -methylguanine DNA methyltransferase Ogt	[L]
2540854031	hypothetical protein	Not in COGs
2540854033	hypothetical protein	Not in COGs
2540854043	predicted integral membrane protein	[S]
2540854044	predicted integral membrane protein	[S]
2540854045	adhesin-like protein	[unclassified]
2540854049	adhesin-like protein	[unclassified]
2540854051	MFS transporter	[P]
2540854052	transcriptional regulator, TetR family	[K]
2540854058	hypothetical protein	Not in COGs
2540854064	adhesin-like protein with transglutaminase and PMBR domains	[E]
2540854067	hypothetical protein	Not in COGs
2540854068	hypothetical protein	Not in COGs
2540854070	cell wall biosynthesis protein Mur ligase family	[M]
2540854076	hypothetical protein	Not in COGs
2540854077	DNA double-strand break repair protein Rad50	[L]
2540854080	NurA domain-containing protein	[S]
2540854084	hypothetical protein	Not in COGs
2540854101	carbohydrate kinase PfkB family	[G]
2540854110	Protein of unknown function (DUF3194)	[unclassified]
2540854128	hypothetical protein	Not in COGs
2540854135	energy-converting hydrogenase A subunit R EhaR	[S]
2540854154	hypothetical protein	[unclassified]
2540854163	hypothetical protein	[unclassified]
2540854188	hypothetical protein	Not in COGs
2540854191	uncharacterized protein conserved in archaea	[S]
2540854209	hypothetical protein	[M]
2540854226	hypothetical protein	Not in COGs
2540854228	hydrolase HAD superfamily	[R]
2540854231	hypothetical protein	Not in COGs
2540854234	Domain of unknown function (DUF955)	[E]
2540854239	hydrolase HAD superfamily	[R]
2540854243	hydrolase HAD superfamily	[R]
2540854244	hydrolase HAD superfamily	[R]
2540854247	hypothetical protein	Not in COGs
2540854249	hypothetical protein	Not in COGs
2540854262	hypothetical protein	Not in COGs
2540854271	hypothetical protein	Not in COGs
2540854323	uncharacterized conserved protein (DUF2304)	Not in COGs
2540854368	short repeat of unknown function (DUF308)	[S]
2540854383	hypothetical protein	Not in COGs
2540854396	adhesin-like protein	[P]
2540854413	hypothetical protein	Not in COGs
2540854414	hypothetical protein	Not in COGs
2540854482	hypothetical protein	[unclassified]
2540854485	hypothetical protein	[unclassified]
2540854509	polysaccharide biosynthesis protein	[R]
2540854538	CAAX amino terminal protease family protein	[unclassified]
2540854548	SIR2 family protein	[K]
2540854560	mechanosensitive ion channel protein	[P]
2540854565	zinc-ribbon domain	[O]

2540854574	uncharacterized protein conserved in archaea	[S]
2540854575	flavodoxin	[C]
2540854576	hypothetical protein	[R]
2540854593	peptidase U32 family	[O]
2540854595	hypothetical protein	[L]
2540854597	trpD anthranilate phosphoribosyltransferase	[E]
2540854598	trpA tryptophan synthase, alpha chain	[E]
2540854600	trpF phosphoribosylanthranilate isomerase	[E]
2540854601	trpC indole-3-glycerol phosphate synthase	[E]
2540854603	trpE anthranilate synthase, component I"	[E]
2540854604	hypothetical protein	[unclassified]
2540854615	NADP oxidoreductase coenzyme F ₄₂₀ -dependent	[I]
2540854625	ppx exopolyphosphatase Ppx	[F]
2540854633	phosphate uptake regulator PhoU1	[P]
2540854639	hypothetical protein	[unclassified]
2540854643	hypothetical protein	[unclassified]
2540854649	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	[C]
2540854660	CAAX amino terminal protease family protein	[R]
2540854722	metallophosphoesterase	[R]
2540854729	hypothetical protein	Not in COGs
2540854730	metallo-beta-lactamase superfamily protein	[R]
2540854754	hypothetical protein	[unclassified]
2540854755	hypothetical protein	[unclassified]
2540854763	CRISPR-associated protein Cas4	[L]
2540854787	energy-converting hydrogenase B subunit J EhbJ	[unclassified]
2540854802	acetyltransferase GNAT family	[R]
2540854809	EamA-like transporter family protein	[P]
2540854810	EamA-like transporter family protein	[P]
2540854812	hypothetical protein	[unclassified]
2540854893	predicted membrane protein	[S]
2540854907	predicted membrane protein	[S]
2540854915	zinc-ribbon domain	[T]
2540854923	cobalamin biosynthesis protein CbiG	[H]
2540854924	cobalamin biosynthesis protein CbiB	[H]

*only one gene from AbM4 for each gene family is represented

Table A.6.08 Predicted *Methanobrevibacter* sp. D5 genes unique to the *Methanobrevibacter* sp. D5 genome

Locus_tag	Predicted gene product	COG category
D5_0009	hypothetical transmembrane protein	[S]
D5_0020	hypothetical protein	Not in COGs
D5_0034	hypothetical secreted protein	[unclassified]
D5_0035	hypothetical transmembrane protein	Not in COGs
D5_0036	adhesin-like protein	[unclassified]
D5_0038	adhesin-like protein	[unclassified]
D5_0051	adhesin-like protein	[unclassified]
D5_0060	hypothetical protein	Not in COGs
D5_0073	hypothetical protein	[R]
D5_0082	hypothetical protein	[unclassified]
D5_0083	hypothetical protein	[unclassified]
D5_0093	pyridoxamine 5'-phosphate oxidase family protein	[S]

D5_0110	hypothetical protein	Not in COGs
D5_0111	adhesin-like protein	[unclassified]
D5_0115	NADH oxidase Nox	[R]
D5_0123	hypothetical protein	[unclassified]
D5_0124	hypothetical protein	[unclassified]
D5_0125	hypothetical protein	Not in COGs
D5_0181	hypothetical protein	[unclassified]
D5_0198	hypothetical protein	Not in COGs
D5_0211	conserved hypothetical secreted protein	[unclassified]
D5_0218	adhesin-like protein	[unclassified]
D5_0219	adhesin-like protein	[unclassified]
D5_0223	glycosyl transferase GT2 family	[M]
D5_0262	adhesin-like protein	Not in COGs
D5_0306	hypothetical protein	Not in COGs
D5_0340	hydrolase alpha/beta fold family	[R]
D5_0344	aldo/keto reductase family protein	[R]
D5_0345	aldo/keto reductase family protein	[R]
D5_0346	aldo/keto reductase family protein	[R]
D5_0354	hypothetical protein	[S]
D5_0355	hypothetical protein	Not in COGs
D5_0378	conserved hypothetical secreted protein	Not in COGs
D5_0387	hypothetical protein	[R]
D5_0392	adhesin-like protein with cysteine protease domain	Not in COGs
D5_0393	adhesin-like protein with cysteine protease domain	[E]
D5_0394	adhesin-like protein	[E]
D5_0431	hypothetical protein	[J]
D5_0432	hypothetical transmembrane protein	[G]
D5_0433	hypothetical protein	Not in COGs
D5_0437	hypothetical protein	Not in COGs
D5_0438	hypothetical protein	Not in COGs
D5_0443	transposase	[L]
D5_0445	hypothetical transmembrane protein	Not in COGs
D5_0449	hypothetical transmembrane protein	[unclassified]
D5_0450	hypothetical transmembrane protein	Not in COGs
D5_0451	hypothetical protein	Not in COGs
D5_0452	adhesin-like protein	[unclassified]
D5_0454	hypothetical protein	Not in COGs
D5_0455	hypothetical protein	Not in COGs
D5_0456	hypothetical protein	Not in COGs
D5_0457	hypothetical transmembrane protein	[S]
D5_0458	adhesin-like protein	Not in COGs
D5_0459	adhesin-like protein	[M]
D5_0460	conserved hypothetical transmembrane protein	[S]
D5_0462	glycosyl transferase GT2 family	[M]
D5_0463	glycosyl transferase	[M]
D5_0476	hypothetical protein	[L]
D5_0478	adhesin-like protein	Not in COGs
D5_0480	hypothetical protein	[L]
D5_0482	non-ribosomal surfactin synthetase SrfAA	[Q]
D5_0483	hypothetical protein	Not in COGs
D5_0484	glycosyl transferase GT2 family	[M]
D5_0486	hypothetical protein	Not in COGs
D5_0487	hypothetical protein	[unclassified]
D5_0488	glycosyl transferase GT2 family	[M]
D5_0491	hypothetical protein	Not in COGs
D5_0492	hypothetical protein	[unclassified]
D5_0494	hypothetical protein	[M]
D5_0495	hypothetical protein	[unclassified]
D5_0496	hypothetical protein	Not in COGs
D5_0497	transposase	[unclassified]
D5_0499	acetyltransferase	[R]
D5_0502	hypothetical transmembrane protein	Not in COGs
D5_0507	phosphatase PAP2 family	[I]
D5_0512	type I restriction-modification enzyme S subunit HsdS	[V]
D5_0513	type I restriction-modification system M subunit, HsdM	[V]
D5_0514	hypothetical protein	[unclassified]
D5_0528	conserved hypothetical secreted protein	Not in COGs
D5_0529	hypothetical protein	Not in COGs
D5_0530	hypothetical transmembrane protein	Not in COGs
D5_0541	hypothetical protein	Not in COGs

D5_0605	conserved hypothetical protein	[R]
D5_0613	hypothetical protein	[E]
D5_0618	exodeoxyribonuclease VII large subunit, XseA	[L]
D5_0637	phosphodiesterase, MJ0936 family	[R]
D5_0640	adhesin-like protein	Not in COGs
D5_0645	conserved hypothetical transmembrane protein	Not in COGs
D5_0671	conserved hypothetical protein	[L]
D5_0715	adhesin-like protein with cysteine protease domain	[unclassified]
D5_0716	conserved hypothetical transmembrane protein	Not in COGs
D5_0756	ATPase	Not in COGs
D5_0767	acetyltransferase GNAT family	[K]
D5_0788	hypothetical protein	[K]
D5_0793	MATE efflux family protein	[V]
D5_0798	nitroreductase family protein	[C]
D5_0821	adhesin-like protein	[M]
D5_0826	hypothetical protein	[unclassified]
D5_0827	hypothetical protein	Not in COGs
D5_0828	ROK family protein	[K]
D5_0841	sialic acid synthase	[M]
D5_0842	UDP- <i>N</i> -acetylglucosamine 2-epimerase	[M]
D5_0843	oxidoreductase domain-containing protein	[R]
D5_0844	oxidoreductase GFO/IDH/MOCA family	[R]
D5_0845	cytidyltransferase-related domain-containing protein	[M]
D5_0846	hypothetical protein	[R]
D5_0847	aminotransferase DegT/DnrJ/EryC1/StrS family	[M]
D5_0849	glycosyl transferase	[unclassified]
D5_0850	hypothetical protein	[unclassified]
D5_0857	hypothetical protein	Not in COGs
D5_0858	hypothetical protein	Not in COGs
D5_0861	hypothetical protein	Not in COGs
D5_0869	hypothetical protein	Not in COGs
D5_0876	hypothetical protein	[unclassified]
D5_0884	polysaccharide biosynthesis protein	[R]
D5_0885	hypothetical protein	Not in COGs
D5_0886	conserved hypothetical protein	[M]
D5_0888	hypothetical protein	Not in COGs
D5_0890	conserved hypothetical protein	[unclassified]
D5_0891	conserved hypothetical protein	[unclassified]
D5_0895	hypothetical protein	[C]
D5_0897	hypothetical protein	[T]
D5_0898	hypothetical protein	[M]
D5_0900	hypothetical protein	Not in COGs
D5_0901	hypothetical protein	[L]
D5_0902	hypothetical protein	Not in COGs
D5_0905	hypothetical protein	[M]
D5_0907	hypothetical protein	[T]
D5_0910	hypothetical protein	[O]
D5_0913	hypothetical protein	Not in COGs
D5_0917	hypothetical protein	Not in COGs
D5_0918	hypothetical protein	Not in COGs
D5_0922	hypothetical protein	Not in COGs
D5_0925	hypothetical protein	Not in COGs
D5_0926	hypothetical protein	[unclassified]
D5_0927	hypothetical protein	Not in COGs
D5_0928	hypothetical protein	[M]
D5_0962	acetyltransferase GNAT family	[K]
D5_0963	hypothetical protein	Not in COGs
D5_0965	adhesin-like protein	Not in COGs
D5_0971	adhesin-like protein	[M]
D5_0973	adhesin-like protein	[unclassified]
D5_0974	adhesin-like protein with cysteine protease domain	[O]
D5_0976	adhesin-like protein	[unclassified]
D5_0978	adhesin-like protein	[unclassified]
D5_0979	adhesin-like protein	[unclassified]
D5_1015	hypothetical transmembrane protein	[S]
D5_1016	CAAX amino terminal protease family protein	[R]
D5_1020	hypothetical protein	Not in COGs

D5_1022	hypothetical protein	Not in COGs
D5_1023	TPR repeat-containing protein	[R]
D5_1024	hypothetical protein	Not in COGs
D5_1035	hypothetical protein	Not in COGs
D5_1038	hypothetical protein	Not in COGs
D5_1040	phosphatidylglycerophosphate synthase, PgsA	[I]
D5_1041	hypothetical transmembrane protein	Not in COGs
D5_1042	succinate dehydrogenase/fumarate reductase flavoprotein subunit, SdhA2	[C]
D5_1044	succinate dehydrogenase/fumarate reductase iron-sulfur protein, SdhB1	[C]
D5_1049	hypothetical transmembrane protein	[G]
D5_1054	short-chain dehydrogenase family protein	[I]
D5_1063	hypothetical protein	[unclassified]
D5_1066	hypothetical transmembrane protein	[V]
D5_1071	adhesin-like protein	[R]
D5_1087	hypothetical transmembrane protein	[unclassified]
D5_1101	hypothetical transmembrane protein	Not in COGs
D5_1105	hypothetical protein	[unclassified]
D5_1106	hypothetical protein	Not in COGs
D5_1107	hypothetical protein	Not in COGs
D5_1108	hypothetical protein	Not in COGs
D5_1109	hypothetical protein	Not in COGs
D5_1110	hypothetical protein	Not in COGs
D5_1112	hypothetical protein	Not in COGs
D5_1113	hypothetical protein	Not in COGs
D5_1118	hypothetical protein	Not in COGs
D5_1119	hypothetical transmembrane protein	[unclassified]
D5_1132	hypothetical transmembrane protein	[unclassified]
D5_1147	hypothetical protein	Not in COGs
D5_1151	hypothetical protein	[H]
D5_1154	hypothetical protein	[C]
D5_1157	WD40 repeat-containing protein	Not in COGs
D5_1158	hypothetical protein	Not in COGs
D5_1159	hypothetical protein	Not in COGs
D5_1160	hypothetical protein	Not in COGs
D5_1162	hypothetical protein	[R]
D5_1165	ADP-ribosylglycohydrolase family protein	[O]
D5_1166	hypothetical protein	Not in COGs
D5_1167	hypothetical protein	Not in COGs
D5_1168	hypothetical protein mru	Not in COGs
D5_1169	conserved hypothetical protein	Not in COGs
D5_1174	hypothetical protein	Not in COGs
D5_1178	hypothetical protein	Not in COGs
D5_1180	hypothetical protein	[I]
D5_1182	hypothetical protein	Not in COGs
D5_1183	conserved hypothetical protein	[S]
D5_1185	conserved hypothetical protein	Not in COGs
D5_1187	hypothetical protein	Not in COGs
D5_1188	hypothetical protein	Not in COGs
D5_1190	hypothetical protein	Not in COGs
D5_1192	hypothetical protein	Not in COGs
D5_1193	hypothetical protein	Not in COGs
D5_1194	hypothetical protein	Not in COGs
D5_1195	hypothetical protein	[C]
D5_1197	hypothetical protein	[S]
D5_1200	hypothetical protein	[unclassified]
D5_1207	ion transport protein	[P]
D5_1212	hypothetical protein	Not in COGs
D5_1215	hypothetical protein	Not in COGs
D5_1216	conserved hypothetical protein	[L]
D5_1217	hypothetical protein	Not in COGs
D5_1218	ATPase	[V]
D5_1219	hypothetical protein	Not in COGs
D5_1222	DNA-cytosine methyltransferase, Dcm	[L]
D5_1223	hypothetical protein	Not in COGs
D5_1224	hypothetical protein	[D]
D5_1226	hypothetical protein	Not in COGs
D5_1227	hypothetical protein	Not in COGs
D5_1229	hypothetical protei	Not in COGs
D5_1230	hypothetical transmembrane protein	Not in COGs
D5_1233	hypothetical protein	Not in COGs
D5_1235	exodeoxyribonuclease VII large subunit, XseA	[L]

D5_1237	hypothetical protein	Not in COGs
D5_1238	hypothetical protein	[D]
D5_1239	hypothetical protein	Not in COGs
D5_1240	ATP-dependent DNA helicase UvrD/REP family	Not in COGs
D5_1244	TPR domain-containing protein	[R]
D5_1245	hypothetical protein	Not in COGs
D5_1246	hypothetical protein	Not in COGs
D5_1247	ATP-dependent DNA helicase UvrD/REP family	[L]
D5_1249	hypothetical transmembrane protein	Not in COGs
D5_1250	hypothetical protein	Not in COGs
D5_1251	hypothetical protein	Not in COGs
D5_1252	hypothetical protein	Not in COGs
D5_1253	hypothetical protein	Not in COGs
D5_1254	hypothetical protein	Not in COGs
D5_1256	hypothetical protein	Not in COGs
D5_1259	hypothetical protein	[D]
D5_1260	hypothetical protein	[S]
D5_1262	hypothetical protein	[S]
D5_1264	hypothetical protein	Not in COGs
D5_1266	hypothetical protein	Not in COGs
D5_1268	hypothetical transmembrane protein	Not in COGs
D5_1270	TPR repeat-containing protein	[R]
D5_1274	hypothetical protein	[unclassified]
D5_1280	hypothetical protein	Not in COGs
D5_1282	hypothetical protein	[O]
D5_1285	hypothetical transmembrane protein	[S]
D5_1289	hypothetical protein	[S]
D5_1297	glycosyl transferase GT2 family	Not in COGs
D5_1303	hypothetical protein	[E]
D5_1305	LPS biosynthesis protein	[M]
D5_1306	glycosyl transferase GT2 family	Not in COGs
D5_1314	hypothetical protein	[M]
D5_1322	hypothetical protein	Not in COGs
D5_1337	hypothetical transmembrane protein	[unclassified]
D5_1343	CAAX amino terminal protease family protein	[S]
D5_1349	ACT domain-containing protein	[S]
D5_1366	DNA mismatch repair ATPase MutS family	[unclassified]
D5_1390	hypothetical protein	Not in COGs
D5_1393	hypothetical transmembrane protein	[O]
D5_1394	hypothetical transmembrane protein	[O]
D5_1406	adhesin-like protein	Not in COGs
D5_1410	hypothetical transmembrane protein	[E]
D5_1412	adhesin-like protein	[unclassified]
D5_1413	adhesin-like protein	[unclassified]
D5_1416	adhesin-like protein	[O]
D5_1417	hypothetical transmembrane protein	[unclassified]
D5_1423	adhesin-like protein	[unclassified]
D5_1424	adhesin-like protein	[unclassified]
D5_1425	chaperone protein DnaJ, <i>dnaJ</i>	[O]
D5_1428	hypothetical protein	Not in COGs
D5_1429	hypothetical protein	Not in COGs
D5_1430	hypothetical protein	Not in COGs
D5_1431	hypothetical protein	Not in COGs
D5_1432	hypothetical protein	Not in COGs
D5_1433	hypothetical protein	[unclassified]
D5_1434	hypothetical protein	Not in COGs
D5_1435	hypothetical protein	Not in COGs
D5_1436	hypothetical protein	Not in COGs
D5_1437	hypothetical protein	Not in COGs
D5_1438	hypothetical protein	Not in COGs
D5_1439	hypothetical protein	Not in COGs
D5_1440	hypothetical protein	Not in COGs
D5_1441	hypothetical protein	Not in COGs
D5_1442	hypothetical protein	Not in COGs
D5_1443	hypothetical protein	Not in COGs
D5_1444	hypothetical protein	Not in COGs
D5_1445	hypothetical protein	Not in COGs
D5_1446	hypothetical protein	Not in COGs
D5_1447	hypothetical protein	Not in COGs
D5_1448	hypothetical protein	Not in COGs
D5_1449	hypothetical protein	Not in COGs
D5_1450	hypothetical protein	Not in COGs

D5_1451	hypothetical protein	[R]
D5_1452	hypothetical protein	Not in COGs
D5_1453	hypothetical transmembrane protein	[unclassified]
D5_1454	hypothetical protein	Not in COGs
D5_1455	hypothetical protein	[unclassified]
D5_1456	hypothetical protein	Not in COGs
D5_1457	hypothetical protein	[L]
D5_1458	hypothetical protein	Not in COGs
D5_1459	hypothetical protein	Not in COGs
D5_1463	hypothetical protein	Not in COGs
D5_1464	hypothetical transmembrane protein	[M]
D5_1473	adhesin-like protein	[unclassified]
D5_1476	adhesin-like protein	Not in COGs
D5_1480	hypothetical protein	Not in COGs
D5_1481	CAAX amino terminal protease family protein	[R]
D5_1486	hypothetical protein	[R]
D5_1491	hypothetical transmembrane protein	[unclassified]
D5_1494	adhesin-like protein	Not in COGs
D5_1515	WD40 repeat-containing protein	Not in COGs
D5_1554	hypothetical protein	Not in COGs
D5_1582	hypothetical protein	Not in COGs
D5_1603	hypothetical transmembrane protein	[R]
D5_1604	hypothetical transmembrane protein	Not in COGs
D5_1605	hypothetical transmembrane protein	[S]
D5_1606	hypothetical transmembrane protein	[O]
D5_1618	adhesin-like protein	[unclassified]
D5_1619	adhesin-like protein	[unclassified]
D5_1625	hypothetical protein	Not in COGs
D5_1627	hypothetical protein	Not in COGs
D5_1628	hypothetical protein	[R]
D5_1629	hypothetical protein	Not in COGs
D5_1630	hypothetical protein	Not in COGs
D5_1631	hypothetical protein	Not in COGs
D5_1632	hypothetical protein	[M]
D5_1633	hypothetical transmembrane protein	Not in COGs
D5_1634	hypothetical protein	Not in COGs
D5_1637	hypothetical protein	Not in COGs
D5_1638	hypothetical transmembrane protein	Not in COGs
D5_1707	hypothetical transmembrane protein	Not in COGs
D5_1711	hypothetical protein	[unclassified]
D5_1735	conserved hypothetical protein	[T]
D5_1736	repeat domain containing protein	[M]
D5_1737	hypothetical protein	Not in COGs
D5_1738	hypothetical transmembrane protein	[S]
D5_1742	nitroreductase family protein	[C]
D5_1744	hypothetical	[unclassified]
D5_1745	hypothetical transmembrane protein	Not in COGs
D5_1764	adhesin-like protein	Not in COGs
D5_1800	hypothetical protein	Not in COGs
D5_1801	hypothetical transmembrane protein	Not in COGs
D5_1802	hypothetical protein	Not in COGs
D5_1833	hypothetical protein	[K]
D5_1837	hypothetical protein	Not in COGs
D5_1838	conserved hypothetical transmembrane protein	[S]
D5_1841	5,10-methenyltetrahydromethanopterin hydrogenase Hmd	[C]
D5_1879	TPR repeat-containing protein	[R]
D5_1884	hypothetical transmembrane protein	[unclassified]
D5_1892	hypothetical transmembrane protein	Not in COGs
D5_1896	adhesin-like protein	[unclassified]
D5_1912	adhesin-like protein	Not in COGs
D5_1930	hypothetical protein	Not in COGs
D5_1970	hypothetical protein	Not in COGs
D5_1971	hypothetical protein	Not in COGs
D5_1972	hypothetical protein	Not in COGs
D5_1973	hypothetical transmembrane protein	[S]
D5_1981	conserved hypothetical	Not in COGs
D5_1982	hypothetical transmembrane protein	Not in COGs
D5_1983	hypothetical transmembrane protein	[S]
D5_1985	hypothetical transmembrane protein	Not in COGs
D5_1988	hypothetical transmembrane protein	Not in COGs
D5_1996	homoserine <i>O</i> -acetyltransferase, MetX	[E]
D5_2016	short chain dehydrogenase	[I]

D5_2025	hypothetical transmembrane protein	Not in COGs
D5_2046	hypothetical protein	[E]
D5_2050	hypothetical protein	Not in COGs
D5_2055	hypothetical protein	Not in COGs
D5_2056	hypothetical protein	[unclassified]
D5_2057	hypothetical protein	[D]
D5_2059	conserved hypothetical protein	[S]
D5_2063	hypothetical protein	Not in COGs
D5_2065	hypothetical protein	Not in COGs
D5_2074	hypothetical protein	Not in COGs
D5_2078	restriction endonuclease	[V]
D5_2082	DNA repair photolyase	[L]
D5_2083	type I site-specific deoxyribonuclease HsdR family, HsdR	[V]
D5_2084	type I restriction endonuclease subunit S, HdsS	[V]
D5_2085	type I restriction endonuclease subunit M, HsdM	[V]
D5_2086	GIY-YIG catalytic domain-containing endonuclease	[unclassified]
D5_2093	hypothetical transmembrane protein	Not in COGs
D5_2099	hypothetical transmembrane protein	Not in COGs
D5_2120	adhesin-like protein	Not in COGs
D5_2164	type III restriction endonuclease res subunit	[unclassified]
D5_2165	type III restriction endonuclease methylation subunit	[L]
D5_2166	hypothetical protein	Not in COGs
D5_2171	hypothetical transmembrane protein	Not in COGs
D5_2173	adhesin-like protein	[M]
D5_2174	hypothetical transmembrane protein	[M]
D5_2175	adhesin-like protein	[unclassified]
D5_2176	adhesin-like protein	Not in COGs
D5_2193	hypothetical protein	[unclassified]
D5_2194	hypothetical transmembrane protein	Not in COGs
D5_2209	hypothetical transmembrane protein	[S]
D5_2210	hypothetical protein	[R]
D5_2247	metallo-beta-lactamase superfamily protein	[R]
D5_2248	hypothetical transmembrane protein	[unclassified]
D5_2265	adhesin-like protein	[unclassified]
D5_2266	adhesin-like protein	[unclassified]
D5_2268	hypothetical protein	Not in COGs
D5_2281	hypothetical protein	Not in COGs
D5_2282	hypothetical transmembrane protein	Not in COGs
D5_2289	hypothetical protein	Not in COGs
D5_2293	hypothetical transmembrane protein	Not in COGs
D5_2294	hypothetical transmembrane protein	Not in COGs
D5_2295	hypothetical protein	[M]
D5_2296	hypothetical transmembrane protein	Not in COGs
D5_2297	hypothetical protein	Not in COGs
D5_2300	hypothetical protein	Not in COGs
D5_2301	hypothetical transmembrane protein	[unclassified]
D5_2309	hypothetical transmembrane protein	[unclassified]
D5_2311	repeat domain containing protein	[M]
D5_2312	potassium channel protein	Not in COGs
D5_2313	potassium channel protein	[P]
D5_2316	conserved hypothetical transmembrane protein	[S]
D5_2317	hypothetical protein	[unclassified]
D5_2322	hypothetical protein	[C]
D5_2323	hypothetical protein	Not in COGs
D5_2325	conserved hypothetical protein	[Q]
D5_2326	hypothetical protein	Not in COGs
D5_2328	hypothetical protein	[S]
D5_2329	hypothetical transmembrane protein	[unclassified]
D5_2330	conserved hypothetical protein	[unclassified]
D5_2331	hypothetical protein	Not in COGs
D5_2335	adhesin-like protein with cysteine protease domain	[unclassified]
D5_2353	hypothetical protein	[unclassified]
D5_2354	adhesin-like protein	[O]
D5_2355	conserved hypothetical protein	[O]
D5_2356	adhesin-like protein	Not in COGs
D5_2357	adhesin-like protein	[unclassified]
D5_2358	hypothetical protein	Not in COGs
D5_2359	hypothetical protein	Not in COGs

D5_2365	hypothetical protein	[T]
D5_2371	conserved hypothetical protein	[H]
D5_2406	hypothetical protein	Not in COGs
D5_2407	adhesin-like protein with cysteine protease domain	[O]
D5_2415	hypothetical transmembrane protein	Not in COGs
D5_2419	hypothetical protein	Not in COGs
D5_2445	hypothetical protein	Not in COGs
D5_2446	hypothetical protein	Not in COGs

D5_2451	hypothetical transmembrane protein	Not in COGs
D5_2460	hypothetical protein	[unclassified]
D5_2461	hypothetical protein	Not in COGs
D5_2465	transposase	[L]

*only one gene from D5 for each gene family is represented

Table A.6.9 Genes involved in methanogenesis and energy generation in *Mbb.* spp. genomes analysed

	D5	YE315	ZA-10 ^T *	SM9	HO ^T *	PS ^T	JMR01*	M1 ^T	KM1H5-1P ^T *	YLM1#	SH ^T *	AbM4*	JH1 ^T *	RFM-1 ^T *	RFM-2 ^T *	RFM-3 ^T *	ATM ^T *	ANOR1*
Formate metabolism																		
<i>fdhC</i>	D5_2393	TL18_00915	2595204654	mbs_2229	2657040815	Msm_1403	2620725525	MRU_RS01705	2595158485	YLM1_0029	2558933326	2540853337	2553937917	Ga0074191_10501	Ga0074190_111836	Ga0078795_10806	Ga0078798_108220	2618697655, 2618697091
<i>fdhA</i>	D5_2392	TL18_00920 (pseud o)	2595204653	mbs_2228	2657040816	Msm_1404	2620725524	MRU_RS01710	2595158484	YLM1_0030	2558933327	2540853338	2553937918	Ga0074191_10502	Ga0074190_111837	Ga0078795_10805	Ga0078798_108219	2618697656
<i>fdhB</i>	D5_2391	TL18_00925	2595204652	mbs_2227	2657040817	Msm_1405	2620725523	MRU_RS01715	2595158483	YLM1_0031	2558933328	2540853339	2553937919	Ga0074191_10503	Ga0074190_111838	Ga0078795_10804	Ga0078798_108218	2618697657
<i>fdhD</i>	D5_0772, D5_2394	TL18_00875, TL18_07080	2595204656, 2595203780	mbs_1636, mbs_2231	2657040813	Msm_1392, Msm_0295	2620725176	MRU_RS03460, MRU_RS09705	2595158965	YLM1_0328	2558934145	2540854360	2553936931	Ga0074191_10513	Ga0074190_111835	Ga0078795_10809	Ga0078798_121524	2618697650, 2618698474
<i>flpE-like</i>	D5_0737	TL18_01665 (pseud o)	2595205493	mbs_1376	-	Msm_1464	2620726189	-	-	-	-	-	-	-	-	-	-	-
<i>flpA</i>	D5_0738	TL18_01670	2595205494	mbs_1375	-	Msm_1463	2620726188	MRU_RS10425	2595158368, 2595159808	YLM1_1118, YLM1_1559	-	2540854057	2553937228	-	-	-	-	-
<i>flpB</i>	D5_0739	TL18_01675	2595205495	mbs_1374	2657041195	Msm_1462	2620726187	MRU_RS10430	2595158369, 2595159809	YLM1_1117, YLM1_1558	-	2540854056	2553937229	-	-	-	-	-
<i>flpD</i>	D5_0740	TL18_01680	2595205496	mbs_1373	2657041194	Msm_1461	2620726186	MRU_RS10435	2595158370, 2595159810	YLM1_1116, YLM1_1557	-	2540854055	2553937230	-	-	-	-	-
Tungsten formylmethanofuran dehydrogenase																		
<i>fwdE</i>	D5_1751	TL18_00895	2595204655	mbs_2230	2657040814	Msm_1396	2620724795, 2620726394	MRU_RS01355	2595158492	YLM1_0022	2558933343	2540853352	2553937932	Ga0074191_109211	Ga0074190_111026	Ga0078795_10642	Ga0078798_121528	2618697653
<i>fwdC</i>	D5_2382	TL18_00990	2595204643	mbs_2217	2657040826	Msm_1414	2620725513	MRU_RS01770	2595158473	YLM1_0041	2558933338	2540853350	2553937930	Ga0074191_105012	Ga0074190_104511	Ga0078795_13898	Ga0078798_10829	2618697660
<i>fwdA</i>	D5_2383	TL18_00985	2595204644	mbs_2218	2657040825	Msm_1413	2620725514	MRU_RS01765	2595158474	YLM1_0040	2558933337	2540853349	2553937929	Ga0074191_105011	Ga0074190_104510	Ga0078795_13897	Ga0078798_108210	2618697661

<i>fwdB</i>	D5_2384	TL18_00980	2595204645	mbs_2219	2657040824	Msm_1412	2620725515	MRU_R S01760	2595158475	YLM1_0039	2558933336	2540853348	2553937928	Ga0074191_105010	Ga0074190_10459	Ga0078795_13896	Ga0078798_108211	2618697662
<i>fwdD</i>	D5_2385	TL18_00975	2595204646	mbs_2220	2657040823	Msm_1411	2620725516	MRU_R S01755	2595158476	YLM1_0038	2558933335	2540853347	2553937927	Ga0074191_10509	Ga0074190_10458	Ga0078795_13895	Ga0078798_108212	2618697663
<i>fwdG</i>	D5_2386	TL18_00970	2595204647	mbs_2221	2657040822	Msm_1410	2620725517	MRU_R S01750	2595158477	YLM1_0037	2558933334	2540853346	2553937926	Ga0074191_10508	Ga0074190_10457	Ga0078795_13894	Ga0078798_108213	2618697664
<i>fwdF</i>	D5_2387	TL18_00965	2595204648	mbs_2222	2657040821	Msm_1409	2620725518	MRU_R S01745	2595158478	YLM1_0036	2558933333	2540853345	2553937925	Ga0074191_10507	Ga0074190_10456	Ga0078795_13893	Ga0078798_108214	2618697666
<i>fwdH</i>	D5_2388	TL18_00960	2595204649	mbs_2223	2657040820	Msm_1408	2620725519	MRU_R S01740	2595158479	YLM1_0035	2558933332	2540853344	2553937924	Ga0074191_10506	Ga0074190_10455	Ga0078795_13892	Ga0078798_108215	2618697667
Formylmethanofuran-tetrahydromethanopterin formyltransferase																		
<i>ptr</i>	D5_0210	TL18_03515	2595204243	mbs_0743	2657039708	Msm_0308	2620724610	MRU_R S06965	2595159281	YLM1_0902	2558933862	2540854134	2553937147	Ga0074191_107324	Ga0074190_111131	Ga0078795_102513	Ga0078798_125770	2618697292
	D5_1769	TL18_09675	2595205618	mbs_2147	2657040050	Msm_1092	2620725209	MRU_R S10125	2595159591	YLM1_1480	2558934229	2540854788	2553937646	Ga0074191_111353	Ga0074190_110921	Ga0078795_116217	Ga0078798_109535	2618698615
Methenyltetrahydromethanopterin cyclohydrolase																		
<i>mch</i>	D5_1626	TL18_04360	2595205554	mbs_1355	2657040207	Msm_1723	2620724969	MRU_R S08105	2595158371	YLM1_1115	2558933616	2540854399	2553936892	Ga0074191_109714	Ga0074190_113227	Ga0078795_14478	Ga0078798_106416	2618698730
H₂ forming methenyltetrahydromethanopterin dehydrogenase																		
<i>hmd</i>	D5_2132	TL18_01650	2595205021	mbs_0405	2657040574	Msm_0572	2620725265	MRU_R S02670	2595159020	YLM1_0194	2558933466	2540853216	2553937792	-	-	-	-	-
F₄₂₀-dependent methylenetetrahydromethanopterin dehydrogenase Mtd																		
<i>mtd</i>	D5_0079	TL18_10280	2595203961	mbs_0086	2657039932	Msm_1204	2620724741	MRU_R S10770	2595159382	YLM1_1696	2558934910	2540853248	2553937824	Ga0074191_10304	Ga0074190_106626	Ga0078795_11587	Ga0078798_1095116	2618697459
5,10-methylenetetrahydromethanopterin reductase Mer																		
<i>mer</i>	D5_2110	TL18_02180	2595205053	mbs_0427	2657040596	Msm_0542	2620726500	MRU_R S02895	2595159063	YLM1_0234	2558934989	2540854611	2553937467	Ga0074191_111924	Ga0074190_11272	Ga0078795_12443	Ga0078798_11093	2618697110
Tetrahydromethanopterin S-methyltransferase																		
<i>mtrE</i>	D5_0289	TL18_09273	2595205127	mbs_2065	2657040125	Msm_1014	2620724514	MRU_R S09625	2595158116	YLM1_1394	2558933935	2540854715	2553937572	Ga0074191_103411	Ga0074190_108988	Ga0078795_108120	Ga0078798_1257141	2618697767
<i>mtrD</i>	D5_0290	TL18_09274	2595205128	mbs_2064	2657040126	Msm_1013	2620724513	MRU_R S09620	2595158115	YLM1_1393	2558933936	2540854714	2553937571	Ga0074191_103412	Ga0074190_108989	Ga0078795_108119	Ga0078798_1257142	2618697768
<i>mtrC</i>	D5_0291	TL18_09275	2595205129	mbs_2063	2657040127	Msm_1012	2620724512	MRU_R S09615	2595158114	YLM1_1392	2558933937	2540854713	2553937570	Ga0074191_103413	Ga0074190_108990	Ga0078795_108118	Ga0078798_1257143	2618697769
<i>mtrB</i>	D5_0292	TL18_09276	2595205130	mbs_2062	2657040128	Msm_1011	2620724511	MRU_R S09610	2595158113	YLM1_1391	2558933938	2540854712	2553937569	Ga0074191_103414	Ga0074190_108991	Ga0078795_108117	Ga0078798_1257144	2618697770

<i>mtrA</i>	D5_0293	TL18_09277	2595205131	mbs_2061	2657040129	Msm_1010	2620724510	MRU_R S09605	2595158112	YLM1_1390	2558933939	2540854711	2553937568	Ga0074191_103415	Ga0074190_108992	Ga0078795_108116	Ga0078798_1257145	2618697771
<i>mtrF</i>	D5_0294	TL18_09278	2595205132	mbs_2060	2657040130	Msm_1009	2620724509	MRU_R S09600	2595158111	YLM1_1389	2558933940	2540854710	2553937567	Ga0074191_103416	Ga0074190_108993	Ga0078795_108115	Ga0078798_1257146	2618697772
<i>mtrG</i>	D5_0295	TL18_09279	2595205133	mbs_2059	2657040131	Msm_1008	2620724508	MRU_R S09595	2595158110	YLM1_1388	2558933941	2540854709	2553937566	Ga0074191_103417	Ga0074190_108994	Ga0078795_108114	Ga0078798_1257147	2618697773
<i>mtrH</i>	D5_0296 , D5_0350	TL18_09280	2595205134, 2595204141	mbs_2058 , mbs_1954	2657040132, 2657040180	Msm_1007	2620724507	MRU_R S09590	2595158109, 2595158108	YLM1_1387, YLM1_1386	2558933942, 4060	2540854708	2553937565	Ga0074191_103418	Ga0074190_108995	Ga0078795_108113	Ga0078798_1257148	2618697774
Methyl-CoM reductase I/II																		
<i>mcrB</i>	D5_0284	TL18_09340	2595205122	mbs_2070	2657040120	Msm_1019	2620724520	MRU_R S09650	2595158121	YLM1_1399	2558933930	2540854720	2553937577	Ga0074191_10346	Ga0074190_108983	Ga0078795_108125	Ga0078798_1257136	2618697762
<i>mcrD</i>	D5_0285	TL18_09335	2595205123	mbs_2069	2657040121	Msm_1018	2620724519	MRU_R S09645	2595158120	YLM1_1398	2558933931	2540854719	2553937576	Ga0074191_10347	Ga0074190_108984	Ga0078795_108124	Ga0078798_1257137	2618697763
<i>mcrC</i>	D5_0286	TL18_09330	2595205124	mbs_2068	2657040122	Msm_1017	2620724518	MRU_R S09640	2595158119	YLM1_1397	2558933932	2540854718	2553937575	Ga0074191_10348	Ga0074190_108985	Ga0078795_108123	Ga0078798_1257138	2618697764
<i>mcrG</i>	D5_0287	TL18_09325	2595205125	mbs_2067	2657040123	Msm_1016	2620724517	MRU_R S09635	2595158118	YLM1_1396	2558933933	2540854717	2553937574	Ga0074191_10349	Ga0074190_108986	Ga0078795_108122	Ga0078798_1257139	2618697765
<i>mcrA</i>	D5_0288	TL18_09320	2595205126	mbs_2066	2657040124	Msm_1015	2620724515(C - termina l)- 2620724516(N - termina l)	MRU_R S09630	2595158117	YLM1_1395	2558933934	2540854716	2553937573	Ga0074191_103410	Ga0074190_108987	Ga0078795_108121	Ga0078798_1257140	2618697766
<i>atwA</i>	D5_0328	TL18_09125	2595203934	mbs_1973 , mbs_1409	2657040164, 2657041025	Msm_0971, Msm_1698	2620724442	MRU_R S09260	2595158296	YLM1_0536, YLM1_0551	2558933974	2540854674, 2540853976	2553937531	Ga0074191_105912, Ga0074191_11579	Ga0074190_116229, Ga0074190_10729	Ga0078795_132016, Ga0078795_12083	Ga0078798_1257238, Ga0078798_1257557	2618697892
<i>mrtB</i>	D5_0742	-	2595203957	mbs_1381	2657041190	Msm_0905	2620726409	-	2595158366	YLM1_1120	-	-	-	-	-	-	-	-
<i>mrtD</i>	D5_0743	-	2595203958	mbs_1380	2657041191	Msm_0904	2620726410	-	2595158365	YLM1_1121	-	-	-	-	-	-	-	-
<i>mrtG</i>	D5_0744	-	2595203959	mbs_1379	2657041192	Msm_0903	2620726411	-	2595158364	YLM1_1122	-	-	-	-	-	-	-	-
<i>mrtA</i>	D5_0745	-	2595203960	mbs_1378	2657041193	Msm_0902	2620726412	-	2595158363	YLM1_1123	-	-	-	-	-	-	-	-
CoB--CoM heterodisulfide reductase																		
<i>hdrA</i>	D5_1502 ,	TL18_00375	2595203696	mbs_1003 ,	2657039812	Msm_0082	2620726078	MRU_R S00595	2595158659	YLM1_0883	2558934522	2540853897	2553937394	Ga0074191_103422	Ga0074190_118171	Ga0078795_12357	Ga0078798_1257522	2618697374

	D5_2467	TL18_05450	2595204522	mbs_2297	2657040761	Msm_1336	2620725595		2595159533	YLM1_1573	2558934537	2540854877	2553937738	Ga0074191_114662	Ga0074190_11912	Ga0078795_117114	Ga0078798_101962	2618697781
<i>hdrB</i>	D5_0650 , D5_1005 , D5_1503	TL18_04030, TL18_05455, TL18_3633 07635	259520 , 259520 3633	mbs_1002 , mbs_1427 , mbs_1746	265703 , 265703 9550	Msm_0083, Msm_0795	262072 6076, 262072 4228	MRU_R S04120	259515 9493, 259515 9534	YLM1_0884, YLM1_0408, YLM1_0627	255893 4521, 255893 3761	254085 3896, 254085 3960, 254085 4504	255393 7395, 255393 6788, 255393 7325	Ga0074191_103423, Ga0074191_112813	Ga0074190_100425, Ga0074190_118170	Ga0078795_11535, Ga0078795_12358	Ga0078798_109744, Ga0078798_125752	261869 6945, 261869 7782
<i>hdrC</i>	D5_0649 , D5_1504	TL18_05460, TL18_259520 07640	259520 3698, 259520 3632	mbs_1001 , mbs_1747	265703 9810, 265703 9549	Msm_0084, Msm_0796	262072 6075, 262072 4229	MRU_R S04115	259515 9494	YLM1_0885, YLM1_0407	255893 4520, 255893 3762	254085 3895, 254085 4505	255393 7396, 255393 6787	Ga0074191_112814, Ga0074191_11427	Ga0074190_100426, Ga0074190_118169	Ga0078795_11536, Ga0078795_12359	Ga0078798_109745, Ga0078798_1257520	261869 6946, 261869 7783
Methyl viologen-reducing hydrogenase																		
<i>mvhD</i>	D5_0302 , D5_0740	TL18_09250, TL18_5140 01680	259520 5140	mbs_1373 , mbs_2052	265704 0138, 265704 1194	Msm_1001, Msm_1461	262072 S09550, 4501 S10435	MRU_R S09550, MRU_R S10435	259515 8102, 259515 8370	YLM1_1380, YLM1_1116	255893 255893 3948	254085 4702, 254085 4055	255393 7559, 255393 7230	Ga0074191_10499, Ga0074191_10499	Ga0074190_10208	Ga0078795_11467	Ga0078798_1257158	261869 7786
<i>mvhG</i>	D5_0303	TL18_09245	2595205141	mbs_2051	2657040139	Msm_1000	2620724500	MRU_R S09545	2595158101	YLM1_1379	2558933949	2540854701	2553937558	Ga0074191_10498	Ga0074190_10207	Ga0078795_11468	Ga0078798_1257159	2618697787
<i>mvhA</i>	D5_0304	TL18_09240	2595205142	mbs_2050	2657040140	Msm_0999	2620724499	MRU_R S09540	2595158100	YLM1_1378	2558933950	2540854700	2553937557	Ga0074191_10497	Ga0074190_10206	Ga0078795_11469	Ga0078798_1257160	2618697788
<i>mvhB</i>	D5_0305	TL18_09235	2595205143	mbs_2049	2657040141	Msm_0998	2620724498	MRU_R S09535	2595158099	YLM1_1377	2558933951	2540854699	2553937556	Ga0074191_10496	Ga0074190_10205	Ga0078795_114610	Ga0078798_1257161	2618697789
Coenzyme F₄₂₀ hydrogenase																		
<i>frhA</i>	D5_0174	TL18_09880	2595205289	mbs_0195	2657040009	Msm_1124	2620724656	MRU_R S10375	2595159549	YLM1_1825	2558934591	2540854823	2553937682	Ga0074191_10899	Ga0074190_113617	Ga0078795_123415	Ga0078798_125732	2618697332
<i>frhD</i>	D5_0175	TL18_09875	2595205288	mbs_0196 , mbs_0194	2657040010	Msm_1123	2620724655	MRU_R S10370	2595159550	YLM1_1826	2558934592	2540854822	2553937681	Ga0074191_10898	Ga0074190_113618	Ga0078795_123414	Ga0078798_125733	2618697331
<i>frhG</i>	D5_0176	TL18_09870	2595205287	mbs_0197 ,	2657040011	Msm_1122	2620724654	MRU_R S10365	2595159551	YLM1_1827	2558934593	2540854821	2553937680	Ga0074191_10897	Ga0074190_113619	Ga0078795_123413	Ga0078798_125734	2618697330
<i>frhB</i>	D5_0177	TL18_09865	2595205286	mbs_0198 , mbs_1479	2657040012	Msm_1121	2620724653	MRU_R S10360	2595159552	YLM1_1828	2558934594	2540854820	2553937679	Ga0074191_10896	Ga0074190_113620	Ga0078795_123412	Ga0078798_125735	2618697329
Energy-converting hydrogenase A																		
<i>ehaA</i>	D5_1770	TL18_03425	2595204261	mbs_0725	2657039726	Msm_0326	2620725227	MRU_R S07055	2595159300	YLM1_0921	2558934211	2540854152	2553937129	Ga0074191_107342	Ga0074190_11093	Ga0078795_10112	Ga0078798_109517	2618698633

<i>ehaB</i>	D5_1771	TL18_03430	2595204260	mbs_0726	2657039725	Msm_0325	2620725226	MRU_R_S07050	2595159299	YLM1_0920	2558934212	2540854151	2553937130	Ga0074191_107341	Ga0074190_11094	Ga0078795_10113	Ga0078798_109518	2618698632
<i>ehaC</i>	D5_1772	TL18_03435	2595204259	mbs_0727	2657039724	Msm_0324	2620725225	MRU_R_S07045	2595159298	YLM1_0919	2558934213	2540854150	2553937131	Ga0074191_107340	Ga0074190_11095	Ga0078795_10114	Ga0078798_109519	2618698631
<i>ehaD</i>	D5_1773	TL18_03440	2595204258	mbs_0728	2657039723	Msm_0323	2620725224	MRU_R_S07040	2595159297	YLM1_0918	2558934214	2540854149	2553937132	Ga0074191_107339	Ga0074190_11096	Ga0078795_10115	Ga0078798_109520	2618698630
<i>ehaE</i>	D5_1774	TL18_03445	2595204257	mbs_0729	2657039722	Msm_0322	2620725223	MRU_R_S07035	2595159296	YLM1_0917	2558934215	2540854148	2553937133	Ga0074191_107338	Ga0074190_11097	Ga0078795_10116	Ga0078798_109521	2618698629
<i>ehaF</i>	D5_1775	TL18_03450	2595204256	mbs_0730	2657039721	Msm_0321	2620725222	MRU_R_S07030	2595159295	YLM1_0916	2558934216	2540854147	2553937134	Ga0074191_107337	Ga0074190_11098	Ga0078795_10117	Ga0078798_109522	2618698628
<i>ehaG</i>	D5_1776	TL18_03455	2595204255	mbs_0731	2657039720	Msm_0320	2620725221	MRU_R_S07025	2595159294	YLM1_0915	2558934217	2540854146	2553937135	Ga0074191_107336	Ga0074190_11099	Ga0078795_10118	Ga0078798_109523	2618698627
<i>ehaH</i>	D5_1777	TL18_03460	2595204254	mbs_0732	2657039719	Msm_0319	2620725220	MRU_R_S07020	2595159293	YLM1_0914	2558934218	2540854145	2553937136	Ga0074191_107335	Ga0074190_110910	Ga0078795_10119	Ga0078798_109524	2618698626
<i>ehaI</i>	D5_1778	TL18_03465	2595204253	mbs_0733	2657039718	Msm_0318	2620725219	MRU_R_S07015	2595159292	YLM1_0913	2558934219	2540854144	2553937137	Ga0074191_107334	Ga0074190_110911	Ga0078795_101110	Ga0078798_109525	2618698625
<i>ehaJ</i>	D5_1779	TL18_03470	2595204252	mbs_0734	2657039717	Msm_0317	2620725218	MRU_R_S07010	2595159291	YLM1_0912	2558934220	2540854143	2553937138	Ga0074191_107333	Ga0074190_110912	Ga0078795_101111	Ga0078798_109526	2618698624
<i>ehaK</i>	D5_1780	TL18_03475	2595204251	mbs_0735	2657039716	Msm_0316	2620725217	MRU_R_S07005	2595159290	YLM1_0911	2558934221	2540854142	2553937139	Ga0074191_107332	Ga0074190_110913	Ga0078795_116227	Ga0078798_109527	2618698623
<i>ehaL</i>	D5_1781	TL18_03480	2595204250	mbs_0736	2657039715	Msm_0315	2620725216	MRU_R_S07000	2595159289	YLM1_0910	2558934222	2540854141	2553937140	Ga0074191_107331	Ga0074190_110914	Ga0078795_116226	Ga0078798_109528	2618698622
<i>ehaM</i>	D5_1782	TL18_03485	2595204249	mbs_0737	2657039714	Msm_0314	2620725215	MRU_R_S06995	2595159288	YLM1_0909	2558934223	2540854140	2553937141	Ga0074191_107330	Ga0074190_110915	Ga0078795_116225	Ga0078798_109529	2618698621
<i>ehaN</i>	D5_1783	TL18_03490	2595204248	mbs_0738	2657039713	Msm_0313	2620725214	MRU_R_S06990	2595159287	YLM1_0908	2558934224	2540854139	2553937142	Ga0074191_107329	Ga0074190_110916	Ga0078795_116224	Ga0078798_109530	2618698620
<i>ehaO</i>	D5_1784	TL18_03495	2595204247	mbs_0739	2657039712	Msm_0312	2620725213	MRU_R_S06985	2595159286	YLM1_0907	2558934225	2540854138	2553937143	Ga0074191_107328	Ga0074190_110917	Ga0078795_116223	Ga0078798_109531	2618698619
<i>ehaP</i>	D5_1785	TL18_03500	2595204246	mbs_0740	2657039711	Msm_0311	2620725212	MRU_R_S06980	2595159285	YLM1_0906	2558934226	2540854137	2553937144	Ga0074191_107327	Ga0074190_110918	Ga0078795_116222	Ga0078798_109532	2618698618
<i>ehaQ</i>	D5_1786	TL18_03505	2595204245	mbs_0741	2657039710	Msm_0310	2620725211	MRU_R_S06975	2595159283	YLM1_0905	2558934227	2540854136	2553937145	Ga0074191_107326	Ga0074190_110919	Ga0078795_116221	Ga0078798_109533	2618698617
<i>ehaR</i>	D5_1787	TL18_03510	2595204244	mbs_0742	2657039709	Msm_0309	2620725210	MRU_R_S06970	2595159282	YLM1_0904	2558934228	2540854135	2553937146	Ga0074191_107325	Ga0074190_110920	Ga0078795_116220	Ga0078798_109534	2618698616
<i>ehaS-like</i>	D5_1766	TL18_03530	2595204240	mbs_0746	2657039705	Msm_0305	2620725206	MRU_R_S06950	2595159278	YLM1_0899	2558934232	2540854131	2553937150	Ga0074191_107321	Ga0074190_110924	Ga0078795_116214	Ga0078798_109538	2618698612
<i>ehaT</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Energy-converting hydrogenase B

<i>ehbA</i>	D5_0225	TL18_09630	2595205602	mbs_2131	2657040060	Msm_1076	2620724599	MRU_R_S10085	2595158190	YLM1_1471	2558933869	2540854780	2553937638	Ga0074191_109041	Ga0074190_106936	Ga0078795_109118	Ga0078798_125778	2618697708
<i>ehbB</i>	D5_0226	TL18_09625	2595205601	mbs_2130	2657040061	Msm_1075	2620724598	MRU_R_S10080	2595158189	YLM1_1470	2558933870	2540854779	2553937637	Ga0074191_109040	Ga0074190_106937	Ga0078795_109117	Ga0078798_125779	2618697707
<i>ehbC</i>	D5_0227	TL18_09620	2595205600	mbs_2129	2657040062	Msm_1074	2620724597	MRU_R_S10075	2595158188	YLM1_1469	2558933871	2540854778	2553937636	Ga0074191_109039	Ga0074190_106938	Ga0078795_109116	Ga0078798_125780	2618697706
<i>ehbD</i>	D5_0228	TL18_09615	2595205599	mbs_2128	2657040063	Msm_1073	2620724596	MRU_R_S10070	2595158187	YLM1_1468	-	2540854777	2553937635	Ga0074191_109038	Ga0074190_106939	Ga0078795_109115	Ga0078798_125781	2618697705

<i>ehbE</i>	D5_0229	TL18_09610	2595205598	mbs_2127	2657040064	Msm_1072	2620724595	MRU_R_S10065	2595158186	YLM1_1467	2558933872	2540854776	2553937634	Ga0074191_109037	Ga0074190_106940	Ga0078795_109114	Ga0078798_125782	2618697704
<i>ehbF</i>	D5_0230	TL18_09605	2595205597	mbs_2126	2657040065	Msm_1071	2620724594	MRU_R_S10060	2595158185	YLM1_1466	2558933873	2540854775	2553937633	Ga0074191_109036	Ga0074190_106941	Ga0078795_109113	Ga0078798_125783	2618697703
<i>ehbG</i>	D5_0231	TL18_09600	2595205596	mbs_2125	2657040066	Msm_1070	2620724593	MRU_R_S10055	2595158184	YLM1_1465	2558933874	2540854774	2553937632	Ga0074191_109035	Ga0074190_106942	Ga0078795_109112	Ga0078798_125784	2618697702
<i>ehbH</i>	D5_0232	TL18_09595	2595205595	mbs_2124	2657040067	Msm_1069	2620724592	MRU_R_S10050	2595158183	YLM1_1464	2558933875	2540854773	2553937631	Ga0074191_109034	Ga0074190_106943	Ga0078795_109111	Ga0078798_125785	2618697701
<i>ehbI</i>	D5_0233	TL18_09590	2595205594	mbs_2123	2657040068	Msm_1068	2620724591	MRU_R_S10045	2595158182	YLM1_1463	2558933876	2540854772	2553937630	Ga0074191_109033	Ga0074190_106944	Ga0078795_109110	Ga0078798_125786	2618697700
<i>ehbJ</i>	D5_0234	TL18_09585	2595205593	mbs_2122	2657040069	Msm_1067	2620724590	MRU_R_S10040	2595158181	YLM1_1462	2558933877	2540854771	2553937629	Ga0074191_109032	Ga0074190_106945	Ga0078795_10919	Ga0078798_125787	2618697699
<i>ehbK</i>	D5_0235	TL18_09580	2595205592	mbs_2121	2657040070	Msm_1066	2620724589	MRU_R_S10035	2595158180	YLM1_1461	2558933878	2540854770	2553937628	Ga0074191_109031	Ga0074190_106946	Ga0078795_10918	Ga0078798_125788	2618697698
<i>ehbL</i>	D5_0236	TL18_09575	2595205591	mbs_2120	2657040071	Msm_1065	2620724588	MRU_R_S10030	2595158179	YLM1_1460	2558933879	2540854769	2553937627	Ga0074191_109030	Ga0074190_106947	Ga0078795_10917	Ga0078798_125789	2618697697
<i>ehbM</i>	D5_0237	TL18_09570	2595205590	mbs_2119	2657040072	Msm_1064	2620724587	MRU_R_S10025	2595158178	YLM1_1459	2558933880	2540854768	2553937626	Ga0074191_109029	Ga0074190_106948	Ga0078795_10916	Ga0078798_125790	2618697696
<i>ehbN</i>	D5_0238	TL18_09565	2595205589	mbs_2118	2657040073	Msm_1063	2620724586	MRU_R_S10020	2595158177	YLM1_1458	2558933881	2540854767	2553937625	Ga0074191_109028	Ga0074190_106949	Ga0078795_10915	Ga0078798_125791	2618697695
<i>ehbO</i>	D5_0239	TL18_09560	2595205588	mbs_2117	2657040074	Msm_1062	2620724585	MRU_R_S10015	2595158176	YLM1_1457	2558933882	2540854766	2553937624	Ga0074191_109027	Ga0074190_106950	Ga0078795_10914	Ga0078798_125792	2618697694
<i>ehbP</i>	D5_0240	TL18_09555	2595205587	mbs_2116	2657040075	Msm_1061	2620724584	MRU_R_S10010	2595158175	YLM1_1456	2558933883	2540854765	2553937623	Ga0074191_109026	Ga0074190_106951	Ga0078795_10913	Ga0078798_125793	2618697693
<i>ehbQ</i>	D5_0241	TL18_09550	2595205586	mbs_2115	2657040076	Msm_1060	2620724583	MRU_R_S10005	2595158174	YLM1_1455	2558933884	2540854764	2553937622	Ga0074191_109025	Ga0074190_106952	Ga0078795_10912	Ga0078798_125794	2618697692
Hydrogenase helper genes									2595158367, 2595158351	YLM1_1119, YLM1_1135	2558934039	2540853801	2553938447	Ga0074191_11337	Ga0074190_113218	Ga0078795_12974	Ga0078798_1257424	2618698226
<i>hypA</i>	D5_1528	TL18_05565	2595203723	mbs_0965	2657039642	Msm_0108	2620724989	MRU_R_S08165	2595158367, 2595158351	YLM1_1119, YLM1_1135	2558934039	2540853801	2553938447	Ga0074191_11337	Ga0074190_113218	Ga0078795_12974	Ga0078798_1257424	2618698226
<i>hypB</i>	D5_1527	TL18_05560	2595203722	mbs_0966	2657039641	Msm_0107	2620724988	MRU_R_S08160	2595158352	YLM1_1134	2558934038	2540853802	2553938448	Ga0074191_11336	Ga0074190_113219	Ga0078795_12975	Ga0078798_1257425	2618698227
<i>hypC</i>	D5_2235	TL18_01440	2595204947	mbs_0341	2657040511	Msm_0636	2620725430	MRU_R_S02400	2595158889	YLM1_0147	2558933425	2540853449	2553938025	Ga0074191_116429	Ga0074190_118520	Ga0078795_11845	Ga0078798_111535	2618697216
<i>hypD</i>	D5_0364	TL18_08960	2595203981	mbs_1938	2657040189	Msm_0945	2620724406	MRU_R_S09385	2595158065	YLM1_1342	2558933475	2540853492	2553938068	Ga0074191_11584	Ga0074190_11722	Ga0078795_10657	Ga0078798_1257206	2618697858
<i>hypE</i>	D5_0144	TL18_10050,	2595205183,	mbs_0155	2657039979,	Msm_1492,	2620724691,	MRU_R_S07745,	2595159121,	YLM1_1048,	2558933321,	2540853330,	2553937910,	Ga0074191_11186,	Ga0074190_10275,	Ga0078795_12916,	Ga0078798_101912,	2618697386,
	D5_0807	TL18_06970	2595204603	mbs_1610	2657041146	Msm_1158	2620725807	MRU_R_S00955	2595159866	YLM1_1506	2558933573	2540854339	2553936955	Ga0074191_112842	Ga0074190_113232	Ga0078795_128722	Ga0078798_102420	2618698237
<i>hypF</i>	D5_0194	TL18_09780	2595205183	mbs_2165	2657040028	Msm_1106	2620724639	MRU_R_S10220	2595159572	YLM1_1493	2558933845	2540854804	2553937662	Ga0074191_113543	Ga0074190_11084	Ga0078795_11564	Ga0078798_125751	2618697316
<i>hycl</i>	D5_1825	TL18_03185	2595205815	mbs_0680	2657039397	Msm_0362	2620726449	MRU_R_S05225	2595159150	YLM1_0589	2558934177	2540854184	2553937097	Ga0074191_10534	Ga0074190_100948	Ga0078795_107142	Ga0078798_102455	2618698684

Alternative reducing potential from alcohol																	
<i>npdG</i>	D5_	TL18_	259520				262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191			
	1461	05575_	5557_	mbs_	265704	Msm_0	4964,	S07215,	9766,	_0542,	4599,	4816,	7440,	_11677,	Ga0074190	Ga007879	Ga0078798_
		TL18_	259520	1352	1207	049	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	_11184	5_10972	11359
		05310	5861				6112	S04990	8790	_0957	4474	3851	7675	_117027			8283
<i>adh</i> (NA DP depe ndent)	-	TL18_	-	-	-	-	-	MRU_R	259515	YLM1	-	-	-	-	-	-	-
		05985						S09245	8215	_1244							
A ₁ A ₀ ATP synthase																	
<i>ahaD</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1938	02715	4423	0591	0901	433	5948	S03565	8944	_0349	34772	3630	8215	_10809	_10443	5_124816	1257337
<i>ahaB</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1939	02710	4424	0590	0902	434	5947	S03560	8945	_0348	34773	3631	8214	_108010	_10444	5_124815	1257336
<i>ahaA</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1940	02705	4425	0589	0903	435	5946	S03555	8946	_0347	34774	3632	8213	_108011	_10445	5_124814	1257335
<i>ahaF</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1941	02700	4426	0588	0904	436	5945	S03550	8947	_0346	34775	3633	8212	_108012	_10446	5_124813	1257334
<i>ahaC</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1942	02695	4427	0587	0905	437	5944	S03545	8948	_0345	34776	3634	8211	_108013	_10447	5_124812	1257333
<i>ahaE</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1943	02690	4428	0586	0906	438	5943	S03540	8949	_0344	34777	3635	8210	_108014	_10448	5_124811	1257332
<i>ahaK</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1944	02685	4429	0585	0907	439	5942	S03535	8950	_0343	34778	3636	8209	_108015	_10449	5_124810	1257331
<i>ahaI</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1945	02680	4430	0584	0908	440	5941	S03530	8951	_0342	34779	3637	8208	_10667	_104410	5_12489	1257330
<i>ahaH</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255839	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1946	02675	4431	0583	0909	441	5940	S03525	8952	_0341	34780	3638	8207	_10666	_104411	5_12488	1257329
Methanogenesis Marker proteins																	
<i>mmp</i> <i>1</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	2000	02440	4464	0549	0939	480	5905	S03395	8676	_0311	4966	3605	8182	_11773	_115372	5_115314	1257304
<i>mmp</i> <i>4</i>	D5_	TL18_	259520	mbs_	265703	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	1511	05490	3707	0994	9804	095	4975	S05055	9186	_0550	4502	3879	7412	_111612	_114937	5_11997	1257534
<i>mmp</i> <i>17</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	0635	07705	3606	1767	0725	809	4242	S08850	8217	_1246	3774	4515	6776	_109125	_105952	5_14603	12313
<i>mmp</i> <i>15</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	0634	07710	3605	1768	0724	810	4243	S08855	8218	_1247	3775	4516	6775	_109115	_105953	5_14604	12312
<i>mmp</i> <i>5</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	0633	07715,	3604	1769	0723	811,	4244,	MRU_R	259515	YLM1	255893	4517,	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
		TL18_	09905	mbs_	0723	Msm_1	262072	S08860	8219	_1248	3776	254085	6774	_109114	_105954	5_14605	12311
		0171		0189	130	5242						3526					6984
<i>mmp</i> <i>6</i>	D5_	TL18_	259520	mbs_	265704	Msm_0	262072	MRU_R	259515	YLM1	255893	254085	255393	Ga0074191	Ga0074190	Ga007879	Ga0078798_
	0632	07720	3603	1770	0722	812	4245	S08865	8220	_1249	3777	4518	6773	_109113	_105958	5_14606	122813

<i>mmp</i> 3	D5_ 0631	TL18_ 07725	259520 3602	mbs_ 1771	265704 0721	Msm_0 813	262072 4246	MRU_R S08870	259515 8221	YLM1 _1250	255893 3778	254085 4519	255393 6772	Ga0074191 _109112	Ga0074190 _105959	Ga007879 5_14607	Ga0078798_ 122812	261869 6986
<i>mmp</i> 2	D5_ 0627	TL18_ 07740	259520 3600	mbs_ 1772	265704 0718	Msm_0 814	262072 4248	MRU_R S08890	259515 8225	YLM1 _1251	255893 3779	254085 4520	255393 6771	Ga0074191 _109111	Ga0074190 _105960	Ga007879 5_14608	Ga0078798_ 122811	261869 6987
<i>mmp</i> 7	D5_ 0282	TL18_ 09350	259520 5120	mbs_ 2072	265704 0118	Msm_0 815, Msm_1 021	262072 4523	MRU_R S09665	259515 8123	YLM1 _1401	255893 3927	254085 4723	255393 7580	Ga0074191 _10327	Ga0074190 _106920	Ga007879 5_12915	Ga0078798_ 1257133	261869 7751
<i>mmp</i> 10	D5_ 0283	TL18_ 09345	259520 5121	mbs_ 2071	265704 0119	Msm_1 020	262072 4521	MRU_R S09655	259515 8122	YLM1 _1400	255893 3929	254085 4721	255393 7578	Ga0074191 _10345	Ga0074190 _11181	Ga007879 5_108126	Ga0078798_ 1257135	261869 7761
<i>mmp</i> 8	D5_ 2244	TL18_ 01400	259520 5337	mbs_ 0333	265704 0449	Msm_0 643	262072 4850	MRU_R S02215	259515 9237	YLM1 _0106	255893 4421	254085 4313	255393 6981	Ga0074191 _11034	Ga0074190 _111411	Ga007879 5_115416	Ga0078798_ 1257629	261869 7231
<i>mmp</i> 9	D5_ 0332	TL18_ 09115	259520 3941	mbs_ 1970	265704 0166	Msm_0 969	262072 4439	MRU_R S09265	259515 8297	YLM1 _1321	255893 3975	254085 4673	255393 7530	Ga0074191 _105911	Ga0074190 _116230	Ga007879 5_132015	Ga0078798_ 1257237	261869 7893
<i>mmp</i> 11	D5_ 2489	TL18_ 00260	259520 4773	mbs_ 2335	265704 0737	Msm_1 295	262072 5630	MRU_R S00495	259515 8642	YLM1 _1590	255893 4693	254085 4901	255393 7763	Ga0074191 _10153	Ga0074190 _111844	Ga007879 5_11337	Ga0078798_ 101995	261869 7533
<i>mmp</i> 12	D5_ 0062	TL18_ 10390	259520 4725	mbs_ 0064	265703 9909	Msm_1 221	262072 6351	MRU_R S10605	259515 9458	YLM1 _1730	255893 3290	254085 3273	255393 7850	Ga0074191 _10707	Ga0074190 _11352	Ga007879 5_113010	Ga0078798_ 1095141	261869 7480
<i>mmp</i> 13	D5_ 0142	TL18_ 10060	259520 4601	mbs_ 0153	265703 9977	Msm_1 160	262072 4693	MRU_R S00910	259515 9111	YLM1 _1516	255893 3319	254085 3328	255393 7908	Ga0074191 _11272	Ga0074190 _11112	Ga007879 5_10302	Ga0078798_ 101915	261869 7387
<i>mmp</i> 14	D5_ 0297	TL18_ 09275	259520 5135	mbs_ 2057	265704 0133	Msm_1 006	262072 4506	MRU_R S09585	259515 8107	YLM1 _1385	255893 3943	254085 4707	255393 7564	Ga0074191 _103419	Ga0074190 _102011	Ga007879 5_10818	Ga0078798_ 1257149	261869 7777
<i>mmp</i> 16	D5_ 0150	TL18_ 05465, TL18_ 10010	259520 3699, 259520 5319	mbs_ 1000 , mbs_ 0163	265703 9809, 265703 9985	Msm_0 085	262072 4679, 262072 6074	MRU_R S09680	259515 8125, 259515 9536	YLM1 _0886, YLM1 _1403	255893 3494, 255893 4519	254085 3519, 254085 3894	255393 7397, 255393 8099	Ga0074191 _107212	Ga0074190 _118166	Ga007879 5_123512	Ga0078798_ 1257523	261869 7195
Cofactor F₄₂₀ biosynthesis																		
<i>cofA</i>	D5_ 1974	TL18_ 02565	259520 4453	mbs_ 0557	265704 0931	Msm_0 467	262072 5913	MRU_R S03415	259515 8976	YLM1 _0316	255893 4971	254085 3609	255393 8186	Ga0074191 _117710	Ga0074190 _109324	Ga007879 5_12159	Ga0078798_ 1257306	261869 7968
<i>fucA</i>	D5_ 2508	TL18_ 00160	259520 4800	mbs_ 2363	265703 9858	Msm_1 270	262072 6296	MRU_R S11110	259515 8600	YLM1 _1634	255893 4713	254085 4921	255393 7781	Ga0074191 _102614	Ga0074190 _103430	Ga007879 5_11833	Ga0078798_ 1019112	261869 7520
<i>cofC</i>	D5_ 1723	TL18_ 06430	259520 5421	mbs_ 0786	265704 0342	Msm_0 288	262072 5166	MRU_R S04805	259515 8831	YLM1 _0517	255893 3627	254085 4406	255393 6885	Ga0074191 _114657	Ga0074190 _105627	Ga007879 5_118516	Ga0078798_ 1257210	261869 8829
<i>cofH</i>	D5_ 1498	TL18_ 05430	259520 5699	mbs_ 1010	265703 9815	Msm_0 079	262072 6081	MRU_R S06335	259515 9655	YLM1 _0646	255893 4853	254085 3974	255393 7310	Ga0074191 _10448	Ga0074190 _115329	Ga007879 5_12238	Ga0078798_ 1257555	261869 8143
<i>cofD</i>	D5_ 0325	TL18_ 09140	259520 3931	mbs_ 1976	265704 0161	Msm_0 974	262072 4446	MRU_R S09230	259515 8292	YLM1 _1316	255893 3971	254085 4677	255393 7534	Ga0074191 _105915	Ga0074190 _11626	Ga007879 5_12644	Ga0078798_ 1257243	261869 7889
<i>cofE</i>	D5_ 0324 , D5_ 0503 , 2229	TL18_ 01485, TL18_ 07135, TL18_ 09145	259520 3908, 259520 3930, 259520 4954	mbs_ 0348 , mbs_ 1590 , mbs_ 1977	265703 9374, 265704 0160, 265704 0520	Msm_0 630, Msm_0 975	262072 4447, 262072 5418	MRU_R S02435, MRU_R S09220, MRU_R S04775	259515 8290, 259515 8896	YLM1 _0154, YLM1 _1314	255893 3432, 255893 3970	254085 3457, 254085 4680	255393 7537, 255393 8033	Ga0074191 _116414	Ga0074190 _11627	Ga007879 5_12643	Ga0078798_ 111526	261869 7207, 261869 7900

<i>cofG</i>	D5_ 0268	TL18_ 09420	259520 5679	mbs_ 2086	265704 0104	Msm_1 035	262072 4550	MRU_R S09880	259515 8151	YLM1 _1429	255893 3912	25408 54737	255393 7594	Ga0074191 _103211	Ga0074190 _106618	Ga007879 5_11188	Ga0078798_ 1257118	261869 7743
<i>cofF</i>	-	-	-	-	-	-	-	-	-	-	-	-	-					-
Cofactor F₄₃₀ biosynthesis																		
<i>ftsA</i>	D5_ 1885	TL18_ 02950	259520 4385	mbs_ 0629	265703 9354	Msm_0 387	262072 5990	MRU_R S08925	259515 8232	YLM1 _1261	255893 3786	254085 4528	255393 6761	Ga0074191 _113716, Ga0074191 _115715	Ga0074190 _10593, Ga0074190 _10936	Ga007879 5_12463, Ga007879 5_11315	Ga0078798_ 12283, Ga0078798_ 109544	261869 6998
CoM biosynthesis																		
<i>comA</i>	D5_ 1506	TL18_ 05470	259520 3700	mbs_ 0999	265703 9808	Msm_0 086	262072 6073	-	259515 9537	YLM1 _0887	255893 4518	254085 3893	255393 7398	Ga0074191 _116413	Ga0074190 _10706	Ga007879 5_11527	Ga0078798_ 1257524	261869 7206
<i>comB</i>	D5_ 0280	TL18_ 09360	259520 5118	mbs_ 2074	265704 0116	Msm_1 023	262072 4525	MRU_R S09755	259515 8138	YLM1 _1416	255893 3925	254085 4725	255393 7582	Ga0074191 _10325	Ga0074190 _118153	Ga007879 5_12133	Ga0078798_ 1257131	261869 7749
<i>comC</i>	D5_ 0263	TL18_ 09445	259520 5671	mbs_ 2091	265704 0099	Msm_1 040	262072 4555	MRU_R S09915	259515 8156	YLM1 _1434	255893 3907	254085 4742	255393 7599	Ga0074191 _103217	Ga0074190 _112510	Ga007879 5_11183	Ga0078798_ 1257113	261869 7728
<i>comD</i>	D5_ 1500	TL18_ 05435	259520 5698	mbs_ 1009	265703 9814	Msm_0 080	262072 6080	-	259515 9268	YLM1 _0891	255893 4526	254085 3900	255393 7391	Ga0074191 _103218	Ga0074190 _118172	Ga007879 5_12353	Ga0078798_ 1257526	261869 7729
<i>comE</i>	D5_ 1501	TL18_ 05440	259520 5697	mbs_ 1008	265703 9813	Msm_0 081	262072 6079	-	259515 9269	YLM1 _0892	255893 4525	254085 3899	255393 7392	Ga0074191 _103219	Ga0074190 _118174	Ga007879 5_12352	Ga0078798_ 1257525	261869 7731 (interpreted)
CoB biosynthesis																		
<i>aksA</i>	D5_ 2368	TL18_ 01070	259520 4630	mbs_ 2204	265704 0840	Msm_0 722	262072 5500	MRU_R S01960	259515 8457	YLM1 _0056	255893 3368	254085 3386	255393 7967	Ga0074191 _10333	Ga0074190 _108982	Ga007879 5_108016	Ga0078798_ 111593	261869 7687
<i>aksD</i>	D5_ 2369	TL18_ 01065	259520 4631	mbs_ 2205	265704 0839	Msm_0 723	262072 5501	MRU_R S01955	259515 8458	YLM1 _0055	255893 3367	254085 3385	255393 7966	Ga0074191 _10334	Ga0074190 _108981	Ga007879 5_108015	Ga0078798_ 111594	261869 7686
<i>aksE</i>	D5_ 0588	TL18_ 07930	259520 3567	mbs_ 1805	265704 0684	Msm_0 847	262072 5628	MRU_R S08455	259515 9789	YLM1 _1170	255893 4092	254085 3716	255393 8362	Ga0074191 _11133	Ga0074190 _115326	Ga007879 5_12235	Ga0078798_ 1257397	261869 8130
<i>aksF</i>	D5_ 1844	TL18_ 03130	259520 5711	mbs_ 0656	265703 9388	Msm_0 373	262072 6405	MRU_R S05195	259515 9156	YLM1 _0583	255893 4387	254085 4197	255393 7084	Ga0074191 _117019	Ga0074190 _108054	Ga007879 5_121413	Ga0078798_ 102445	261869 7536
Methanofuran biosynthesis																		
<i>mf nA</i>	D5_ 0313	TL18_ 09200	259520 3920	mbs_ 1987	265704 0149	Msm_0 987	262072 4462	MRU_R S09490	259515 8090	YLM1 _1368	255893 3959	254085 4691	255393 7548	Ga0074191 _11761	Ga0074190 _108932	Ga007879 5_115117	Ga0078798_ 1257174	261869 7806
<i>mf nB</i>	D5_ 1007	TL18_ 04040	259520 5086	mbs_ 1425	265704 1043	Msm_1 628	262072 5653	MRU_R S06050	259515 8980	YLM1 _0629	255893 4836	254085 3962	255393 7323	Ga0074191 _11033	Ga0074190 _10735	Ga007879 5_120812	Ga0078798_ 12062	261869 8343
<i>mf nD</i>	D5_ 0584	TL18_ 07950	259520 3561	mbs_ 1811	265704 0680	Msm_0 852	262072 4294	MRU_R S08490	259515 9782	YLM1 _1178	255893 4099	254085 3707	255393 8352	Ga0074191 _10818	Ga0074190 _105611	Ga007879 5_10753	Ga0078798_ 1257390	261869 8123
<i>mf nF</i>	D5_ 0585	TL18_ 07945	259520 3562	mbs_ 1810	265704 0681	Msm_0 851	262072 4292	MRU_R S08485	259515 9783	YLM1 _1177	255893 4098	254085 3708	255393 8353	Ga0074191 _10817	Ga0074190 _105612	Ga007879 5_10752	Ga0078798_ 1257391	261869 8125
<i>mf nE</i>	D5_ 2202	TL18_ 01695	259520 4993	mbs_ 0377	265704 0545	Msm_0 604	262072 5298	MRU_R S02630	259515 8925	YLM1 _0186	255893 3993	254085 4652	255393 7509	Ga0074191 _10592	Ga0074190 _111418	Ga007879 5_11576	Ga0078798_ 11155	261869 7171
H₄MPT biosynthesis																		
<i>arfA/ mptA</i>	D5_ 0270	TL18_ 09410	259520 5681	mbs_ 2084	265704 0106	Msm_1 033	262072 4548	MRU_R S09820	259515 8148	YLM1 _1426	255893 3914	254085 4735	255393 7592	Ga0074191 _10329	Ga0074190 _106930	Ga007879 5_111810	Ga0078798_ 1257120	261869 7741

<i>arfB</i>	D5_1597	TL18_05910	2595203798	mbs_0884	2657041003	Msm_0184	2620725062	MRU_R_S06415	2595159602	YLM1_0803	2558934885	2540853998	2553937285	Ga0074191_109215	Ga0074190_108012	Ga0078795_11255	Ga0078798_1257631	2618698554
<i>mptD</i>	D5_0314	TL18_09195	2595203921	mbs_1986	2657040150	Msm_0985	2620724461	MRU_R_S09165	2595158280	YLM1_1304	2558933960	2540854690	2553937547	Ga0074191_10223	Ga0074190_116224	Ga0078795_11217	Ga0078798_1257256	2618697910
<i>mptE</i>	D5_2280	TL18_01270	2595205894	mbs_0300	2657040423	Msm_0672	2620725465	MRU_R_S02140	2595158424	YLM1_0089	2558933394	2540853417	2553937993	Ga0074191_10356	Ga0074190_116117	Ga0078795_100722	Ga0078798_111566	2618697259
<i>mptG</i>	D5_1075	TL18_04245	2595203621	mbs_1758	2657040225	Msm_0848	2620726063	MRU_R_S08460	2595159788	YLM1_1171	2558934095	2540853715	2553938360	Ga0074191_11132	Ga0074190_111174	Ga0078795_12234	Ga0078798_1257396	2618698129
<i>mptH</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>citG</i>	D5_0790	TL18_07015	2595205783	mbs_1619	2657041157	Msm_1477	2620725818	MRU_R_S07785	2595159704	YLM1_1056	2558933585	2540854369	2553936922	Ga0074191_11497	Ga0074190_100941	Ga0078795_107148	Ga0078798_102414	2618698691
<i>dmrX</i>	D5_2463	TL18_00390	2595204524	mbs_2294	2657040764	Msm_1338	2620725593	MRU_R_S00625	2595158661	YLM1_1571	2558934539	2540854875	2553937736	Ga0074191_114660	Ga0074190_111464	Ga0078795_13164	Ga0078798_101960	2618697576

*JGI IMG gene ID number is shown instead of locus_tag. # Temporary locus_tag is displayed as this draft genome has not been submitted. Temporary locus_tag is subject to change once genome completes. Formate dehydrogenase (*fdhAB/flpAB*), formate transporter (*fdhC*), formate dehydrogenase accessory protein (*fdhD*), formylmethanofuran dehydrogenase (*fwdA-H*), formylmethanofuran-tetrahydromethanopterin formyl transferase (*ftr*), N⁵,N¹⁰-methenyl-H₄MPT cyclohydrolase (*mch*), F₄₂₀-dependent methylene-H₄MPT dehydrogenase (*mtd*), F₄₂₀ reducing hydrogenase (*frhABDG*), methylene-H₄MPT reductase (*mer*), tetrahydromethanopterin S-methyltransferase (*mtrA-H*), H₂-dependent methylene-H₄MPT dehydrogenase (*hmd*), methyl-CoM reductase (*mcr/mrtA-G*), heterodisulfide reductase (*hdrABC*), methyl-viologen hydrogenase (*mvhABDG*), energy conserving hydrogenase (*eha/ehbA-T*), hydrogenase nickel insertion protein (*hypA*), hydrogenase accessory protein (*hypB*), hydrogenase assembly chaperone (*hypC*), hydrogenase expression/formation protein (*hypDEI*), hydrogenase maturation factor (*hypF*), NADP-dependent F₄₂₀ reductase (*npdG*), alcohol dehydrogenase (*adh*), Na⁺/H⁺ antiporter (*nha*), A₁A₀ ATP synthase subunits are present (*ahaA-K*), methanogenesis marker protein (*mmp1-17*), lactaldehyde dehydrogenase (*cofA*), L-fucose phosphate aldolase (*fucA*), 2-phospho-L-lactate guanylyltransferase (*cofC*), LPPG:FO 2-phospho-L-lactate transferase (*cofD*), F₄₂₀-O:gamma-glutamyl ligase (*cofE*), γ-F₄₂₀-2:α-L-glutamate ligase (*cofF*), FO synthase (*cofGH*), coenzyme F₃₉₀ synthetase (*ftsA*), (2R)-phospho-3-sulfolactate synthase (*comA*), 2-phosphosulfolactate phosphohydrolase (*comB*), (2R)3-sulfolactate dehydrogenase (*comC*), sulfopyruvate decarboxylase (*comDE*), (R)-homocitrate synthase (*aksA*), (R)-homocitrate dehydratase (*aksDE*), Threo-isohomocitrate dehydrogenase (*aksF*), aspartate 1-decarboxylase/L-tyrosine decarboxylase (*mfnA*), 2-furaldehyde phosphate synthase (*mfnA*), tyramine—L-glutamate ligase (*mfnD*), (4-{4-[2-(γ-L-glutamylamino)ethyl]phenoxyethyl}furan-2-yl)methanamine synthase (*mfnF*), [5-(aminomethyl)furan-3-yl]methyl phosphate kinase (*mfnE*), GTP cyclohydrolase III/IV (*arfA/mptA*), 2-amino-5-formylamino-6-ribosylaminopyrimidin-4(3H)-one 5'-monophosphate deformylase (*arfB*), dihydroneopterin aldolase (*mptD*), 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase (*mptE*), beta-ribofuranosylaminobenzene 5-phosphate synthase (*mptG*), dihydropteroate synthase (*mptH*), triphosphoribosyl-dephospho-CoA synthase (*citG*), dihydromethanopterin reductase (*dmrX*).