COG	Function		Functional Category
COG1828	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component	F	Nucleotide transport and metabolism
COG3194	Ureidoglycolate hydrolase	F	Nucleotide transport and metabolism
COG5515	Uncharacterized conserved small protein	S	Function unknown
COG1489	DNA-binding protein, stimulates sugar fermentation	R	General function prediction only
COG1058	Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA	R	General function prediction only
COG0006	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG2192	Predicted carbamoyl transferase, NodU family	O	Posttranslational modification, protein turnover, chaperones
COG0418	Dihydroorotase	F	Nucleotide transport and metabolism
COG1570	Exonuclease VII, large subunit	L	Replication, recombination and repair
COG0435	Predicted glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0717	Deoxycytidine deaminase	F	Nucleotide transport and metabolism
COG0777	Acetyl-CoA carboxylase beta subunit	I	Lipid transport and metabolism
COG1984	Allophanate hydrolase subunit 2	E	Amino acid transport and metabolism
COG2049	Allophanate hydrolase subunit 1	E	Amino acid transport and metabolism
COG1540	Uncharacterized proteins, homologs of lactam utilization protein B	R	General function prediction only
COG4336	Uncharacterized conserved protein	S	Function unknown
COG0159	Tryptophan synthase alpha chain	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0280	Phosphotransacetylase	C	Energy production and conversion
COG0133	Tryptophan synthase beta chain	E	Amino acid transport and metabolism
COG2055	Malate/L-lactate dehydrogenases	C	Energy production and conversion
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG1937	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1233	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG1022	Long-chain acyl-CoA synthetases (AMP-forming)	I	Lipid transport and metabolism
COG0518	GMP synthase - Glutamine amidotransferase domain	F	Nucleotide transport and metabolism
COG2252	Permeases	R	General function prediction only
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0764	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	I	Lipid transport and metabolism
COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	I	Lipid transport and metabolism
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG5508	Uncharacterized conserved small protein	S	Function unknown
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG0520	Selenocysteine lyase	E	Amino acid transport and metabolism
COG2133	Glucose/sorbosone dehydrogenases	G	Carbohydrate transport and metabolism
COG3221	ABC-type phosphate/phosphonate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG1899	Deoxyhypusine synthase	O	Posttranslational modification, protein turnover, chaperones
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG1073	Hydrolases of the alpha/beta superfamily	R	General function prediction only
COG3802	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3491	Isopenicillin N synthase and related dioxygenases	R	General function prediction only
COG1086	Predicted nucleoside-diphosphate sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2089	Sialic acid synthase	M	Cell wall/membrane/envelope biogenesis
COG0612	Predicted Zn-dependent peptidases	R	General function prediction only
COG0461	Orotate phosphoribosyltransferase	F	Nucleotide transport and metabolism
COG3178	Predicted phosphotransferase related to Ser/Thr protein kinases	R	General function prediction only
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation	M	Cell wall/membrane/envelope biogenesis
COG2127	Uncharacterized conserved protein	S	Function unknown
COG3484	Predicted proteasome-type protease	O	Posttranslational modification, protein turnover, chaperones
COG0739	Membrane proteins related to metalloendopeptidases	M	Cell wall/membrane/envelope biogenesis
COG1686	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
COG2998	ABC-type tungstate transport system, permease component	H	Coenzyme transport and metabolism
COG4662	ABC-type tungstate transport system, periplasmic component	H	Coenzyme transport and metabolism
COG1526	Uncharacterized protein required for formate dehydrogenase activity	C	Energy production and conversion
COG0746	Molybdopterin-guanine dinucleotide biosynthesis protein A	H	Coenzyme transport and metabolism
COG0397	Uncharacterized conserved protein	S	Function unknown
COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	G	Carbohydrate transport and metabolism
COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport and metabolism
COG0711	F0F1-type ATP synthase, subunit b	C	Energy production and conversion
COG0711	F0F1-type ATP synthase, subunit b	C	Energy production and conversion
COG5336	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG4338	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG2154	Pterin-4a-carbinolamine dehydratase	H	Coenzyme transport and metabolism
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG2225	Malate synthase	C	Energy production and conversion
COG0270	Site-specific DNA methylase	L	Replication, recombination and repair
COG4783	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
COG2025	Electron transfer flavoprotein, alpha subunit	C	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG3288	NAD/NADP transhydrogenase alpha subunit	C	Energy production and conversion
COG1182	Acyl carrier protein phosphodiesterase	I	Lipid transport and metabolism
COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0006	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport and metabolism
COG2721	Altronate dehydratase	G	Carbohydrate transport and metabolism

COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG1475	Predicted transcriptional regulators	K	Transcription
COG1840	ABC-type Fe3+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG0816	Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. sub	L	Replication, recombination and repair
COG0558	Phosphatidylglycerophosphate synthase	I	Lipid transport and metabolism
COG0839	NADH:ubiquinone oxidoreductase subunit 6 (chain J)	C	Energy production and conversion
COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Energy production and conversion
COG0343	Queuine/archaeosine tRNA-ribosyltransferase	J	Translation, ribosomal structure and biogenesis
COG0101	Pseudouridylate synthase	J	Translation, ribosomal structure and biogenesis
COG0150	Phosphoribosylaminoimidazole (AIR) synthetase	F	Nucleotide transport and metabolism
COG1006	Multisubunit Na+/H+ antiporter, MnhC subunit	P	Inorganic ion transport and metabolism
COG2111	Multisubunit Na+/H+ antiporter, MnhB subunit	P	Inorganic ion transport and metabolism
COG1320	Multisubunit Na+/H+ antiporter, MnhG subunit	P	Inorganic ion transport and metabolism
COG1385	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0196	FAD synthase	H	Coenzyme transport and metabolism
COG0623	Enoyl-[acyl-carrier-protein] reductase (NADH)	I	Lipid transport and metabolism
COG2104	Sulfur transfer protein involved in thiamine biosynthesis	H	Coenzyme transport and metabolism
COG0663	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	R	General function prediction only
COG0018	Arginyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0670	Integral membrane protein, interacts with FtsH	R	General function prediction only
COG1005	NADH:ubiquinone oxidoreductase subunit 1 (chain H)	C	Energy production and conversion
COG2823	Predicted periplasmic or secreted lipoprotein	R	General function prediction only
COG0184	Ribosomal protein S15P/S13E	J	Translation, ribosomal structure and biogenesis
COG0015	Adenylosuccinate lyase	F	Nucleotide transport and metabolism
COG0359	Ribosomal protein L9	J	Translation, ribosomal structure and biogenesis
COG0360	Ribosomal protein S6	J	Translation, ribosomal structure and biogenesis
COG0226	ABC-type phosphate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0590	Cytosine/adenosine deaminases	F	Nucleotide transport and metabolism
COG0223	Methionyl-tRNA formyltransferase	J	Translation, ribosomal structure and biogenesis
COG0130	Pseudouridine synthase	J	Translation, ribosomal structure and biogenesis
COG1530	Ribonucleases G and E	J	Translation, ribosomal structure and biogenesis
COG0157	Nicotinate-nucleotide pyrophosphorylase	H	Coenzyme transport and metabolism
COG0228	Ribosomal protein S16	J	Translation, ribosomal structure and biogenesis
COG0806	RimM protein, required for 16S rRNA processing	J	Translation, ribosomal structure and biogenesis
COG0805	Sec-independent protein secretion pathway component TatC	U	Intracellular trafficking, secretion, and vesicular transport
COG2890	Methylase of polypeptide chain release factors	J	Translation, ribosomal structure and biogenesis
COG0712	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)	C	Energy production and conversion
COG0212	5-formyltetrahydrofolate cyclo-ligase	H	Coenzyme transport and metabolism
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G	Carbohydrate transport and metabolism
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG0564	Pseudouridylate synthases, 23S RNA-specific	J	Translation, ribosomal structure and biogenesis
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0044	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
COG1734	DnaK suppressor protein	T	Signal transduction mechanisms
COG1351	Predicted alternative thymidylate synthase	F	Nucleotide transport and metabolism
COG0330	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification, protein turnover, chaperones
COG0330	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification, protein turnover, chaperones
COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	O	Posttranslational modification, protein turnover, chaperones
COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)	L	Replication, recombination and repair
COG0612	Predicted Zn-dependent peptidases	R	General function prediction only
COG5405	ATP-dependent protease HslVU (ClpYQ), peptidase subunit	O	Posttranslational modification, protein turnover, chaperones
COG0167	Dihydroorotate dehydrogenase	F	Nucleotide transport and metabolism
COG0128	5-enolpyruvylshikimate-3-phosphate synthase	E	Amino acid transport and metabolism
COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)	F	Nucleotide transport and metabolism
COG0189	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism
COG0593	ATPase involved in DNA replication initiation	L	Replication, recombination and repair
COG0841	Cation/multidrug efflux pump	V	Defense mechanisms
COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)	J	Translation, ribosomal structure and biogenesis
COG1195	Recombinational DNA repair ATPase (RecF pathway)	L	Replication, recombination and repair
COG0742	N6-adenine-specific methylase	L	Replication, recombination and repair
COG0271	Stress-induced morphogen (activity unknown)	T	Signal transduction mechanisms
COG0278	Glutaredoxin-related protein	O	Posttranslational modification, protein turnover, chaperones
COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase	L	Replication, recombination and repair
COG0576	Molecular chaperone GrpE (heat shock protein)	O	Posttranslational modification, protein turnover, chaperones
COG0180	Tryptophanyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0291	Ribosomal protein L35	J	Translation, ribosomal structure and biogenesis
COG0292	Ribosomal protein L20	J	Translation, ribosomal structure and biogenesis
COG0016	Phenylalanyl-tRNA synthetase alpha subunit	J	Translation, ribosomal structure and biogenesis
COG0698	Ribose 5-phosphate isomerase RpiB	G	Carbohydrate transport and metabolism
COG0352	Thiamine monophosphate synthase	H	Coenzyme transport and metabolism
COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)	E	Amino acid transport and metabolism
COG0312	Predicted Zn-dependent proteases and their inactivated homologs	R	General function prediction only
COG0104	Adenylosuccinate synthase	F	Nucleotide transport and metabolism
COG0240	Glycerol-3-phosphate dehydrogenase	C	Energy production and conversion
COG1396	Predicted transcriptional regulators	K	Transcription
COG0041	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase	F	Nucleotide transport and metabolism
COG0533	Metal-dependent proteases with possible chaperone activity	O	Posttranslational modification, protein turnover, chaperones
COG2358	TRAP-type uncharacterized transport system, periplasmic component	R	General function prediction only
COG0142	Geranylgeranyl pyrophosphate synthase	H	Coenzyme transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG0769	UDP-N-acetylmuramyl tripeptide synthase	M	Cell wall/membrane/envelope biogenesis
COG0177	Predicted EndoIII-related endonuclease	L	Replication, recombination and repair
COG1183	Phosphatidylserine synthase	I	Lipid transport and metabolism
COG0688	Phosphatidylserine decarboxylase	I	Lipid transport and metabolism

COG0319	Predicted metal-dependent hydrolase	R	General function prediction only
COG0074	Succinyl-CoA synthetase, alpha subunit	C	Energy production and conversion
COG0045	Succinyl-CoA synthetase, beta subunit	C	Energy production and conversion
COG0611	Thiamine monophosphate kinase	H	Coenzyme transport and metabolism
COG0149	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
COG1054	Predicted sulfurtransferase	R	General function prediction only
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG3175	Cytochrome oxidase assembly factor	O	Posttranslational modification, protein turnover, chaperones
COG0593	ATPase involved in DNA replication initiation	L	Replication, recombination and repair
COG0136	Aspartate-semialdehyde dehydrogenase	E	Amino acid transport and metabolism
COG0566	rRNA methylases	J	Translation, ribosomal structure and biogenesis
COG0087	Ribosomal protein L3	J	Translation, ribosomal structure and biogenesis
COG0088	Ribosomal protein L4	J	Translation, ribosomal structure and biogenesis
COG0089	Ribosomal protein L23	J	Translation, ribosomal structure and biogenesis
COG0090	Ribosomal protein L2	J	Translation, ribosomal structure and biogenesis
COG0091	Ribosomal protein L22	J	Translation, ribosomal structure and biogenesis
COG0092	Ribosomal protein S3	J	Translation, ribosomal structure and biogenesis
COG0197	Ribosomal protein L16/L10E	J	Translation, ribosomal structure and biogenesis
COG0186	Ribosomal protein S17	J	Translation, ribosomal structure and biogenesis
COG0093	Ribosomal protein L14	J	Translation, ribosomal structure and biogenesis
COG0094	Ribosomal protein L5	J	Translation, ribosomal structure and biogenesis
COG0199	Ribosomal protein S14	J	Translation, ribosomal structure and biogenesis
COG0096	Ribosomal protein S8	J	Translation, ribosomal structure and biogenesis
COG0097	Ribosomal protein L6P/L9E	J	Translation, ribosomal structure and biogenesis
COG0256	Ribosomal protein L18	J	Translation, ribosomal structure and biogenesis
COG0098	Ribosomal protein S5	J	Translation, ribosomal structure and biogenesis
COG0200	Ribosomal protein L15	J	Translation, ribosomal structure and biogenesis
COG0201	Preprotein translocase subunit SecY	U	Intracellular trafficking, secretion, and vesicular transport
COG0563	Adenylate kinase and related kinases	F	Nucleotide transport and metabolism
COG0099	Ribosomal protein S13	J	Translation, ribosomal structure and biogenesis
COG0100	Ribosomal protein S11	J	Translation, ribosomal structure and biogenesis
COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	K	Transcription
COG0203	Ribosomal protein L17	J	Translation, ribosomal structure and biogenesis
COG0789	Predicted transcriptional regulators	K	Transcription
COG1267	Phosphatidylglycerophosphatase A and related proteins	I	Lipid transport and metabolism
COG0290	Translation initiation factor 3 (IF-3)	J	Translation, ribosomal structure and biogenesis
COG0633	Ferredoxin	C	Energy production and conversion
COG0316	Uncharacterized conserved protein	S	Function unknown
COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	E	Amino acid transport and metabolism
COG1178	ABC-type Fe3+ transport system, permease component	P	Inorganic ion transport and metabolism
COG1825	Ribosomal protein L25 (general stress protein Ctc)	J	Translation, ribosomal structure and biogenesis
COG0193	Peptidyl-tRNA hydrolase	J	Translation, ribosomal structure and biogenesis
COG0237	Dephospho-CoA kinase	H	Coenzyme transport and metabolism
COG0061	Predicted sugar kinase	G	Carbohydrate transport and metabolism
COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	K	Transcription
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0354	Predicted aminomethyltransferase related to GcvT	R	General function prediction only
COG0854	Pyridoxal phosphate biosynthesis protein	H	Coenzyme transport and metabolism
COG0227	Ribosomal protein L28	J	Translation, ribosomal structure and biogenesis
COG0320	Lipoate synthase	H	Coenzyme transport and metabolism
COG2867	Oligoketide cyclase/lipid transport protein	I	Lipid transport and metabolism
COG1806	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1253	Hemolysins and related proteins containing CBS domains	R	General function prediction only
COG1146	Ferredoxin	C	Energy production and conversion
COG0215	Cysteinyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0036	Pentose-5-phosphate-3-epimerase	G	Carbohydrate transport and metabolism
COG0024	Methionine aminopeptidase	J	Translation, ribosomal structure and biogenesis
COG2941	Ubiquinone biosynthesis protein COQ7	H	Coenzyme transport and metabolism
COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	K	Transcription
COG0162	Tyrosyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG1981	Predicted membrane protein	S	Function unknown
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG1327	Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains	K	Transcription
COG0210	Superfamily I DNA and RNA helicases	L	Replication, recombination and repair
COG0084	Mg-dependent DNase	L	Replication, recombination and repair
COG1952	Preprotein translocase subunit SecB	U	Intracellular trafficking, secretion, and vesicular transport
COG4395	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0030	Dimethyladenosine transferase (rRNA methylation)	J	Translation, ribosomal structure and biogenesis
COG0442	Prolyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	G	Carbohydrate transport and metabolism
COG0259	Pyridoxamine-phosphate oxidase	H	Coenzyme transport and metabolism
COG0029	Aspartate oxidase	H	Coenzyme transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG0181	Porphobilinogen deaminase	H	Coenzyme transport and metabolism
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0242	N-formylmethionyl-tRNA deformylase	J	Translation, ribosomal structure and biogenesis
COG0113	Delta-aminolevulinic acid dehydratase	H	Coenzyme transport and metabolism
COG0356	F0F1-type ATP synthase, subunit a	C	Energy production and conversion
COG0054	Riboflavin synthase beta-chain	H	Coenzyme transport and metabolism
COG0706	Preprotein translocase subunit YidC	U	Intracellular trafficking, secretion, and vesicular transport
COG1253	Hemolysins and related proteins containing CBS domains	R	General function prediction only
COG0216	Protein chain release factor A	J	Translation, ribosomal structure and biogenesis
COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	I	Lipid transport and metabolism
COG0539	Ribosomal protein S1	J	Translation, ribosomal structure and biogenesis
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms

COG0209	Ribonucleotide reductase, alpha subunit	F	Nucleotide transport and metabolism
COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	F	Nucleotide transport and metabolism
COG0708	Exonuclease III	L	Replication, recombination and repair
COG0341	Preprotein translocase subunit SecF	U	Intracellular trafficking, secretion, and vesicular transport
COG0465	ATP-dependent Zn proteases	O	Posttranslational modification, protein turnover, chaperones
COG0072	Phenylalanyl-tRNA synthetase beta subunit	J	Translation, ribosomal structure and biogenesis
COG0849	Actin-like ATPase involved in cell division	D	Cell cycle control, cell division, chromosome partitioning
COG0838	NADH:ubiquinone oxidoreductase subunit 3 (chain A)	C	Energy production and conversion
COG0377	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases	C	Energy production and conversion
COG0852	NADH:ubiquinone oxidoreductase 27 kD subunit	C	Energy production and conversion
COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	G	Carbohydrate transport and metabolism
COG0126	3-phosphoglycerate kinase	G	Carbohydrate transport and metabolism
COG0761	Penicillin tolerance protein	I	Lipid transport and metabolism
COG1587	Uroporphyrinogen-III synthase	H	Coenzyme transport and metabolism
COG0743	1-deoxy-D-xylulose 5-phosphate reductoisomerase	I	Lipid transport and metabolism
COG0536	Predicted GTPase	R	General function prediction only
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain	F	Nucleotide transport and metabolism
COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	I	Lipid transport and metabolism
COG0408	Coproporphyrinogen III oxidase	H	Coenzyme transport and metabolism
COG0232	dGTP triphosphohydrolase	F	Nucleotide transport and metabolism
COG1381	Recombinational DNA repair protein (RecF pathway)	L	Replication, recombination and repair
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related e	C	Energy production and conversion
COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)	P	Inorganic ion transport and metabolism
COG0482	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain	J	Translation, ribosomal structure and biogenesis
COG0847	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	L	Replication, recombination and repair
COG0006	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
COG2945	Predicted hydrolase of the alpha/beta superfamily	R	General function prediction only
COG3474	Cytochrome c2	C	Energy production and conversion
COG0299	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	F	Nucleotide transport and metabolism
COG0260	Leucyl aminopeptidase	E	Amino acid transport and metabolism
COG0581	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG2022	Uncharacterized enzyme of thiazole biosynthesis	H	Coenzyme transport and metabolism
COG0294	Dihydropteroate synthase and related enzymes	H	Coenzyme transport and metabolism
COG0801	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	H	Coenzyme transport and metabolism
COG0192	S-adenosylmethionine synthetase	H	Coenzyme transport and metabolism
COG0718	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2812	DNA polymerase III, gamma/tau subunits	L	Replication, recombination and repair
COG5424	Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C	H	Coenzyme transport and metabolism
COG0815	Apolipoprotein N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0117	Pyrimidine deaminase	H	Coenzyme transport and metabolism
COG0505	Carbamoylphosphate synthase small subunit	E	Amino acid transport and metabolism
COG0254	Ribosomal protein L31	J	Translation, ribosomal structure and biogenesis
COG3820	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0755	ABC-type transport system involved in cytochrome c biogenesis, permease component	O	Posttranslational modification, protein turnover, chaperones
COG0540	Aspartate carbamoyltransferase, catalytic chain	F	Nucleotide transport and metabolism
COG0208	Ribonucleotide reductase, beta subunit	F	Nucleotide transport and metabolism
COG0195	Transcription elongation factor	K	Transcription
COG0516	IMP dehydrogenase/GMP reductase	F	Nucleotide transport and metabolism
COG1463	ABC-type transport system involved in resistance to organic solvents, periplasmic component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0349	Ribonuclease D	J	Translation, ribosomal structure and biogenesis
COG0468	RecA/RadA recombinase	L	Replication, recombination and repair
COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	C	Energy production and conversion
COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O	Posttranslational modification, protein turnover, chaperones
COG1160	Predicted GTPases	R	General function prediction only
COG0461	Orotate phosphoribosyltransferase	F	Nucleotide transport and metabolism
COG0541	Signal recognition particle GTPase	U	Intracellular trafficking, secretion, and vesicular transport
COG0552	Signal recognition particle GTPase	U	Intracellular trafficking, secretion, and vesicular transport
COG0293	23S rRNA methylase	J	Translation, ribosomal structure and biogenesis
COG0125	Thymidylate kinase	F	Nucleotide transport and metabolism
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related e	C	Energy production and conversion
COG0312	Predicted Zn-dependent proteases and their inactivated homologs	R	General function prediction only
COG1999	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems	R	General function prediction only
COG0305	Replicative DNA helicase	L	Replication, recombination and repair
COG0564	Pseudouridylate synthases, 23S RNA-specific	J	Translation, ribosomal structure and biogenesis
COG0492	Thioredoxin reductase	O	Posttranslational modification, protein turnover, chaperones
COG0450	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0105	Nucleoside diphosphate kinase	F	Nucleotide transport and metabolism
COG0728	Uncharacterized membrane protein, putative virulence factor	R	General function prediction only
COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Energy production and conversion
COG0172	Seryl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase	J	Translation, ribosomal structure and biogenesis
COG1138	Cytochrome c biogenesis factor	O	Posttranslational modification, protein turnover, chaperones
COG1235	Metal-dependent hydrolases of the beta-lactamase superfamily I	R	General function prediction only
COG0522	Ribosomal protein S4 and related proteins	J	Translation, ribosomal structure and biogenesis
COG0302	GTP cyclohydrolase I	H	Coenzyme transport and metabolism
COG0224	F0F1-type ATP synthase, gamma subunit	C	Energy production and conversion
COG0812	UDP-N-acetylmuramate dehydrogenase	M	Cell wall/membrane/envelope biogenesis
COG1494	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase and related proteins	G	Carbohydrate transport and metabolism
COG4122	Predicted O-methyltransferase	R	General function prediction only
COG1048	Aconitase A	C	Energy production and conversion
COG1565	Uncharacterized conserved protein	S	Function unknown
COG0525	Valyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG1186	Protein chain release factor B	J	Translation, ribosomal structure and biogenesis
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Coenzyme transport and metabolism

COG1622	Heme/copper-type cytochrome/quinol oxidases, subunit 2	C	Energy production and conversion
COG0843	Heme/copper-type cytochrome/quinol oxidases, subunit 1	C	Energy production and conversion
COG0109	Polyprenyltransferase (cytochrome oxidase assembly factor)	O	Posttranslational modification, protein turnover, chaperones
COG0723	Rieske Fe-S protein	C	Energy production and conversion
COG1290	Cytochrome b subunit of the bc complex	C	Energy production and conversion
COG2857	Cytochrome c1	C	Energy production and conversion
COG0342	Preprotein translocase subunit SecD	U	Intracellular trafficking, secretion, and vesicular transport
COG2227	2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase	H	Coenzyme transport and metabolism
COG0416	Fatty acid/phospholipid biosynthesis enzyme	I	Lipid transport and metabolism
COG0333	Ribosomal protein L32	J	Translation, ribosomal structure and biogenesis
COG1905	NADH:ubiquinone oxidoreductase 24 kD subunit	C	Energy production and conversion
COG0661	Predicted unusual protein kinase	R	General function prediction only
COG0776	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
COG0217	Uncharacterized conserved protein	S	Function unknown
COG0459	Chaperonin GroEL (HSP60 family)	O	Posttranslational modification, protein turnover, chaperones
COG0234	Co-chaperonin GroES (HSP10)	O	Posttranslational modification, protein turnover, chaperones
COG0617	tRNA nucleotidyltransferase/poly(A) polymerase	J	Translation, ribosomal structure and biogenesis
COG0764	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0328	Ribonuclease HI	L	Replication, recombination and repair
COG0782	Transcription elongation factor	K	Transcription
COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains	L	Replication, recombination and repair
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
COG0081	Ribosomal protein L1	J	Translation, ribosomal structure and biogenesis
COG0080	Ribosomal protein L11	J	Translation, ribosomal structure and biogenesis
COG0250	Transcription antiterminator	K	Transcription
COG0049	Ribosomal protein S7	J	Translation, ribosomal structure and biogenesis
COG0048	Ribosomal protein S12	J	Translation, ribosomal structure and biogenesis
COG1008	NADH:ubiquinone oxidoreductase subunit 4 (chain M)	C	Energy production and conversion
COG1007	NADH:ubiquinone oxidoreductase subunit 2 (chain N)	C	Energy production and conversion
COG0340	Biotin-(acetyl-CoA carboxylase) ligase	H	Coenzyme transport and metabolism
COG0142	Geranylgeranyl pyrophosphate synthase	H	Coenzyme transport and metabolism
COG0767	ABC-type transport system involved in resistance to organic solvents, permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1127	ABC-type transport system involved in resistance to organic solvents, ATPase component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0802	Predicted ATPase or kinase	R	General function prediction only
COG0164	Ribonuclease HII	L	Replication, recombination and repair
COG0021	Transketolase	G	Carbohydrate transport and metabolism
COG0651	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	C	Energy production and conversion
COG0608	Single-stranded DNA-specific exonuclease	L	Replication, recombination and repair
COG0285	Folylpolyglutamate synthase	H	Coenzyme transport and metabolism
COG4775	Outer membrane protein/protective antigen OMA87	M	Cell wall/membrane/envelope biogenesis
COG0750	Predicted membrane-associated Zn-dependent proteases 1	M	Cell wall/membrane/envelope biogenesis
COG1947	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase	I	Lipid transport and metabolism
COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0194	Guanylate kinase	F	Nucleotide transport and metabolism
COG0372	Citrate synthase	C	Energy production and conversion
COG0148	Enolase	G	Carbohydrate transport and metabolism
COG0008	Glutamyl- and glutaminyl-tRNA synthetases	J	Translation, ribosomal structure and biogenesis
COG0344	Predicted membrane protein	S	Function unknown
COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	O	Posttranslational modification, protein turnover, chaperones
COG0740	Protease subunit of ATP-dependent Clp proteases	O	Posttranslational modification, protein turnover, chaperones
COG0751	Glycyl-tRNA synthetase, beta subunit	J	Translation, ribosomal structure and biogenesis
COG0752	Glycyl-tRNA synthetase, alpha subunit	J	Translation, ribosomal structure and biogenesis
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG0629	Single-stranded DNA-binding protein	L	Replication, recombination and repair
COG5590	Uncharacterized conserved protein	S	Function unknown
COG0176	Transaldolase	G	Carbohydrate transport and metabolism
COG1384	Lysyl-tRNA synthetase (class I)	J	Translation, ribosomal structure and biogenesis
COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	H	Coenzyme transport and metabolism
COG0492	Thioredoxin reductase	O	Posttranslational modification, protein turnover, chaperones
COG0124	Histidyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG0271	Stress-induced morphogen (activity unknown)	T	Signal transduction mechanisms
COG0681	Signal peptidase I	U	Intracellular trafficking, secretion, and vesicular transport
COG0621	2-methylthioadenine synthetase	J	Translation, ribosomal structure and biogenesis
COG0276	Protoheme ferro-lyase (ferrochelatase)	H	Coenzyme transport and metabolism
COG0268	Ribosomal protein S20	J	Translation, ribosomal structure and biogenesis
COG0284	Orotidine-5'-phosphate decarboxylase	F	Nucleotide transport and metabolism
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG0821	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis	I	Lipid transport and metabolism
COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	G	Carbohydrate transport and metabolism
COG1071	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit	C	Energy production and conversion
COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	H	Coenzyme transport and metabolism
COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R	General function prediction only
COG1117	ABC-type phosphate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0691	tmRNA-binding protein	O	Posttranslational modification, protein turnover, chaperones
COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	F	Nucleotide transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0462	Phosphoribosylpyrophosphate synthetase	F	Nucleotide transport and metabolism
COG0694	Thioredoxin-like proteins and domains	O	Posttranslational modification, protein turnover, chaperones
COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C	Energy production and conversion
COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	H	Coenzyme transport and metabolism
COG0156	7-keto-8-aminopelargonate synthetase and related enzymes	H	Coenzyme transport and metabolism
COG2332	Cytochrome c-type biogenesis protein CcmE	O	Posttranslational modification, protein turnover, chaperones
COG0595	Predicted hydrolase of the metallo-beta-lactamase superfamily	R	General function prediction only
COG0621	2-methylthioadenine synthetase	J	Translation, ribosomal structure and biogenesis

COG0415	Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
COG0103	Ribosomal protein S9	J	Translation, ribosomal structure and biogenesis
COG0102	Ribosomal protein L13	J	Translation, ribosomal structure and biogenesis
COG4666	TRAP-type uncharacterized transport system, fused permease components	R	General function prediction only
COG0605	Superoxide dismutase	P	Inorganic ion transport and metabolism
COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport and metabolism
COG4992	Ornithine/acetylornithine aminotransferase	E	Amino acid transport and metabolism
COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	O	Posttranslational modification, protein turnover, chaperones
COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	F	Nucleotide transport and metabolism
COG0307	Riboflavin synthase alpha chain	H	Coenzyme transport and metabolism
COG0682	Prolipoprotein diacylglyceryltransferase	M	Cell wall/membrane/envelope biogenesis
COG1612	Uncharacterized protein required for cytochrome oxidase assembly	O	Posttranslational modification, protein turnover, chaperones
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG0424	Nucleotide-binding protein implicated in inhibition of septum formation	D	Cell cycle control, cell division, chromosome partitioning
COG0361	Translation initiation factor 1 (IF-1)	J	Translation, ribosomal structure and biogenesis
COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0519	GMP synthase, PP-ATPase domain/subunit	F	Nucleotide transport and metabolism
COG0489	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG2945	Predicted hydrolase of the alpha/beta superfamily	R	General function prediction only
COG0143	Methionyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG3118	Thioredoxin domain-containing protein	O	Posttranslational modification, protein turnover, chaperones
COG0335	Ribosomal protein L19	J	Translation, ribosomal structure and biogenesis
COG0336	tRNA-(guanine-N1)-methyltransferase	J	Translation, ribosomal structure and biogenesis
COG0211	Ribosomal protein L27	J	Translation, ribosomal structure and biogenesis
COG0261	Ribosomal protein L21	J	Translation, ribosomal structure and biogenesis
COG0353	Recombinational DNA repair protein (RecF pathway)	L	Replication, recombination and repair
COG1651	Protein-disulfide isomerase	O	Posttranslational modification, protein turnover, chaperones
COG0012	Predicted GTPase, probable translation factor	J	Translation, ribosomal structure and biogenesis
COG0597	Lipoprotein signal peptidase	M	Cell wall/membrane/envelope biogenesis
COG2317	Zn-dependent carboxypeptidase	E	Amino acid transport and metabolism
COG0571	dsRNA-specific ribonuclease	K	Transcription
COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0220	Predicted S-adenosylmethionine-dependent methyltransferase	R	General function prediction only
COG4105	DNA uptake lipoprotein	R	General function prediction only
COG0151	Phosphoribosylamine-glycine ligase	F	Nucleotide transport and metabolism
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG3038	Cytochrome B561	C	Energy production and conversion
COG2853	Surface lipoprotein	M	Cell wall/membrane/envelope biogenesis
COG2854	ABC-type transport system involved in resistance to organic solvents, auxiliary component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0371	Glycerol dehydrogenase and related enzymes	C	Energy production and conversion
COG0575	CDP-diglyceride synthetase	I	Lipid transport and metabolism
COG0020	Undecaprenyl pyrophosphate synthase	I	Lipid transport and metabolism
COG0233	Ribosome recycling factor	J	Translation, ribosomal structure and biogenesis
COG0528	Uridylate kinase	F	Nucleotide transport and metabolism
COG4586	ABC-type uncharacterized transport system, ATPase component	R	General function prediction only
COG0264	Translation elongation factor Ts	J	Translation, ribosomal structure and biogenesis
COG0052	Ribosomal protein S2	J	Translation, ribosomal structure and biogenesis
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related e	C	Energy production and conversion
COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	H	Coenzyme transport and metabolism
COG0039	Malate/lactate dehydrogenases	C	Energy production and conversion
COG0756	dUTPase	F	Nucleotide transport and metabolism
COG1159	GTPase	R	General function prediction only
COG0331	(acyl-carrier-protein) S-malonyltransferase	I	Lipid transport and metabolism
COG0358	DNA primase (bacterial type)	L	Replication, recombination and repair
COG0736	Phosphopantetheinyl transferase (holo-ACP synthase)	I	Lipid transport and metabolism
COG0717	Deoxycytidine deaminase	F	Nucleotide transport and metabolism
COG0026	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)	F	Nucleotide transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0407	Uroporphyrinogen-III decarboxylase	H	Coenzyme transport and metabolism
COG0379	Quinolinate synthase	H	Coenzyme transport and metabolism
COG0669	Phosphopantetheine adenylyltransferase	H	Coenzyme transport and metabolism
COG0334	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0247	Fe-S oxidoreductase	C	Energy production and conversion
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG1083	CMP-N-acetylneuraminic acid synthetase	M	Cell wall/membrane/envelope biogenesis
COG2154	Pterin-4a-carbinolamine dehydratase	H	Coenzyme transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0009	Putative translation factor (SUA5)	J	Translation, ribosomal structure and biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2605	Predicted kinase related to galactokinase and mevalonate kinase	R	General function prediction only
COG2377	Predicted molecular chaperone distantly related to HSP70-fold metalloproteases	O	Posttranslational modification, protein turnover, chaperones
COG1045	Serine acetyltransferase	E	Amino acid transport and metabolism
COG1959	Predicted transcriptional regulator	K	Transcription
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG0530	Ca2+/Na+ antiporter	P	Inorganic ion transport and metabolism
COG0762	Predicted integral membrane protein	S	Function unknown
COG1664	Integral membrane protein CcmA involved in cell shape determination	M	Cell wall/membrane/envelope biogenesis
COG4221	Short-chain alcohol dehydrogenase of unknown specificity	R	General function prediction only
COG3427	Uncharacterized conserved protein	S	Function unknown
COG0432	Uncharacterized conserved protein	S	Function unknown

COG2951	Membrane-bound lytic murein transglycosylase B	M	Cell wall/membrane/envelope biogenesis
COG1454	Alcohol dehydrogenase, class IV	C	Energy production and conversion
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0019	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2717	Predicted membrane protein	S	Function unknown
COG4215	ABC-type arginine transport system, permease component	E	Amino acid transport and metabolism
COG0386	Glutathione peroxidase	O	Posttranslational modification, protein turnover, chaperones
COG0205	6-phosphofructokinase	G	Carbohydrate transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG2068	Uncharacterized MobA-related protein	R	General function prediction only
COG0345	Pyrroline-5-carboxylate reductase	E	Amino acid transport and metabolism
COG2606	Uncharacterized conserved protein	S	Function unknown
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG3011	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0661	Predicted unusual protein kinase	R	General function prediction only
COG0739	Membrane proteins related to metalloendopeptidases	M	Cell wall/membrane/envelope biogenesis
COG1164	Oligoendopeptidase F	E	Amino acid transport and metabolism
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG4133	ABC-type transport system involved in cytochrome c biogenesis, ATPase component	O	Posttranslational modification, protein turnover, chaperones
COG3288	NAD/NADP transhydrogenase alpha subunit	C	Energy production and conversion
COG3288	NAD/NADP transhydrogenase alpha subunit	C	Energy production and conversion
COG1282	NAD/NADP transhydrogenase beta subunit	C	Energy production and conversion
COG5470	Uncharacterized conserved protein	S	Function unknown
COG0413	Ketopantoate hydroxymethyltransferase	H	Coenzyme transport and metabolism
COG0828	Ribosomal protein S21	J	Translation, ribosomal structure and biogenesis
COG0651	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	C	Energy production and conversion
COG3914	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family	O	Posttranslational modification, protein turnover, chaperones
COG0560	Phosphoserine phosphatase	E	Amino acid transport and metabolism
COG0440	Acetolactate synthase, small (regulatory) subunit	E	Amino acid transport and metabolism
COG0059	Ketol-acid reductoisomerase	E	Amino acid transport and metabolism
COG1077	Actin-like ATPase involved in cell morphogenesis	D	Cell cycle control, cell division, chromosome partitioning
COG1792	Cell shape-determining protein	M	Cell wall/membrane/envelope biogenesis
COG0768	Cell division protein FtsI/penicillin-binding protein 2	M	Cell wall/membrane/envelope biogenesis
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG3845	ABC-type uncharacterized transport systems, ATPase components	R	General function prediction only
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG1529	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	C	Energy production and conversion
COG1863	Multisubunit Na+/H+ antiporter, MnhE subunit	P	Inorganic ion transport and metabolism
COG2135	Uncharacterized conserved protein	S	Function unknown
COG1525	Micrococcal nuclease (thermonuclease) homologs	L	Replication, recombination and repair
COG1733	Predicted transcriptional regulators	K	Transcription
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG1442	Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases	M	Cell wall/membrane/envelope biogenesis
COG3088	Uncharacterized protein involved in biosynthesis of c-type cytochromes	O	Posttranslational modification, protein turnover, chaperones
COG0521	Molybdopterin biosynthesis enzymes	H	Coenzyme transport and metabolism
COG1238	Predicted membrane protein	S	Function unknown
COG0469	Pyruvate kinase	G	Carbohydrate transport and metabolism
COG1238	Predicted membrane protein	S	Function unknown
COG0239	Integral membrane protein possibly involved in chromosome condensation	D	Cell cycle control, cell division, chromosome partitioning
COG4603	ABC-type uncharacterized transport system, permease component	R	General function prediction only
COG1079	Uncharacterized ABC-type transport system, permease component	R	General function prediction only
COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein	R	General function prediction only
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG4301	Uncharacterized conserved protein	S	Function unknown
COG1109	Phosphomannomutase	G	Carbohydrate transport and metabolism
COG0347	Nitrogen regulatory protein PII	E	Amino acid transport and metabolism
COG0137	Argininosuccinate synthase	E	Amino acid transport and metabolism
COG0713	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)	C	Energy production and conversion
COG0820	Predicted Fe-S-cluster redox enzyme	R	General function prediction only
COG1043	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3494	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0763	Lipid A disaccharide synthetase	M	Cell wall/membrane/envelope biogenesis
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG3806	Anti-sigma factor	T	Signal transduction mechanisms
COG1974	SOS-response transcriptional repressors (RecA-mediated autopeptidases)	K	Transcription
COG0303	Molybdopterin biosynthesis enzyme	H	Coenzyme transport and metabolism
COG0315	Molybdenum cofactor biosynthesis enzyme	H	Coenzyme transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG0134	Indole-3-glycerol phosphate synthase	E	Amino acid transport and metabolism
COG0547	Anthranilate phosphoribosyltransferase	E	Amino acid transport and metabolism
COG0512	Anthranilate/para-aminobenzoate synthases component II	E	Amino acid transport and metabolism
COG0147	Anthranilate/para-aminobenzoate synthases component I	E	Amino acid transport and metabolism
COG0149	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
COG2877	3-deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase	M	Cell wall/membrane/envelope biogenesis
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1729	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0705	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	R	General function prediction only
COG0678	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG4448	L-asparaginase II	E	Amino acid transport and metabolism

COG2897	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG1171	Threonine dehydratase	E	Amino acid transport and metabolism
COG0659	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport and metabolism
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG1324	Uncharacterized protein involved in tolerance to divalent cations	P	Inorganic ion transport and metabolism
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
COG1832	Predicted CoA-binding protein	R	General function prediction only
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG0002	Acetylglutamate semialdehyde dehydrogenase	E	Amino acid transport and metabolism
COG3243	Poly(3-hydroxyalkanoate) synthetase	I	Lipid transport and metabolism
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG0460	Homoserine dehydrogenase	E	Amino acid transport and metabolism
COG1953	Cytosine/uracil/thiamine/allantoin permeases	F	Nucleotide transport and metabolism
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG1893	Ketopantoate reductase	H	Coenzyme transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG1802	Transcriptional regulators	K	Transcription
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG5477	Predicted small integral membrane protein	S	Function unknown
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0388	Predicted amidohydrolase	R	General function prediction only
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1609	Transcriptional regulators	K	Transcription
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG0787	Alanine racemase	M	Cell wall/membrane/envelope biogenesis
COG2230	Cyclopropane fatty acid synthase and related methyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0238	Ribosomal protein S18	J	Translation, ribosomal structure and biogenesis
COG0236	Acyl carrier protein	I	Lipid transport and metabolism
COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG0686	Alanine dehydrogenase	E	Amino acid transport and metabolism
COG0518	GMP synthase - Glutamine amidotransferase domain	F	Nucleotide transport and metabolism
COG1975	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	O	Posttranslational modification, protein turnover, chaperones
COG1975	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	O	Posttranslational modification, protein turnover, chaperones
COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs	C	Energy production and conversion
COG2080	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs	C	Energy production and conversion
COG0139	Phosphoribosyl-AMP cyclohydrolase	E	Amino acid transport and metabolism
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
COG4765	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG4597	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG0079	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	E	Amino acid transport and metabolism
COG0623	Enoyl-[acyl-carrier-protein] reductase (NADH)	I	Lipid transport and metabolism
COG2897	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG2872	Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain	R	General function prediction only
COG0031	Cysteine synthase	E	Amino acid transport and metabolism
COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	O	Posttranslational modification, protein turnover, chaperones
COG0818	Diacylglycerol kinase	M	Cell wall/membrane/envelope biogenesis
COG2835	Uncharacterized conserved protein	S	Function unknown
COG2518	Protein-L-isoaspartate carboxylmethyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG1434	Uncharacterized conserved protein	S	Function unknown
COG1686	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
COG4337	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2847	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2957	Peptidylarginine deiminase and related enzymes	E	Amino acid transport and metabolism
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1329	Transcriptional regulators, similar to M. xanthus CarD	K	Transcription
COG2113	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
COG4176	ABC-type proline/glycine betaine transport system, permease component	E	Amino acid transport and metabolism
COG4175	ABC-type proline/glycine betaine transport system, ATPase component	E	Amino acid transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism

COG0314	Molybdopterin converting factor, large subunit	H	Coenzyme transport and metabolism
COG1763	Molybdopterin-guanine dinucleotide biosynthesis protein	H	Coenzyme transport and metabolism
COG0322	Nuclease subunit of the excinuclease complex	L	Replication, recombination and repair
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	E	Amino acid transport and metabolism
COG3027	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1692	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0824	Predicted thioesterase	R	General function prediction only
COG0811	Biopolymer transport proteins	U	Intracellular trafficking, secretion, and vesicular transport
COG0848	Biopolymer transport protein	U	Intracellular trafficking, secretion, and vesicular transport
COG0823	Periplasmic component of the Tol biopolymer transport system	U	Intracellular trafficking, secretion, and vesicular transport
COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	M	Cell wall/membrane/envelope biogenesis
COG1086	Predicted nucleoside-diphosphate sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG5255	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0006	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase	M	Cell wall/membrane/envelope biogenesis
COG2076	Membrane transporters of cations and cationic drugs	P	Inorganic ion transport and metabolism
COG1133	ABC-type long-chain fatty acid transport system, fused permease and ATPase components	I	Lipid transport and metabolism
COG2802	Uncharacterized protein, similar to the N-terminal domain of Lon protease	R	General function prediction only
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0529	Adenylylsulfate kinase and related kinases	P	Inorganic ion transport and metabolism
COG4764	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG4581	Superfamily II RNA helicase	L	Replication, recombination and repair
COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	G	Carbohydrate transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG0176	Transaldolase	G	Carbohydrate transport and metabolism
COG1218	3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase	P	Inorganic ion transport and metabolism
COG3840	ABC-type thiamine transport system, ATPase component	H	Coenzyme transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0685	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport and metabolism
COG1486	Alpha-galactosidases/6-phospho-beta-glucosidases, family 4 of glycosyl hydrolases	G	Carbohydrate transport and metabolism
COG0824	Predicted thioesterase	R	General function prediction only
COG1357	Uncharacterized low-complexity proteins	S	Function unknown
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG0169	Shikimate 5-dehydrogenase	E	Amino acid transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG1207	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0546	Predicted phosphatases	R	General function prediction only
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0414	Panthothenate synthetase	H	Coenzyme transport and metabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related e	C	Energy production and conversion
COG1488	Nicotinic acid phosphoribosyltransferase	H	Coenzyme transport and metabolism
COG0040	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
COG2761	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0685	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport and metabolism
COG1072	Panthothenate kinase	H	Coenzyme transport and metabolism
COG2928	Uncharacterized conserved protein	S	Function unknown
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent	C	Energy production and conversion
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	F	Nucleotide transport and metabolism
COG1764	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones
COG0005	Purine nucleoside phosphorylase	F	Nucleotide transport and metabolism
COG1278	Cold shock proteins	K	Transcription
COG3118	Thioredoxin domain-containing protein	O	Posttranslational modification, protein turnover, chaperones
COG0108	3,4-dihydroxy-2-butanone 4-phosphate synthase	H	Coenzyme transport and metabolism
COG0334	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
COG0781	Transcription termination factor	K	Transcription
COG0776	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG2895	GTPases - Sulfate adenylate transferase subunit 1	P	Inorganic ion transport and metabolism
COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase	H	Coenzyme transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG1520	FOG: WD40-like repeat	S	Function unknown
COG3803	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1360	Flagellar motor protein	N	Cell motility
COG0509	Glycine cleavage system H protein (lipoate-binding)	E	Amino acid transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG3369	Uncharacterized conserved protein	S	Function unknown
COG2334	Putative homoserine kinase type II (protein kinase fold)	R	General function prediction only
COG0678	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0498	Threonine synthase	E	Amino acid transport and metabolism
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG3346	Uncharacterized conserved protein	S	Function unknown
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG0704	Phosphate uptake regulator	P	Inorganic ion transport and metabolism
COG0385	Predicted Na+-dependent transporter	R	General function prediction only

COG2008	Threonine aldolase	E	Amino acid transport and metabolism
COG0168	Trk-type K+ transport systems, membrane components	P	Inorganic ion transport and metabolism
COG1932	Phosphoserine aminotransferase	H	Coenzyme transport and metabolism
COG0082	Chorismate synthase	E	Amino acid transport and metabolism
COG0573	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG3063	Tfp pilus assembly protein PilF	N	Cell motility
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG1610	Uncharacterized conserved protein	S	Function unknown
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG1611	Predicted Rossmann fold nucleotide-binding protein	R	General function prediction only
COG0538	Isocitrate dehydrogenases	C	Energy production and conversion
COG5352	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2329	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related e	C	Energy production and conversion
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
COG3794	Plastocyanin	C	Energy production and conversion
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0071	Molecular chaperone (small heat shock protein)	O	Posttranslational modification, protein turnover, chaperones
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0198	Ribosomal protein L24	J	Translation, ribosomal structure and biogenesis
COG0255	Ribosomal protein L29	J	Translation, ribosomal structure and biogenesis
COG0185	Ribosomal protein S19	J	Translation, ribosomal structure and biogenesis
COG0051	Ribosomal protein S10	J	Translation, ribosomal structure and biogenesis
COG3651	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0222	Ribosomal protein L7/L12	J	Translation, ribosomal structure and biogenesis
COG0244	Ribosomal protein L10	J	Translation, ribosomal structure and biogenesis
COG0690	Preprotein translocase subunit SecE	U	Intracellular trafficking, secretion, and vesicular transport
COG1940	Transcriptional regulator/sugar kinase	K	Transcription
COG0241	Histidinol phosphatase and related phosphatases	E	Amino acid transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG1696	Predicted membrane protein involved in D-alanine export	M	Cell wall/membrane/envelope biogenesis
COG2021	Homoserine acetyltransferase	E	Amino acid transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG3572	Gamma-glutamylcysteine synthetase	H	Coenzyme transport and metabolism
COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	I	Lipid transport and metabolism
COG2908	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1519	3-deoxy-D-manno-octulosonic-acid transferase	M	Cell wall/membrane/envelope biogenesis
COG1663	Tetraacyldisaccharide-1-P 4'-kinase	M	Cell wall/membrane/envelope biogenesis
COG1560	Lauroyl/myristoyl acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3761	NADH:ubiquinone oxidoreductase 17.2 kD subunit	C	Energy production and conversion
COG0439	Biotin carboxylase	I	Lipid transport and metabolism
COG0511	Biotin carboxyl carrier protein	I	Lipid transport and metabolism
COG0757	3-dehydroquinate dehydratase II	E	Amino acid transport and metabolism
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG1834	N-Dimethylarginine dimethylaminohydrolase	E	Amino acid transport and metabolism
COG1380	Putative effector of murein hydrolase LrgA	R	General function prediction only
COG1346	Putative effector of murein hydrolase	M	Cell wall/membrane/envelope biogenesis
COG1033	Predicted exporters of the RND superfamily	R	General function prediction only
COG0616	Periplasmic serine proteases (ClpP class)	O	Posttranslational modification, protein turnover, chaperones
COG4123	Predicted O-methyltransferase	R	General function prediction only
COG2128	Uncharacterized conserved protein	S	Function unknown
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG1076	DnaJ-domain-containing proteins 1	O	Posttranslational modification, protein turnover, chaperones
COG0488	ATPase components of ABC transporters with duplicated ATPase domains	R	General function prediction only
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG3023	Negative regulator of beta-lactamase expression	V	Defense mechanisms
COG2001	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0768	Cell division protein FtsI/penicillin-binding protein 2	M	Cell wall/membrane/envelope biogenesis
COG0770	UDP-N-acetylmuramyl pentapeptide synthase	M	Cell wall/membrane/envelope biogenesis
COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	M	Cell wall/membrane/envelope biogenesis
COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase	M	Cell wall/membrane/envelope biogenesis
COG0772	Bacterial cell division membrane protein	D	Cell cycle control, cell division, chromosome partitioning
COG0773	UDP-N-acetylmuramate-alanine ligase	M	Cell wall/membrane/envelope biogenesis
COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes	M	Cell wall/membrane/envelope biogenesis
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG0206	Cell division GTPase	D	Cell cycle control, cell division, chromosome partitioning
COG0774	UDP-3-O-acyl-N-acetylglucosamine deacetylase	M	Cell wall/membrane/envelope biogenesis
COG0266	Formamidopyrimidine-DNA glycosylase	L	Replication, recombination and repair
COG0497	ATPase involved in DNA repair	L	Replication, recombination and repair
COG4103	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG3239	Fatty acid desaturase	I	Lipid transport and metabolism
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2520	Predicted methyltransferase	R	General function prediction only
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2896	Molybdenum cofactor biosynthesis enzyme	H	Coenzyme transport and metabolism
COG3180	Putative ammonia monooxygenase	R	General function prediction only
COG1403	Restriction endonuclease	V	Defense mechanisms
COG1495	Disulfide bond formation protein DsbB	O	Posttranslational modification, protein turnover, chaperones
COG1131	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms

COG1052	Lactate dehydrogenase and related dehydrogenases	C	Energy production and conversion
COG3564	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2925	Exonuclease I	L	Replication, recombination and repair
COG3474	Cytochrome c2	C	Energy production and conversion
COG3807	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0225	Peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG1592	Rubrerythrin	C	Energy production and conversion
COG3660	Predicted nucleoside-diphosphate-sugar epimerase	M	Cell wall/membrane/envelope biogenesis
COG2259	Predicted membrane protein	S	Function unknown
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG3004	Na+/H+ antiporter	P	Inorganic ion transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0584	Glycerophosphoryl diester phosphodiesterase	C	Energy production and conversion
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG0078	Ornithine carbamoyltransferase	E	Amino acid transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4663	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4665	TRAP-type mannitol/chloroaromatic compound transport system, small permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0647	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes	M	Cell wall/membrane/envelope biogenesis
COG3502	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0730	Predicted permeases	R	General function prediction only
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1765	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	E	Amino acid transport and metabolism
COG2009	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit	C	Energy production and conversion
COG2076	Membrane transporters of cations and cationic drugs	P	Inorganic ion transport and metabolism
COG1485	Predicted ATPase	R	General function prediction only
COG2240	Pyridoxal/pyridoxine/pyridoxamine kinase	H	Coenzyme transport and metabolism
COG2301	Citrate lyase beta subunit	G	Carbohydrate transport and metabolism
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
COG0066	3-isopropylmalate dehydratase small subunit	E	Amino acid transport and metabolism
COG0253	Diaminopimelate epimerase	E	Amino acid transport and metabolism
COG1702	Phosphate starvation-inducible protein PhoH, predicted ATPase	T	Signal transduction mechanisms
COG2917	Intracellular septation protein A	D	Cell cycle control, cell division, chromosome partitioning
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0513	Superfamily II DNA and RNA helicases	L	Replication, recombination and repair
COG3176	Putative hemolysin	R	General function prediction only
COG3565	Predicted dioxygenase of extradiol dioxygenase family	R	General function prediction only
COG0627	Predicted esterase	R	General function prediction only
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG1250	3-hydroxyacyl-CoA dehydrogenase	I	Lipid transport and metabolism
COG3476	Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog)	T	Signal transduction mechanisms
COG1826	Sec-independent protein secretion pathway components	U	Intracellular trafficking, secretion, and vesicular transport
COG1840	ABC-type Fe3+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG1414	Transcriptional regulator	K	Transcription
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG1807	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	M	Cell wall/membrane/envelope biogenesis
COG0707	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase	M	Cell wall/membrane/envelope biogenesis
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG0589	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
COG1562	Phytoene/squalene synthetase	I	Lipid transport and metabolism
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2086	Electron transfer flavoprotein, beta subunit	C	Energy production and conversion
COG1391	Glutamine synthetase adenylyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG5490	Uncharacterized conserved protein	S	Function unknown
COG2962	Predicted permeases	R	General function prediction only
COG3492	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0289	Dihydrodipicolinate reductase	E	Amino acid transport and metabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0803	ABC-type metal ion transport system, periplasmic component/surface adhesin	P	Inorganic ion transport and metabolism

COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1121	ABC-type Mn/Zn transport systems, ATPase component	P	Inorganic ion transport and metabolism
COG0858	Ribosome-binding factor A	J	Translation, ribosomal structure and biogenesis
COG1108	ABC-type Mn2+/Zn2+ transport systems, permease components	P	Inorganic ion transport and metabolism
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
COG1279	Lysine efflux permease	R	General function prediction only
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG3063	Tfp pilus assembly protein PilF	N	Cell motility
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0367	Asparagine synthase (glutamine-hydrolyzing)	E	Amino acid transport and metabolism
COG0044	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	C	Energy production and conversion
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG2840	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1894	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	C	Energy production and conversion
COG2259	Predicted membrane protein	S	Function unknown
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG4454	Uncharacterized copper-binding protein	P	Inorganic ion transport and metabolism
COG0131	Imidazoleglycerol-phosphate dehydratase	E	Amino acid transport and metabolism
COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	F	Nucleotide transport and metabolism
COG0118	Glutamine amidotransferase	E	Amino acid transport and metabolism
COG1480	Predicted membrane-associated HD superfamily hydrolase	R	General function prediction only
COG0106	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	E	Amino acid transport and metabolism
COG1496	Uncharacterized conserved protein	S	Function unknown
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0107	Imidazoleglycerol-phosphate synthase	E	Amino acid transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG2021	Homoserine acetyltransferase	E	Amino acid transport and metabolism
COG0287	Prephenate dehydrogenase	E	Amino acid transport and metabolism
COG0140	Phosphoribosyl-ATP pyrophosphohydrolase	E	Amino acid transport and metabolism
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG3030	Protein affecting phage T7 exclusion by the F plasmid	R	General function prediction only
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1089	GDP-D-mannose dehydratase	M	Cell wall/membrane/envelope biogenesis
COG1089	GDP-D-mannose dehydratase	M	Cell wall/membrane/envelope biogenesis
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
COG1758	DNA-directed RNA polymerase, subunit K/omega	K	Transcription
COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases	T	Signal transduction mechanisms
COG0119	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport and metabolism
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG0836	Mannose-1-phosphate guanylyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0398	Uncharacterized conserved protein	S	Function unknown
COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2270	Permeases of the major facilitator superfamily	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG1091	dTDP-4-dehydrorhamnose reductase	M	Cell wall/membrane/envelope biogenesis
COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG1209	dTDP-glucose pyrophosphorylase	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2603	Predicted ATPase	R	General function prediction only
COG0424	Nucleotide-binding protein implicated in inhibition of septum formation	D	Cell cycle control, cell division, chromosome partitioning
COG0415	Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
COG2079	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
COG0372	Citrate synthase	C	Energy production and conversion
COG2513	PEP phosphonomutase and related enzymes	G	Carbohydrate transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG0169	Shikimate 5-dehydrogenase	E	Amino acid transport and metabolism
COG2121	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0583	Transcriptional regulator	K	Transcription
COG0772	Bacterial cell division membrane protein	D	Cell cycle control, cell division, chromosome partitioning
COG0350	Methylated DNA-protein cysteine methyltransferase	L	Replication, recombination and repair
COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G	Carbohydrate transport and metabolism
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG0486	Predicted GTPase	R	General function prediction only
COG3959	Transketolase, N-terminal subunit	G	Carbohydrate transport and metabolism
COG3958	Transketolase, C-terminal subunit	G	Carbohydrate transport and metabolism
COG1968	Uncharacterized bacitracin resistance protein	V	Defense mechanisms
COG2166	SufE protein probably involved in Fe-S center assembly	R	General function prediction only
COG0357	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division	M	Cell wall/membrane/envelope biogenesis
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG1192	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism

COG1134	ABC-type polysaccharide/polyol phosphate transport system, ATPase component	G	Carbohydrate transport and metabolism
COG0019	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism
COG0165	Argininosuccinate lyase	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1466	DNA polymerase III, delta subunit	L	Replication, recombination and repair
COG3748	Predicted membrane protein	S	Function unknown
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG0191	Fructose/tagatose bisphosphate aldolase	G	Carbohydrate transport and metabolism
COG0464	ATPases of the AAA+ class	O	Posttranslational modification, protein turnover, chaperones
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG1794	Aspartate racemase	M	Cell wall/membrane/envelope biogenesis
COG0583	Transcriptional regulator	K	Transcription
COG0225	Peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG0381	UDP-N-acetylglucosamine 2-epimerase	M	Cell wall/membrane/envelope biogenesis
COG1846	Transcriptional regulators	K	Transcription
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0325	Predicted enzyme with a TIM-barrel fold	R	General function prediction only
COG3786	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0721	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit	J	Translation, ribosomal structure and biogenesis
COG1459	Type II secretory pathway, component PulF	N	Cell motility
COG2804	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB	N	Cell motility
COG1989	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases	N	Cell motility
COG5360	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1521	Putative transcriptional regulator, homolog of Bvg accessory factor	K	Transcription
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
COG1354	Uncharacterized conserved protein	S	Function unknown
COG1386	Predicted transcriptional regulator containing the HTH domain	K	Transcription
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG2391	Predicted transporter component	R	General function prediction only
COG2391	Predicted transporter component	R	General function prediction only
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG2303	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG4311	Sarcosine oxidase delta subunit	E	Amino acid transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG0527	Aspartokinases	E	Amino acid transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG0345	Pyrroline-5-carboxylate reductase	E	Amino acid transport and metabolism
COG1109	Phosphomannomutase	G	Carbohydrate transport and metabolism
COG1210	UDP-glucose pyrophosphorylase	M	Cell wall/membrane/envelope biogenesis
COG2017	Galactose mutarotase and related enzymes	G	Carbohydrate transport and metabolism
COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0644	Dehydrogenases (flavoproteins)	C	Energy production and conversion
COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG2370	Hydrogenase/urease accessory protein	O	Posttranslational modification, protein turnover, chaperones
COG5266	ABC-type Co2+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0679	Predicted permeases	R	General function prediction only
COG4392	Predicted membrane protein	S	Function unknown
COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2351	Transthyretin-like protein	R	General function prediction only
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
COG2071	Predicted glutamine amidotransferases	R	General function prediction only
COG1862	Preprotein translocase subunit YajC	U	Intracellular trafficking, secretion, and vesicular transport
COG2607	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG1722	Exonuclease VII small subunit	L	Replication, recombination and repair
COG0425	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones
COG0141	Histidinol dehydrogenase	E	Amino acid transport and metabolism
COG3718	Uncharacterized enzyme involved in inositol metabolism	G	Carbohydrate transport and metabolism
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG0006	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
COG3473	Maleate cis-trans isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0415	Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
COG2828	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2079	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1322	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG3307	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1741	Pirin-related protein	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0400	Predicted esterase	R	General function prediction only
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxy	E	Amino acid transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1530	Ribonucleases G and E	J	Translation, ribosomal structure and biogenesis
COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase	E	Amino acid transport and metabolism
COG2844	UTP:GlnB (protein PII) uridylyltransferase	O	Posttranslational modification, protein turnover, chaperones

COG0069	Glutamate synthase domain 2	E	Amino acid transport and metabolism
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG3822	ABC-type sugar transport system, auxiliary component	R	General function prediction only
COG5006	Predicted permease, DMT superfamily	R	General function prediction only
COG1252	NADH dehydrogenase, FAD-containing subunit	C	Energy production and conversion
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
COG0863	DNA modification methylase	L	Replication, recombination and repair
COG0558	Phosphatidylglycerophosphate synthase	I	Lipid transport and metabolism
COG0337	3-dehydroquinate synthetase	E	Amino acid transport and metabolism
COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	J	Translation, ribosomal structure and biogenesis
COG0313	Predicted methyltransferases	R	General function prediction only
COG2961	Protein involved in catabolism of external DNA	R	General function prediction only
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG1194	A/G-specific DNA glycosylase	L	Replication, recombination and repair
COG4391	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4091	Predicted homoserine dehydrogenase	E	Amino acid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0127	Xanthosine triphosphate pyrophosphatase	F	Nucleotide transport and metabolism
COG0689	RNase PH	J	Translation, ribosomal structure and biogenesis
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG4240	Predicted kinase	R	General function prediction only
COG1420	Transcriptional regulator of heat shock gene	K	Transcription
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG2907	Predicted NAD/FAD-binding protein	R	General function prediction only
COG3496	Uncharacterized conserved protein	S	Function unknown
COG2230	Cyclopropane fatty acid synthase and related methyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2211	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R	General function prediction only
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	E	Amino acid transport and metabolism
COG0794	Predicted sugar phosphate isomerase involved in capsule formation	M	Cell wall/membrane/envelope biogenesis
COG2303	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG3127	Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG3791	Uncharacterized conserved protein	S	Function unknown
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG4547	Cobalamin biosynthesis protein CobT (nicotinate-mononucleotide:5, 6-dimethylbenzimidazole phosphoribosyltrans	H	Coenzyme transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG2095	Multiple antibiotic transporter	U	Intracellular trafficking, secretion, and vesicular transport
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG3046	Uncharacterized protein related to deoxyribodipyrimidine photolyase	R	General function prediction only
COG2062	Phosphohistidine phosphatase SixA	T	Signal transduction mechanisms
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0347	Nitrogen regulatory protein PII	E	Amino acid transport and metabolism
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG1213	Predicted sugar nucleotidyltransferases	M	Cell wall/membrane/envelope biogenesis
COG1674	DNA segregation ATPase FtsK/SpoIIIE and related proteins	D	Cell cycle control, cell division, chromosome partitioning
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG4341	Predicted HD phosphohydrolase	R	General function prediction only
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG4341	Predicted HD phosphohydrolase	R	General function prediction only
COG0637	Predicted phosphatase/phosphohexomutase	R	General function prediction only
COG3217	Uncharacterized Fe-S protein	R	General function prediction only
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG0246	Mannitol-1-phosphate/altronate dehydrogenases	G	Carbohydrate transport and metabolism
COG2721	Altronate dehydratase	G	Carbohydrate transport and metabolism
COG2236	Predicted phosphoribosyltransferases	R	General function prediction only
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG1546	Uncharacterized protein (competence- and mitomycin-induced)	R	General function prediction only
COG2947	Uncharacterized conserved protein	S	Function unknown
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Coenzyme transport and metabolism
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0714	MoxR-like ATPases	R	General function prediction only
COG5000	Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation	T	Signal transduction mechanisms
COG2224	Isocitrate lyase	C	Energy production and conversion
COG3800	Predicted transcriptional regulator	R	General function prediction only
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism

COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG5135	Uncharacterized conserved protein	S	Function unknown
COG4583	Sarcosine oxidase gamma subunit	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxy	E	Amino acid transport and metabolism
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG0620	Methionine synthase II (cobalamin-independent)	E	Amino acid transport and metabolism
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	E	Amino acid transport and metabolism
COG1414	Transcriptional regulator	K	Transcription
COG5394	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG2151	Predicted metal-sulfur cluster biosynthetic enzyme	R	General function prediction only
COG0822	NifU homolog involved in Fe-S cluster formation	C	Energy production and conversion
COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component	O	Posttranslational modification, protein turnover, chaperones
COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component	O	Posttranslational modification, protein turnover, chaperones
COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component	O	Posttranslational modification, protein turnover, chaperones
COG3836	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	G	Carbohydrate transport and metabolism
COG0321	Lipoate-protein ligase B	H	Coenzyme transport and metabolism
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG5267	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4102	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2346	Truncated hemoglobins	R	General function prediction only
COG0279	Phosphoheptose isomerase	G	Carbohydrate transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0349	Ribonuclease D	J	Translation, ribosomal structure and biogenesis
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG0578	Glycerol-3-phosphate dehydrogenase	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG2081	Predicted flavoproteins	R	General function prediction only
COG2863	Cytochrome c553	C	Energy production and conversion
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1539	Dihydroneopterin aldolase	H	Coenzyme transport and metabolism
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG0248	Exopolyphosphatase	F	Nucleotide transport and metabolism
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG0647	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG3347	Uncharacterized conserved protein	S	Function unknown
COG4176	ABC-type proline/glycine betaine transport system, permease component	E	Amino acid transport and metabolism
COG2113	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0535	Predicted Fe-S oxidoreductases	R	General function prediction only
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG2510	Predicted membrane protein	S	Function unknown
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG3769	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG1452	Organic solvent tolerance protein OstA	M	Cell wall/membrane/envelope biogenesis
COG0795	Predicted permeases	R	General function prediction only
COG0795	Predicted permeases	R	General function prediction only
COG1995	Pyridoxal phosphate biosynthesis protein	H	Coenzyme transport and metabolism
COG0122	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	L	Replication, recombination and repair
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG1321	Mn-dependent transcriptional regulator	K	Transcription
COG1254	Acylphosphatases	C	Energy production and conversion
COG0045	Succinyl-CoA synthetase, beta subunit	C	Energy production and conversion
COG0074	Succinyl-CoA synthetase, alpha subunit	C	Energy production and conversion
COG0229	Conserved domain frequently associated with peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG0141	Histidinol dehydrogenase	E	Amino acid transport and metabolism
COG0040	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
COG3703	Uncharacterized protein involved in cation transport	P	Inorganic ion transport and metabolism
COG3573	Predicted oxidoreductase	R	General function prediction only
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG0015	Adenylosuccinate lyase	F	Nucleotide transport and metabolism
COG0073	EMAP domain	R	General function prediction only
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG3917	2-hydroxychromene-2-carboxylate isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism

COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0010	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family	E	Amino acid transport and metabolism
COG3246	Uncharacterized conserved protein	S	Function unknown
COG1250	3-hydroxyacyl-CoA dehydrogenase	I	Lipid transport and metabolism
COG4147	Predicted symporter	R	General function prediction only
COG1062	Zn-dependent alcohol dehydrogenases, class III	C	Energy production and conversion
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG1522	Transcriptional regulators	K	Transcription
COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair	L	Replication, recombination and repair
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs	C	Energy production and conversion
COG4154	Fucose dissimilation pathway protein FucU	G	Carbohydrate transport and metabolism
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG3624	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG3625	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG3627	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG4778	ABC-type phosphonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG3454	Metal-dependent hydrolase involved in phosphonate metabolism	P	Inorganic ion transport and metabolism
COG2188	Transcriptional regulators	K	Transcription
COG2113	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
COG4176	ABC-type proline/glycine betaine transport system, permease component	E	Amino acid transport and metabolism
COG2510	Predicted membrane protein	S	Function unknown
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1002	Type II restriction enzyme, methylase subunits	V	Defense mechanisms
COG1349	Transcriptional regulators of sugar metabolism	K	Transcription
COG3347	Uncharacterized conserved protein	S	Function unknown
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0861	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion transport and metabolism
COG0633	Ferredoxin	C	Energy production and conversion
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG2137	Uncharacterized protein conserved in bacteria	R	General function prediction only
COG1434	Uncharacterized conserved protein	S	Function unknown
COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E	Amino acid transport and metabolism
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG4206	Outer membrane cobalamin receptor protein	H	Coenzyme transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG1748	Saccharopine dehydrogenase and related proteins	E	Amino acid transport and metabolism
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0406	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)	E	Amino acid transport and metabolism
COG3342	Uncharacterized conserved protein	S	Function unknown
COG0153	Galactokinase	G	Carbohydrate transport and metabolism
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
COG0791	Cell wall-associated hydrolases (invasion-associated proteins)	M	Cell wall/membrane/envelope biogenesis
COG0730	Predicted permeases	R	General function prediction only
COG3380	Predicted NAD/FAD-dependent oxidoreductase	R	General function prediction only
COG0695	Glutaredoxin and related proteins	O	Posttranslational modification, protein turnover, chaperones
COG0388	Predicted amidohydrolase	R	General function prediction only
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG1268	Uncharacterized conserved protein	R	General function prediction only
COG5319	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent	C	Energy production and conversion
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
COG0182	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	J	Translation, ribosomal structure and biogenesis
COG0847	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	L	Replication, recombination and repair
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxy	E	Amino acid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG3588	Fructose-1,6-bisphosphate aldolase	G	Carbohydrate transport and metabolism
COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle control, cell division, chromosome partitioning
COG1738	Uncharacterized conserved protein	S	Function unknown
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG2855	Predicted membrane protein	S	Function unknown
COG0405	Gamma-glutamyltransferase	E	Amino acid transport and metabolism
COG0283	Cytidylate kinase	F	Nucleotide transport and metabolism
COG0776	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
COG1802	Transcriptional regulators	K	Transcription
COG1609	Transcriptional regulators	K	Transcription
COG4608	ABC-type oligopeptide transport system, ATPase component	E	Amino acid transport and metabolism

COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	C	Energy production and conversion
COG0135	Phosphoribosylanthranilate isomerase	E	Amino acid transport and metabolism
COG1741	Pirin-related protein	R	General function prediction only
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0714	MoxR-like ATPases	R	General function prediction only
COG0778	Nitroreductase	C	Energy production and conversion
COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O	Posttranslational modification, protein turnover, chaperones
COG2303	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member	L	Replication, recombination and repair
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG0517	FOG: CBS domain	R	General function prediction only
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG0337	3-dehydroquinate synthetase	E	Amino acid transport and metabolism
COG0703	Shikimate kinase	E	Amino acid transport and metabolism
COG1974	SOS-response transcriptional repressors (RecA-mediated autopeptidases)	K	Transcription
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG3221	ABC-type phosphate/phosphonate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG2364	Predicted membrane protein	S	Function unknown
COG3638	ABC-type phosphate/phosphonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0406	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG0166	Glucose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG1196	Chromosome segregation ATPases	D	Cell cycle control, cell division, chromosome partitioning
COG3333	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG3152	Predicted membrane protein	S	Function unknown
COG0171	NAD synthase	H	Coenzyme transport and metabolism
COG0579	Predicted dehydrogenase	R	General function prediction only
COG0181	Porphobilinogen deaminase	H	Coenzyme transport and metabolism
COG1605	Chorismate mutase	E	Amino acid transport and metabolism
COG5000	Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation	T	Signal transduction mechanisms
COG0825	Acetyl-CoA carboxylase alpha subunit	I	Lipid transport and metabolism
COG4968	Tfp pilus assembly protein PilE	N	Cell motility
COG4972	Tfp pilus assembly protein, ATPase PilM	N	Cell motility
COG2805	Tfp pilus assembly protein, pilus retraction ATPase PilT	N	Cell motility
COG2813	16S RNA G1207 methylase RsmC	J	Translation, ribosomal structure and biogenesis
COG5524	Bacteriorhodopsin	R	General function prediction only
COG4696	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	M	Cell wall/membrane/envelope biogenesis
COG2940	Proteins containing SET domain	R	General function prediction only
COG0306	Phosphate/sulphate permeases	P	Inorganic ion transport and metabolism
COG1392	Phosphate transport regulator (distant homolog of PhoU)	P	Inorganic ion transport and metabolism
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG5010	Flp pilus assembly protein TadD, contains TPR repeats	U	Intracellular trafficking, secretion, and vesicular transport
COG1666	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG3223	Predicted membrane protein	S	Function unknown
COG0548	Acetylglutamate kinase	E	Amino acid transport and metabolism
COG0646	Methionine synthase I (cobalamin-dependent), methyltransferase domain	E	Amino acid transport and metabolism
COG0218	Predicted GTPase	R	General function prediction only
COG0759	Uncharacterized conserved protein	S	Function unknown
COG3785	Uncharacterized conserved protein	S	Function unknown
COG2301	Citrate lyase beta subunit	G	Carbohydrate transport and metabolism
COG0646	Methionine synthase I (cobalamin-dependent), methyltransferase domain	E	Amino acid transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG3225	ABC-type uncharacterized transport system involved in gliding motility, auxiliary component	N	Cell motility
COG1277	ABC-type transport system involved in multi-copper enzyme maturation, permease component	R	General function prediction only
COG0617	tRNA nucleotidyltransferase/poly(A) polymerase	J	Translation, ribosomal structure and biogenesis
COG0394	Protein-tyrosine-phosphatase	T	Signal transduction mechanisms
COG3313	Predicted Fe-S protein	R	General function prediction only
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG0069	Glutamate synthase domain 2	E	Amino acid transport and metabolism
COG0070	Glutamate synthase domain 3	E	Amino acid transport and metabolism
COG0067	Glutamate synthase domain 1	E	Amino acid transport and metabolism
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG4583	Sarcosine oxidase gamma subunit	E	Amino acid transport and metabolism
COG0510	Predicted choline kinase involved in LPS biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG2212	Multisubunit Na+/H+ antiporter, MnhF subunit	P	Inorganic ion transport and metabolism
COG0150	Phosphoribosylaminoimidazole (AIR) synthetase	F	Nucleotide transport and metabolism
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation	M	Cell wall/membrane/envelope biogenesis
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG4487	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis

COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0397	Uncharacterized conserved protein	S	Function unknown
COG0677	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	M	Cell wall/membrane/envelope biogenesis
COG3448	CBS-domain-containing membrane protein	T	Signal transduction mechanisms
COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG2208	Serine phosphatase RsbU, regulator of sigma subunit	T	Signal transduction mechanisms
COG1366	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)	T	Signal transduction mechanisms
COG4567	Response regulator consisting of a CheY-like receiver domain and a Fis-type HTH domain	T	Signal transduction mechanisms
COG4266	Allantoicase	F	Nucleotide transport and metabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG4311	Sarcosine oxidase delta subunit	E	Amino acid transport and metabolism
COG1131	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0069	Glutamate synthase domain 2	E	Amino acid transport and metabolism
COG0070	Glutamate synthase domain 3	E	Amino acid transport and metabolism
COG0067	Glutamate synthase domain 1	E	Amino acid transport and metabolism
COG1511	Predicted membrane protein	S	Function unknown
COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O	Posttranslational modification, protein turnover, chaperones
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	E	Amino acid transport and metabolism
COG2171	Tetrahydrodipicolinate N-succinyltransferase	E	Amino acid transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG0730	Predicted permeases	R	General function prediction only
COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0042	tRNA-dihydrouridine synthase	J	Translation, ribosomal structure and biogenesis
COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	C	Energy production and conversion
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG5454	Predicted secreted protein	S	Function unknown
COG1522	Transcriptional regulators	K	Transcription
COG0065	3-isopropylmalate dehydratase large subunit	E	Amino acid transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG3791	Uncharacterized conserved protein	S	Function unknown
COG4663	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1396	Predicted transcriptional regulators	K	Transcription
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production and conversion
COG1051	ADP-ribose pyrophosphatase	F	Nucleotide transport and metabolism
COG0819	Putative transcription activator	K	Transcription
COG3205	Predicted membrane protein	S	Function unknown
COG3284	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3971	2-keto-4-pentenoate hydratase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1035	Coenzyme F420-reducing hydrogenase, beta subunit	C	Energy production and conversion
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	R	General function prediction only
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG5350	Predicted protein tyrosine phosphatase	R	General function prediction only
COG0584	Glycerophosphoryl diester phosphodiesterase	C	Energy production and conversion
COG5395	Predicted membrane protein	S	Function unknown
COG0260	Leucyl aminopeptidase	E	Amino acid transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG3908	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E	Amino acid transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	G	Carbohydrate transport and metabolism
COG0077	Prephenate dehydratase	E	Amino acid transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG4665	TRAP-type mannitol/chloroaromatic compound transport system, small permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1212	CMP-2-keto-3-deoxyoctulosonic acid synthetase	M	Cell wall/membrane/envelope biogenesis
COG2967	Uncharacterized protein affecting Mg2+/Co2+ transport	P	Inorganic ion transport and metabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2258	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0316	Uncharacterized conserved protein	S	Function unknown
COG0355	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG0793	Periplasmic protease	M	Cell wall/membrane/envelope biogenesis
COG0785	Cytochrome c biogenesis protein	O	Posttranslational modification, protein turnover, chaperones
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG1576	Uncharacterized conserved protein	S	Function unknown
COG0799	Uncharacterized homolog of plant Iojap protein	S	Function unknown

COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG1057	Nicotinic acid mononucleotide adenylyltransferase	H	Coenzyme transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG0014	Gamma-glutamyl phosphate reductase	E	Amino acid transport and metabolism
COG0637	Predicted phosphatase/phosphohexomutase	R	General function prediction only
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG0263	Glutamate 5-kinase	E	Amino acid transport and metabolism
COG0598	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
COG0569	K+ transport systems, NAD-binding component	P	Inorganic ion transport and metabolism
COG1211	4-diphosphocytidyl-2-methyl-D-erithritol synthase	I	Lipid transport and metabolism
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG3705	ATP phosphoribosyltransferase involved in histidine biosynthesis	E	Amino acid transport and metabolism
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG1807	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	M	Cell wall/membrane/envelope biogenesis
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0119	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport and metabolism
COG0565	rRNA methylase	J	Translation, ribosomal structure and biogenesis
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG0219	Predicted rRNA methylase (SpoU class)	J	Translation, ribosomal structure and biogenesis
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG2962	Predicted permeases	R	General function prediction only
COG3333	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism