

NCBI ID	COG(s)	Locus	Gene	Functional category	Subcategory	Putative function	A vs 7d (T1)	A	B	C	D	E	F	G	H	A vs 7d (T2)	A	B	C	D	E	F	G	H	
1029804	COG0593L	gbs0001	dnaA	Cellular processes	DNA replication, recombination and repair	Chromosomal replication initiator protein dnaA	2,315	P	P	P	P	P	P	P	P	1,780	P	P	P	P	P	P	P	P	
1029808	COG0592L	gbs0002	dnaN	Cellular processes	DNA replication, recombination and repair	DNA polymerase III, beta chain (EC 2.7.7.7)	1,806	P	P	P	P	P	P	P	P	1,579	P	P	P	P	P	P	P	P	
1029799	COG1597IR	gbs0003		Hypothetical		Hypothetical protein	2,367	P	A	P	M	P	P	M	A	1,517	P	A	A	M	A	A	A	A	
1029797	-	gbs0004		Hypothetical		Hypothetical cytosolic protein	2,072	P	A	A	A	A	A	A	A	2,088	P	A	A	A	A	A	A	A	
1029795	-	gbs0005		Hypothetical		Hypothetical protein	2,043	P	P	P	P	P	P	P	P	1,930	P	A	P	P	A	P	A	P	
1030675	COG0012J	gbs0006	ychF	Cellular processes	Translation, ribosomal structure and biogenesis	GTP-binding protein, probable translation factor	1,744	P	P	P	P	P	P	P	P	0,759	P	P	P	P	P	P	P	P	
1030987	-	gbs0007	pth	Cellular processes	Translation, ribosomal structure and biogenesis	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	7,592	M	A	A	A	A	A	A	A	0,205	A	A	A	A	A	A	A	A	A
1029794	COG1197LK	gbs0008	trcF	Cellular processes	DNA replication, recombination and repair	Transcription-repair coupling factor	5,373	A	A	A	A	A	A	A	A	0,675	A	A	A	A	A	A	A	A	A
1029790	COG1188J	gbs0009	HSP15	Cellular processes	Translation, ribosomal structure and biogenesis	Heat shock protein 15	1,616	P	P	P	P	P	P	P	P	1,256	P	A	M	A	A	A	A	A	
1029787	COG2919D	gbs0010	divIC	Cellular processes	Cell division	Cell division protein DIVIC	1,876	P	P	P	A	P	P	P	P	0,885	P	A	P	P	P	P	A	P	
1030424	-	gbs0011		Hypothetical		Hypothetical protein	3,462	P	P	P	P	P	P	P	P	1,608	P	A	P	A	P	P	A	P	
1029782	COG2367V	gbs0012		Cellular processes	Toxin production and resistance	Beta-lactamase (EC 3.5.2.6)	2,410	P	P	P	M	P	P	P	P	0,890	P	A	A	A	A	P	P	A	
1029802	COG0037D	gbs0013	tiIS	Cellular processes	Translation, ribosomal structure and biogenesis	tRNA(Ile)-lysine synthetase TiIS	2,234	P	A	P	A	P	P	A	A	0,662	P	A	P	A	A	P	M	A	
1030991	COG0634F	gbs0014	hpt	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Purine, pyrimidine, nucleoside, and nucleotide	1,717	P	P	P	P	P	P	P	1,275	P	A	P	P	P	P	P	P	P	
1030977	COG0465O	gbs0015	ftsH	Cellular processes	Posttranslational modification, protein turnover, chaperones	Cell division protein ftsH (EC 3.4.24.-)	1,549	P	P	P	P	P	P	P	1,524	P	A	P	A	P	P	P	P	P	
1031481	3883S, COG3	gbs0016	pcsB	Cell Envelope	Other	Glucan-binding protein B	1,454	P	P	P	P	P	P	P	0,773	P	P	P	P	P	P	P	P	P	
1031120	COG0462FE	gbs0017	prsA.2	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	2,160	P	P	P	P	P	P	P	1,270	P	P	P	P	P	P	P	P	P	
1031047	COG0436E	gbs0018	aspB	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Aromatic amino acid aminotransferase (EC 2.6.1.57) Acetylglutamate amin	1,417	P	P	P	P	P	P	P	1,684	P	A	P	M	P	P	P	P	P	
1030999	COG1381L	gbs0019	recO	Cellular processes	DNA replication, recombination and repair	DNA repair protein recO	2,436	P	P	P	P	P	P	P	1,477	P	A	P	M	M	P	P	P	P	
1031000	-	gbs0020		Cellular processes	Posttranslational modification, protein turnover, chaperones	CAAX amino terminal protease family	0,248	A	A	A	A	A	A	A	P	0,145	A	P	A	A	A	A	A	A	
1031476	COG0416I	gbs0021	plsX	Metabolism and transport	Fatty acid and phospholipids	Fatty acid phospholipid synthesis protein plsX	2,831	P	P	P	P	P	P	P	1,619	P	A	P	P	P	P	A	P	A	
1031477	COG0236IQ	gbs0022	acpP.2	Metabolism and transport	Fatty acid and phospholipids	Acyl carrier protein	2,238	P	P	P	P	P	P	P	1,257	P	A	P	A	A	P	P	A	P	
1031217	-	gbs0023	purC	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	1,620	P	P	P	P	P	P	P	0,476	A	A	A	A	P	A	P	A	P	
1030849	30046F, COG0	gbs0024		Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylformylglycinamide synthase (EC 6.3.5.3)	0,995	P	P	P	P	P	P	P	0,619	P	P	P	P	P	P	M	P	P	
1031315	COG0034F	gbs0025	purF	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Amidophosphoribosyltransferase (EC 2.4.2.14)	1,502	P	P	P	P	P	P	P	1,845	P	A	A	A	P	A	P	A	P	
1029830	COG0150F	gbs0026	purM	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)	0,989	P	P	P	P	P	P	P	0,845	P	M	P	P	P	P	P	P	P	
1030771	-	gbs0027	purN	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	1,741	P	M	P	P	P	P	P	2,252	P	A	A	A	A	A	A	A	A	
1031482	-	gbs0028		Hypothetical		Zwittermucin A resistance protein zmaR	1,920	P	P	P	P	P	P	P	3,580	P	M	A	A	P	A	P	A	A	
1031413	-	gbs0029	purH	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) IMP c	1,145	P	P	P	P	P	P	P	1,761	P	A	P	A	P	P	P	P	P	
1031034	COG0739M	gbs0030		Cellular processes	Posttranslational modification, protein turnover, chaperones	Peptidoglycan-specific endopeptidase, M23 family	1,373	P	A	A	A	A	A	A	0,083	A	A	A	A	A	A	A	A	A	
1031483	-	gbs0031	slp	Hypothetical		Surface antigen	1,099	P	P	P	P	P	P	P	0,853	P	P	P	P	P	P	P	P	P	
1029831	COG3010G	gbs0032		Metabolism and transport	Carbohydrates, organic alcohols, and acids	N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)	0,612	P	A	P	A	A	A	A	A	8,317	P	P	P	P	P	P	P	P	
1030981	COG1653G	gbs0033		Metabolism and transport	Carbohydrates, organic alcohols, and acids	N-acetylneuraminate-binding protein	0,803	A	A	A	A	A	A	A	A	7,517	P	A	P	A	P	M	A	A	
1029979	COG1175G	gbs0034		Metabolism and transport	Carbohydrates, organic alcohols, and acids	N-acetylneuraminate transport system permease protein	0,658	A	A	A	A	A	A	A	A	7,252	P	A	M	A	A	A	A	A	
1031470	COG0395G	gbs0035		Metabolism and transport	Carbohydrates, organic alcohols, and acids	N-acetylneuraminate transport system permease protein	0,176	A	A	A	A	A	A	A	A	4,372	P	A	P	A	A	A	A	A	
1031485	-	gbs0036		Hypothetical		Hypothetical cytosolic protein	0,420	A	A	M	A	A	A	A	A	4,450	P	A	P	A	P	P	A	A	
1031486	-	gbs0037		Hypothetical		Hypothetical membrane spanning protein	2,058	A	A	A	A	A	A	A	A	2,842	P	A	P	A	A	P	A	A	
1030355	COG0329EM	gbs0038	nanH	Cell Envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	N-acetylneuraminate lyase (EC 4.1.3.3)	0,243	A	A	A	A	A	A	A	A	3,891	P	A	A	A	A	A	A	A	
1030984	COG1940KG	gbs0039		Cellular processes	Signal transduction	N-acetylmannosamine kinase (EC 2.7.1.60) Transcriptional regulator	0,727	A	A	A	A	A	A	A	A	1,828	P	A	A	A	A	A	A	A	
1031495	COG3458Q	gbs0040		Metabolism and transport	Secondary metabolites	Cephalosporin-C deacetylase (EC 3.1.1.41)	0,658	A	A	A	A	A	A	A	A	1,542	P	A	M	A	A	A	A	A	
1030478	COG1737K	gbs0041		Cellular processes	Transcription	Transcriptional regulator, RpiR family	2,221	P	P	P	P	P	P	P	1,641	P	P	P	P	P	P	P	P	P	
1031720	COG00151F	gbs0042	purD	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylamine-glycine ligase (EC 6.3.4.13)	0,535	P	P	P	P	P	P	P	0,302	A	A	M	A	A	M	P	A	P	
1030779	COG0041F	gbs0043	purE	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylaminoimidazole carboxylase carboxyltransferase subunit (EC 4.1.1.1)	0,670	P	P	P	P	P	P	P	0,495	P	A	A	A	A	P	M	M	A	
1030263	COG0026F	gbs0044	purK	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Phosphoribosylaminoimidazole carboxylase NCAIR mutase subunit (EC 4.1.1.21)	0,611	P	P	P	P	P	P	P	0,561	P	A	M	A	A	P	M	A	A	
1030998	-	gbs0045		Hypothetical		Hypothetical protein	0,847	P	P	P	P	P	P	P	1,526	P	P	P	P	P	P	P	P	P	
1030996	-	gbs0046		Hypothetical		Hypothetical protein	0,869	P	P	P	P	P	P	P	1,559	P	P	P	P	P	P	P	P	P	
1030994	COG0015F	gbs0047	purB	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Adenylosuccinate lyase (EC 4.3.2.2)	0,787	P	P	P	P	P	P	P	0,945	P	P	P	P	P	P	P	P	P	
1030979	-	gbs0048		Cellular processes	Transcription	Transcriptional regulator	1,625	P	P	P	P	P	P	P	1,978	P	A	P	P	P	P	A	M	A	
1030989	COG2255L	gbs0049	ruvB	Cellular processes	DNA replication, recombination and repair	Holliday junction DNA helicase ruvB	1,175	P	A	A	A	A	A	A	A	0,847	P	A	A	A	A	A	A	A	
1030982	COG0394T	gbs0050		Cellular processes	Signal transduction	Protein tyrosine phosphatase (EC 3.1.3.48)	0,940	P	P	P	P	P	P	P	1,256	P	P	P	P	P	P	P	M	A	
1030978	COG4642S	gbs0051		Hypothetical		Hypothetical membrane associated protein	1,199	P	P	P	P	P	P	P	2,411	P	A	P	A	M	A	A	A	A	
1030985	COG1835I	gbs0052		Metabolism and transport	Fatty acid and phospholipids	Acyltransferase family	1,648	P	P	P	P	P	P	P	1,596	P	P	P	P	P	P	P	P	P	
1030824	1012C, COG1	gbs0053	adh2	Metabolism and transport	Energy production and conversion	Alcohol dehydrogenase (EC 1.1.1.1) Acetaldehyde dehydrogenase [acetylating] (0,660	P	A	A	P	P	P	A	0,346	P	P	A	P	P	A	P	A	P	
1030992	COG1064R	gbs0054	adhA	Metabolism and transport	Energy production and conversion	Alcohol dehydrogenase (EC 1.1.1.1)	0,360	P	A	P	M	P	P	P	0,530	P	P	P	P	P	P	P	P	P	
1031381	COG0498E	gbs0055	thrC	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Threonine synthase (EC 4.2.3.1)	2,542	P	A	P	A	M	A	M	1,673	P	A	A	A	A	A	A	A	A	
1030757	COG0534V	gbs0056		Cellular processes	Toxin production and resistance	Na+ driven multidrug efflux pump	1,777	P	M	P	P	P	P	P	0,628	P	P	P	P	P	P	P	P	P	
1030755	COG0051J	gbs0057	rpsJ	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S10P	1,241	P	P	P	P	P	P	P	0,682	P	P	A	P	P	P	P	P	P	
1030743	-	gbs0058	rplC	Cellular processes	Translation, ribosomal structure and biogenesis	LSU ribosomal protein L3P	1,038	P	P	P	P	P</													

1031238	COG0171H	gbs0286	nadE	Metabolism and transport	Cofactors, prosthetic groups, and carriers	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)	1.103	P	P	P	A	P	P	M	P	0.952	P	A	A	A	A	A	A	A	A
1030350	COG3579E	gbs0287	pepC	Metabolism and transport	Amino acids, peptides, aminoglycos and amines	Aminopeptidase C (EC 3.4.22.40)	1.003	P	P	P	P	P	P	P	P	1.586	P	P	P	P	P	P	P	P	P
1031240	COG0744M	gbs0288	ponA	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	Multimodular transpeptidase-transglycosylase PBP 1A	1.637	P	P	P	P	P	P	P	P	1.433	P	P	P	P	P	P	P	P	P
1031247	COG3331R	gbs0289	recU	Cellular processes	DNA replication, recombination, and repair	Recombination protein recU	3.435	P	P	P	P	P	P	P	P	1.589	P	P	P	P	P	P	P	P	P
1031242	-	gbs0290	-	Hypothetical	Hypothetical cytosolic protein	Hypothetical cytosolic protein	0.717	P	A	A	A	A	A	A	A	0.415	P	A	A	A	A	A	A	A	A
1030697	COG3599D	gbs0291	-	Cellular processes	Cell division	Cell division initiation protein DivIVA	2.054	P	P	P	P	P	P	P	P	1.033	P	P	P	P	P	P	P	P	P
1031245	COG0116L	gbs0292	-	Metabolism and transport	Central intermediary metabolism	Methyltransferase (EC 2.1.1.-)	1.681	P	A	P	A	A	P	A	A	0.634	P	A	M	A	A	M	A	A	A
1031248	-	gbs0293	-	Hypothetical	Hypothetical protein	Hypothetical protein	1.533	P	P	P	P	P	P	P	P	0.905	P	M	P	P	P	P	P	P	P
1030700	-	gbs0294	luxS	Cellular processes	Signal transduction	Autoinducer-2 production protein luxS (EC 3.13.1.-)	1.546	P	P	P	P	P	P	P	P	1.986	P	A	P	A	M	P	A	A	A
1031251	COG1418R	gbs0295	-	Metabolism and transport	Central intermediary metabolism	Hydrolase (HAD superfamily)	2.209	P	P	P	A	P	P	P	P	0.888	P	P	A	A	P	P	P	P	P
1031256	COG1131V	gbs0296	-	Transport and binding proteins	Unknown substrate	ABC transporter ATP-binding protein	1.658	P	A	M	A	P	A	A	A	1.098	A	A	A	A	A	A	A	A	A
1031254	COG0842V	gbs0297	-	Transport and binding proteins	Unknown substrate	ABC transporter permease	0.820	M	A	A	A	A	A	A	A	0.925	A	A	A	A	A	A	A	A	A
1031261	COG4585T	gbs0298	-	Cellular processes	Signal transduction	Sensory Transduction Histidine Kinase (EC 2.7.3.-)	1.526	P	A	P	P	P	P	A	A	0.618	P	A	P	A	M	P	A	A	A
1030718	COG2197TK	gbs0299	-	Cellular processes	Signal transduction	Two-component response regulator	1.662	P	A	P	A	P	P	P	A	0.832	P	A	A	A	A	A	A	A	A
1030702	-	gbs0300	-	Hypothetical	Hypothetical membrane spanning protein	Hypothetical membrane spanning protein	1.181	P	A	P	P	P	P	A	P	0.475	P	A	A	M	P	A	A	A	A
1031266	COG0194F	gbs0301	gmk	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Guanylate kinase (EC 2.7.4.8)	3.205	P	P	P	P	P	P	P	P	1.719	P	P	P	P	P	P	P	P	P
1031267	COG1758K	gbs0302	-	Cellular processes	Transcription	DNA-directed RNA polymerase omega chain (EC 2.7.7.6)	1.401	P	P	P	A	P	P	P	P	1.198	P	A	P	A	P	P	P	P	P
1031268	COG1198L	gbs0303	priA	Cellular processes	DNA replication, recombination and repair	Primosomal protein N	2.221	P	A	P	A	A	A	A	A	1.957	A	A	A	A	A	A	A	A	A
1031270	COG0223J	gbs0304	fnt	Cellular processes	Translation, ribosomal structure and biogenesis	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	0.881	P	P	P	P	P	P	P	P	0.798	P	A	M	P	P	A	A	A	A
1030722	COG0144J	gbs0305	sunL	Cellular processes	Translation, ribosomal structure and biogenesis	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	1.546	P	P	P	M	P	P	P	P	1.268	P	M	P	A	M	P	A	A	A
1031295	COG0631T	gbs0306	stp1/pppI	Cellular processes	Signal transduction	Protein phosphatase 2C (EC 3.1.3.16)	1.962	P	P	P	P	P	P	P	P	1.268	P	P	P	P	P	P	P	P	P
1030725	15fRRTL, COC	gbs0307	stk1	Cellular processes	Signal transduction	Serine threonine protein kinase (EC 2.7.1.37)	1.945	P	P	P	P	P	P	P	P	1.330	P	P	P	P	P	P	P	P	P
1030188	COG4758S	gbs0308	yyvF	Transport and binding proteins	Unknown substrate	Transporter yyvF	1.493	P	A	P	A	P	P	A	A	1.062	P	A	P	M	P	A	P	A	A
1031297	COG4585T	gbs0309	yyvE	Cellular processes	Signal transduction	Two-component sensor protein yyvE (EC 2.7.3.-)	3.980	P	A	A	A	A	A	A	A	1.893	P	A	A	A	A	A	A	A	A
1031299	COG2197TK	gbs0310	yyvC	Cellular processes	Signal transduction	Two-component response regulator yyvC	1.016	P	A	P	M	P	P	P	P	0.866	P	A	P	A	A	P	P	A	A
1031439	0561R, COGO	gbs0311	-	Metabolism and transport	Central intermediary metabolism	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	1.665	P	P	P	P	P	P	P	P	0.792	P	P	P	P	P	P	P	P	P
1030520	COG1098J	gbs0312	-	Cellular processes	Translation, ribosomal structure and biogenesis	S1-type RNA-binding domain	1.689	P	P	P	P	P	P	P	P	0.827	P	A	P	A	P	P	A	A	A
1030470	COG1180O	gbs0313	-	Metabolism and transport	Energy production and conversion	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	0.051	P	P	P	P	P	P	P	P	0.572	P	P	P	P	P	P	P	P	P
1031443	COG1349KG	gbs0314	-	Cellular processes	Transcription	Transcriptional regulator, DeoR family	0.723	P	P	P	P	P	P	P	P	1.389	P	A	P	A	P	P	P	P	P
1031449	COG2390K	gbs0315	-	Cellular processes	Transcription	Transcriptional regulatory protein	1.235	P	P	P	P	P	P	P	P	1.706	P	P	P	A	M	P	A	P	P
1031313	-	gbs0316	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	0.429	P	P	P	P	P	P	P	P	0.922	P	A	P	A	M	A	P	A	A
1031316	COG1440G	gbs0317	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	0.315	P	M	P	P	P	P	P	A	0.759	P	A	A	A	A	A	A	A	A
1030527	COG1455G	gbs0318	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, cellobiose-specific IIC component (EC 2.7.1.69)	0.240	A	A	A	A	A	A	A	A	0.361	A	A	A	A	A	A	A	A	A
1030546	COG1882C	gbs0319	pflD	Metabolism and transport	Energy production and conversion	Formate acetyltransferase (EC 2.3.1.54)	0.102	P	P	P	P	P	P	P	P	0.245	P	P	P	P	P	P	P	P	P
1031318	-	gbs0320	mipB	Metabolism and transport	Energy production and conversion	Transaldolase (EC 2.2.1.2)	0.039	A	A	P	P	P	P	A	P	0.219	P	P	P	P	P	P	P	P	P
1030547	COG0371C	gbs0321	gldA	Metabolism and transport	Energy production and conversion	Glycerol dehydrogenase (EC 1.1.1.6)	0.172	A	P	P	P	P	P	A	P	0.237	P	P	P	P	P	P	P	P	P
1031319	COG0031E	gbs0322	cysK	Metabolism and transport	Amino acids, peptides, aminoglycos and amines	Cysteine synthase (EC 2.5.1.47)	1.487	P	P	M	P	P	P	A	A	0.923	P	A	A	A	P	M	P	A	A
1030550	COG1739S	gbs0323	-	Hypothetical	Hypothetical protein	Hypothetical protein	5.515	P	A	A	A	A	A	A	A	0.750	A	A	A	A	A	A	A	A	A
1031416	COG4098L	gbs0324	comFA	Cellular processes	DNA transformation	COMF operon protein 1	0.100	A	A	A	A	A	A	A	A	0.035	A	A	A	A	A	A	A	A	A
1031320	COG1040R	gbs0325	comFC	General function predicted only	General function predicted only	COMF operon protein 3	0.445	A	A	A	A	M	A	A	A	0.387	P	A	A	A	A	A	A	A	A
1030561	COG1544J	gbs0326	-	Cellular processes	Translation, ribosomal structure and biogenesis	Ribosome-associated factor Y	0.241	P	P	P	P	P	P	P	P	0.281	P	P	P	P	P	P	P	P	P
1031329	COG0527E	gbs0327	lysC	Metabolism and transport	Amino acids, peptides, aminoglycos and amines	Aspartokinase (EC 2.7.2.4)	2.125	P	A	A	A	A	A	A	A	0.625	M	A	A	A	A	A	A	A	A
1031799	COG0637R	gbs0328	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Beta-phosphoglucomutase (EC 5.4.2.6)	3.166	P	P	P	P	P	A	A	P	1.223	P	A	A	P	A	A	A	A	A
1031330	COG1024I	gbs0329	phaB	Metabolism and transport	Fatty acid and phospholipids	Enoyl-CoA hydratase (EC 4.2.1.17)	1.164	P	P	P	P	P	P	P	P	0.454	P	P	P	A	A	P	P	P	P
1031333	COG1846K	gbs0330	-	Cellular processes	Transcription	Transcriptional regulator, MarR family	1.606	P	P	P	P	P	P	P	P	1.056	P	P	P	P	P	P	P	P	P
1030728	COG0332I	gbs0331	fabH	Metabolism and transport	Fatty acid and phospholipids	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	1.472	P	P	P	P	P	P	P	P	1.011	P	P	P	P	P	P	P	P	P
1031336	COG0236IQ	gbs0332	acpP	Metabolism and transport	Fatty acid and phospholipids	Acyl carrier protein	1.155	P	P	P	P	P	P	P	P	1.172	P	P	P	P	P	P	P	P	P
1031832	COG2070R	gbs0333	fabK	Metabolism and transport	Fatty acid and phospholipids	Enoyl-[acyl-carrier protein] reductase (NADH) (EC 1.3.1.9)	1.698	P	P	P	P	P	P	P	P	1.188	P	A	P	P	A	P	P	P	P
1031797	COG0331I	gbs0334	fabD	Metabolism and transport	Fatty acid and phospholipids	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	1.715	P	A	P	P	M	P	P	P	1.157	P	A	P	A	A	M	P	A	A
1030587	COG1028IQR	gbs0335	fabG	Metabolism and transport	Fatty acid and phospholipids	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	1.878	P	A	P	P	P	P	P	P	0.893	P	A	P	A	P	P	P	P	P
1031339	COG0304IQ	gbs0336	fabF	Metabolism and transport	Fatty acid and phospholipids	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)	1.599	P	A	P	P	P	P	P	P	0.702	P	P	P	A	P	P	P	P	P
1030727	COG0511I	gbs0337	accB	Metabolism and transport	Fatty acid and phospholipids	Biotin carboxyl carrier protein of acetyl-CoA carboxylase (EC 6.4.1.2)	1.520	P	P	P	P	P	P	P	P	0.824	P	P	P	P	P	P	P	P	P
1031344	COG0764I	gbs0338	abZ/clpA	Metabolism and transport	Fatty acid and phospholipids	(3R)-hydroxyacyl-[acyl carrier protein] dehydratase (EC 4.2.1.60)	2.662	P	P	P	P	P	P	P	P	0.883	P	P	P	P	P	P	P	P	P
1030589	COG0439I	gbs0339	accC	Metabolism and transport	Fatty acid and phospholipids	Biotin carboxylase (EC 6.3.4.14)	1.746	P	A	P	A	A	A	P	A	0.791	P	A	P	A	M	P	A	A	A
1031347	COG0777I	gbs0340	accA	Metabolism and transport	Fatty acid and phospholipids	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2)	1.331	P	A	P	P	P	P	P	P	0.806	P	P	P	P	P	P	P	P	P
1031345	COG0825I	gbs0341	accD	Metabolism and transport	Fatty acid and phospholipids	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	1.456	P	P	P	P	P	P	P	P	0.865	P	P	P	P	P	P	P	P	P
1030828	-	gbs0342	-	Hypothetical	Hypothetical protein	Hypothetical protein	0.658	P	P	P	P	P	P	P	P	0.872	P	P	P	P	P	P	P	P	P
1031352	COG0172J	gbs0343	serS	Cellular processes	Translation, ribosomal structure and biogenesis	Seryl-tRNA synthetase (EC 6.1.1.11)	0.778	P	P	P	P	P	P	P	P	1.000	P	M	P	A	P	P	M	P	M
1030671	COG3274S	gbs0344	-	Hypothetical	Hypothetical protein	Integral membrane protein	2.467	P	P	P	P	P	P	P	P	1.002	P	A	P	P	P	A	P	A	P
1030667	-	gbs0345	manO	Hypothetical	Hypothetical cytosolic protein	Hypothetical cytosolic protein	1.773	P	P	P	P	P	P	P	P	2.578	P	P	P	P	P	P	P	P	P
1030670	-	gbs0346	manN	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IID component (EC 2.7.1.69)	1.109	P	P	P	P	P	P	P	P	2.048	P	P	P	P	P	P	P	P	P
1030669	-	gbs0347	manM	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IIC component (EC 2.7.1.69)	1.211	P	P	P	P	P	P	P	P	2.091	P	P	P	P	P	P	P	P	P
1030489	COG2893G	gbs0348	manL	Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IIB component (EC 2.7.1.69)	0.794	P	P	P	P	P	P	P	P	2.068	P	P	P	P	P	P	P	P	P
1030672	COG0561R	gbs0349	-	Metabolism and transport	Central intermediary metabolism	Hydrolase (HAD superfamily)	3.961	P	A	A	A	P	A	A	A	1.129	P	A	P	A	M	A	A	A	A
1031417	-	gbs0350	-	Hypothetical	Hypothetical protein	Hypothetical protein	1.692	P	P	A	A	P	P	P	P	1.243	P	A	P	A	P	P	A	P	A

1030880	-	gbs0619		Hypothetical	Hypothetical protein	1.055	A	A	A	A	A	A	A	A	A	0.621	P	A	A	A	A	A	A	A	A	
1031243	COG2963L	gbs0621		Mobile and extrachromosomal elements	Transposase	3.062	P	A	P	P	P	P	P	P	P	1.418	P	P	P	P	P	P	P	P	P	
1031262	-	gbs0622		Hypothetical	Hypothetical protein	1.078	P	A	A	A	A	A	A	A	A	0.880	A	A	A	A	A	A	A	A	A	
1031121	-	gbs0625		Cellular processes	Posttranslational modification, protein turnover, chaperones	2.020	P	P	P	P	P	P	P	P	P	1.018	P	P	P	P	P	P	P	P	P	
1030901	-	gbs0627	araC	Cellular processes	Transcription	1.036	P	P	P	P	P	P	P	P	P	1.023	P	P	P	P	P	P	P	P	P	
1031310	COG4932M	gbs0628		Hypothetical	IPXtG Hypothetical protein	0.343	P	A	M	M	M	M	M	M	P	0.230	P	A	P	M	A	P	A	A	A	
1031068	COG4932M	gbs0629		Cellular processes	Posttranslational modification, protein turnover, chaperones	1.063	A	A	A	A	A	A	A	A	A	0.141	A	A	A	A	A	A	A	A	A	
1031473	COG3764M	gbs0630		Cellular processes	Posttranslational modification, protein turnover, chaperones	0.307	A	A	A	A	A	A	A	A	A	0.079	A	A	A	A	A	A	A	A	A	
1031341	COG3764M	gbs0631		Cellular processes	Posttranslational modification, protein turnover, chaperones	0.485	A	A	A	P	A	A	A	A	A	0.242	M	A	A	A	A	A	A	A	A	
1031148	COG4932M	gbs0632		Cell Envelope	Other	0.097	A	A	A	A	A	A	A	A	A	0.559	A	A	A	A	A	A	A	A	A	
1030835	COG4932M	gbs0636		Metabolism and transport	Energy production and conversion	0.542	A	A	A	A	A	A	A	A	A	0.127	A	A	A	A	A	A	A	A	A	
1031305	-	gbs0638		Hypothetical	Hypothetical protein	4.509	P	A	P	P	P	P	P	P	P	2.005	P	A	P	A	A	A	A	A	P	
1031469	-	gbs0639		Hypothetical	Hypothetical protein	1.635	A	A	A	A	A	A	A	A	A	0.064	A	A	A	A	A	A	A	A	A	
1030886	COG1680V	gbs0640		Cellular processes	Toxin production and resistance	3.279	P	P	A	A	P	P	A	M	0.747	P	A	P	A	A	P	A	A	A	A	
1030753	COG4586R	gbs0641	drfA	General function predicted only	Daunorubicin resistance ATP-binding protein drfA	2.331	P	A	A	A	A	A	A	A	A	1.677	P	M	P	P	P	P	P	P	P	
1031475	COG4587R	gbs0642		General function predicted only	Daunorubicin resistance transmembrane protein	5.732	P	A	A	A	A	A	A	A	A	1.768	P	A	P	A	A	P	A	P	P	
1031396	COG3694R	gbs0643		Transport and binding proteins	Unknown substrate	2.608	P	A	A	A	A	A	A	A	A	1.748	P	A	M	A	A	P	A	A	A	
1031464	-	gbs0644	cyX	Hypothetical	Hypothetical protein	0.938	P	P	P	P	P	P	P	P	P	2.654	P	P	P	P	P	P	P	P	P	
1031688	COG0331I	gbs0645	cyD	Metabolism and transport	Fatty acid and phospholipids	0.653	P	P	P	P	P	P	P	P	P	1.817	P	P	P	P	P	P	P	P	P	
1031686	COG1028QR	gbs0646	cyG	Metabolism and transport	Fatty acid and phospholipids	0.635	P	P	P	P	P	P	P	P	P	1.926	P	P	P	P	P	P	P	P	P	
1031687	COG0236IQ	gbs0647	acpC	Metabolism and transport	Fatty acid and phospholipids	0.829	P	P	P	P	P	P	P	P	P	2.304	P	M	P	P	P	P	P	P	P	
1031692	COG0764I	gbs0648	cyZ	Metabolism and transport	Fatty acid and phospholipids	0.844	P	P	P	P	P	P	P	P	P	1.700	P	P	P	M	P	P	A	A	A	
1031693	COG1131V	gbs0649	cyA	Transport and binding proteins	Unknown substrate	1.274	P	A	P	P	P	P	P	P	P	1.984	P	P	P	P	P	P	P	P	P	
1031691	-	gbs0650	cyB	Transport and binding proteins	Unknown substrate	1.782	P	P	P	P	P	P	P	P	P	2.377	P	A	P	A	P	P	A	M	A	
1031430	-	gbs0651	cyE	Hypothetical	Hypothetical protein	1.877	P	P	P	P	P	P	P	P	P	2.034	P	M	A	P	P	P	P	P	P	
1031690	COG0404E	gbs0652	cyF	Metabolism and transport	Amino acids, peptides, aminosugars and amines	1.537	P	P	P	P	P	P	P	P	P	2.556	P	P	P	P	P	P	P	P	P	
1031699	COG0304IQ	gbs0653	cyll	Metabolism and transport	Fatty acid and phospholipids	0.957	P	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)	Chain length factor	1.959	P	P	P	P	P	P	1.959	P	P	P	P	P	P	P	P	P
1031696	COG1819GC	gbs0654	cyJ	Metabolism and transport	Carbohydrates, organic alcohols, and acids	2.798	P	P	P	P	P	P	P	P	P	2.845	P	P	A	P	P	P	P	P	P	
1031698	-	gbs0655	cyK	Hypothetical	Hypothetical protein	3.902	P	P	P	P	P	P	P	P	P	3.087	P	P	P	P	P	P	P	P	P	
1031700	COG0577V	gbs0657		Transport and binding proteins	Unknown substrate	1.690	A	A	A	A	A	A	A	A	A	0.405	A	A	A	A	A	A	A	A	A	
1031695	-	gbs0658		Hypothetical	Hypothetical protein	0.966	A	A	A	A	A	A	A	A	A	0.805	A	A	A	A	A	A	A	A	A	
1031701	COG1136V	gbs0659		Transport and binding proteins	Unknown substrate	1.426	A	A	A	A	A	A	A	A	A	0.079	A	A	A	A	A	A	A	A	A	
1031115	COG4529S	gbs0660		Hypothetical	Hypothetical exported protein	0.359	P	A	P	A	M	A	A	A	A	0.919	P	A	A	A	A	A	A	A	A	
1031706	-	gbs0661		Cellular processes	DNA transformation	0.636	P	P	P	P	P	P	P	P	P	2.443	P	P	P	P	P	P	P	P	P	
1031702	COG0586S	gbs0662		General function predicted only	DedA family protein	1.269	P	M	A	A	A	P	A	P	A	1.291	A	A	A	A	A	A	A	A	A	
1031703	COG4619R	gbs0663		Transport and binding proteins	Unknown substrate	0.606	P	A	P	A	P	M	P	P	P	0.617	A	A	A	A	A	A	A	A	A	
1031704	COG0390R	gbs0664		Transport and binding proteins	Unknown substrate	0.674	P	A	M	A	A	A	A	A	A	0.804	A	A	A	A	A	A	A	A	A	
1031705	-	gbs0665		Hypothetical	Hypothetical protein	0.780	P	A	P	P	P	P	P	P	P	0.557	P	A	P	A	A	A	A	A	A	
1031707	COG0583K	gbs0666		Cellular processes	Transcription	0.962	P	A	P	P	P	P	P	P	P	1.125	P	A	A	A	A	A	A	A	A	
1031052	COG3641R	gbs0667		Hypothetical	Hypothetical membrane spanning protein	1.105	P	P	P	P	P	P	P	P	P	0.316	P	A	P	P	P	P	P	P	P	
1031708	COG1052CHF	gbs0668	ddh	Metabolism and transport	Central intermediary metabolism	1.304	P	P	P	P	P	P	P	P	P	0.315	P	A	P	P	P	P	P	M	A	
1031711	COG2211G	gbs0669		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.394	A	A	A	A	A	A	A	A	A	0.372	A	A	A	A	A	A	A	A	A	
1031712	COG0524G	gbs0670		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.324	A	A	A	A	A	A	A	A	A	0.056	A	A	A	A	A	A	A	A	A	
1031721	COG3250G	gbs0671	lacZ	Metabolism and transport	Carbohydrates, organic alcohols, and acids	1.882	P	A	A	A	A	A	A	A	A	0.833	A	A	A	A	A	A	A	A	A	
1031715	COG2186K	gbs0672		Cellular processes	Transcription	0.720	P	A	A	A	A	A	A	A	A	1.003	A	A	A	A	A	A	A	A	A	
1031709	COG0800G	gbs0673		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.394	P	P	P	M	P	A	P	A	A	1.802	P	A	M	M	A	A	A	A	A	
1030888	COG1904G	gbs0674		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.935	P	A	A	A	A	A	A	A	A	1.329	P	A	A	A	A	A	A	A	A	
1031717	COG1312G	gbs0675		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.749	A	A	A	A	A	A	A	A	A	0.496	A	A	A	A	A	A	A	A	A	
1031719	COG1028QR	gbs0676		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.529	P	M	P	A	P	P	A	A	A	0.566	P	A	P	P	P	A	A	A	A	
1031716	COG0546R	gbs0677		Metabolism and transport	Central intermediary metabolism	1.005	P	A	A	A	A	A	A	A	A	0.777	P	A	A	P	A	A	A	A	A	
1031371	-	gbs0678		Metabolism and transport	Carbohydrates, organic alcohols, and acids	0.567	A	A	A	A	A	A	A	A	A	3.168	A	A	A	A	A	A	A	A	A	
1031724	COG0006E	gbs0679	pepQ	Metabolism and transport	Amino acids, peptides, aminosugars and amines	0.760	P	P	P	P	P	P	P	P	P	1.690	P	A	P	P	P	P	P	P	P	
1031718	COG1609K	gbs0680	ccpA	Cellular processes	Transcription	1.397	P	P	P	P	P	P	P	P	P	0.778	P	P	P	P	P	P	P	P	P	
1031212	-	gbs0681		Metabolism and transport	Carbohydrates, organic alcohols, and acids	1.295	P	P	A	P	P	P	P	P	P	1.135	P	A	P	P	P	P	P	P	P	
1031321	COG0438M	gbs0682		Metabolism and transport	Central intermediary metabolism	2.410	P	P	P	P	P	P	P	P	P	1.723	P	A	P	A	A	P	A	A	A	
1031722	COG0438M	gbs0683		Metabolism and transport	Central intermediary metabolism	2.146	P	P	P	P	P	P	P	P	P	1.399	P	A	P	A	P	P	P	P	P	
1031726	COG0441J	gbs0684	thrS	Cellular processes	Translation, ribosomal structure and biogenesis	1.103	P	P	P	P	P	P	P	P	P	0.631	P	P	P	A	P	P	P	M	A	
1031725	COG0745TK	gbs0685		Cellular processes	Transcription	4.461	P	A	A	A	A	A	A	A	A	5.149	P	A	A	A	A	A	A	A	A	A
1031730	-	gbs0686		Hypothetical	Hypothetical cytosolic protein	1.518	P	P	P	P	P	P	P	P	P	0.853	P	A	P	A	P	P	P	P	P	
1031723	-	gbs0687		Hypothetical	Hypothetical membrane associated protein	0.154	P	P	P	P	P	P	P	P	P	0.142	P	P	P	P	P	P	P	P	P	
1031728	COG0765E	gbs0688		Metabolism and transport	Amino acids, peptides, aminosugars and amines	8.312	P	A	P	P	P	M	P	A	A	4.488	P	A	A	A	P	A	A	A	A	
1031732	COG0765E	gbs0689		Metabolism and transport	Amino acids, peptides, aminosugars and amines	15.956	P	A	A	A	A	A	A	A	A	5.152	P	A	A	A	A	A	A	A	A	
1031714	COG0834ET	gbs0690		Metabolism and transport	Amino acids, peptides, aminosugars and amines	10.446	P	A	A	A	A	A	A	A	A	5.471	P	A	A	A	A	A	A	A	A	
1031301	COG1126E	gbs0691		Metabolism and transport	Amino acids, peptides, aminosugars and amines	10.191	P	A	A	A	A	A	A	A	A	1.968	A	A	A	A	A	A	A	A	A	
1031731	-	gbs0692		Hypothetical	Hypothetical protein	0.271	P	A	A	A	A	A	A	A	A	0.307	A	A	A	A	A	A	A	A	A	
1031733	-	gbs0693		Hypothetical	Hypothetical protein	0.713	P	A	A	A	A	A	M	A	A	0.361	P	A	A	A	A	A	A	A	A	
1031727	-	gbs0694		Hypothetical	Hypothetical protein	0.213	A	A	P	P	A	A	A	A	A	0.228	P	A	P	A	P	A	A	A	A	
1031740	-	gbs0695		Hypothetical	Hypothetical protein	0.305	A	A	A	A	A	A	A	A	A	0.323	A	A	A	A	A	A	A	A	A	
1031737	-	gbs0696		Hypothetical	Hypothetical protein	1.416	A	A	A	A	A	A	A	A	A	0.450	A	A	A	A	A	A	A	A	A	
1031741	-	gbs0697		Hypothetical	Hypothetical protein	0.928	M	A	A	A	A	A	A	A	A	0.354	A	A	A	A	A	A	A	A	A	
1031735	-	gbs0698		General function predicted only	RepR protein	0.646	A	A	P	A	A	A	A	A	A	0.084	A	M	A	A	A	A	A	A	A	
1031745	-	gbs0699		Hyp																						

1031151	COG2141C	gbs0753		Metabolism and transport	Energy production and conversion	Luciferase-like monooxygenase (EC 1.14.-.-)	0.448	P	A	A	A	A	A	A	A	A	A	0.483	A	A	A	A	A	A	A	A	A
1031205	COG2183K	gbs0754		Cellular processes	Transcription	TRANSCRIPTION ACCESSORY PROTEIN (S1 RNA binding domain)	3.709	P	A	A	A	A	A	A	A	A	A	1.549	P	A	A	A	A	A	A	A	A
1031050	-	gbs0755		Cellular processes	Toxin production and resistance	Metallopeptidase, SprT family (EC 3.4.24.-)	1.749	P	P	P	P	P	P	P	P	P	P	1.126	P	A	P	A	P	P	P	P	P
1031462	COG1983KT	gbs0756		Cellular processes	Transcription	Stress-responsive transcriptional regulator PspC	0.932	P	P	P	P	P	P	P	P	P	P	0.396	P	P	P	P	P	P	P	P	P
1031783	COG1493T	gbs0757	ptsK	Cellular processes	Signal transduction	HPR(SER) KINASE (EC 2.7.1.-) PHOSPHATASE (EC 3.1.3.-)	0.550	P	P	P	P	P	P	P	P	P	P	0.720	P	P	P	P	P	P	P	P	P
1031041	-	gbs0758	lgt	Cellular processes	Posttranslational modification, protein turnover, chaperones	Prolipoprotein diacylglycerol transferase (EC 2.4.99.-)	0.741	P	P	P	P	P	P	P	P	P	P	0.801	P	P	P	P	P	P	P	P	P
1031264	COG4768R	gbs0759		Hypothetical		Hypothetical protein	0.559	P	P	P	P	P	P	P	P	P	P	0.626	P	P	P	P	P	P	P	P	P
1031781	-	gbs0760		Hypothetical		Hypothetical exported protein	0.574	P	P	P	P	P	P	P	P	P	P	0.665	P	P	P	P	P	P	P	P	P
1031786	-	gbs0761		Hypothetical		Hypothetical protein	2.905	P	P	P	P	P	P	P	P	P	P	0.769	P	P	P	P	P	P	P	P	P
1031183	-	gbs0762		Cellular processes	Posttranslational modification, protein turnover, chaperones	Peptidase family U32	5.227	P	A	P	P	P	P	P	P	P	P	0.946	P	A	P	P	P	P	P	P	P
1031342	-	gbs0763		Cellular processes	Posttranslational modification, protein turnover, chaperones	Peptidase family U32	6.688	P	A	A	A	A	A	A	A	A	A	1.041	A	A	P	A	A	A	A	A	A
1031363	COG4443S	gbs0764		Hypothetical		Hypothetical cytosolic protein	0.619	P	A	P	A	P	P	P	P	P	P	0.793	A	A	P	A	A	A	A	A	A
1031785	-	gbs0765		Hypothetical		Hypothetical protein	0.694	P	P	P	P	P	P	P	P	P	P	0.503	P	P	P	P	P	P	P	P	P
1031379	COG1914P	gbs0766		Metabolism and transport	Inorganic ion transport and metabolism	Manganese transport protein mntH	2.452	P	P	P	P	P	P	P	P	P	P	1.237	P	A	P	A	P	P	A	A	A
1031104	0117H, COG1	gbs0767		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) 5-amin	2.048	P	P	P	P	P	P	P	P	P	P	2.390	P	A	P	A	P	A	P	A	P
1031789	COG0307H	gbs0768		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Riboflavin synthase alpha chain (EC 2.5.1.9)	1.119	P	P	P	P	P	P	P	P	P	P	2.414	P	A	P	P	P	P	A	P	A
1031790	COG0807H	gbs0769		Metabolism and transport	Cofactors, prosthetic groups, and carriers	GTP cyclohydrolase II (EC 3.5.4.25) 3,4-dihydroxy-2-butanone-4-phosphate syntn	1.037	P	P	P	P	P	P	P	P	P	P	2.786	P	A	P	P	P	P	A	P	A
1031373	-	gbs0770		Metabolism and transport	Cofactors, prosthetic groups, and carriers	6,7-dimethyl-8-ribitylmazine synthase (EC 2.5.1.9)	0.841	P	P	P	P	P	P	P	P	P	P	3.188	P	P	P	P	P	P	P	P	P
1031784	COG1190J	gbs0771	lysS	Cellular processes	Translation, ribosomal structure and biogenesis	Lysyl-tRNA synthetase (EC 6.1.1.6)	2.529	P	P	P	P	P	P	P	P	P	P	1.137	P	P	P	P	P	P	P	P	P
1031788	COG1011R	gbs0772		Metabolism and transport	Central intermediary metabolism	Haloacetyl dehalogenase-like hydrolase	2.286	P	A	A	A	A	A	A	A	A	A	1.343	P	A	A	A	A	A	A	A	A
1031445	COG0406G	gbs0773		Metabolism and transport	Carbohydrates, organic alcohols, and acids	Phosphoglycerate mutase family protein	0.350	P	P	P	P	P	P	P	P	P	P	0.683	P	P	P	P	P	P	P	P	P
1031793	COG2606S	gbs0774		Cellular processes	Transcription	Transcriptional regulator	0.126	P	P	P	P	P	P	P	P	P	P	1.044	P	P	P	P	P	P	P	P	P
1031787	51MG, COG0	gbs0775		General function predicted only		NADH-ubiquinone oxidoreductase 39-40 kDa subunit homolog	5.511	P	A	P	A	A	A	A	A	A	1.966	P	A	P	A	A	A	A	A	A	A
1031042	COG3757M	gbs0776		Cellular processes	Posttranslational modification, protein turnover, chaperones	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	2.058	P	P	P	P	P	P	P	P	P	P	1.262	P	P	P	P	P	P	P	P	P
1031791	-	gbs0777		Hypothetical		Integral membrane protein	1.029	P	P	P	P	P	P	P	P	P	P	0.760	P	A	P	A	A	A	A	A	A
1030905	-	gbs0778		Hypothetical		Hypothetical exported protein	0.653	P	P	P	P	P	P	P	P	P	P	0.558	P	P	P	P	P	P	P	P	P
1031466	COG1164E	gbs0779	pepF	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Oligoendopeptidase F (EC 3.4.24.-)	1.105	P	P	P	P	P	P	P	P	P	P	0.725	P	P	P	P	P	P	P	P	P
1031917	COG2352C	gbs0780	ppc	Metabolism and transport	Energy production and conversion	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	1.865	P	P	P	P	P	P	P	P	P	P	1.272	P	A	P	A	P	A	P	A	P
1031792	-	gbs0781	ftsW	Cellular processes	Cell division	Cell division protein ftsW	3.193	P	A	P	A	M	A	A	A	A	0.624	P	A	P	A	A	A	A	A	A	A
1031913	COG0050J	gbs0782	tuf	Cellular processes	Translation, ribosomal structure and biogenesis	Protein Translation Elongation Factor Tu (EF-TU)	0.767	P	P	P	P	P	P	P	P	P	P	0.529	P	P	P	P	P	P	P	P	P
1031916	COG0149G	gbs0783	tpiA	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Triosephosphate isomerase (EC 5.3.1.1)	0.463	P	P	P	P	P	P	P	P	P	P	0.717	P	P	P	P	P	P	P	P	P
1031918	COG0588G	gbs0784	gpmA	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Phosphoglycerate mutase (EC 5.4.2.1)	0.907	P	P	P	P	P	P	P	P	P	P	0.945	P	P	P	P	P	P	P	P	P
1031914	COG0768M	gbs0785		Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	Penicillin-binding protein	3.027	P	P	P	P	P	P	P	P	P	P	1.077	P	A	P	A	P	P	A	P	A
1031920	COG0353L	gbs0786	recR	Cellular processes	DNA replication, recombination and repair	Recombination protein recR	2.711	P	P	P	P	P	P	P	P	P	P	0.752	P	P	A	P	P	P	A	P	A
1031911	COG1181M	gbs0787	ddl	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	D-alanine--D-alanine ligase (EC 6.3.2.4)	3.030	P	A	A	M	A	A	A	A	A	1.058	P	A	P	A	A	A	A	A	A	A
1031919	COG0770M	gbs0788	murF	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)	1.915	P	P	P	M	P	P	P	P	P	1.076	P	P	P	P	P	P	P	P	P	P
1031915	-	gbs0789		Transport and binding proteins	Unknown substrate	Transporter, MFS superfamily	0.723	P	P	P	P	P	P	P	P	P	P	0.608	P	A	P	A	P	P	A	P	A
1031924	COG5522S	gbs0790		Hypothetical		Hypothetical membrane spanning protein	3.466	P	P	P	A	P	P	P	P	P	1.917	P	A	M	A	P	P	A	P	A	P
1031910	-	gbs0791		Hypothetical		LPXTG Surface anchor protein	1.396	P	M	P	P	P	P	P	P	P	P	0.872	P	A	P	M	P	P	A	P	A
1031905	COG4108J	gbs0792	prfC	Cellular processes	Translation, ribosomal structure and biogenesis	Bacterial Peptide Chain Release Factor 3 (RF-3)	1.718	P	P	P	M	P	P	P	P	P	0.685	P	A	P	P	P	P	M	P	P	P
1031912	-	gbs0793		Hypothetical		Hypothetical cytosolic protein	1.491	P	P	P	P	P	P	P	P	P	P	1.963	P	A	P	A	P	P	A	P	A
1031922	COG1135P	gbs0794		Metabolism and transport	Inorganic ion transport and metabolism	Probable D-methionine transport ATP-binding protein metN	1.758	P	P	P	A	P	P	P	P	P	P	0.932	P	A	A	A	P	P	M	P	M
1031921	COG2011P	gbs0795		Transport and binding proteins	Unknown substrate	ABC transporter permease protein	3.548	P	P	P	A	P	P	P	P	P	P	1.189	P	A	P	A	P	A	P	A	P
1031923	COG1464P	gbs0796		Transport and binding proteins	Unknown substrate	ABC transporter substrate-binding protein	1.561	P	P	P	A	P	P	P	P	P	P	1.138	P	P	P	A	P	P	P	P	P
1031907	COG0513KJ	gbs0797	deaD	Cellular processes	DNA replication, recombination and repair	ATP-dependent RNA helicase	2.957	P	P	A	A	P	P	P	M	P	0.773	A	A	A	A	A	P	A	P	A	P
1031909	COG2827L	gbs0798		Hypothetical		Hypothetical protein with endo excinuclease domain	1.337	P	A	P	M	P	P	P	A	P	1.313	P	A	P	A	A	M	A	P	A	P
1031906	COG4123R	gbs0799		Metabolism and transport	Central intermediary metabolism	Methyltransferase (EC 2.1.1.-)	1.850	P	A	A	A	A	A	A	A	A	1.518	P	A	A	A	A	A	A	A	A	A
1031926	COG0204I	gbs0800		Metabolism and transport	Fatty acid and phospholipids	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	1.292	P	P	P	P	P	P	P	P	P	0.662	P	P	P	P	P	P	P	P	P	P
1031925	COG1555L	gbs0801		Cellular processes	DNA transformation	COME operon protein 1	0.194	A	A	A	A	A	A	A	A	A	0.083	A	A	A	A	A	A	A	A	A	A
1031903	0658R, COG2	gbs0802	comEC	General function predicted only		COME operon protein 3	1.091	P	A	A	A	A	A	A	A	A	0.240	A	A	A	A	A	A	A	A	A	A
1031902	COG0561R	gbs0803		Metabolism and transport	Central intermediary metabolism	Hydrolase (HAD superfamily)	1.185	P	A	P	P	A	P	A	M	0.924	P	A	A	A	A	A	A	A	A	A	A
1031904	COG1609K	gbs0804		Cellular processes	Transcription	Catabolite control protein B	1.374	P	P	P	P	P	P	P	P	P	0.641	P	A	P	M	P	P	A	P	A	P
1031908	COG0657I	gbs0805		Metabolism and transport	Fatty acid and phospholipids	Esterase (EC 3.1.1.-)	4.525	A	A	A	A	A	A	A	A	A	0.639	A	A	A	A	A	A	A	A	A	A
1031888	COG0500QR	gbs0806		Metabolism and transport	Secondary metabolites	Biotin synthesis protein bioC	0.438	P	P	P	P	P	P	P	P	P	0.606	P	P	P	P	P	P	A	P	A	P
1031901	COG1466L	gbs0807		Cellular processes	DNA replication, recombination and repair	DNA polymerase III, delta subunit (EC 2.7.7.7)	1.566	P	P	P	P	P	P	P	P	P	0.887	P	M	P	P	P	P	P	P	P	P
1031927	COG0605P	gbs0808	soeA	Metabolism and transport	Inorganic ion transport and metabolism	Superoxide dismutase (EC 1.15.1.1)	0.387	P	P	P	P	P	P	P	P	P	0.403	P	P	P	P	P	P	P	P	P	P
1031900	COG3711K	gbs0809	licT	Cellular processes	Transcription	Transcription antiterminator, BglG family	0.506	P	A	P	A	A	A	A	A	A	1.792	P	P	P	A	A	A	A	P	A	P
1031929	COG1263G	gbs0810		Metabolism and transport	Carbohydrates, organic alcohols, and acids	PTS system, beta-glucosidase-specific IIABC component (EC 2.7.1.69)	0.307	A	A	A	A	A	A	A	A	A	1.047	P	A	A	A	A	A	A	A	A	A
1031897	-	gbs0811	bgIA	Metabolism and transport	Carbohydrates, organic alcohols, and acids	6-phospho-beta-glucosidase (EC 3.2.1.86)	1.520	P	A	A	A	A	A	A	A	A	1.900	P	A	P	A	A	A	A	P	A	P
1031899	COG3835KT	gbs0812		Cellular processes	Transcription	Transcriptional regulatory protein	1.109	P	A	M	A	A	A	M	P	1.796	P	A	A	P	A	A	A	A	A	A	A
1031896	-	gbs0813		Metabolism and transport	Energy production and conversion	Glycerate kinase (EC 2.7.1.31)	0.728	A	A	A	A	A	A	A	A	A	0.262	A	A	A	A	A	A	A	A	A	A
1031898	COG2610GE	gbs0814		Metabolism and transport	Carbohydrates, organic alcohols, and acids	Glucanate permease	0.498	P	A	A	A	A	A	A	A	A	0.514	P	A	P	A	P	M	A	P	A	P
1031893	1686M, COG2	gbs0815		Cellular processes	Posttranslational modification, protein turnover, chaperones	Peptidase family S11	3.068	P	A	A	A	A	A	A	A	A	1.253	P	A	P	A	A	A	A	A	A	A
1031928	COG1846K	gbs0816		Cellular processes</																							

1029826	0340H, COG1	gbs0848	birA	Cellular processes	Transcription	Biotin operon repressor Biotin-[acetyl-CoA-carboxylase] synthetase (EC 6.3.4.15)	1.398	P	A	A	A	A	A	A	A	A	A	0.801	P	A	A	A	A	A	A	A	A
1029821	COG0192H	gbs0849	metK2	Metabolism and transport	Cofactors, prosthetic groups, and carriers	S-adenosylmethionine synthetase (EC 2.5.1.6)	2.007	P	P	M	A	P	P	P	M			1.485	P	A	P	A	P	P	M	A	
1029828	-	gbs0850	ftsB	Hypothetical		Hypothetical protein	1.196	P	A	A	A	A	A	A	A			1.316	A	A	A	A	A	A	A	A	
1029823	-	gbs0851		Hypothetical		Hypothetical protein	1.152	P	A	A	A	A	A	A	A			0.828	A	A	A	A	A	A	A	A	
1029834	-	gbs0852		Hypothetical		Hypothetical protein	1.144	P	A	A	A	A	A	A	A			0.350	A	A	A	A	A	A	A	A	
1029824	COG4732S	gbs0853		Transport and binding proteins	Unknown substrate	Hydroxyethylthiazole permease	0.186	A	A	A	A	A	A	A	A			0.273	A	A	A	A	A	A	A	A	
1029833	COG4721S	gbs0854		Transport and binding proteins	Unknown substrate	Hydroxymethylpyrimidine transport system permease protein	1.630	A	A	A	A	A	A	A	A			0.570	A	A	A	A	A	A	A	A	
1029836	COG1122P	gbs0855		Metabolism and transport	Inorganic ion transport and metabolism	Transporter	2.649	A	A	A	A	A	A	A	A			0.848	A	A	A	A	A	A	A	A	
1029832	COG0619P	gbs0856		Metabolism and transport	Inorganic ion transport and metabolism	Hydroxymethylpyrimidine transport system permease protein	1.472	A	A	A	A	A	A	A	A			0.404	A	A	A	A	A	A	A	A	
1029838	COG0819K	gbs0857		Cellular processes	Transcription	Transcriptional activator tenA	0.511	A	A	A	A	A	A	A	A			0.477	P	A	A	A	A	A	A	A	
1029827	COG0351H	gbs0858		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	0.934	A	A	A	A	A	A	A	A			0.745	A	A	A	A	A	A	A	A	
1029837	COG2145H	gbs0859		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Hydroxyethylthiazole kinase (EC 2.7.1.50)	0.549	P	A	A	M	A	A	A	A			0.381	P	A	A	M	A	A	A	P	
1029839	COG0352H	gbs0860		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	0.958	M	A	A	A	A	A	A	A			0.745	P	A	A	A	A	A	A	A	
1029841	COG0766M	gbs0861	murZ	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	3.465	P	A	A	A	P	A	A	A			1.190	P	A	A	A	A	A	A	A	
1029840	COG1670J	gbs0862		Cellular processes	Transcription	Ribosomal-protein-S5-alanine acetyltransferase (EC 2.3.1.128)	2.247	P	A	P	P	P	P	M			1.446	P	A	P	A	P	P	P	P		
1029848	COG4109K	gbs0863		Cellular processes	Transcription	Cytosolic protein containing multiple CBS domains	1.995	P	A	M	A	P	A	A	A			1.182	P	A	M	A	A	P	M	A	
1029845	COG0024J	gbs0864	map	Cellular processes	Transcription	Methionine aminopeptidase (EC 3.4.11.18)	1.971	P	P	P	P	P	P	P			1.307	P	P	P	P	P	P	P	P		
1029846	COG1295S	gbs0865		Cellular processes	Transcription	Ribonuclease BN (EC 3.1.-.-)	2.949	P	P	P	P	P	P	P			1.199	P	M	P	P	P	P	P	P		
1029847	COG2246S	gbs0866		General function predicted only		Bacteronol-linked monosaccharide translocase (flippase type)	1.014	P	A	A	A	A	M	A			0.594	P	A	A	A	P	A	A			
1029842	COG4708S	gbs0867		Hypothetical		Hypothetical membrane spanning protein	1.015	P	P	P	P	P	P	P			0.508	P	A	P	A	P	P	A			
1029844	COG0272L	gbs0868	lig	Cellular processes	DNA replication, recombination and repair	NAD-dependent DNA ligase (EC 6.5.1.2)	1.078	P	A	A	A	A	A	A			1.358	P	A	A	A	A	A	A	A		
1029843	COG1597R	gbs0869		Metabolism and transport	Fatty acid and phospholipids	Dialcylglycerol kinase family protein	1.305	P	A	P	P	P	P	P			1.433	P	P	P	A	P	P	A			
1029853	COG1523G	gbs0870		Metabolism and transport	Carbohydrates, organic alcohols, and acids	Pullulanase (EC 3.2.1.41)	1.337	P	A	P	M	M	A	A			1.650	P	A	P	A	M	M	A			
1029852	COG0296G	gbs0871		Metabolism and transport	Carbohydrates, organic alcohols, and acids	1,4-alpha-glucan branching enzyme (EC 2.4.1.18)	1.056	P	P	P	P	P	P	P			1.269	P	P	P	P	P	P	P			
1029849	COG0448G	gbs0872	glgC	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Glucose-1-phosphate adenylyltransferase catalytic subunit (EC 2.7.7.27)	0.800	P	P	P	P	P	P	P			1.219	P	P	P	P	P	P	P			
1029851	COG0448G	gbs0873		Metabolism and transport	Carbohydrates, organic alcohols, and acids	Glucose-1-phosphate adenylyltransferase regulatory subunit (EC 2.7.7.27)	0.805	P	P	P	P	P	P	P			1.154	P	P	P	P	P	P	P			
1029850	COG0297G	gbs0874		Metabolism and transport	Carbohydrates, organic alcohols, and acids	Glycogen synthase (EC 2.4.1.21)	1.294	P	P	P	P	P	P	P			1.159	P	P	P	P	P	P	P			
1029854	-	gbs0875	atpE	Metabolism and transport	Energy production and conversion	ATP synthase C chain (EC 3.6.3.14)	1.114	P	P	P	P	P	P	P			0.884	P	M	P	P	P	P	P			
1029856	-	gbs0876	atpB	Metabolism and transport	Energy production and conversion	ATP synthase A chain (EC 3.6.3.14)	1.806	P	P	P	P	P	P	P			1.295	P	P	P	P	P	P	P			
1029857	COG0711C	gbs0877	atpF	Metabolism and transport	Energy production and conversion	ATP synthase B chain (EC 3.6.3.14)	1.859	P	P	P	P	P	P	P			1.220	P	P	P	P	P	P	P			
1029859	COG0712C	gbs0878	atpH	Metabolism and transport	Energy production and conversion	ATP synthase delta chain (EC 3.6.3.14)	2.636	P	P	P	P	P	P	P			1.406	P	P	P	P	P	P	P			
1029855	COG0056C	gbs0879	atpA	Metabolism and transport	Energy production and conversion	ATP synthase alpha chain (EC 3.6.3.14)	1.646	P	P	P	P	P	P	P			1.389	P	P	P	P	P	P	P			
1029865	COG0224C	gbs0880	atpG	Metabolism and transport	Energy production and conversion	ATP synthase gamma chain (EC 3.6.3.14)	1.841	P	P	P	P	P	P	P			1.358	P	P	P	P	P	P	P			
1029858	COG0055C	gbs0881	atpD	Metabolism and transport	Energy production and conversion	ATP synthase beta chain (EC 3.6.3.14)	1.499	P	P	P	P	P	P	P			1.273	P	P	P	P	P	P	P			
1029863	-	gbs0882	atpC	Metabolism and transport	Energy production and conversion	ATP synthase epsilon chain (EC 3.6.3.14)	1.093	P	P	P	P	P	P	P			0.962	P	P	P	P	P	P	P			
1029866	COG0766M	gbs0883	murA	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	1.551	P	P	P	A	P	P	P			0.965	P	A	P	M	P	P	P	M		
1029867	-	gbs0884	eupA	General function predicted only		EupA protein	0.868	P	P	P	A	P	P	P			0.591	P	A	P	A	P	A				
1029861	-	gbs0885	endA	Cellular processes	DNA transformation	DNA-entry nuclease (EC 3.1.30.-)	3.358	P	A	A	M	A	A	A			1.672	P	A	A	A	A	A	A			
1029860	COG0016J	gbs0886	pheS	Cellular processes	Transcription, ribosomal structure and biogenesis	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	1.710	P	P	P	P	P	P	P			1.272	P	A	A	A	P	P	A			
1029864	-	gbs0887	pheT	Metabolism and transport	Central intermediary metabolism	Acetyltransferase, GNAT family	1.665	P	P	P	P	P	P	P			1.328	P	A	A	A	P	M	A			
1029872	0072J, COG0	gbs0888	pheT	Cellular processes	Transcription, ribosomal structure and biogenesis	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	1.421	P	P	P	P	P	P	P			0.882	P	P	P	P	P	P				
1029871	COG3857L	gbs0890	rexB	Cellular processes	DNA replication, recombination and repair	ATP-dependent nuclease subunit B	1.218	P	A	A	P	A	A	A			1.794	P	A	A	A	A	A	A			
1029875	COG1074L	gbs0891	rexA	Cellular processes	DNA replication, recombination and repair	ATP-dependent nuclease subunit A	1.059	M	A	A	A	A	A	A			0.846	M	A	A	A	A	A	A			
1029873	COG0598P	gbs0892		Metabolism and transport	Inorganic ion transport and metabolism	Magnesium and cobalt transport protein corA	4.120	A	A	A	A	A	A	A			3.541	P	A	A	A	A	A	A			
1029874	COG0486R	gbs0893	thdF	Cellular processes	Transcription, ribosomal structure and biogenesis	tRNA (5-carboxymethylaminomethyl-2-thiouridylyl) synthase	1.441	P	M	P	P	P	P	P			0.583	P	P	A	A	P	A				
1029870	COG0488R	gbs0894		Transport and binding proteins	Unknown substrate	ABC transporter ATP-binding protein	3.672	P	A	A	A	A	A	A			2.327	P	A	P	A	A	A	A			
1029869	COG1071C	gbs0895	acoA	Metabolism and transport	Energy production and conversion	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	0.713	P	P	P	P	P	P	P			0.695	P	P	P	P	P	P				
1029876	COG0022C	gbs0896	acoB	Metabolism and transport	Energy production and conversion	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	0.963	P	P	P	P	P	P	P			0.724	P	P	P	P	P	P				
1029878	COG0508C	gbs0897	acoC	Metabolism and transport	Energy production and conversion	Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex	1.321	P	P	P	P	P	P	P			0.909	P	P	P	P	P	P				
1029879	COG1249C	gbs0898	acoL	Metabolism and transport	Energy production and conversion	Dihydropyrimidine dehydrogenase (EC 1.8.1.4)	1.112	P	P	P	P	P	P	P			0.905	P	P	P	P	P	P				
1029885	COG0095H	gbs0899	lipB	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Lipoate-protein ligase A (EC 6.3.2.-)	1.702	P	P	P	A	P	P	P			1.290	P	P	P	P	P	P				
1029877	COG3442R	gbs0900		General function predicted only		CobB CobQ-like glutamine amidotransferase domain	1.382	P	P	P	P	P	P	P			1.117	P	A	P	A	P	P				
1029887	COG0769M	gbs0901		Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase (EC 6.3.2.-)	2.137	P	M	A	A	P	M	P	A			0.719	P	A	A	A	A	A	A		
1029881	-	gbs0902		Hypothetical		Hypothetical membrane spanning protein	0.666	P	P	P	P	P	P	P			1.068	P	P	P	P	P	P				
1029884	COG4856S	gbs0903		Hypothetical		Hypothetical membrane associated protein	0.646	P	P	P	P	P	P	P			1.063	P	P	P	P	P	P				
1029882	COG1109G	gbs0904	fermD	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Phosphoglucosamine mutase (EC 5.4.2.10)	1.067	P	P	P	P	P	P	P													

1030073	-	gbs1071		Hypothetical		Hypothetical protein	12.675	P	A	P	A	P	P	A	A	17.038	P	A	A	A	A	A	A	A	A
1030071	-	gbs1072		Hypothetical		Hypothetical protein	7.790	P	P	P	P	P	P	P	P	6.331	P	A	P	A	A	M	A	A	A
1030077	COG1511S	gbs1073		Mobile and extrachromosomal elements		Phage infection protein	3.680	P	P	P	P	P	P	P	P	3.647	P	A	A	A	A	A	A	A	A
1030076	COG4842S	gbs1074		Hypothetical		Hypothetical protein	2.494	P	P	P	P	P	P	P	P	6.520	P	A	P	A	A	P	A	A	A
1030074	COG5153U	gbs1075		Hypothetical		Hypothetical cytosolic protein	5.007	P	P	P	P	P	P	P	P	9.794	P	A	P	A	P	P	A	M	
1030082	-	gbs1076		Hypothetical		Hypothetical secreted protein	3.703	P	P	P	P	P	P	P	P	8.187	P	A	P	A	M	P	A	P	
1030084	COG0458EF	gbs1077	carB	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	2.112	P	P	P	P	P	P	P	P	2.226	P	P	A	P	P	P	P	P	
1030081	COG0505EF	gbs1078	carA	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	1.940	P	P	P	P	P	P	P	P	2.707	P	A	P	A	P	P	A	M	
1030083	COG0540F	gbs1079	pyrB	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Aspartate carbamoyltransferase (EC 2.1.3.2)	1.982	P	P	P	P	P	P	P	P	1.421	P	A	P	P	P	P	P	P	
1030072	COG0044F	gbs1080	pyrC	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Dihydroorotase (EC 3.5.2.3)	1.200	P	P	P	P	P	P	P	P	1.285	P	A	P	M	P	P	P	P	
1030087	COG0461F	gbs1081	pyrE	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Orotate phosphoribosyltransferase (EC 2.4.2.10)	1.549	P	P	P	P	P	P	P	P	0.885	P	A	P	A	P	P	P	P	
1030080	COG0284F	gbs1082	pyrF	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Orotidine 5-phosphate decarboxylase (EC 4.1.1.23)	1.662	P	P	P	P	P	P	P	P	1.056	P	P	P	P	P	P	P	P	
1030085	Z966S, COG3	gbs1083		Transport and binding proteins	Unknown substrate	Threonine Serine Exporter	1.729	P	P	P	A	P	P	A	A	1.026	P	A	P	A	A	M	A	M	A
1030093	COG0488R	gbs1084		Transport and binding proteins	Unknown substrate	ABC transporter ATP-binding protein	3.350	P	A	A	A	A	A	A	A	1.778	P	A	A	A	A	A	A	A	A
1030086	COG1328F	gbs1085	mhB	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	0.463	P	A	A	A	P	P	P	P	0.627	P	A	P	P	P	P	P	P	
1030088	COG0136E	gbs1086		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	2.738	P	P	P	P	P	P	P	P	4.794	P	A	P	A	A	P	A	P	
1030097	-	gbs1087	ftsA	Hypothetical		LPXTG Hypothetical protein	0.654	P	P	P	P	P	P	P	P	2.824	P	A	P	P	P	P	P	P	
1030090	COG1502I	gbs1088		Metabolism and transport	Fatty acid and phospholipids	Cardiolipin synthetase (EC 2.7.8.-)	1.452	P	P	P	P	P	P	P	P	1.390	P	A	P	A	M	P	M	A	
1030094	COG2759F	gbs1089	fts.1	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Formate-tetrahydrofolate ligase (EC 6.3.4.3)	0.885	P	P	P	P	P	P	P	P	0.737	P	A	P	P	P	P	P	P	
1030091	COG0095H	gbs1090	lplA	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Lipoate-protein ligase A (EC 6.3.2.-)	2.747	P	A	P	A	P	A	A	A	0.959	P	A	M	A	A	M	A	M	A
1030092	COG0846K	gbs1091		Cellular processes	Transcription	SIR2 family protein	4.364	P	A	P	A	P	P	P	A	1.059	P	A	P	A	A	P	P	P	
1030095	-	gbs1092		Cellular processes	Posttranslational modification, protein turnover, chaperones	ATPase associated with chromosome architecture replication	2.398	P	M	M	A	P	P	P	A	0.837	P	A	P	A	P	P	A	A	
1030102	COG0509E	gbs1093		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Glycine cleavage system H protein	2.531	P	P	P	A	P	P	P	P	0.983	P	M	P	A	P	P	A	A	
1030100	COG2141C	gbs1094		Metabolism and transport	Energy production and conversion	Luciferase-like monooxygenase (EC 1.14.-.-)	3.564	P	A	A	A	A	A	A	A	0.667	P	A	P	A	A	A	P	A	
1030096	COG1902C	gbs1095		Metabolism and transport	Energy production and conversion	Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	2.311	P	A	A	A	A	A	A	A	0.734	P	A	A	A	A	A	A	A	
1030101	COG0095H	gbs1096		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Lipoate-protein ligase A (EC 6.3.2.-)	3.355	P	A	P	A	P	P	A	P	0.914	P	A	P	A	P	P	M	A	
1030107	COG0452H	gbs1097	dpfB	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Phosphopantothenate-cysteine ligase (EC 6.3.2.5)	2.984	P	A	A	A	A	A	A	A	1.439	P	A	A	A	A	A	P	A	
1030103	COG0452H	gbs1098	dfp	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Phosphopantothencysteine decarboxylase (EC 4.1.1.36)	1.478	P	A	M	A	P	P	A	M	0.719	P	A	A	A	A	A	A	A	
1030098	COG4684S	gbs1099		Hypothetical		Integral membrane protein	1.861	P	P	P	P	P	P	P	P	1.050	P	A	P	P	P	P	P	P	
1030099	COG1109G	gbs1100	pgmA	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Phosphoglucomutase (EC 5.4.2.2) Phosphomannomutase (EC 5.4.2.8)	0.781	P	P	P	P	P	P	P	P	1.166	P	M	P	A	P	P	P	P	
1030108	-	gbs1101		Hypothetical		Hypothetical protein	2.816	P	P	P	A	P	P	P	M	1.378	P	A	P	A	P	P	A	P	
1030115	COG1132V	gbs1102		Cellular processes	Toxin production and resistance	Multidrug protein lipid ABC transporter family, ATP-binding and permease protein	2.821	P	A	A	A	P	A	A	A	1.748	P	A	A	A	A	A	A	A	A
1030106	COG1132V	gbs1103		Cellular processes	Toxin production and resistance	Multidrug resistance ABC transporter ATP-binding and permease protein	2.541	P	A	A	A	A	A	A	A	1.613	P	A	A	A	A	A	A	A	A
1030105	-	gbs1104		Hypothetical		Antigen	2.708	P	A	P	A	P	P	A	P	1.697	P	A	P	A	P	P	A	A	
1030119	-	gbs1105		Hypothetical		Hypothetical protein	3.144	P	P	P	A	P	P	P	A	3.545	P	A	A	A	P	A	A	A	
1030114	COG0112E	gbs1106	glyA	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Serine hydroxymethyltransferase (EC 2.1.2.1)	2.088	P	P	P	P	P	P	P	P	1.616	P	A	P	A	P	P	P	P	
1030116	COG0009J	gbs1107		Cellular processes	Translation, ribosomal structure and biogenesis	Sua5 YciO YrdC YwlC family protein	2.104	P	P	P	P	P	P	P	P	1.318	P	A	P	A	P	P	P	P	
1030111	COG2890J	gbs1108	hemK	Cellular processes	Translation, ribosomal structure and biogenesis	Peptide release factor-glutamine N5-methyltransferase (EC 2.1.1.-)	2.652	P	P	P	P	P	P	P	P	1.883	P	A	P	P	P	P	P	P	
1030109	COG0216J	gbs1109	prfA	Cellular processes	Translation, ribosomal structure and biogenesis	Bacterial Peptide Chain Release Factor 1 (RF-1)	2.230	P	P	M	P	P	P	P	P	2.418	P	A	P	A	A	A	A	A	
1030113	COG1435F	gbs1110	tdk2	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Thymidine kinase (EC 2.7.1.21)	1.952	P	P	P	P	P	P	P	P	1.323	P	A	P	P	P	P	P	P	
1030117	COG1942R	gbs1111		Metabolism and transport	Energy production and conversion	4-oxalocrotonate tautomerase (EC 5.3.2.-)	0.373	P	P	P	P	P	P	P	P	0.240	P	P	A	P	A	M	A		
1030118	-	gbs1112	apbE	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Iron-sulfur cluster assembly repair protein ApbE	1.213	P	P	P	P	P	P	P	P	2.348	P	A	P	P	P	P	P	P	
1030120	COG0431R	gbs1113		Metabolism and transport	Central intermediary metabolism	NADPH-dependent FMN reductase family protein	0.689	P	P	P	P	P	P	P	P	1.790	P	A	P	P	P	P	P	P	
1030123	0431R, COG2	gbs1114		Metabolism and transport	Central intermediary metabolism	Oxidoreductase (EC 1.1.1.-)	0.751	P	M	P	P	P	P	A	P	2.624	P	A	P	P	P	P	P	P	
1030125	COG2116P	gbs1115		Metabolism and transport	Inorganic ion transport and metabolism	Formate nitrite transporter family protein	1.177	P	M	P	P	P	P	M	P	1.447	P	A	P	P	P	P	P	P	
1030122	COG2233F	gbs1116		Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Xanthine permease	1.328	P	P	P	P	P	P	P	P	0.899	P	A	P	P	P	M	P	P	
1030114	COG0503F	gbs1117	xpt	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Xanthine phosphoribosyltransferase (EC 2.4.2.-)	1.167	P	P	P	A	P	M	P	0.680	P	A	M	A	A	P	A	A		
1030130	-	gbs1118		Hypothetical		Hypothetical protein	1.510	A	A	A	A	A	A	A	A	0.291	A	A	A	A	A	A	A	A	
1030126	-	gbs1119		Hypothetical		hypothetical phage protein	0.951	P	A	A	A	A	A	A	A	0.782	P	A	A	A	A	A	A	A	
1030127	0863L, COG1	gbs1120		Cellular processes	DNA replication, recombination and repair	Chromosome partitioning protein parB Adenine-specific methyltransferase (EC 2.	0.455	A	A	A	A	A	A	A	A	0.265	A	A	A	A	A	A	A	A	
1030132	COG3843U	gbs1121		General function predicted only		Relaxase	0.153	A	A	A	A	A	A	A	A	0.099	A	A	A	A	A	A	A	A	
1030128	-	gbs1122		Mobile and extrachromosomal elements		Mobilisation protein	0.269	A	A	A	A	A	A	A	A	0.054	A	A	A	A	A	A	A	A	
1030133	-	gbs1123		Hypothetical		Hypothetical protein	0.339	A	A	A	A	A	A	A	A	0.070	A	A	A	A	A	A	A	A	
1030129	-	gbs1124		Hypothetical		Hypothetical protein	0.476	A	A	A	A	A	A	A	A	0.410	A	A	A	A	A	A	A	A	
1030135	-	gbs1125		Hypothetical		Hypothetical protein	0.148	A	A	A	A	A	A	A	A	0.091	A	A	A	A	A	A	A	A	
1030134	-	gbs1126		General function predicted only		LtrC-like protein	0.318	A	A	A	A	A	A	A	A	0.347	A	A	A	A	A	A	A	A	
1030137	-	gbs1127		Hypothetical		Hypothetical protein	0.910	A	A	A	A	A	A	A	A	0.288	A	A	A	A	A	A	A	A	
1030131	COG3505U	gbs1128		Mobile and extrachromosomal elements		TraG TraD family	0.197	A	A	A	A	A	A	A	A	0.126	A	A	A	A	A	A	A	A	
1030141	-	gbs1129		Hypothetical		Hypothetical protein	0.246	A	A	A	A	A	A	A	A	0.463	A	A	A	A	A	A	A	A	
1030138	-	gbs1130		Hypothetical		Hypothetical protein	0.604	A	A	A	A	A	A	A	A	0.634	A	A	A	A	A	A	A	A	
1030143	-	gbs1131		Hypothetical		Hypothetical protein	0.335	A	A	A	A	M	A	A	A	0.698	A	A	A	A	A	A	A	A	
1030142	-	gbs1132		Hypothetical		Hypothetical protein	0.304	A	A	A	A	A	A	A	A	0.103	A	A	A	A	A	A	A	A	
1030145	COG3942R	gbs1133		Hypothetical		Hypothetical protein	0.497	A	A	A	A	A	A	A	A	0.325	A	A	A	A	A	A	A	A	
1030140	-	gbs1134		Hypothetical		Hypothetical protein	1.183	P	A	A	A	A	A	A	A	0.852	A	A	A	A	A	A	A	A	
1030146	COG3451U	gbs1135		Hypothetical		TRSE PROTEIN	0.484	A	A	A	A	A	A	A	A	0.127	A	A	A	A	A	A	A	A	
1030150	-	gbs1136		Hypothetical		Hypothetical protein	0.352	P	A	P	P	P	P	M	A	0.312	M	A	A	A	A	P	A	A	
1030147	-	gbs1137		Hypothetical		Hypothetical protein	0.678	A	A	M	A	P	A	A	A	0.327	A	A	A	A	A	A	A	A	
1030139	-	gbs1138		Hypothetical		Hypothetical protein	0.493	A	A	A	A	A	A	A	A	1.047	A	A	A	A	A	A	A	A	
1030151	-	gbs1139		Hypothetical																					

1030285	COG1293K	gbs1263	fbp	Cell Envelope	Other	Fibronectin-binding protein	1.432	P	P	P	P	P	P	P	P	P	P	1.747	P	A	A	A	A	A	A	A	A	
1030284	COG3527Q	gbs1264		Metabolism and transport	Secondary metabolites	Alpha-acetolactate decarboxylase (EC 4.1.1.5)	1.584	P	P	P	P	P	P	P	P	P	P	1.543	P	P	P	P	P	P	P	P	P	
1030291	COG0028EH	gbs1265		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Acetolactate synthase (EC 2.2.1.6)	0.949	P	P	P	P	P	P	P	P	P	P	0.869	P	P	P	P	P	P	P	P	P	
1030293	-	gbs1266		Hypothetical		Tetratricopeptide repeat family protein	2.186	P	A	P	A	P	A	P	A	P	A	1.463	P	A	A	A	A	P	A	A	A	
1030289	COG0628R	gbs1267		Hypothetical		Hypothetical membrane spanning protein	1.848	P	M	P	P	P	P	P	P	P	P	0.985	P	A	P	A	P	P	P	P	P	
1030295	COG0494LR	gbs1268		Cellular processes	DNA replication, recombination and repair	Phosphohydrolase (MutT nudix family protein)	1.329	P	P	P	A	M	P	A	A	A	0.809	P	A	A	A	A	M	A	A	A	A	
1030296	COG0494LR	gbs1269		General function predicted only		7,8-dihydro-8-oxoguanine-triphosphatase (EC 3.6.1.-)	1.162	P	D	P	P	P	P	P	P	P	1.002	P	A	P	A	P	M	P	P	P		
1030294	-	gbs1270	hylB/A	General function predicted only		Hyaluronate lyase precursor (EC 4.2.2.1)	1.027	P	A	P	A	A	A	P	A	P	A	0.903	P	A	A	A	A	P	A	P	A	
1030292	COG1088M	gbs1271	cpsF/Q	Metabolism and transport		Carbohydrates, organic alcohols, and acids	1.120	P	P	P	A	P	P	P	P	P	1.363	P	A	P	M	A	P	P	A	P	A	
1030299	COG1898M	gbs1272	rmlC	Metabolism and transport		Carbohydrates, organic alcohols, and acids	1.200	P	P	P	P	P	P	P	P	P	1.302	P	P	P	P	P	P	P	P	P	P	
1030298	COG1209M	gbs1273	rmlA	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.877	P	P	P	P	P	P	P	P	P	1.222	P	P	P	M	P	P	P	P	P	P	
1030300	COG0665E	gbs1274		Metabolism and transport		Amino acids, peptides, aminosugars and amines	2.082	P	A	A	A	A	A	A	A	A	1.306	P	A	A	A	A	A	A	A	A	A	
1030297	COG0327S	gbs1275		General function predicted only		NIF3-related protein	1.173	P	M	P	A	P	P	A	M	1.058	P	A	A	A	A	P	A	P	A	P	A	
1030303	COG2384R	gbs1276		Hypothetical		Hypothetical cytosolic protein	2.067	P	M	P	P	P	P	P	P	1.030	P	A	P	A	A	P	A	P	A	P	A	
1030302	COG3935L	gbs1277	dnaD	Cellular processes	DNA replication, recombination and repair	DNA replication protein dnaD	5.373	P	A	A	A	A	A	A	A	1.168	P	A	A	A	A	A	A	A	A	A	A	
1030304	COG0503F	gbs1278	apt	Metabolism and transport		Purines, pyrimidines, nucleosides, and nucleotides	1.680	P	P	P	P	P	P	P	P	0.696	P	P	P	P	P	P	P	P	P	P	P	
1030301	-	gbs1279		Cell Envelope		M protein	0.956	P	P	P	P	P	P	P	P	1.913	P	A	P	P	P	P	P	P	P	P	P	
1030307	COG0608L	gbs1280	recJ	Cellular processes	DNA replication, recombination and repair	Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-)	1.900	P	A	A	A	A	P	A	P	A	0.838	P	A	M	A	A	M	A	A	A	A	
1030308	COG0300R	gbs1281		Metabolism and transport		Short chain dehydrogenase	1.615	P	P	P	P	P	P	P	P	0.910	P	M	P	P	P	P	P	P	P	P	P	
1030306	COG1234R	gbs1282	elaC	Cellular processes		Transcription	1.452	P	P	P	P	P	P	P	P	0.976	P	P	P	P	P	P	P	P	P	P	P	
1030305	-	gbs1283		Metabolism and transport		Carbohydrates, organic alcohols, and acids	2.484	P	P	P	P	P	P	P	P	1.427	P	P	P	P	P	P	P	P	P	P	P	
1030311	COG2262R	gbs1284	hflX	General function predicted only		GTP-binding protein hflX	1.088	P	P	P	P	P	P	P	P	0.817	P	P	P	P	P	P	P	P	P	P	P	
1030309	COG0324J	gbs1285	miaA	Cellular processes		Translation, ribosomal structure and biogenesis	0.511	P	M	delta(2)	-isopentenylpyrophosphate transferase (EC 2.5.1.8)	0.511	P	M	delta(2)	-isopentenylpyrophosphate transferase (EC 2.5.1.8)	0.511	P	A	P	P	P	A	P	A	P	A	P
1030310	-	gbs1286		Hypothetical		Hypothetical protein	0.415	P	P	P	P	P	P	P	P	0.544	P	P	P	P	P	P	P	P	P	P	P	
1030314	COG1275P	gbs1287	exfA	Hypothetical		Hypothetical membrane-spanning protein	0.963	P	A	A	A	A	A	A	A	0.784	P	A	P	A	P	A	A	P	A	A	A	
1030315	COG1523G	gbs1288		Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.335	A	A	A	A	P	A	A	A	1.747	P	P	A	A	A	P	P	A	P	A	A	
1030313	COG1387ER	gbs1289		Metabolism and transport		Amino acids, peptides, aminosugars and amines	2.666	P	A	P	A	P	A	A	A	4.167	P	A	A	A	A	A	A	A	A	A	A	A
1030312	COG1573L	gbs1290		Cellular processes		DNA replication, recombination and repair	2.828	P	P	P	A	P	M	P	M	3.926	P	A	M	A	A	A	A	A	A	A	A	A
1030317	COG0624E	gbs1291		Metabolism and transport		Amino acids, peptides, aminosugars and amines	0.889	P	P	P	P	P	P	P	P	1.409	P	P	P	P	P	P	P	P	P	P	P	
1030316	COG0778C	gbs1292		Metabolism and transport		Energy production and conversion	1.131	P	P	P	P	P	P	P	P	1.916	P	P	P	P	P	P	P	P	P	P	P	
1030319	0584C, COG4	gbs1293		Metabolism and transport		Energy production and conversion	1.584	P	P	P	M	M	A	A	P	0.534	P	A	P	A	P	A	P	A	P	A	P	A
1030322	COG0322L	gbs1294	uvrC	Cellular processes		DNA replication, recombination and repair	2.123	P	A	A	A	A	A	A	A	1.111	P	A	A	A	A	A	A	A	A	A	A	A
1030320	COG1636S	gbs1295		Hypothetical		Hypothetical cytosolic protein	1.906	M	A	A	A	A	A	A	A	1.663	A	A	A	A	A	A	A	A	A	A	A	A
1030321	COG0534V	gbs1296		Cellular processes		Toxin production and resistance	1.789	P	A	A	A	A	A	A	A	1.135	A	A	A	A	A	A	A	A	A	A	A	A
1030318	COG2764S	gbs1297		Metabolism and transport		Energy production and conversion	1.090	P	P	P	P	P	P	P	P	0.866	P	P	P	P	P	P	P	P	P	P	P	
1030327	-	gbs1298		Hypothetical		putohtical protein	2.300	P	P	P	P	P	P	P	P	0.890	P	P	P	P	P	P	P	P	P	P	P	P
1030325	-	gbs1299		Mobile and extrachromosomal elements		PUTATIVE HOST CELL SURFACE-EXPOSED LIPOPROTEIN	2.618	P	A	M	A	P	P	M	A	1.645	P	A	A	A	A	A	A	A	A	A	A	A
1030323	COG2801L	gbs1301		Mobile and extrachromosomal elements		Transposase	0.273	A	A	A	A	A	A	A	A	0.162	A	A	A	A	A	A	A	A	A	A	A	A
1030324	-	gbs1302		Mobile and extrachromosomal elements		Transposase	1.035	A	A	A	A	A	A	A	A	0.126	A	A	A	A	A	A	A	A	A	A	A	A
1030329	-	gbs1306		Mobile and extrachromosomal elements		Streptococcal histidine triad protein	4.656	A	A	A	A	A	A	A	A	3.449	A	A	A	A	A	A	A	A	A	A	A	A
1030333	COG0803P	gbs1307	lmb	Metabolism and transport		Inorganic ion transport and metabolism	0.871	P	A	A	A	A	A	A	A	1.312	P	A	A	A	A	M	A	A	A	A	A	A
1030336	COG1404O	gbs1308	scpB	Cellular processes		Posttranslational modification, protein turnover, chaperones	1.928	P	M	P	M	P	P	P	P	1.628	P	A	P	M	M	P	A	P	A	P	A	P
1030332	COG2176L	gbs1312		Hypothetical		Hypothetical protein	4.233	P	A	A	A	A	A	A	A	1.294	A	A	A	A	A	A	A	A	A	A	A	A
1030342	-	gbs1313		Hypothetical		Hypothetical protein	2.835	P	P	A	P	A	P	M	0.689	P	A	P	A	A	P	P	A	P	P	P	P	P
1030339	COG0582L	gbs1314		Mobile and extrachromosomal elements		DNA integration recombination inversion protein	1.160	P	P	P	P	P	P	P	P	2.731	P	P	P	P	P	P	P	P	P	P	P	P
1030338	-	gbs1315		Hypothetical		Hypothetical protein	1.091	P	P	P	P	P	P	P	P	1.900	P	P	P	P	P	P	P	P	P	P	P	P
1030351	-	gbs1316		Mobile and extrachromosomal elements		Replication protein	0.346	M	A	A	A	P	M	A	A	0.361	A	A	A	A	A	A	A	A	A	A	A	A
1030348	-	gbs1318		Hypothetical		Hypothetical protein	0.152	A	A	A	A	A	A	A	A	0.141	A	A	A	A	A	A	A	A	A	A	A	A
1030343	COG1674D	gbs1320		Cellular processes		Cell division	0.455	A	A	A	A	A	A	A	A	0.104	A	A	A	A	A	A	A	A	A	A	A	A
1030357	-	gbs1321		Hypothetical		Hypothetical protein	0.435	P	M	A	P	A	A	A	A	0.113	A	A	A	A	A	A	A	A	A	A	A	A
1030354	-	gbs1322		Hypothetical		Hypothetical protein	1.371	P	A	A	A	A	A	A	A	1.904	P	A	A	A	A	A	A	A	A	A	A	A
1030361	-	gbs1323		Hypothetical		Hypothetical protein	1.624	M	A	A	A	A	A	A	A	1.165	P	A	A	A	A	A	A	A	A	A	A	A
1030353	-	gbs1324	hsmD	Mobile and extrachromosomal elements		TYPE II RESTRICTION-MODIFICATION SYSTEM MODIFICATION SUBUNIT	0.375	A	A	A	A	A	A	A	A	0.220	A	A	A	A	A	A	A	A	A	A	A	A
1030364	COG0582L	gbs1325		Mobile and extrachromosomal elements		DNA integration recombination inversion protein	1.225	P	P	P	P	P	P	P	P	1.977	P	P	P	P	P	P	P	P	P	P	P	P
1030363	-	gbs1326		Hypothetical		Hypothetical protein	0.753	P	P	P	P	P	P	P	P	1.251	P	A	P	A	P	P	A	P	A	P	A	P
1030360	COG1396K	gbs1327		Cellular processes		Transcriptional regulator, Cro CI family	0.173	A	A	A	A	A	A	A	A	0.347	A	A	A	A	A	A	A	A	A	A	A	A
1030368	COG2017G	gbs1328		Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.445	P	A	A	A	P	A	A	P	0.567	P	A	M	A	A	A	A	P	A	P	A	P
1030367	-	gbs1329	lacG	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.642	P	A	A	A	A	A	A	A	2.211	P	A	P	A	A	M	P	A	P	A	P	A
1030369	COG1455G	gbs1330	lacE	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.368	P	P	M	M	P	M	2.344	P	A	P	A	P	A	P	P	P	P	P	P	P	P
1030366	-	gbs1331	lacF	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.290	A	A	P	A	A	M	A	2.756	P	M	P	A	A	A	P	A	P	A	P	A	P
1030373	COG3711K	gbs1332		Cellular processes		Transcription	0.349	P	A	A	A	A	P	A	3.539	P	A	M	P	A	P	P	A	P	P	P	P	P
1030371	COG3684G	gbs1333	lacD.2	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.400	P	P	P	P	P	P	P	0.443	P	M	P	P	P	P	P	P	P	P	P	P	P
1030372	COG1105G	gbs1334	lacC.2	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.365	A	A	A	A	A	A	A	1.022	A	A	A	A	A	A	A	P	A	P	A	P	A
1030370	COG0698G	gbs1335	lacB.1	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.547	A	A	A	A	A	A	A	0.773	P	A	A	A	A	A	A	A	A	A	A	A	A
1030376	COG0698G	gbs1336	lacA.2	Metabolism and transport		Carbohydrates, organic alcohols, and acids	0.495	P	A	A	A	P	M	A	0.960	P	A	A	A	A	A	A	A	A	A	A	A	A
1030375	COG1349KG	gbs1337		Cellular processes		Transcription	2.038																					

1030523	COG1120PH	gbs1462	fhuA	Metabolism and transport	Inorganic ion transport and metabolism	Ferrichrome transport ATP-binding protein fhuC	6.917	P	A	A	A	P	M	A	A	1.275	P	A	P	A	A	P	A	A
1030524	COG0614P	gbs1463	fhuD	Metabolism and transport	Inorganic ion transport and metabolism	Ferrichrome-binding protein	2.223	P	P	P	P	P	P	P	P	0.828	P	P	P	P	P	P	P	P
1030528	COG0609P	gbs1464	fhuB	Metabolism and transport	Inorganic ion transport and metabolism	Ferrichrome transport system permease protein fhuB	1.562	P	A	P	M	P	P	A	A	0.621	P	A	P	A	A	P	A	A
1030533	COG0609P	gbs1465	fhuG	Metabolism and transport	Inorganic ion transport and metabolism	Ferrichrome transport system permease protein fhuG	10.270	P	A	A	A	A	A	A	A	2.397	P	A	A	A	A	A	A	A
1030525	-	gbs1466	-	Hypothetical	-	Hypothetical cytosolic protein	2.104	P	P	P	P	P	P	P	1.274	P	A	A	A	A	P	P	P	
1030534	COG1227C	gbs1467	ppaC	Metabolism and transport	Energy production and conversion	Inorganic pyrophosphatase (EC 3.6.1.1)	0.883	P	P	P	P	P	P	P	0.913	P	P	P	P	P	P	P	P	
1030531	COG1180O	gbs1468	pfIC	Metabolism and transport	Energy production and conversion	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	0.975	P	P	P	P	P	P	P	1.554	P	P	P	P	P	P	P	P	
1030539	COG1253R	gbs1469	hlyX	General function predicted only	-	Magnesium and cobalt efflux protein corC	2.062	P	P	P	P	P	P	P	1.071	P	P	P	P	P	P	P	P	
1030537	-	gbs1470	-	Metabolism and transport	Central intermediary metabolism	SAM-dependent methyltransferase (EC 2.1.-.-)	1.680	P	P	P	P	P	P	P	1.118	P	A	P	A	P	P	P	M	
1030543	COG1242R	gbs1471	-	General function predicted only	-	Radical SAM superfamily protein	1.989	P	A	P	P	P	P	A	2.066	P	A	P	A	A	M	A	A	
1030536	COG0671I	gbs1472	-	Metabolism and transport	Fatty acid and phospholipids	Membrane-associated phospholipid phosphatase	0.665	P	P	P	P	P	P	P	1.730	P	A	P	P	P	P	P	P	
1030535	COG3601S	gbs1473	-	Transport and binding proteins	Unknown substrate	Riboflavin transporter	0.559	P	P	P	P	P	P	P	1.041	P	A	P	P	P	P	P	P	
1030548	COG4932M	gbs1474	piIC	hypothetical	-	LPXTG Hypothetical protein	1.896	P	A	P	P	P	P	P	2.547	P	A	P	A	P	A	M	A	
1030545	COG3764M	gbs1475	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	Sortase	3.932	P	A	P	A	P	P	A	3.413	P	A	P	A	A	A	A	A	
1030542	COG3764M	gbs1476	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	Sortase	2.719	P	P	P	P	P	P	P	1.784	P	P	P	A	P	M	P	P	
1030552	-	gbs1477	piIB	Hypothetical	-	IPXTG Cell wall surface anchor family protein	0.639	P	P	P	P	P	P	P	4.661	P	A	P	A	A	P	P	A	
1030551	COG4932M	gbs1478	piIA	Cell Envelope	Other	IPXTG Collagen adhesion protein	3.320	P	A	P	A	A	A	A	6.161	P	A	A	A	A	A	A	A	
1030555	-	gbs1479	rogB	Cellular processes	Transcription	Transcriptional regulator RogB	2.564	P	P	A	P	M	P	P	2.312	P	A	A	A	A	A	A	A	
1030549	COG0438M	gbs1480	-	Cell Envelope	Biosynthesis and degradation of surface polysaccharides and lipoproteins	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein	2.621	P	A	P	A	P	A	A	2.220	P	A	A	A	A	P	A	A	
1030556	COG1216R	gbs1481	-	General function predicted only	-	dTDP-rhamnosyl transferase rfbF (EC 2.-.-.-)	4.220	P	A	P	M	P	P	A	2.589	P	A	P	A	P	P	P	P	
1030557	COG2244R	gbs1482	-	General function predicted only	-	Oligosaccharide translocase (flippase)	3.438	P	A	A	A	A	A	A	1.687	P	A	A	A	M	A	A	A	
1030553	-	gbs1483	-	Hypothetical	-	Hypothetical protein	3.286	P	P	P	P	P	A	P	1.281	P	P	A	P	P	P	P	P	
1030563	COG0463M	gbs1484	-	Metabolism and transport	Central intermediary metabolism	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	2.584	P	P	P	P	P	P	P	1.566	P	P	P	P	P	P	P	P	
1030560	COG0463M	gbs1485	-	Metabolism and transport	Central intermediary metabolism	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	2.474	P	P	P	P	P	P	P	1.187	P	P	P	P	P	P	P	P	
1030566	COG0451MG	gbs1486	-	Hypothetical	-	UDP-D-glucuronate carboxy-lyase (EC 4.1.1.35)	2.314	P	P	P	P	P	P	P	1.313	P	P	P	P	P	P	P	P	
1030559	COG1211I	gbs1487	-	Metabolism and transport	Fatty acid and phospholipids	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)	1.656	P	P	P	A	P	P	P	1.262	P	A	P	A	P	P	A	A	
1030567	COG3475M	gbs1488	-	Cell Envelope	Biosynthesis and degradation of surface polysaccharides and lipoproteins	Lipo oligosaccharide cholinephosphotransferase (EC 2.7.8.-)	1.866	P	P	P	P	P	P	P	0.748	P	P	P	P	P	P	P	P	
1030565	-	gbs1489	-	Hypothetical	-	Hypothetical protein	4.095	P	A	A	A	A	A	A	1.862	P	A	A	A	A	A	A	A	
1030564	COG2456S	gbs1490	-	Hypothetical	-	Hypothetical membrane spanning protein	4.094	P	P	P	P	P	P	P	1.682	P	A	P	P	P	P	P	P	
1030570	COG0463M	gbs1491	-	Metabolism and transport	Central intermediary metabolism	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	2.703	P	A	P	A	P	A	A	0.967	P	A	A	A	M	M	A	A	
1030568	COG0463M	gbs1492	rgpBC	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	2.834	P	A	A	A	A	A	A	1.800	P	A	A	A	A	A	A	A	
1030571	COG0438M	gbs1493	rgpAC	Cell Envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	alpha-D-GlcNAc alpha-1,2-L-rhamnosyltransferase (EC 2.4.1.-)	3.018	P	A	P	A	A	A	A	1.258	P	A	A	A	A	A	A	A	
1030575	COG1091M	gbs1494	rmdID	Metabolism and transport	Carbohydrates, organic alcohols, and acids	dTDP-4-dehydrohamnose reductase (EC 1.1.1.133)	1.175	P	P	P	A	P	P	P	1.085	P	A	A	A	A	A	A	A	
1030577	-	gbs1495	-	Hypothetical	-	Hypothetical cytosolic protein	1.577	P	P	P	P	P	P	P	0.943	P	A	P	M	M	P	P	A	
1030574	COG0568K	gbs1496	ropD	Cellular processes	Transcription	RNA polymerase sigma factor ropD	2.372	P	P	P	P	P	P	P	1.227	P	A	P	A	P	P	A	A	
1030576	COG0358L	gbs1497	dnaG	Cellular processes	DNA replication, recombination and repair	DNA primase (EC 2.7.7.-)	3.439	P	A	A	A	M	A	A	1.070	P	A	P	A	P	P	A	A	
1030572	-	gbs1498	mscL	Transport and binding proteins	Unknown substrate	Large-conductance mechanosensitive channel	0.439	P	P	A	P	P	P	P	0.548	P	A	P	P	P	P	P	P	
1030581	COG0828J	gbs1499	rpsU	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S21P	0.568	P	P	P	P	P	P	P	0.608	P	P	P	P	P	P	P	P	
1030579	COG0727R	gbs1500	-	Hypothetical	-	Hypothetical protein	1.128	P	A	P	A	P	A	A	0.690	A	A	A	A	A	A	A	A	
1030580	COG0834E	gbs1501	-	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Arginine-binding protein	0.674	P	P	P	M	P	M	P	0.325	P	A	P	A	M	P	A	A	
1030578	-	gbs1502	-	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Ammonium transporter	0.455	P	P	P	P	P	M	P	0.191	P	A	P	M	A	A	A	P	
1030584	COG0492O	gbs1503	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	Oxidoreductase (EC 1.1.1.-)	1.149	P	A	A	A	A	A	A	0.400	A	A	A	A	A	A	A	A	
1030583	COG1054R	gbs1504	-	Metabolism and transport	Central intermediary metabolism	Rhodanese-related sulfurtransferases	1.231	P	P	A	A	P	P	P	0.815	P	A	P	A	M	P	P	A	
1030582	-	gbs1505	-	Hypothetical	-	Hypothetical protein	0.771	P	P	P	P	P	P	P	0.608	P	A	P	A	P	P	P	P	
1030586	COG2271G	gbs1506	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Transporter	0.969	A	A	A	A	A	A	A	1.795	P	A	A	A	A	A	A	A	
1030592	COG0508G	gbs1507	glgP	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Maltodextrin phosphorylase (EC 2.4.1.1)	0.636	P	P	P	P	P	P	P	3.406	P	P	P	P	P	P	P	P	
1030595	-	gbs1508	malM	Metabolism and transport	Carbohydrates, organic alcohols, and acids	4-alpha-glucanotransferase (EC 2.4.1.25)	0.353	P	P	P	P	P	P	P	2.730	P	A	P	M	A	P	P	P	
1030593	COG1609K	gbs1509	malR	Cellular processes	Transcription	Transcriptional regulator, LacI family	2.693	P	P	P	A	P	P	A	1.434	P	A	A	A	A	A	A	A	
1030597	COG2182G	gbs1510	malE	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Maltose maltodextrin-binding protein	0.242	P	P	P	P	P	P	P	0.967	P	A	P	P	P	P	P	P	
1030591	COG1175G	gbs1511	malF	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Maltodextrin transport system permease protein malC	0.482	P	M	P	P	P	P	P	1.757	P	P	P	P	P	P	P	P	
1030599	COG3833G	gbs1512	malG	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Maltose transport system permease protein malG	0.663	P	P	P	P	P	P	P	2.179	P	P	P	P	P	P	P	P	
1030600	COG3104E	gbs1513	-	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Di- tripeptide transporter	2.751	P	M	P	P	M	P	A	1.047	P	A	P	A	P	A	A	A	
1030598	COG0494LR	gbs1514	-	Cellular processes	DNA replication, recombination and repair	Phosphohydrolase (MutT nudix family protein)	4.039	P	A	A	A	A	A	A	2.023	P	A	A	A	A	A	A	A	
1030603	-	gbs1515	-	Hypothetical	-	Hypothetical protein	4.143	P	A	A	A	A	A	A	2.247	P	A	A	A	M	A	A	P	
1030602	-	gbs1516	-	Hypothetical	-	surface protein PIs	1.840	P	M	P	P	P	A	P	1.212	P	A	P	A	P	P	A	P	
1030607	COG0438M	gbs1517	-	Metabolism and transport	Central intermediary metabolism	Probable poly(Glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52)	2.859	P	A	A	A	A	A	A	2.594	P	A	A	A	A	A	A	A	
1030610	COG0653U	gbs1518	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	Protein translocase subunit secA	2.282	P	A	A	A	A	A	A	0.944	P	A	P	A	M	A	A	A	
1030609	-	gbs1519	-	Hypothetical	-	Hypothetical protein	2.148	P	A	A	A	A	A	A	1.751	P	A	P	A	A	P	A	A	
1030608	-	gbs1520	-	Hypothetical	-	Hypothetical protein	3.016	P	P	A	A	P	M	P	1.048	P	M	P	M	P	P	A	P	
1030605	-	gbs1521	-	Hypothetical	-	Hypothetical protein	19.176	P	A	A	A	A	A	A	2.181	P	A	A	A	A	A	A	A	
1030604	COG0201U	gbs1522	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	Protein translocase subunit secY	2.476	P	M	P	A	M	P	A	1.676	P	A	P	P	P	A	P	P	
1030612	-	gbs1523	-	Hypothetical	-	Hypothetical protein	1.952	P	A	P	M	P	A	A	1.119	P	P	P	P	P	M	P	P	
1030613	COG0463M	gbs1524	-	Metabolism and transport	Central intermediary metabolism	Glycosyltransferase (EC 2.4.1.-)	2.747	P	A	A	A	A	A	A	1.840	P	A	P	A	A	A	A	A	
1030614	COG1442M	gbs1525	-	Metabolism and transport	Central intermediary metabolism	Glycosyl transferase, family 8	5.160	P	A	A	A	A	A	A	1.701	P	A	A	A	A	A	A	A	
1030611	COG1442M	gbs1526	-	Metabolism and transport	Central intermediary metabolism	Glycosyl transferase, family 8	6.786	M	A	A	A	A	A	A	2.074	P	A	A	A	A	A	A	A	
1030617	COG1442M	gbs1527	-	Metabolism and transport	Central intermediary metabolism	Glycosyl transferase, family 8	1.499	P	M	P	A	A	A	A	0.732	P	A	M	A	A	A	A	A	
1030616	-	gbs1528	-	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Putative galactofuranosyltransferase (EC 2.4.1.-)	1.998	P	A	A	A	A	A	A	2.950	P	A	A	A	A	A	A	A	
1030619	-	gbs1529	-	Cell Envelope	Other	LPXTG Fibronectin-binding protein	1.279	P	A	A	A	P	A	A	0.341	P	A	A	A	M	P	P	A	
1030615	-	gbs1530	rofA	Cellular processes	Transcription	Transcriptional regulator RogB	2.722	P	A	P	A	P	P	A	1.062	P	A	P	A	A	P	A	A	
1030621	COG0556L	gbs1531	UvrB	Cellular processes	DNA replication, recombination and repair	Excinuclease ABC subunit B	1.213	P	A	P	A	P	P	A	0.868	P	A	A	A	P	A	A	A	
1030620	-	gbs1532	-	Cellular processes	Posttranslational modification, protein turnover, chaperones	CAAX amino terminal protease family	2.636	P	P	P	P	P	P	P	1.049	P	A	P	A	M	P	P	M	

1030683	COG1321K	gbs1749		Cellular processes	Transcription	Iron-dependent repressor	3.031	P	A	P	A	A	P	A	P	3.089	P	A	A	A	A	A	A	A	A
1030685	COG2131F	gbs1750	comEB	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	ComE operon protein 2	1.911	P	M	P	A	P	P	P	A	3.418	P	A	A	A	A	A	A	A	A
1030715	COG0006E	gbs1751		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Xaa-Pro dipeptidase (EC 3.4.13.9)	1.331	P	P	P	P	P	P	P	P	1.992	P	A	A	A	A	M	A	A	A
1030708	-	gbs1752		Hypothetical		Hypothetical protein	1.603	P	A	A	A	A	A	A	A	1.044	P	A	A	A	A	A	A	A	A
1030687	-	gbs1753		Cellular processes	Toxin production and resistance	Multidrug resistance protein B	1.505	P	A	A	A	A	A	A	A	0.583	P	A	A	A	A	A	A	A	A
1030705	COG0178L	gbs1754	uvrA	Cellular processes	DNA replication, recombination and repair	Excinuclease ABC subunit A	1.540	P	A	A	A	A	A	A	A	1.045	P	A	A	A	A	A	A	A	A
1030719	-	gbs1755		Hypothetical		Hypothetical membrane spanning protein	1.712	P	P	P	A	M	P	A	A	0.568	M	A	P	A	A	P	A	A	A
1030723	COG0598P	gbs1756	corA	Metabolism and transport	Inorganic ion transport and metabolism	Magnesium and cobalt transport protein corA	2.008	P	P	P	M	P	P	P	P	0.568	P	A	P	A	A	P	A	A	A
1030704	-	gbs1757	rpsR	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S18P	0.715	P	P	P	P	P	P	P	P	0.378	P	P	P	P	P	P	P	P	P
1030713	COG0629L	gbs1758	ssb3	Cellular processes	DNA replication, recombination and repair	Single strand binding protein	1.012	P	P	P	P	P	P	P	P	0.424	P	P	P	P	P	P	P	P	P
1030730	COG0360J	gbs1759	rpsF	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S6P	0.797	P	P	P	P	P	P	P	P	0.396	P	P	P	P	P	P	P	P	P
1030720	COG1194L	gbs1760	mutY	Cellular processes	DNA replication, recombination and repair	A.G-specific adenine DNA glycosylase (EC 3.2.2.-)	1.505	P	P	P	A	P	P	P	P	0.922	P	A	P	A	A	P	M	A	A
1030726	COG1396K	gbs1761		Cellular processes	Transcription	Transcriptional regulator	0.795	P	M	P	P	P	P	P	P	0.841	P	A	A	A	A	A	A	A	A
1030744	COG0526OC	gbs1762	trx	Metabolism and transport	Energy production and conversion	Thioredoxin	1.273	P	P	P	P	P	P	P	P	1.033	P	P	P	P	P	P	P	P	P
1031017	-	gbs1763		Metabolism and transport	Fatty acid and phospholipids	Phosphatidylglycerophosphatase B (EC 3.1.3.27)	2.334	P	P	P	P	P	P	P	P	1.332	P	P	P	P	P	P	P	P	P
1030736	COG1193L	gbs1764	mutS2	Cellular processes	DNA replication, recombination and repair	DNA mismatch repair protein mutS	2.578	P	A	A	A	A	A	A	A	1.849	P	A	A	A	A	A	A	A	A
1031828	-	gbs1765		General function predicted only		CvpA family membrane protein	1.542	P	P	P	P	P	P	P	P	1.035	P	A	P	P	P	P	P	A	A
1030758	-	gbs1766		Hypothetical		Hypothetical cytosolic protein	2.718	P	P	P	P	P	P	P	P	2.041	P	A	P	P	P	P	P	P	P
1031367	COG1039L	gbs1767		Cellular processes	Transcription	Ribonuclease HIII (EC 3.1.26.4)	5.060	P	A	P	A	P	P	P	P	1.381	P	A	P	A	P	P	P	P	A
1030794	COG0681U	gbs1768	spi	Cellular processes	Posttranslational modification, protein turnover, chaperones	Signal peptidase I (EC 3.4.21.89)	1.330	P	P	P	P	P	P	P	P	0.712	P	A	P	A	P	P	P	P	P
1030802	COG0507L	gbs1769	recD	Cellular processes	DNA replication, recombination and repair	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	0.910	P	A	A	A	A	A	A	A	0.622	A	A	A	A	A	A	A	A	A
1030764	-	gbs1770		Hypothetical		Hypothetical protein	0.505	P	P	P	P	P	P	P	P	1.297	P	P	P	P	P	P	P	P	P
1031309	COG0389L	gbs1771	dinP	Cellular processes	DNA replication, recombination and repair	DNA polymerase IV (EC 2.7.7.7)	1.125	P	P	P	P	P	P	P	P	0.760	P	A	P	P	P	M	P	P	P
1030768	COG1882C	gbs1772	pfl	Metabolism and transport	Energy production and conversion	Formate acetyltransferase (EC 2.3.1.54)	0.368	P	P	P	P	P	P	P	P	0.533	P	P	P	P	P	P	P	P	P
1030831	-	gbs1773		General function predicted only		FMN-binding protein	0.590	P	P	P	P	P	P	P	P	0.871	P	P	P	P	P	P	P	P	P
1030769	COG1680V	gbs1774		Cellular processes	Toxin production and resistance	Beta-lactamase family protein	2.309	P	P	P	A	P	P	A	P	0.631	P	A	A	A	M	A	A	A	A
1030770	-	gbs1775		Hypothetical		Hypothetical cytosolic protein	1.464	P	P	P	M	P	P	A	P	0.525	P	A	P	A	P	P	A	A	A
1030773	-	gbs1776		Hypothetical		Hypothetical membrane spanning protein	2.502	P	P	P	A	P	P	P	P	0.523	P	A	P	A	P	P	A	A	A
1030776	-	gbs1777	glpF.2	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Aquaporin Glycerol uptake facilitator protein	1.812	P	P	P	P	P	P	P	P	0.884	P	A	P	P	P	P	P	A	A
1030777	COG0589T	gbs1778		Cellular processes	Posttranslational modification, protein turnover, chaperones	Universal stress protein family	2.426	A	A	A	A	A	A	A	A	0.512	A	A	A	A	A	A	A	A	A
1031468	-	gbs1779	norA	Transport and binding proteins	Unknown substrate	Transporter, MFS superfamily	0.907	P	A	A	A	A	M	A	A	0.734	A	A	A	A	A	A	A	A	A
1030778	COG0664T	gbs1780	srv	Cellular processes	Transcription	Transcription regulator, crp family	1.266	P	P	P	P	P	P	P	P	1.716	P	A	P	A	M	P	A	P	A
1030789	COG2936R	gbs1781	pepXP	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Xaa-Pro dipeptidyl-peptidase (EC 3.4.14.11)	1.434	P	P	P	P	P	P	P	P	1.015	P	A	P	P	P	P	P	P	P
1031410	-	gbs1782		Hypothetical		Hypothetical protein	3.450	P	P	P	A	P	P	P	P	2.986	P	A	P	A	P	P	A	P	A
1030790	COG0142H	gbs1783		Metabolism and transport	Cofactors, prosthetic groups, and carriers	Farnesyl pyrophosphate synthetase (EC 2.5.1.1) Geranyltransferase (EC 2.5.1.10)	2.004	P	P	P	P	P	P	P	P	1.154	P	A	P	A	M	P	P	M	P
1030803	COG4987CO	gbs1784		Metabolism and transport	Energy production and conversion	Transport ATP-binding protein cydC	13.095	A	A	A	A	A	A	A	A	2.010	A	A	A	A	A	A	A	A	A
1030795	COG4988CO	gbs1785		Metabolism and transport	Energy production and conversion	Transport ATP-binding protein cydD	2.182	P	A	A	A	A	A	A	A	1.770	P	A	A	A	A	A	A	A	A
1030801	COG1294C	gbs1786		Metabolism and transport	Energy production and conversion	Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)	1.912	P	P	P	P	P	P	P	P	1.220	P	P	P	P	P	P	P	P	P
1030701	COG1271C	gbs1787		Metabolism and transport	Energy production and conversion	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)	1.837	P	P	P	P	P	P	P	P	1.011	P	P	P	P	P	P	P	P	P
1030807	COG1523C	gbs1788		Metabolism and transport	Energy production and conversion	NADH dehydrogenase family	1.446	P	A	P	A	P	A	P	A	0.838	P	A	P	A	A	P	P	A	A
1030761	COG1575H	gbs1789		Metabolism and transport	Cofactors, prosthetic groups, and carriers	1,4-dihydroxy-2-naphthoate polypropenyltransferase (EC 2.5.1.-)	1.823	P	A	A	A	A	A	A	A	0.972	P	A	M	A	A	A	P	P	A
1030847	-	gbs1790		Hypothetical		Hypothetical protein	0.637	P	P	P	P	P	P	P	P	0.782	P	P	P	P	P	P	P	P	P
1030848	COG0718S	gbs1791		Hypothetical		Hypothetical cytosolic protein	1.815	P	P	P	P	P	P	P	P	0.865	P	A	P	P	P	P	P	P	P
1030850	COG2230M	gbs1792		Cell Envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	1.467	P	P	P	P	P	P	P	P	0.448	P	A	A	A	A	A	A	A	A
1030851	COG0789K	gbs1793		Cellular processes	Transcription	Transcriptional regulator, MerR family	0.681	P	P	P	P	P	P	P	P	0.929	P	A	P	A	P	P	P	P	P
1030859	COG0847L	gbs1794	dnaQ	Cellular processes	DNA replication, recombination and repair	DNA polymerase III, epsilon chain (EC 2.7.7.7)	1.583	P	P	P	P	P	P	P	P	1.451	P	A	A	A	A	P	A	P	A
1030852	-	gbs1795		Hypothetical		Hypothetical cytosolic protein	2.967	P	P	P	P	P	P	P	P	1.207	P	P	P	P	P	P	P	P	P
1030856	COG2081R	gbs1796		General function predicted only		NAD(FAD)-utilizing dehydrogenases	1.132	P	A	P	A	P	A	A	A	0.710	M	A	A	A	A	A	A	A	A
1030860	COG1085C	gbs1797		Metabolism and transport	Energy production and conversion	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	1.121	P	P	P	P	P	P	M	0.677	P	A	P	A	P	P	A	A	A	A
1030855	COG0199J	gbs1798	rpsN2	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S14P	0.444	P	P	P	P	P	P	P	P	1.668	P	P	P	P	P	P	P	P	P
1030854	COG2008E	gbs1799		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Low-specificity L-threonine aldolase (EC 4.1.2.5)	1.301	P	P	P	P	P	P	P	P	0.982	P	A	P	A	P	M	A	P	A
1030853	COG0533O	gbs1800		Cellular processes	Posttranslational modification, protein turnover, chaperones	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	1.999	P	A	M	A	A	A	A	A	1.027	P	A	A	A	A	P	A	A	A
1030862	COG0456R	gbs1801		Cellular processes	Translation, ribosomal structure and biogenesis	Ribosomal protein-S18-alanine acetyltransferase (EC 2.3.1.128)	2.932	P	P	P	P	P	P	P	P	0.939	P	A	P	A	M	P	A	P	A
1030865	COG1214O	gbs1802		Cellular processes	Posttranslational modification, protein turnover, chaperones	Non-proteolytic protein, peptidase family M22	2.595	P	A	M	A	A	A	A	A	1.250	P	A	A	A	A	P	A	P	A
1030868	-	gbs1803		General function predicted only		Putative transcriptional regulator	2.689	P	P	P	P	P	P	P	P	1.539	P	P	P	P	P	P	P	P	P
1030867	COG0595R	gbs1804		General function predicted only		Zn-dependent hydrolase (EC 3.-.-.-)	2.285	P	P	P	P	P	P	P	P	1.702	P	A	P	A	P	P	P	P	A
1030861	COG3942R	gbs1805		General function predicted only		Secreted protein	2.208	P	A	A	A	A	P	A	A	0.828	A	A	A	A	A	A	A	A	A
1030872	-	gbs1806	glnA	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Glutamine synthetase (EC 6.3.1.2)	6.862	P	M	P	P	P	P	P	P	2.133	P	A	A	A	P	P	A	P	A
1030864	COG0789K	gbs1807		Cellular processes	Transcription	Transcriptional regulator, MerR family	2.655	P	P	P	P	P	P	P	P	0.972	P	A	P	P	P	P	P	P	P
1030866	COG4129S	gbs1808		Hypothetical		Hypothetical protein	1.258	P	M	P	P	P	P	P	P	0.790	P	A	P	A	P	P	A	P	A
1030870	-	gbs1809	pgk	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Phosphoglycerate kinase (EC 2.7.2.3)	0.522	P	P	P	P	P	P	P	P	0.644	P	A	P	P	P	P	P	P	P
1030873	COG2503R	gbs1810	lppC	Metabolism and transport	Cofactors, prosthetic groups, and carriers	Acid phosphatase (EC 3.1.3.2)	0.476	P	P	P	P	P	P	P	P	0.748	P	P	P	P	P	P	P	P	P
1030869	COG0057G	gbs1811	gapC/plr	Metabolism and transport	Carbohydrates, organic alcohols, and acids	Glyceroldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) GAPDH	0.371	P	P	P	P	P	P	P	P	0.418	P	P	P	P	P	P	P	P	P
1030871	COG0480J	gbs1812	fus	Cellular processes	Translation, ribosomal structure and biogenesis	Protein Translation Elongation Factor G (EF-G)	0.951	P	P	P	P	P	P	P	P	0.896	P	P	P	P	P	P	P	P	P
1030883	COG0049J	gbs1813	rpsG	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S7P	1.715	P	P	P	P	P	P	P	P	0.723	P	P	P	P	P	P	P	P	P
1030884	-	gbs1814	rpsL	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S12P	1.545	P	P	P	P	P	P	P	P	0.665	P	P	P	P	P	P	P	P	P
1030890	COG0503F	gbs1815	purR	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	SRU operon repressor	0.592	P	P	P	P	P	P	P	P	1.059	P	P	P	M	P	P	P	P	P
1030876	COG34																								

1031452	COG3022S	gbs2036	yaaA	Hypothetical		Hypothetical cytosolic protein	1.600	P	A	P	P	A	P	A	A	A	1.046	P	A	A	A	A	M	A	A
1031438	COG0602O	gbs2037	nrpG	Cellular processes	Posttranslational modification, protein turnover, chaperones	Anaerobic ribonucleoside-triphosphate reductase activating protein	2.601	P	A	P	P	P	M	A	A	A	1.398	P	A	P	A	A	M	A	A
1031463	COG3981R	gbs2038		Metabolism and transport	Central intermediary metabolism	Acetyltransferase (EC 2.3.1.-)	3.991	P	A	M	A	P	P	A	A	A	3.601	P	A	A	A	A	A	A	A
1031457	COG0673R	gbs2039		Metabolism and transport	Central intermediary metabolism	NAD-dependent oxidoreductase	2.480	P	A	P	A	P	M	A	M	A	2.195	P	A	A	A	A	A	A	A
1031458	-	gbs2040		Hypothetical		Hypothetical protein	1.747	P	P	P	P	P	P	P	P	P	1.903	P	P	P	P	P	P	P	P
1031480	COG1328F	gbs2041	nrpD	Metabolism and transport	Purines, pyrimidines, nucleosides, and nucleotides	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	2.046	P	P	P	P	P	P	P	P	P	0.703	P	P	P	P	P	P	P	P
1031460	-	gbs2042		Hypothetical		Hypothetical membrane spanning protein	3.976	P	A	P	P	P	P	P	P	P	2.491	P	A	P	A	P	A	P	A
1031467	COG3906S	gbs2043		Hypothetical		Hypothetical cytosolic protein	0.625	P	P	P	P	P	P	P	P	P	1.474	P	P	P	P	P	P	P	P
1031487	-	gbs2044		Cellular processes	DNA replication, recombination and repair	Endonuclease involved in recombination	0.528	P	P	P	P	P	P	P	P	P	1.330	P	P	P	P	P	P	P	P
1031478	-	gbs2045		Hypothetical		Hypothetical cytosolic protein	0.434	P	P	P	P	P	P	P	P	P	1.002	P	P	P	P	P	P	P	P
1031465	COG1393P	gbs2046	spxA	Metabolism and transport	Inorganic ion transport and metabolism	Arsenate reductase family protein	0.734	P	P	P	P	P	P	P	P	P	0.679	P	P	P	P	P	P	P	P
1031471	COG0468L	gbs2047	recA	Cellular processes	DNA replication, recombination and repair	RecA protein	1.456	P	A	P	A	M	M	A	P	1.251	P	A	P	A	A	A	M	A	A
1031601	1058R, COG1	gbs2048	cinA	General function predicted only		Colligrin	1.380	P	A	A	M	M	M	A	P	0.476	P	A	P	A	A	A	M	A	A
1031543	-	gbs2049	tag	Cellular processes	DNA replication, recombination and repair	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	2.487	P	M	P	A	P	P	A	P	1.557	P	A	P	A	P	P	A	A	A
1031545	COG0632L	gbs2050	ruvA	Cellular processes	DNA replication, recombination and repair	Holliday junction DNA helicase ruvA	5.742	P	A	A	A	A	P	A	A	3.162	P	A	A	A	A	A	A	A	A
1031501	-	gbs2051	ImrP	Cellular processes	Toxin production and resistance	Multidrug resistance protein ImrP	5.579	P	A	P	A	A	P	A	A	3.410	P	A	P	A	A	P	A	A	A
1031648	COG0323L	gbs2052	mutL	Cellular processes	DNA replication, recombination and repair	DNA mismatch repair protein mutL	2.239	P	A	P	A	A	A	M	A	1.548	P	A	A	A	A	A	A	A	A
1031494	-	gbs2053	csp	Cellular processes	Posttranslational modification, protein turnover, chaperones	Cold shock protein	1.290	P	P	P	P	P	P	P	P	0.751	P	P	P	P	P	P	P	P	P
1031681	COG0249L	gbs2054	mutS	Cellular processes	DNA replication, recombination and repair	DNA mismatch repair protein mutS	0.816	P	A	A	A	A	A	A	A	0.710	P	A	A	A	A	A	A	A	A
1031544	COG1438K	gbs2055	argR2	Cellular processes	Transcription	Arginine repressor, argR	1.336	P	P	P	P	P	P	P	P	1.281	P	A	P	A	A	P	A	A	A
1031682	COG0018J	gbs2056	argS	Cellular processes	Translation, ribosomal structure and biogenesis	Arginyl-tRNA synthetase (EC 6.1.1.19)	1.159	P	P	P	P	P	P	P	P	1.125	P	A	P	P	P	P	P	P	P
1031685	-	gbs2057	uvrB	Hypothetical		Bacteriocin uvrB	1.674	P	P	P	P	P	P	P	P	2.530	P	A	P	A	A	P	A	A	A
1031680	COG1284S	gbs2058		Hypothetical		Hypothetical membrane spanning protein	1.496	P	P	P	P	P	A	P	0.569	P	M	P	M	P	P	A	P	A	P
1030780	COG1284S	gbs2059		Hypothetical		Hypothetical membrane spanning protein	2.959	P	P	P	P	P	P	P	0.967	P	P	P	A	P	P	P	P	P	P
1031827	COG0173J	gbs2060	aspS	Cellular processes	Translation, ribosomal structure and biogenesis	Aspartyl-tRNA synthetase (EC 6.1.1.12)	2.238	P	P	P	M	P	P	P	P	0.928	P	M	A	P	M	P	M	P	M
1031683	COG0124J	gbs2061	hisS	Cellular processes	Translation, ribosomal structure and biogenesis	Histidyl-tRNA synthetase (EC 6.1.1.21)	2.134	P	M	P	A	P	P	P	A	1.301	P	A	A	A	A	A	A	A	A
1031684	COG0333J	gbs2062	rpmF	Cellular processes	Translation, ribosomal structure and biogenesis	LSU ribosomal protein L32P	0.853	P	P	P	P	P	P	P	P	0.683	P	P	P	P	P	P	P	P	P
1030811	COG0267J	gbs2063	rpmG	Cellular processes	Translation, ribosomal structure and biogenesis	LSU ribosomal protein L33P	0.590	P	P	P	P	P	P	P	P	0.638	P	P	P	P	P	P	P	P	P
1030716	-	gbs2064	cadD	Cellular processes	Toxin production and resistance	Cadmium resistance protein	1.456	P	A	A	A	A	M	A	A	1.357	P	A	A	A	A	A	A	A	A
1030808	COG0640K	gbs2065	cadC	Cellular processes	Toxin production and resistance	Cadmium efflux system accessory protein	1.158	P	A	M	A	P	P	A	A	1.398	P	A	A	A	A	A	A	A	A
1030814	-	gbs2066		Hypothetical		Hypothetical protein	1.156	P	M	P	P	P	P	P	2.120	P	A	A	M	A	A	A	A	A	A
1030813	-	gbs2067		Hypothetical		Hypothetical protein	0.567	P	A	M	A	A	A	A	A	0.364	A	A	A	A	A	A	A	A	A
1030815	-	gbs2068		Hypothetical		Hypothetical protein	0.665	P	P	A	A	P	A	P	0.596	P	A	M	P	M	P	P	A	A	A
1030830	COG1674D	gbs2069		Cellular processes	Cell division	FtsK SpoIIIE family	1.037	P	A	A	A	A	A	A	A	0.840	P	A	A	A	A	A	A	A	A
1031433	-	gbs2070		Hypothetical		Hypothetical protein	1.152	P	A	A	A	A	A	A	A	3.029	P	A	A	A	A	A	A	A	A
1030817	-	gbs2071		Mobile and extrachromosomal elements		Replication protein	1.141	A	A	A	A	A	A	A	A	0.326	A	A	A	A	A	A	A	A	A
1030783	-	gbs2072		Mobile and extrachromosomal elements		Phage protein	3.419	P	A	A	A	A	A	A	A	1.351	A	A	A	A	A	A	A	A	A
1030747	COG0582L	gbs2073		Mobile and extrachromosomal elements		DNA integration recombination inversion protein	2.301	P	P	P	P	P	P	P	1.311	P	P	P	P	P	P	P	P	P	P
1030842	-	gbs2074		Hypothetical		Hypothetical cytosolic protein	5.410	P	A	P	A	P	P	A	P	2.221	P	A	P	M	P	A	P	A	P
1030781	-	gbs2076		Hypothetical		Hypothetical protein	1.525	P	M	P	P	P	P	P	1.307	P	A	P	A	M	A	A	A	A	A
1030820	-	gbs2077		Hypothetical		Hypothetical protein	3.107	P	A	A	P	P	P	P	A	0.785	P	A	A	P	A	A	A	A	A
1031055	COG3212S	gbs2080		Hypothetical		Hypothetical protein	1.059	P	A	A	A	A	A	A	A	0.126	A	A	A	A	A	A	A	A	A
1030819	COG0745TK	gbs2081		Cellular processes	Transcription	Transcriptional regulatory protein	1.012	P	P	P	P	P	P	P	1.162	P	A	P	M	M	P	P	A	P	A
1030759	COG0642T	gbs2082		Cellular processes	Signal transduction	Two-component sensor kinase czcS (EC 2.7.3.-)	1.329	P	P	P	P	P	M	P	2.094	P	A	A	A	P	A	A	A	A	A
1030703	COG1288S	gbs2083		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Arginine ornithine antiporter	0.308	A	A	A	A	A	A	A	A	6.813	P	A	A	A	A	A	A	A	A
1030750	COG0549E	gbs2084		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Carbamate kinase (EC 2.7.2.2)	1.249	P	A	A	A	A	P	A	A	3.280	P	A	P	P	A	A	A	A	A
1031013	COG0078E	gbs2085		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Ornithine carbamoyltransferase (EC 2.1.3.3)	0.753	P	A	P	A	P	P	P	P	1.972	P	A	P	A	P	M	P	A	A
1031066	COG0642T	gbs2086		Cellular processes	Signal transduction	Sporulation kinase A (EC 2.7.3.-)	1.675	P	A	A	A	A	A	A	A	1.760	A	A	A	A	A	A	A	A	A
1030729	COG4753T	gbs2087		Cellular processes	Signal transduction	Two-component response regulator	1.391	P	A	A	A	A	A	A	A	1.617	P	A	A	A	A	M	A	A	A
1031098	COG1125E	gbs2088	proV	Metabolism and transport	Amino acids, peptides, aminosugars and amines	Glycine betaine transport-ATP-binding protein	1.815	P	P	P	P	P	P	P	1.524	P	A	P	P	P	P	P	P	P	P
1030749	1174E, COG1	gbs2089		Metabolism and transport	Amino acids, peptides, aminosugars and amines	Glycine betaine transport system permease protein Glycine betaine-binding prote	1.474	P	P	P	P	P	P	P	1.048	P	P	P	P	P	P	P	P	P	P
1031102	0392S, COG2	gbs2090		General function predicted only		Lysylcardiolipin synthase (EC 2.3.2.-) Lysyltransferase (EC 2.3.2.3)	1.595	P	P	P	P	P	P	P	1.521	P	A	P	P	P	P	P	P	P	P
1031088	COG0596R	gbs2091		General function predicted only		Non-heme chloroperoxidase (EC 1.11.1.10)	2.405	P	P	P	P	P	M	P	1.566	P	A	P	P	A	M	A	A	A	A
1030688	COG3759S	gbs2092		Hypothetical		Hypothetical membrane spanning protein	1.475	A	A	A	A	A	A	A	A	0.162	A	A	A	A	A	A	A	A	A
1030562	COG1511S	gbs2093		Mobile and extrachromosomal elements		Phage infection protein	3.144	A	A	A	A	A	A	A	A	0.130	A	A	A	A	A	A	A	A	A
1030957	COG1309K	gbs2094		Cellular processes	Transcription	Transcriptional regulator, TetR family	1.436	P	A	A	A	A	A	A	A	1.060	P	A	A	A	A	A	A	A	A
1030235	-	gbs2095		Hypothetical		Hypothetical protein	3.872	P	A	A	A	A	A	A	A	0.565	A	A	A	A	A	A	A	A	A
1029947	COG0522J	gbs2096	rpsD	Cellular processes	Translation, ribosomal structure and biogenesis	SSU ribosomal protein S4P	1.888	P	P	P	P	P	P	P	0.477	P	P	P	P	P	P	P	P	P	P
1031112	-	gbs2097		Hypothetical		Hypothetical protein	1.943	P	P	P	P	P	P	P	1.504	P	P	P	P	P	P	P	P	P	P
1031046	COG0305L	gbs2098	holB	Cellular processes	DNA replication, recombination and repair	Replicative DNA helicase (EC 3.6.1.-)	2.110	P	P	P	P	P	P	P	1.304	P	A	P	A	P	P	P	P	P	P
1030821	COG0359J	gbs2099	rplI	Cellular processes	Translation, ribosomal structure and biogenesis	LSU ribosomal protein L9P	1.659	P	P	P	P	P	P	P	1.182	P	P	P	P	P	P	P	P	P	P
1030960	COG3887T	gbs2100		Metabolism and transport	Central intermediary metabolism	Phosphoesterase, DHH family protein	2.188	P	P	P	P	P	P	P	1.292	P	P	P	P	P	P	P	P	P	P
1030341	COG0445D	gbs2101	gidA	General function predicted only		Putative tRNA (5-carboxymethylaminomethyl-2-thiouridylylate) synthase subunit Gid	1.420	P	A	M	A	M	A	A	A	1.287	P	A	A	A	A	A	A	A	A
1031036	COG2095U	gbs2102		Cell Envelope	Other	MarC family integral membrane protein	2.776	P	A	A	A	A	A	A	A	0.827	P	A	A	A	A	A	A	A	A
1030810	COG0482J	gbs2103	trmU	Cellular processes	Translation, ribosomal structure and biogenesis	tRNA (5-methylaminomethyl-2-thiouridylylate)-methyltransferase (EC 2.1.1.61)	2.183	P	A	A	A	A	A	A	A	0.767	P	A	A	A	A	A	A	A	A
1031056	COG1760E	gbs2104	sdhB	Metabolism and transport	Amino acids, peptides, aminosugars and amines	L-serine dehydratase beta subunit (EC 4.3.1.17)	3.552	P	A	A	A	A	A	A	A	2.469	P	A	A	A	A	A	A	A	A
1030711	COG1760E	gbs2105	sdhA	Metabolism and transport	Amino acids, peptides, aminosugars and amines	L-serine dehydratase alpha subunit (EC 4.3.1.17)	1.080	P	A	P	A	M	A	A	A	1.023	P	A	M	A	A	A	A	A	A
1031113	-	gbs2106		General function predicted only		Transglycosylase SLT domain family protein	2.358	P	A	A	A	A	A	A	A	1.070	M	A	A	A	A	A	A	A	A
1031059	-	gbs2107		Cell Envelope		peptidoglycan binding protein (LysM domain)	1.																		

1031012	COG1475K	qbs2134	parB	Cellular processess	Transcription	Chromosome partitioning protein parB	1,618	P	P	P	M	P	P	P	P	1,242	P	A	P	A	A	A	A	A	A
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