COG	Function		Functional Category
COG2258	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4251	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	T	Signal transduction mechanisms
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG1828	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component	F	Nucleotide transport and metabolism
COG4113	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG4461	Uncharacterized protein conserved in bacteria, putative lipoprotein	S	Function unknown
COG1309	Transcriptional regulator	K	Transcription
COG0841	Cation/multidrug efflux pump	V	Defense mechanisms
COG0775	Nucleoside phosphorylase	F	Nucleotide transport and metabolism
COG3194	Ureidoglycolate hydrolase	F	Nucleotide transport and metabolism
COG3203	Outer membrane protein (porin)	M	Cell wall/membrane/envelope biogenesis
COG3637	Opacity protein and related surface antigens	M	Cell wall/membrane/envelope biogenesis
COG4208	ABC-type sulfate transport system, permease component	P	Inorganic ion transport and metabolism
COG5515	Uncharacterized conserved small protein	S	Function unknown
COG2003	DNA repair proteins	L	Replication, recombination and repair
COG1122	ABC-type cobalt transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0619	ABC-type cobalt transport system, permease component CbiQ and related transporters	P	Inorganic ion transport and metabolism
COG1268	Uncharacterized conserved protein	R	General function prediction only
COG1489	DNA-binding protein, stimulates sugar fermentation	R	General function prediction only
COG2128	Uncharacterized conserved protein	S	Function unknown
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
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
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG2192	Predicted carbamoyl transferase, NodU family	O	Posttranslational modification, protein turnover, chaperones
COG3505	Type IV secretory pathway, VirD4 components	U	Intracellular trafficking, secretion, and vesicular transport
COG3843	Type IV secretory pathway, VirD2 components (relaxase)	U	Intracellular trafficking, secretion, and vesicular transport
COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
COG4959	Type IV secretory pathway, protease TraF	O	Posttranslational modification, protein turnover, chaperones
COG5534	Plasmid replication initiator protein	L	Replication, recombination and repair
COG5489	Uncharacterized conserved protein	S	Function unknown
COG1487	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG4691	Plasmid stability protein	R	General function prediction only
COG1475	Predicted transcriptional regulators	K	Transcription
COG3177	Uncharacterized conserved protein	S	Function unknown
COG3440	Predicted restriction endonuclease	V	Defense mechanisms
COG3838	Type IV secretory pathway, VirB2 components (pilins)	U	Intracellular trafficking, secretion, and vesicular transport
COG5268	Type IV secretory pathway, TrbD component	N	Cell motility
COG5314	Conjugal transfer/entry exclusion protein	U	Intracellular trafficking, secretion, and vesicular transport
COG3846	Type IV secretory pathway, TrbL components	U	Intracellular trafficking, secretion, and vesicular transport
COG3701	Type IV secretory pathway, TrbF components	U	Intracellular trafficking, secretion, and vesicular transport
COG3504	Type IV secretory pathway, VirB9 components	U	Intracellular trafficking, secretion, and vesicular transport
COG2948	Type IV secretory pathway, VirB10 components	U	Intracellular trafficking, secretion, and vesicular transport
COG5639	Uncharacterized conserved small protein	S	Function unknown
COG2856	Predicted Zn peptidase	E	Amino acid transport and metabolism
COG1813	Predicted transcription factor, homolog of eukaryotic MBF1	K	Transcription
COG0418	Dihydroorotase	F	Nucleotide transport and metabolism
COG4674	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
COG1570	Exonuclease VII, large subunit	L	Replication, recombination and repair
COG1816	Adenosine deaminase	F	Nucleotide transport and metabolism
COG5469	Predicted metal-binding protein	S	Function unknown
COG1429	Cobalamin biosynthesis protein CobN and related Mg-chelatases	H	Coenzyme transport and metabolism
COG1010	Precorrin-3B methylase	H	Coenzyme transport and metabolism
COG0024	Methionine aminopeptidase	J	Translation, ribosomal structure and biogenesis
COG1903	Cobalamin biosynthesis protein CbiD	H	Coenzyme transport and metabolism
COG3360	Uncharacterized conserved protein	S	Function unknown
COG0435	Predicted glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG4615	ABC-type siderophore export system, fused ATPase and permease components	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0717	Deoxycytidine deaminase	F	Nucleotide transport and metabolism
COG0777	Acetyl-CoA carboxylase beta subunit	I	Lipid transport and metabolism
COG0405	Gamma-glutamyltransferase	E	Amino acid transport and metabolism
COG2326	Uncharacterized conserved protein	S	Function unknown
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
COG1075	Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold	R	General function prediction only
COG4336	Uncharacterized conserved protein	S	Function unknown
COG3911	Predicted ATPase	R	General function prediction only
COG3900	Predicted periplasmic protein	S	Function unknown
COG2199	FOG: GGDEF domain	T	Signal transduction mechanisms
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG4674	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3437	Response regulator containing a CheY-like receiver domain and an HD-GYP domain	K	Transcription
COG0583	Transcriptional regulator	K	Transcription
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
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0282	Acetate kinase	C	Energy production and conversion
COG2368	Aromatic ring hydroxylase	Q	Secondary metabolites biosynthesis, transport and catabolism

COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG3403	Uncharacterized conserved protein	S	Function unknown
COG0133	Tryptophan synthase beta chain	E	Amino acid transport and metabolism
COG2055	Malate/L-lactate dehydrogenases	C	Energy production and conversion
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1620	L-lactate permease	C	Energy production and conversion
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
COG2367	Beta-lactamase class A	V	Defense mechanisms
COG1937	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1802	Transcriptional regulators	K	Transcription
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG3473	Maleate cis-trans isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1233	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0252	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D	E	Amino acid transport and metabolism
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	I	Lipid transport and metabolism
COG0609	ABC-type Fe3+-siderophore transport system, permease component	P	Inorganic ion transport and metabolism
COG1712	Predicted dinucleotide-utilizing enzyme	R	General function prediction only
COG1123	ATPase components of various ABC-type transport systems, contain duplicated ATPase	R	General function prediction only
COG0842	ABC-type multidrug transport system, permease component	V	Defense mechanisms
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG4706	Predicted 3-hydroxylacyl-(acyl carrier protein) dehydratase	I	Lipid transport and metabolism
COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	I	Lipid transport and metabolism
COG4258	Predicted exporter	R	General function prediction only
COG3712	Fe2+-dicitrate sensor, membrane component	P	Inorganic ion transport and metabolism
COG0824	Predicted thioesterase	R	General function prediction only
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG0236	Acyl carrier protein	I	Lipid transport and metabolism
COG2199	FOG: GGDEF domain	T	Signal transduction mechanisms
COG0236	Acyl carrier protein	I	Lipid transport and metabolism
COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	I	Lipid transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG3668	Plasmid stabilization system protein	R	General function prediction only
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1541	Coenzyme F390 synthetase	H	Coenzyme transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG3284	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1022	Long-chain acyl-CoA synthetases (AMP-forming)	I	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG3549	Plasmid maintenance system killer protein	R	General function prediction only
COG3093	Plasmid maintenance system antidote protein	R	General function prediction only
COG0518	GMP synthase - Glutamine amidotransferase domain	F	Nucleotide transport and metabolism
COG1873	Uncharacterized conserved protein	S	Function unknown
COG2252	Permeases	R	General function prediction only
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	C	Energy production and conversion
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
COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	R	General function prediction only
COG1357	Uncharacterized low-complexity proteins	S	Function unknown
COG0471	Di- and tricarboxylate transporters	P	Inorganic ion transport and metabolism
COG2936	Predicted acyl esterases	R	General function prediction only
COG4993	Glucose dehydrogenase	G	Carbohydrate transport and metabolism
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG0306	Phosphate/sulphate permeases	P	Inorganic ion transport and metabolism
COG5499	Predicted transcription regulator containing HTH domain	K	Transcription
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
COG3550	Uncharacterized protein related to capsule biosynthesis enzymes	R	General function prediction only
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG5302	Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid	R	General function prediction only
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG0598	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
COG2250	Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN	S	Function unknown
COG0583	Transcriptional regulator	K	Transcription
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
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG1123	ATPase components of various ABC-type transport systems, contain duplicated ATPase	R	General function prediction only
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
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG2133	Glucose/sorbosone dehydrogenases	G	Carbohydrate transport and metabolism
COG4953	Membrane carboxypeptidase/penicillin-binding protein PbpC	M	Cell wall/membrane/envelope biogenesis
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG0640	Predicted transcriptional regulators	K	Transcription
COG2764	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3832	Uncharacterized conserved protein	S	Function unknown
COG3832	Uncharacterized conserved protein	S	Function unknown
COG5564	Predicted TIM-barrel enzyme, possibly a dioxygenase	R	General function prediction only

COG3221	ABC-type phosphate/phosphonate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG1959	Predicted transcriptional regulator	K	Transcription
COG0492	Thioredoxin reductase	O	Posttranslational modification, protein turnover, chaperones
COG1899	Deoxyhypusine synthase	O	Posttranslational modification, protein turnover, chaperones
COG5439	Uncharacterized conserved protein	S	Function unknown
COG5381	Uncharacterized protein conserved in bacteria	S	Function unknown
COG5441	Uncharacterized conserved protein	S	Function unknown
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG4626	Phage terminase-like protein, large subunit	R	General function prediction only
COG4695	Phage-related protein	S	Function unknown
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG2124	Cytochrome P450	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0456	Acetyltransferases	R	General function prediction only
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
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
COG2272	Carboxylesterase type B	I	Lipid transport and metabolism
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
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG2169	Adenosine deaminase	F	Nucleotide transport and metabolism
COG0515	Serine/threonine protein kinase	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
COG0612	Predicted Zn-dependent peptidases	R	General function prediction only
COG1073	Hydrolases of the alpha/beta superfamily	R	General function prediction only
COG0643	Chemotaxis protein histidine kinase and related kinases	N	Cell motility
COG1733	Predicted transcriptional regulators	K	Transcription
COG0461	Orotate phosphoribosyltransferase	F	Nucleotide transport and metabolism
COG0620	Methionine synthase II (cobalamin-independent)	E	Amino acid transport and metabolism
COG3507	Beta-xylosidase	G	Carbohydrate transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG3671	Predicted membrane protein	S	Function unknown
COG0640	Predicted transcriptional regulators	K	Transcription
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2152	Predicted glycosylase	G	Carbohydrate transport and metabolism
COG2201	Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain	N	Cell motility
COG1352	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0644	Dehydrogenases (flavoproteins)	C	Energy production and conversion
COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	O	Posttranslational modification, protein turnover, chaperones
COG3178	Predicted phosphotransferase related to Ser/Thr protein kinases	R	General function prediction only
COG3766	Predicted membrane protein	S	Function unknown
COG2939	Carboxypeptidase C (cathepsin A)	E	Amino acid transport and metabolism
COG3619	Predicted membrane protein	S	Function unknown
COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	M	Cell wall/membrane/envelope biogenesis
COG4251	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	T	Signal transduction mechanisms
COG3334	Uncharacterized conserved protein	S	Function unknown
COG5528	Predicted integral membrane protein	S	Function unknown
COG0590	Cytosine/adenosine deaminases	F	Nucleotide transport and metabolism
COG0517	FOG: CBS domain	R	General function prediction only
COG0139	Phosphoribosyl-AMP cyclohydrolase	E	Amino acid transport and metabolism
COG0040	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG4496	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, g	M	Cell wall/membrane/envelope biogenesis
COG3307	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG2127	Uncharacterized conserved protein	S	Function unknown
COG3484	Predicted proteasome-type protease	O	Posttranslational modification, protein turnover, chaperones
COG3670	Lignostilbene-alpha,beta-dioxygenase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
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
COG0213	Thymidine phosphorylase	F	Nucleotide transport and metabolism
COG1526	Uncharacterized protein required for formate dehydrogenase activity	C	Energy production and conversion
COG1285	Uncharacterized membrane protein	S	Function unknown
COG0746	Molybdopterin-guanine dinucleotide biosynthesis protein A	H	Coenzyme transport and metabolism
COG3381	Uncharacterized component of anaerobic dehydrogenases	R	General function prediction only
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production and conversion
COG0397	Uncharacterized conserved protein	S	Function unknown
COG3237	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1142	Fe-S-cluster-containing hydrogenase components 2	C	Energy production and conversion
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0695	Glutaredoxin and related proteins	O	Posttranslational modification, protein turnover, chaperones
COG2864	Cytochrome b subunit of formate dehydrogenase	C	Energy production and conversion
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG1607	Acyl-CoA hydrolase	I	Lipid transport and metabolism
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	G	Carbohydrate transport and metabolism
COG2135	Uncharacterized conserved protein	S	Function unknown
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
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
COG1418	Predicted HD superfamily hydrolase	R	General function prediction only
COG5336	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG4961	Flp pilus assembly protein TadG	U	Intracellular trafficking, secretion, and vesicular transport
COG2315	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0393	Uncharacterized conserved protein	S	Function unknown
COG3568	Metal-dependent hydrolase	R	General function prediction only
COG5368	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
COG2211	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
COG0850	Septum formation inhibitor	D	Cell cycle control, cell division, chromosome partitioning
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG2894	Septum formation inhibitor-activating ATPase	D	Cell cycle control, cell division, chromosome partitioning
COG0342	Preprotein translocase subunit SecD	U	Intracellular trafficking, secretion, and vesicular transport
COG3338	Carbonic anhydrase	P	Inorganic ion transport and metabolism
COG4961	Flp pilus assembly protein TadG	U	Intracellular trafficking, secretion, and vesicular transport
COG0252	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D	E	Amino acid transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG4338	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG1215	Glycosyltransferases, probably involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG1957	Inosine-uridine nucleoside N-ribohydrolase	F	Nucleotide transport and metabolism
COG3667	Uncharacterized protein involved in copper resistance	P	Inorganic ion transport and metabolism
COG3188	P pilus assembly protein, porin PapC	N	Cell motility
COG2154	Pterin-4a-carbinolamine dehydratase	H	Coenzyme transport and metabolism
COG3040	Bacterial lipocalin	M	Cell wall/membrane/envelope biogenesis
COG0738	Fucose permease	G	Carbohydrate transport and metabolism
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG2225	Malate synthase	C	Energy production and conversion
COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member	L	Replication, recombination and repair
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG3727	DNA G:T-mismatch repair endonuclease	L	Replication, recombination and repair
COG0270	Site-specific DNA methylase	L	Replication, recombination and repair
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	R	General function prediction only
COG2440	Ferredoxin-like protein	C	Energy production and conversion
COG5373	Predicted membrane protein	S	Function unknown
COG0644	Dehydrogenases (flavoproteins)	C	Energy production and conversion
COG4339	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4783	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
COG2025	Electron transfer flavoprotein, alpha subunit	C	Energy production and conversion
COG1846	Transcriptional regulators	K	Transcription
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG2086	Electron transfer flavoprotein, beta subunit	C	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG3288	NAD/NADP transhydrogenase alpha subunit	C	Energy production and conversion
COG3809	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0119	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport and metabolism
COG4709	Predicted membrane protein	S	Function unknown
COG1695	Predicted transcriptional regulators	K	Transcription
COG3324	Predicted enzyme related to lactoylglutathione lyase	R	General function prediction only
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C	Energy production and conversion
COG5420	Uncharacterized conserved small protein containing a coiled-coil domain	S	Function unknown
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1309	Transcriptional regulator	K	Transcription
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG1462	Uncharacterized protein involved in formation of curli polymers	M	Cell wall/membrane/envelope biogenesis
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG2971	Predicted N-acetylglucosamine kinase	G	Carbohydrate transport and metabolism
COG1252	NADH dehydrogenase, FAD-containing subunit	C	Energy production and conversion
COG1959	Predicted transcriptional regulator	K	Transcription
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG3503	Predicted membrane protein	S	Function unknown
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG1348	Nitrogenase subunit NifH (ATPase)	P	Inorganic ion transport and metabolism
COG3609	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain	K	Transcription
COG3668	Plasmid stabilization system protein	R	General function prediction only
COG0001	Glutamate-1-semialdehyde aminotransferase	H	Coenzyme transport and metabolism
COG1393	Arsenate reductase and related proteins, glutaredoxin family	P	Inorganic ion transport and metabolism
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
COG3422	Uncharacterized conserved protein	S	Function unknown
COG0738	Fucose permease	G	Carbohydrate transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG1414	Transcriptional regulator	K	Transcription

COG2721	Altronate dehydratase	G	Carbohydrate transport and metabolism
COG2017	Galactose mutarotase and related enzymes	G	Carbohydrate transport and metabolism
COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG1505	Serine proteases of the peptidase family S9A	E	Amino acid transport and metabolism
COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C	Energy production and conversion
COG4148	ABC-type molybdate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0535	Predicted Fe-S oxidoreductases	R	General function prediction only
COG1475	Predicted transcriptional regulators	K	Transcription
COG0775	Nucleoside phosphorylase	F	Nucleotide transport and metabolism
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. subtilis)	L	Replication, recombination and repair
COG4695	Phage-related protein	S	Function unknown
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
COG1563	Predicted subunit of the Multisubunit Na+/H+ antiporter	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
COG4618	ABC-type protease/lipase transport system, ATPase and permease components	R	General function prediction only
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
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0606	Predicted ATPase with chaperone activity	O	Posttranslational modification, protein turnover, chaperones
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
COG1322	Uncharacterized protein conserved in bacteria	S	Function unknown
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
COG1115	Na+/alanine symporter	E	Amino acid transport and metabolism
COG0044	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
COG0471	Di- and tricarboxylate transporters	P	Inorganic ion 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
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
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
COG2070	Dioxygenases related to 2-nitropropane dioxygenase	R	General function prediction only
COG0593	ATPase involved in DNA replication initiation	L	Replication, recombination and repair
COG0628	Predicted permease	R	General function prediction only
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
COG0573	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase	L	Replication, recombination and repair
COG3932	Uncharacterized ABC-type transport system, permease components	R	General function prediction only
COG3504	Type IV secretory pathway, VirB9 components	U	Intracellular trafficking, secretion, and vesicular transport
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
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
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
COG0267	Ribosomal protein L33	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
COG3604	Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains	K	Transcription
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
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
COG0658	Predicted membrane metal-binding protein	R	General function prediction only
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
COG0206	Cell division GTPase	D	Cell cycle control, cell division, chromosome partitioning
COG1544	Ribosome-associated protein Y (PSrp-1)	J	Translation, ribosomal structure and biogenesis
COG0162	Tyrosyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
COG2193	Bacterioferritin (cytochrome b1)	P	Inorganic ion transport and metabolism
COG0352	Thiamine monophosphate synthase	H	Coenzyme transport and metabolism
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
COG0042	tRNA-dihydrouridine synthase	J	Translation, ribosomal structure and biogenesis
COG0496	Predicted acid phosphatase	R	General function prediction only
COG0029	Aspartate oxidase	H	Coenzyme transport and metabolism
COG0470	ATPase involved in DNA replication	L	Replication, recombination and repair
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
COG0758	Predicted Rossmann fold nucleotide-binding protein involved in DNA uptake	L	Replication, recombination and repair
COG0242	N-formylmethionyl-tRNA deformylase	J	Translation, ribosomal structure and biogenesis
COG0113	Delta-aminolevulinic acid dehydratase	H	Coenzyme transport and metabolism
COG1295	Predicted membrane protein	S	Function unknown
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
COG0616	Periplasmic serine proteases (ClpP class)	O	Posttranslational modification, protein turnover, chaperones
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
COG1040	Predicted amidophosphoribosyltransferases	R	General function prediction only
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
COG0300	Short-chain dehydrogenases of various substrate specificities	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
COG3577	Predicted aspartyl protease	R	General function prediction only
COG0232	dGTP triphosphohydrolase	F	Nucleotide transport and metabolism
COG1381	Recombinational DNA repair protein (RecF pathway)	L	Replication, recombination and repair
COG3814	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)	P	Inorganic ion transport and metabolism
COG4653	Predicted phage phi-C31 gp36 major capsid-like protein	R	General function prediction only
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
COG3706	Response regulator containing a CheY-like receiver domain and a GGDEF domain	T	Signal transduction mechanisms
COG0208	Ribonucleotide reductase, beta subunit	F	Nucleotide transport and metabolism
COG0195	Transcription elongation factor	K	Transcription
COG0429	Predicted hydrolase of the alpha/beta-hydrolase fold	R	General function prediction only
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
COG2070	Dioxygenases related to 2-nitropropane dioxygenase	R	General function prediction only
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 enzymes	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
COG3740	Phage head maturation protease	R	General function prediction only
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
COG0632	Holliday junction resolvasome, DNA-binding subunit	L	Replication, recombination and repair
COG2255	Holliday junction resolvasome, helicase subunit	L	Replication, recombination and repair
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
COG0323	DNA mismatch repair enzyme (predicted ATPase)	L	Replication, recombination and repair
COG0502	Biotin synthase and related enzymes	H	Coenzyme transport and metabolism
COG0156	7-keto-8-aminopelargonate synthetase and related enzymes	H	Coenzyme transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0132	Dethiobiotin synthetase	H	Coenzyme transport and metabolism
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
COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III	I	Lipid 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
COG0760	Parvulin-like peptidyl-prolyl isomerase	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
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
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
COG2834	Outer membrane lipoprotein-sorting protein	M	Cell wall/membrane/envelope biogenesis
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
COG3387	Glucoamylase and related glycosyl hydrolases	G	Carbohydrate transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1947	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase	I	Lipid transport and metabolism

COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0591	Na+/proline symporter	E	Amino acid transport and metabolism
COG0194	Guanylate kinase	F	Nucleotide transport and metabolism
COG0372	Citrate synthase	C	Energy production and conversion
COG0148	Enolase	G	Carbohydrate transport and metabolism
COG0221	Inorganic pyrophosphatase	C	Energy production and conversion
COG0008	Glutamyl- and glutaminyl-tRNA synthetases	J	Translation, ribosomal structure and biogenesis
COG0344	Predicted membrane protein	S	Function unknown
COG4962	Flp pilus assembly protein, ATPase CpaF	U	Intracellular trafficking, secretion, and vesicular transport
COG3736	Type IV secretory pathway, component VirB8	U	Intracellular trafficking, secretion, and vesicular transport
COG0807	GTP cyclohydrolase II	H	Coenzyme transport and metabolism
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
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
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
COG0861	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion 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
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
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
COG3451	Type IV secretory pathway, VirB4 components	U	Intracellular trafficking, secretion, and vesicular transport
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
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
COG0475	Kef-type K+ transport systems, membrane components	P	Inorganic ion transport and metabolism
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
COG0696	Phosphoglyceromutase	G	Carbohydrate transport and metabolism
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
COG1651	Protein-disulfide isomerase	O	Posttranslational modification, protein turnover, chaperones
COG0012	Predicted GTPase, probable translation factor	J	Translation, ribosomal structure and biogenesis
COG0612	Predicted Zn-dependent peptidases	R	General function prediction only
COG0612	Predicted Zn-dependent peptidases	R	General function prediction only
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
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
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
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0371	Glycerol dehydrogenase and related enzymes	C	Energy production and conversion
COG2938	Uncharacterized conserved protein	S	Function unknown
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 enzymes	C	Energy production and conversion
COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	H	Coenzyme transport and metabolism
COG0817	Holliday junction resolvasome, endonuclease subunit	L	Replication, recombination and repair
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
COG5410	Uncharacterized protein conserved in bacteria	S	Function unknown
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
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG4227	Antirestriction protein	L	Replication, recombination and repair
COG0655	Multimeric flavodoxin WrbA	R	General function prediction only
COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG3971	2-keto-4-pentenoate hydratase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG5434	Endopolygalacturonase	M	Cell wall/membrane/envelope biogenesis
COG0247	Fe-S oxidoreductase	C	Energy production and conversion
COG3250	Beta-galactosidase/beta-glucuronidase	G	Carbohydrate transport and metabolism
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
COG3550	Uncharacterized protein related to capsule biosynthesis enzymes	R	General function prediction only
COG2154	Pterin-4a-carbinolamine dehydratase	H	Coenzyme transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG1835	Predicted acyltransferases	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
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1192	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG0157	Nicotinate-nucleotide pyrophosphorylase	H	Coenzyme transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG2605	Predicted kinase related to galactokinase and mevalonate kinase	R	General function prediction only
COG2942	N-acyl-D-glucosamine 2-epimerase	G	Carbohydrate transport and metabolism
COG2377	Predicted molecular chaperone distantly related to HSP70-fold metalloproteases	O	Posttranslational modification, protein turnover, chaperones
COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1	O	Posttranslational modification, protein turnover, chaperones
COG1045	Serine acetyltransferase	E	Amino acid transport and metabolism
COG1959	Predicted transcriptional regulator	K	Transcription
COG1076	DnaJ-domain-containing proteins 1	O	Posttranslational modification, protein turnover, chaperones
COG0598	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
COG2388	Predicted acetyltransferase	R	General function prediction only
COG5006	Predicted permease, DMT superfamily	R	General function prediction only
COG2159	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG3916	N-acyl-L-homoserine lactone synthetase	T	Signal transduction mechanisms
COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
COG2421	Predicted acetamidase/formamidase	C	Energy production and conversion
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0063	Predicted sugar kinase	G	Carbohydrate transport and metabolism
COG4307	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1872	Uncharacterized conserved protein	S	Function unknown
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG3801	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG0530	Ca2+/Na+ antiporter	P	Inorganic ion transport and metabolism
COG3104	Dipeptide/tripeptide permease	E	Amino acid transport and metabolism
COG0584	Glycerophosphoryl diester phosphodiesterase	C	Energy production and conversion
COG0762	Predicted integral membrane protein	S	Function unknown

COG0793	Periplasmic protease	M	Cell wall/membrane/envelope biogenesis
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG3142	Uncharacterized protein involved in copper resistance	P	Inorganic ion transport and metabolism
COG4976	Predicted methyltransferase (contains TPR repeat)	R	General function prediction only
COG1295	Predicted 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
COG0583	Transcriptional regulator	K	Transcription
COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG3427	Uncharacterized conserved protein	S	Function unknown
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG3759	Predicted membrane protein	S	Function unknown
COG0432	Uncharacterized conserved protein	S	Function unknown
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG3339	Uncharacterized conserved protein	S	Function unknown
COG2951	Membrane-bound lytic murein transglycosylase B	M	Cell wall/membrane/envelope biogenesis
COG0546	Predicted phosphatases	R	General function prediction only
COG1801	Uncharacterized conserved protein	S	Function unknown
COG5373	Predicted membrane protein	S	Function unknown
COG3791	Uncharacterized conserved protein	S	Function unknown
COG1454	Alcohol dehydrogenase, class IV	C	Energy production and conversion
COG2962	Predicted permeases	R	General function prediction only
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0019	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism
COG4675	Microcystin-dependent protein	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3022	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1192	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
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
COG0692	Uracil DNA glycosylase	L	Replication, recombination and repair
COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG0386	Glutathione peroxidase	O	Posttranslational modification, protein turnover, chaperones
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG2514	Predicted ring-cleavage extradiol dioxygenase	R	General function prediction only
COG2244	Membrane protein involved in the export of O-antigen and teichoic acid	R	General function prediction only
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG0205	6-phosphofructokinase	G	Carbohydrate transport and metabolism
COG1297	Predicted membrane protein	S	Function unknown
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
COG1874	Beta-galactosidase	G	Carbohydrate transport and metabolism
COG0287	Prephenate dehydrogenase	E	Amino acid transport and metabolism
COG0163	3-polyprenyl-4-hydroxybenzoate decarboxylase	H	Coenzyme transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1714	Predicted membrane protein/domain	S	Function unknown
COG1300	Uncharacterized membrane protein	S	Function unknown
COG1721	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	R	General function prediction only
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG2200	FOG: EAL domain	T	Signal transduction mechanisms
COG2068	Uncharacterized MobA-related protein	R	General function prediction only
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG3508	Homogentisate 1,2-dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1574	Predicted metal-dependent hydrolase with the TIM-barrel fold	R	General function prediction only
COG2382	Enterochelin esterase and related enzymes	P	Inorganic ion transport and metabolism
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0784	FOG: CheY-like receiver	T	Signal transduction mechanisms
COG2273	Beta-glucanase/Beta-glucan synthetase	G	Carbohydrate transport and metabolism
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
COG3938	Proline racemase	E	Amino acid transport and metabolism
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG3663	G:T/U mismatch-specific DNA glycosylase	L	Replication, recombination and repair
COG0809	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)	J	Translation, ribosomal structure and biogenesis
COG0661	Predicted unusual protein kinase	R	General function prediction only
COG0739	Membrane proteins related to metalloendopeptidases	M	Cell wall/membrane/envelope biogenesis
COG4898	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1164	Oligoendopeptidase F	E	Amino acid transport and metabolism
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG1363	Cellulase M and related proteins	G	Carbohydrate transport and metabolism
COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes	M	Cell wall/membrane/envelope biogenesis
COG4133	ABC-type transport system involved in cytochrome c biogenesis, ATPase component	O	Posttranslational modification, protein turnover, chaperones
COG4231	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	C	Energy production and conversion
COG0330	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification, protein turnover, chaperones
COG0147	Anthranilate/para-aminobenzoate synthases component I	E	Amino acid transport and metabolism
COG3750	Uncharacterized protein conserved in bacteria	S	Function unknown
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
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism

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
COG3070	Regulator of competence-specific genes	K	Transcription
COG3914	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family	O	Posttranslational modification, protein turnover, chaperones
COG2984	ABC-type uncharacterized transport system, periplasmic component	R	General function prediction only
COG4120	ABC-type uncharacterized transport system, permease component	R	General function prediction only
COG1101	ABC-type uncharacterized transport system, ATPase component	R	General function prediction only
COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	E	Amino acid transport and metabolism
COG3242	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0560	Phosphoserine phosphatase	E	Amino acid transport and metabolism
COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K	Transcription
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
COG4603	ABC-type uncharacterized transport system, permease component	R	General function prediction only
COG0005	Purine nucleoside phosphorylase	F	Nucleotide transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG4674	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG2200	FOG: EAL domain	T	Signal transduction mechanisms
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
COG2261	Predicted membrane protein	S	Function unknown
COG2005	N-terminal domain of molybdenum-binding protein	R	General function prediction only
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1733	Predicted transcriptional regulators	K	Transcription
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG1171	Threonine dehydratase	E	Amino acid transport and metabolism
COG0546	Predicted phosphatases	R	General function prediction only
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
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG4570	Holliday junction resolvase	L	Replication, recombination and repair
COG1802	Transcriptional regulators	K	Transcription
COG3135	Uncharacterized protein involved in benzoate metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4315	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3131	Periplasmic glucans biosynthesis protein	P	Inorganic ion transport and metabolism
COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG0782	Transcription elongation factor	K	Transcription
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
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
COG2378	Predicted transcriptional regulator	K	Transcription
COG3706	Response regulator containing a CheY-like receiver domain and a GGDEF domain	T	Signal transduction mechanisms
COG1236	Predicted exonuclease of the beta-lactamase fold involved in RNA processing	J	Translation, ribosomal structure and biogenesis
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG3555	Aspartyl/asparaginyl beta-hydroxylase and related dioxygenases	O	Posttranslational modification, protein turnover, chaperones
COG1051	ADP-ribose pyrophosphatase	F	Nucleotide transport and metabolism
COG4301	Uncharacterized conserved protein	S	Function unknown
COG1109	Phosphomannomutase	G	Carbohydrate transport and metabolism
COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K	Transcription
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG0384	Predicted epimerase, PhzC/PhzF homolog	R	General function prediction only
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG2103	Predicted sugar phosphate isomerase	R	General function prediction only
COG0347	Nitrogen regulatory protein PII	E	Amino acid transport and metabolism
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG4125	Predicted membrane protein	S	Function unknown
COG3391	Uncharacterized conserved protein	S	Function unknown
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG0062	Uncharacterized conserved protein	S	Function unknown
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0137	Argininosuccinate synthase	E	Amino acid transport and metabolism
COG0025	NhaP-type Na+/H+ and K+/H+ antiporters	P	Inorganic ion transport and metabolism
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG3201	Nicotinamide mononucleotide transporter	H	Coenzyme transport and metabolism
COG3189	Uncharacterized conserved protein	S	Function unknown
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG3568	Metal-dependent hydrolase	R	General function prediction only
COG0713	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)	C	Energy production and conversion
COG0863	DNA modification methylase	L	Replication, recombination and repair
COG0778	Nitroreductase	C	Energy production and conversion
COG0820	Predicted Fe-S-cluster redox enzyme	R	General function prediction only

COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0640	Predicted transcriptional regulators	K	Transcription
COG1064	Zn-dependent alcohol dehydrogenases	R	General function prediction only
COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
COG0841	Cation/multidrug efflux pump	V	Defense mechanisms
COG2825	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
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
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG1529	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	C	Energy production and conversion
COG0456	Acetyltransferases	R	General function prediction only
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG3806	Anti-sigma factor	T	Signal transduction mechanisms
COG3450	Predicted enzyme of the cupin superfamily	R	General function prediction only
COG2706	3-carboxymuconate cyclase	G	Carbohydrate transport and metabolism
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
COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	G	Carbohydrate transport and metabolism
COG0547	Anthranilate phosphoribosyltransferase	E	Amino acid transport and metabolism
COG1434	Uncharacterized conserved protein	S	Function unknown
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
COG5472	Predicted small integral membrane protein	S	Function unknown
COG0149	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG2877	3-deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase	M	Cell wall/membrane/envelope biogenesis
COG0535	Predicted Fe-S oxidoreductases	R	General function prediction only
COG1309	Transcriptional regulator	K	Transcription
COG4320	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0811	Biopolymer transport proteins	U	Intracellular trafficking, secretion, and vesicular transport
COG1235	Metal-dependent hydrolases of the beta-lactamase superfamily I	R	General function prediction only
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1729	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1112	Superfamily I DNA and RNA helicases and helicase subunits	L	Replication, recombination and repair
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0566	rRNA methylases	J	Translation, ribosomal structure and biogenesis
COG0778	Nitroreductase	C	Energy production and conversion
COG1451	Predicted metal-dependent hydrolase	R	General function prediction only
COG0705	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	R	General function prediction only
COG3205	Predicted membrane protein	S	Function unknown
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG0678	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	E	Amino acid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1971	Predicted membrane protein	S	Function unknown
COG0025	NhaP-type Na+/H+ and K+/H+ antiporters	P	Inorganic ion transport and metabolism
COG5042	Purine nucleoside permease	F	Nucleotide transport and metabolism
COG4122	Predicted O-methyltransferase	R	General function prediction only
COG4448	L-asparaginase II	E	Amino acid transport and metabolism
COG1695	Predicted transcriptional regulators	K	Transcription
COG1032	Fe-S oxidoreductase	C	Energy production and conversion
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism	T	Signal transduction mechanisms
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
COG2897	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG1887	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC	M	Cell wall/membrane/envelope biogenesis
COG0236	Acyl carrier protein	I	Lipid transport and metabolism
COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	I	Lipid transport and metabolism
COG2266	GTP:adenosylcobinamide-phosphate guanylyltransferase	H	Coenzyme transport and metabolism
COG1171	Threonine dehydratase	E	Amino acid transport and metabolism
COG3449	DNA gyrase inhibitor	L	Replication, recombination and repair
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG2352	Phosphoenolpyruvate carboxylase	C	Energy production and conversion
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0659	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport and metabolism
COG0562	UDP-galactopyranose mutase	M	Cell wall/membrane/envelope biogenesis
COG2267	Lysophospholipase	I	Lipid transport and metabolism
COG1209	dTDP-glucose pyrophosphorylase	M	Cell wall/membrane/envelope biogenesis
COG3837	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG4529	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG4717	Uncharacterized conserved protein	S	Function unknown
COG1289	Predicted membrane protein	S	Function unknown
COG0446	Uncharacterized NAD(FAD)-dependent dehydrogenases	R	General function prediction only
COG1324	Uncharacterized protein involved in tolerance to divalent cations	P	Inorganic ion transport and metabolism
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG1479	Uncharacterized conserved protein	S	Function unknown
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
COG1739	Uncharacterized conserved protein	S	Function unknown
COG3667	Uncharacterized protein involved in copper resistance	P	Inorganic ion transport and metabolism
COG0002	Acetylglutamate semialdehyde dehydrogenase	E	Amino acid transport and metabolism
COG3243	Poly(3-hydroxyalkanoate) synthetase	I	Lipid transport and metabolism
COG1846	Transcriptional regulators	K	Transcription
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG0448	ADP-glucose pyrophosphorylase	G	Carbohydrate transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0460	Homoserine dehydrogenase	E	Amino acid transport and metabolism
COG3193	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	R	General function prediction only
COG0511	Biotin carboxyl carrier protein	I	Lipid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG0297	Glycogen synthase	G	Carbohydrate transport and metabolism
COG2837	Predicted iron-dependent peroxidase	P	Inorganic ion transport and metabolism
COG0656	Aldo/keto reductases, related to diketogulonate reductase	R	General function prediction only
COG1953	Cytosine/uracil/thiamine/allantoin permeases	F	Nucleotide transport and metabolism
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG1846	Transcriptional regulators	K	Transcription
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1893	Ketopantoate reductase	H	Coenzyme transport and metabolism
COG0598	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
COG3265	Gluconate kinase	G	Carbohydrate transport and metabolism
COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG0640	Predicted transcriptional regulators	K	Transcription
COG0659	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG1223	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG2801	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG1802	Transcriptional regulators	K	Transcription
COG3470	Uncharacterized protein probably involved in high-affinity Fe2+ transport	P	Inorganic ion transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG0583	Transcriptional regulator	K	Transcription
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0831	Urea amidohydrolase (urease) gamma subunit	E	Amino acid transport and metabolism
COG0832	Urea amidohydrolase (urease) beta subunit	E	Amino acid transport and metabolism
COG2371	Urease accessory protein UreE	O	Posttranslational modification, protein turnover, chaperones
COG0640	Predicted transcriptional regulators	K	Transcription
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
COG1109	Phosphomannomutase	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
COG1396	Predicted transcriptional regulators	K	Transcription
COG3577	Predicted aspartyl protease	R	General function prediction only
COG1803	Methylglyoxal synthase	G	Carbohydrate transport and metabolism
COG0388	Predicted amidohydrolase	R	General function prediction only
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG3952	Predicted membrane protein	S	Function unknown
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
COG1125	ABC-type proline/glycine betaine transport systems, ATPase components	E	Amino acid transport and metabolism
COG1732	Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)	M	Cell wall/membrane/envelope biogenesis
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2	O	Posttranslational modification, protein turnover, chaperones
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
COG2350	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1373	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG1922	Teichoic acid biosynthesis proteins	M	Cell wall/membrane/envelope biogenesis
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
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG0236	Acyl carrier protein	I	Lipid transport and metabolism
COG1683	Uncharacterized conserved protein	S	Function unknown

COG1559	Predicted periplasmic solute-binding protein	R	General function prediction only
COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
COG3214	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG2602	Beta-lactamase class D	V	Defense mechanisms
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG0640	Predicted transcriptional regulators	K	Transcription
COG3543	Uncharacterized conserved protein	S	Function unknown
COG1881	Phospholipid-binding protein	R	General function prediction only
COG0583	Transcriptional regulator	K	Transcription
COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	I	Lipid transport and metabolism
COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG0038	Chloride channel protein EriC	P	Inorganic ion transport and metabolism
COG1487	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG2194	Predicted membrane-associated, metal-dependent hydrolase	R	General function prediction only
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG3860	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG4737	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2944	Predicted transcriptional regulator	K	Transcription
COG0589	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
COG1734	DnaK suppressor protein	T	Signal transduction mechanisms
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG1320	Multisubunit Na+/H+ antiporter, MnhG subunit	P	Inorganic ion transport and metabolism
COG1006	Multisubunit Na+/H+ antiporter, MnhC subunit	P	Inorganic ion transport and metabolism
COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Energy production and conversion
COG4177	ABC-type branched-chain amino acid transport system, permease component	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
COG3553	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2068	Uncharacterized MobA-related protein	R	General function prediction only
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
COG3180	Putative ammonia monooxygenase	R	General function prediction only
COG3552	Protein containing von Willebrand factor type A (vWA) domain	R	General function prediction only
COG1487	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG0714	MoxR-like ATPases	R	General function prediction only
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
COG4729	Uncharacterized conserved protein	S	Function unknown
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG2329	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
COG2199	FOG: GGDEF domain	T	Signal transduction mechanisms
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
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
COG0284	Orotidine-5'-phosphate decarboxylase	F	Nucleotide 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
COG0456	Acetyltransferases	R	General function prediction only
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
COG2195	Di- and tripeptidases	E	Amino acid transport and metabolism
COG0659	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport and metabolism
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
COG1476	Predicted transcriptional regulators	K	Transcription
COG0818	Diacylglycerol kinase	M	Cell wall/membrane/envelope biogenesis
COG2835	Uncharacterized conserved protein	S	Function unknown
COG3293	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG2518	Protein-L-isoaspartate carboxylmethyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG0563	Adenylate kinase and related kinases	F	Nucleotide transport and metabolism
COG1434	Uncharacterized conserved protein	S	Function unknown
COG4222	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4134	ABC-type uncharacterized transport system, periplasmic component	R	General function prediction only
COG1686	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
COG4337	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0010	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family	E	Amino acid transport and metabolism
COG2847	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0631	Serine/threonine protein phosphatase	T	Signal transduction mechanisms
COG5525	Bacteriophage tail assembly protein	R	General function prediction only
COG5511	Bacteriophage capsid protein	R	General function prediction only
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
COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III	R	General function prediction only
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
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate 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
COG4097	Predicted ferric reductase	P	Inorganic ion transport and metabolism
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
COG0861	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion transport and metabolism
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
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
COG2020	Putative protein-S-isoprenylcysteine methyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG1010	Precorrin-3B methylase	H	Coenzyme transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG3609	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain	K	Transcription
COG0314	Molybdopterin converting factor, large subunit	H	Coenzyme transport and metabolism
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid 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
COG0727	Predicted Fe-S-cluster oxidoreductase	R	General function prediction only
COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	E	Amino acid transport and metabolism
COG1231	Monoamine oxidase	E	Amino acid transport and metabolism
COG3027	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1692	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3719	Ribonuclease I	J	Translation, ribosomal structure and biogenesis
COG2942	N-acyl-D-glucosamine 2-epimerase	G	Carbohydrate transport and metabolism
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
COG2932	Predicted transcriptional regulator	K	Transcription
COG1086	Predicted nucleoside-diphosphate sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase	R	General function prediction only
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
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase	M	Cell wall/membrane/envelope biogenesis
COG4424	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3416	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG2017	Galactose mutarotase and related enzymes	G	Carbohydrate transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
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
COG2337	Growth inhibitor	T	Signal transduction mechanisms
COG3237	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
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
COG1846	Transcriptional regulators	K	Transcription
COG2852	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3755	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0529	Adenylylsulfate kinase and related kinases	P	Inorganic ion transport and metabolism
COG4520	Surface antigen	M	Cell wall/membrane/envelope biogenesis
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1230	Co/Zn/Cd efflux system component	P	Inorganic ion transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG4764	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG4427	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG4581	Superfamily II RNA helicase	L	Replication, recombination and repair
COG5607	Uncharacterized conserved protein	S	Function unknown
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
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG2186	Transcriptional regulators	K	Transcription
COG2898	Uncharacterized conserved protein	S	Function unknown
COG3946	Type IV secretory pathway, VirJ component	U	Intracellular trafficking, secretion, and vesicular transport
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG2962	Predicted permeases	R	General function prediction only
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
COG1262	Uncharacterized conserved protein	S	Function unknown
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism

COG3173	Predicted aminoglycoside phosphotransferase	R	General function prediction only
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1218	3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase	P	Inorganic ion transport and metabolism
COG2372	Uncharacterized protein, homolog of Cu resistance protein CopC	R	General function prediction only
COG1276	Putative copper export protein	P	Inorganic ion transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG3840	ABC-type thiamine transport system, ATPase component	H	Coenzyme transport and metabolism
COG1669	Predicted nucleotidyltransferases	R	General function prediction only
COG3562	Capsule polysaccharide export protein	M	Cell wall/membrane/envelope biogenesis
COG0835	Chemotaxis signal transduction protein	N	Cell motility
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0835	Chemotaxis signal transduction protein	N	Cell motility
COG1640	4-alpha-glucanotransferase	G	Carbohydrate transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG1196	Chromosome segregation ATPases	D	Cell cycle control, cell division, chromosome partitioning
COG1475	Predicted transcriptional regulators	K	Transcription
COG1522	Transcriptional regulators	K	Transcription
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport and metabolism
COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase	R	General function prediction only
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1305	Transglutaminase-like enzymes, putative cysteine proteases	E	Amino acid transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG0589	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0590	Cytosine/adenosine deaminases	F	Nucleotide transport and metabolism
COG1305	Transglutaminase-like enzymes, putative cysteine proteases	E	Amino acid transport and metabolism
COG0685	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1486	Alpha-galactosidases/6-phospho-beta-glucosidases, family 4 of glycosyl hydrolases	G	Carbohydrate transport and metabolism
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG0824	Predicted thioesterase	R	General function prediction only
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG1357	Uncharacterized low-complexity proteins	S	Function unknown
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG2070	Dioxygenases related to 2-nitropropane dioxygenase	R	General function prediction only
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0644	Dehydrogenases (flavoproteins)	C	Energy production and conversion
COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein	R	General function prediction only
COG1079	Uncharacterized ABC-type transport system, permease component	R	General function prediction only
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG4566	Response regulator	T	Signal transduction mechanisms
COG2186	Transcriptional regulators	K	Transcription
COG0754	Glutathionylspermidine synthase	E	Amino acid transport and metabolism
COG4188	Predicted dienelactone hydrolase	R	General function prediction only
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG2116	Formate/nitrite family of transporters	P	Inorganic ion transport and metabolism
COG4032	Predicted thiamine-pyrophosphate-binding protein	R	General function prediction only
COG1522	Transcriptional regulators	K	Transcription
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
COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG1207	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	M	Cell wall/membrane/envelope biogenesis
COG0546	Predicted phosphatases	R	General function prediction only
COG4565	Response regulator of citrate/malate metabolism	K	Transcription
COG1162	Predicted GTPases	R	General function prediction only
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG0414	Panthothenate synthetase	H	Coenzyme transport and metabolism
COG0467	RecA-superfamily ATPases implicated in signal transduction	T	Signal transduction mechanisms
COG1414	Transcriptional regulator	K	Transcription
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
COG1488	Nicotinic acid phosphoribosyltransferase	H	Coenzyme transport and metabolism
COG3411	Ferredoxin	C	Energy production and conversion
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0054	Riboflavin synthase beta-chain	H	Coenzyme transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	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
COG3345	Alpha-galactosidase	G	Carbohydrate 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

COG0511	Biotin carboxyl carrier protein	I	Lipid transport and metabolism
COG2049	Allophanate hydrolase subunit 1	E	Amino acid transport and metabolism
COG3509	Poly(3-hydroxybutyrate) depolymerase	Q	Secondary metabolites biosynthesis, transport and catabolism
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
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG3758	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1072	Panthothenate kinase	H	Coenzyme transport and metabolism
COG1940	Transcriptional regulator/sugar kinase	K	Transcription
COG1522	Transcriptional regulators	K	Transcription
COG0401	Uncharacterized homolog of Blt101	S	Function unknown
COG0160	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
COG2928	Uncharacterized conserved protein	S	Function unknown
COG3424	Predicted naringenin-chalcone synthase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4559	ABC-type hemin transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	F	Nucleotide transport and metabolism
COG0798	Arsenite efflux pump ACR3 and related permeases	P	Inorganic ion transport and metabolism
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG1840	ABC-type Fe3+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG5309	Exo-beta-1,3-glucanase	G	Carbohydrate transport and metabolism
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
COG5662	Predicted transmembrane transcriptional regulator (anti-sigma factor)	K	Transcription
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG2911	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG0005	Purine nucleoside phosphorylase	F	Nucleotide transport and metabolism
COG1108	ABC-type Mn2+/Zn2+ transport systems, permease components	P	Inorganic ion transport and metabolism
COG2094	3-methyladenine DNA glycosylase	L	Replication, recombination and repair
COG2153	Predicted acyltransferase	R	General function prediction only
COG5483	Uncharacterized conserved protein	S	Function unknown
COG3685	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG1278	Cold shock proteins	K	Transcription
COG3118	Thioredoxin domain-containing protein	O	Posttranslational modification, protein turnover, chaperones
COG1174	ABC-type proline/glycine betaine transport systems, permease component	E	Amino acid transport and metabolism
COG1174	ABC-type proline/glycine betaine transport systems, permease component	E	Amino acid transport and metabolism
COG0108	3,4-dihydroxy-2-butanone 4-phosphate synthase	H	Coenzyme transport and metabolism
COG5514	Uncharacterized conserved protein	S	Function unknown
COG0334	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
COG0781	Transcription termination factor	K	Transcription
COG2913	Small protein A (tmRNA-binding)	J	Translation, ribosomal structure and biogenesis
COG4757	Predicted alpha/beta hydrolase	R	General function prediction only
COG3306	Glycosyltransferase involved in LPS biosynthesis	M	Cell wall/membrane/envelope biogenesis
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
COG1648	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)	H	Coenzyme transport and metabolism
COG2895	GTPases - Sulfate adenylate transferase subunit 1	P	Inorganic ion transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate 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
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3255	Putative sterol carrier protein	I	Lipid transport and metabolism
COG2336	Growth regulator	T	Signal transduction mechanisms
COG0789	Predicted transcriptional regulators	K	Transcription
COG0824	Predicted thioesterase	R	General function prediction only
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG3021	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase	H	Coenzyme transport and metabolism
COG3126	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0464	ATPases of the AAA+ class	O	Posttranslational modification, protein turnover, chaperones
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG1520	FOG: WD40-like repeat	S	Function unknown
COG3514	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1020	Non-ribosomal peptide synthetase modules and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG1233	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3918	Predicted membrane protein	S	Function unknown
COG4226	Uncharacterized protein encoded in hypervariable junctions of pilus gene clusters	S	Function unknown
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG3803	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0730	Predicted permeases	R	General function prediction only
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1360	Flagellar motor protein	N	Cell motility
COG5446	Predicted integral membrane protein	S	Function unknown
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
COG2374	Predicted extracellular nuclease	R	General function prediction only
COG4702	Uncharacterized conserved protein	S	Function unknown
COG2334	Putative homoserine kinase type II (protein kinase fold)	R	General function prediction only
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism

COG0678	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG1678	Putative transcriptional regulator	K	Transcription
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
COG3153	Predicted acetyltransferase	R	General function prediction only
COG3346	Uncharacterized conserved protein	S	Function unknown
COG4608	ABC-type oligopeptide transport system, ATPase component	E	Amino acid transport and metabolism
COG5349	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG0704	Phosphate uptake regulator	P	Inorganic ion transport and metabolism
COG5271	AAA ATPase containing von Willebrand factor type A (vWA) domain	R	General function prediction only
COG0385	Predicted Na+-dependent transporter	R	General function prediction only
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1802	Transcriptional regulators	K	Transcription
COG2008	Threonine aldolase	E	Amino acid transport and metabolism
COG5508	Uncharacterized conserved small protein	S	Function unknown
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2329	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
COG0168	Trk-type K+ transport systems, membrane components	P	Inorganic ion transport and metabolism
COG1932	Phosphoserine aminotransferase	H	Coenzyme transport and metabolism
COG1295	Predicted membrane protein	S	Function unknown
COG0082	Chorismate synthase	E	Amino acid transport and metabolism
COG0573	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
COG2128	Uncharacterized conserved protein	S	Function unknown
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1352	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
COG2271	Sugar phosphate permease	G	Carbohydrate 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
COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG1610	Uncharacterized conserved protein	S	Function unknown
COG0684	Demethylmenaquinone methyltransferase	H	Coenzyme transport and metabolism
COG3916	N-acyl-L-homoserine lactone synthetase	T	Signal transduction mechanisms
COG4821	Uncharacterized protein containing SIS (Sugar ISomerase) phosphosugar binding domain	R	General function prediction only
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG5383	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1393	Arsenate reductase and related proteins, glutaredoxin family	P	Inorganic ion transport and metabolism
COG0149	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases	V	Defense mechanisms
COG0732	Restriction endonuclease S subunits	V	Defense mechanisms
COG0286	Type I restriction-modification system methyltransferase subunit	V	Defense mechanisms
COG1611	Predicted Rossmann fold nucleotide-binding protein	R	General function prediction only
COG0538	Isocitrate dehydrogenases	C	Energy production and conversion
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG5352	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1178	ABC-type Fe3+ transport system, permease component	P	Inorganic ion transport and metabolism
COG5662	Predicted transmembrane transcriptional regulator (anti-sigma factor)	K	Transcription
COG2329	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases	T	Signal transduction mechanisms
COG4323	Predicted membrane protein	S	Function unknown
COG2217	Cation transport ATPase	P	Inorganic ion transport and metabolism
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	C	Energy production and conversion
COG1309	Transcriptional regulator	K	Transcription
COG0348	Polyferredoxin	C	Energy production and conversion
COG2257	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB	S	Function unknown
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
COG0826	Collagenase and related proteases	O	Posttranslational modification, protein turnover, chaperones
COG0826	Collagenase and related proteases	O	Posttranslational modification, protein turnover, chaperones
COG3794	Plastocyanin	C	Energy production and conversion
COG1477	Membrane-associated lipoprotein involved in thiamine biosynthesis	H	Coenzyme transport and metabolism
COG4314	Predicted lipoprotein involved in nitrous oxide reduction	C	Energy production and conversion
COG1277	ABC-type transport system involved in multi-copper enzyme maturation, permease component	R	General function prediction only
COG1131	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
COG3420	Nitrous oxidase accessory protein	P	Inorganic ion transport and metabolism
COG4263	Nitrous oxide reductase	C	Energy production and conversion
COG2132	Putative multicopper oxidases	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4548	Nitric oxide reductase activation protein	P	Inorganic ion transport and metabolism
COG0714	MoxR-like ATPases	R	General function prediction only
COG3256	Nitric oxide reductase large subunit	P	Inorganic ion transport and metabolism
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
COG3143	Chemotaxis protein	N	Cell motility
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG2827	Predicted endonuclease containing a URI domain	L	Replication, recombination and repair
COG1580	Flagellar basal body-associated protein	N	Cell motility
COG2366	Protein related to penicillin acylase	R	General function prediction only
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG3232	5-carboxymethyl-2-hydroxymuconate isomerase	E	Amino acid transport and metabolism
COG1846	Transcriptional regulators	K	Transcription
COG0160	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2030	Acyl dehydratase	I	Lipid transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism

COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	O	Posttranslational modification, protein turnover, chaperones
COG0071	Molecular chaperone (small heat shock protein)	O	Posttranslational modification, protein turnover, chaperones
COG0420	DNA repair exonuclease	L	Replication, recombination and repair
COG4717	Uncharacterized conserved protein	S	Function unknown
COG3001	Fructosamine-3-kinase	G	Carbohydrate transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1237	Metal-dependent hydrolases of the beta-lactamase superfamily II	R	General function prediction only
COG2170	Uncharacterized conserved protein	S	Function unknown
COG2962	Predicted permeases	R	General function prediction only
COG2186	Transcriptional regulators	K	Transcription
COG1841	Ribosomal protein L30/L7E	J	Translation, ribosomal structure and biogenesis
COG2085	Predicted dinucleotide-binding enzymes	R	General function prediction only
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG2132	Putative multicopper oxidases	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG3794	Plastocyanin	C	Energy production and conversion
COG4637	Predicted ATPase	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
COG1861	Spore coat polysaccharide biosynthesis protein F, CMP-KDO synthetase homolog	M	Cell wall/membrane/envelope biogenesis
COG0051	Ribosomal protein S10	J	Translation, ribosomal structure and biogenesis
COG3651	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG1994	Zn-dependent proteases	R	General function prediction only
COG1251	NAD(P)H-nitrite reductase	C	Energy production and conversion
COG0222	Ribosomal protein L7/L12	J	Translation, ribosomal structure and biogenesis
COG0244	Ribosomal protein L10	J	Translation, ribosomal structure and biogenesis
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0690	Preprotein translocase subunit SecE	U	Intracellular trafficking, secretion, and vesicular transport
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
COG2132	Putative multicopper oxidases	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4422	Bacteriophage protein gp37	S	Function unknown
COG1846	Transcriptional regulators	K	Transcription
COG1881	Phospholipid-binding protein	R	General function prediction only
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG2312	Erythromycin esterase homolog	R	General function prediction only
COG1940	Transcriptional regulator/sugar kinase	K	Transcription
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG4674	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	H	Coenzyme transport and metabolism
COG0241	Histidinol phosphatase and related phosphatases	E	Amino acid transport and metabolism
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG4292	Predicted membrane protein	S	Function unknown
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0512	Anthranilate/para-aminobenzoate synthases component II	E	Amino acid transport and metabolism
COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	M	Cell wall/membrane/envelope biogenesis
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3556	Predicted membrane protein	S	Function unknown
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG0753	Catalase	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
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG4783	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
COG2932	Predicted transcriptional regulator	K	Transcription
COG1695	Predicted transcriptional regulators	K	Transcription
COG3572	Gamma-glutamylcysteine synthetase	H	Coenzyme transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG3631	Ketosteroid isomerase-related protein	R	General function prediction only
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases	H	Coenzyme transport and metabolism
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2259	Predicted membrane protein	S	Function unknown
COG5654	Uncharacterized conserved protein	S	Function unknown
COG2856	Predicted Zn peptidase	E	Amino acid transport and metabolism
COG4185	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
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
COG3166	Tfp pilus assembly protein PilN	N	Cell motility
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

COG4549	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3811	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3761	NADH:ubiquinone oxidoreductase 17.2 kD subunit	C	Energy production and conversion
COG2361	Uncharacterized conserved protein	S	Function unknown
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
COG1276	Putative copper export protein	P	Inorganic ion transport and metabolism
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1544	Ribosome-associated protein Y (PSrp-1)	J	Translation, ribosomal structure and biogenesis
COG0296	1,4-alpha-glucan branching enzyme	G	Carbohydrate transport and metabolism
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG2353	Uncharacterized conserved protein	S	Function unknown
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
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
COG1621	Beta-fructosidases (levanase/invertase)	G	Carbohydrate transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
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
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
COG3023	Negative regulator of beta-lactamase expression	V	Defense mechanisms
COG2001	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
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
COG1589	Cell division septal protein	M	Cell wall/membrane/envelope biogenesis
COG1251	NAD(P)H-nitrite reductase	C	Energy production and conversion
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG0206	Cell division GTPase	D	Cell cycle control, cell division, chromosome partitioning
COG1283	Na+/phosphate symporter	P	Inorganic ion transport and metabolism
COG0774	UDP-3-O-acyl-N-acetylglucosamine deacetylase	M	Cell wall/membrane/envelope biogenesis
COG0605	Superoxide dismutase	P	Inorganic ion transport and metabolism
COG0266	Formamidopyrimidine-DNA glycosylase	L	Replication, recombination and repair
COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	I	Lipid transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0497	ATPase involved in DNA repair	L	Replication, recombination and repair
COG4753	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	T	Signal transduction mechanisms
COG1724	Predicted periplasmic or secreted lipoprotein	N	Cell motility
COG1598	Uncharacterized conserved protein	S	Function unknown
COG4103	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG5622	Protein required for attachment to host cells	N	Cell motility
COG3239	Fatty acid desaturase	I	Lipid transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG3304	Predicted membrane protein	S	Function unknown
COG4992	Ornithine/acetylornithine aminotransferase	E	Amino acid transport and metabolism
COG0280	Phosphotransacetylase	C	Energy production and conversion
COG2520	Predicted methyltransferase	R	General function prediction only
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1309	Transcriptional regulator	K	Transcription
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2896	Molybdenum cofactor biosynthesis enzyme	H	Coenzyme transport and metabolism
COG3180	Putative ammonia monooxygenase	R	General function prediction only
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0330	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification, protein turnover, chaperones
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG4986	ABC-type anion transport system, duplicated permease component	P	Inorganic ion transport and metabolism
COG5507	Uncharacterized conserved protein	S	Function unknown
COG1733	Predicted transcriptional regulators	K	Transcription
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
COG2718	Uncharacterized conserved protein	S	Function unknown
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
COG1878	Predicted metal-dependent hydrolase	R	General function prediction only
COG1403	Restriction endonuclease	V	Defense mechanisms
COG1495	Disulfide bond formation protein DsbB	O	Posttranslational modification, protein turnover, chaperones
COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG3474	Cytochrome c2	C	Energy production and conversion

COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG4993	Glucose dehydrogenase	G	Carbohydrate transport and metabolism
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG5501	Predicted secreted protein	S	Function unknown
COG2031	Short chain fatty acids transporter	I	Lipid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG3391	Uncharacterized conserved protein	S	Function unknown
COG1131	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG2963	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG1052	Lactate dehydrogenase and related dehydrogenases	C	Energy production and conversion
COG3287	Uncharacterized conserved protein	S	Function unknown
COG3564	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1476	Predicted transcriptional regulators	K	Transcription
COG5489	Uncharacterized conserved protein	S	Function unknown
COG1476	Predicted transcriptional regulators	K	Transcription
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
COG3435	Gentisate 1,2-dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1893	Ketopantoate reductase	H	Coenzyme transport and metabolism
COG0225	Peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG0372	Citrate synthase	C	Energy production and conversion
COG1285	Uncharacterized membrane protein	S	Function unknown
COG3256	Nitric oxide reductase large subunit	P	Inorganic ion transport and metabolism
COG1522	Transcriptional regulators	K	Transcription
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG1592	Rubrerythrin	C	Energy production and conversion
COG1525	Micrococcal nuclease (thermonuclease) homologs	L	Replication, recombination and repair
COG0412	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3660	Predicted nucleoside-diphosphate-sugar epimerase	M	Cell wall/membrane/envelope biogenesis
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG0066	3-isopropylmalate dehydratase small subunit	E	Amino acid transport and metabolism
COG0065	3-isopropylmalate dehydratase large subunit	E	Amino acid transport and metabolism
COG2259	Predicted membrane protein	S	Function unknown
COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)	P	Inorganic ion transport and metabolism
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
COG0480	Translation elongation factors (GTPases)	J	Translation, ribosomal structure and biogenesis
COG3004	Na+/H+ antiporter	P	Inorganic ion transport and metabolism
COG5470	Uncharacterized conserved protein	S	Function unknown
COG3658	Cytochrome b	C	Energy production and conversion
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport and metabolism
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG3011	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG3832	Uncharacterized conserved protein	S	Function unknown
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG4458	Uncharacterized protein conserved in bacteria, putative virulence factor	S	Function unknown
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG3791	Uncharacterized conserved protein	S	Function unknown
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
COG1262	Uncharacterized conserved protein	S	Function unknown
COG0606	Predicted ATPase with chaperone activity	O	Posttranslational modification, protein turnover, chaperones
COG0606	Predicted ATPase with chaperone activity	O	Posttranslational modification, protein turnover, chaperones
COG0730	Predicted permeases	R	General function prediction only
COG0739	Membrane proteins related to metalloendopeptidases	M	Cell wall/membrane/envelope biogenesis
COG0730	Predicted permeases	R	General function prediction only
COG1144	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit	C	Energy production and conversion
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG0584	Glycerophosphoryl diester phosphodiesterase	C	Energy production and conversion
COG1146	Ferredoxin	C	Energy production and conversion
COG3917	2-hydroxychromene-2-carboxylate isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2852	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG2818	3-methyladenine DNA glycosylase	L	Replication, recombination and repair
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG3764	Sortase (surface protein transpeptidase)	M	Cell wall/membrane/envelope biogenesis
COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain	R	General function prediction only
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG2514	Predicted ring-cleavage extradiol dioxygenase	R	General function prediction only
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG1846	Transcriptional regulators	K	Transcription

COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG0703	Shikimate kinase	E	Amino acid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG3396	Uncharacterized conserved protein	S	Function unknown
COG0549	Carbamate kinase	E	Amino acid transport and metabolism
COG0078	Ornithine carbamoyltransferase	E	Amino acid transport and metabolism
COG0531	Amino acid transporters	E	Amino acid transport and metabolism
COG4763	Predicted membrane protein	S	Function unknown
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG3957	Phosphoketolase	G	Carbohydrate transport and metabolism
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG1846	Transcriptional regulators	K	Transcription
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0492	Thioredoxin reductase	O	Posttranslational modification, protein turnover, chaperones
COG1309	Transcriptional regulator	K	Transcription
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
COG0583	Transcriptional regulator	K	Transcription
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG1946	Acyl-CoA thioesterase	I	Lipid transport and metabolism
COG1475	Predicted transcriptional regulators	K	Transcription
COG1475	Predicted transcriptional regulators	K	Transcription
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
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG5616	Predicted integral membrane protein	S	Function unknown
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2128	Uncharacterized conserved protein	S	Function unknown
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0412	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1231	Monoamine oxidase	E	Amino acid transport and metabolism
COG3145	Alkylated DNA repair protein	L	Replication, recombination and repair
COG0863	DNA modification methylase	L	Replication, recombination and repair
COG1842	Phage shock protein A (IM30), suppresses sigma54-dependent transcription	K	Transcription
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
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
COG0412	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3502	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0730	Predicted permeases	R	General function prediction only
COG4297	Uncharacterized protein containing double-stranded beta helix domain	S	Function unknown
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
COG0640	Predicted transcriptional regulators	K	Transcription
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG4119	Predicted NTP pyrophosphohydrolase	L	Replication, recombination and repair
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG2159	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG3653	N-acyl-D-aspartate/D-glutamate deacylase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0779	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2124	Cytochrome P450	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4783	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
COG3795	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1359	Uncharacterized conserved protein	S	Function unknown
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0225	Peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG1733	Predicted transcriptional regulators	K	Transcription
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG2124	Cytochrome P450	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1317	Flagellar biosynthesis/type III secretory pathway protein	N	Cell motility
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
COG1080	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	G	Carbohydrate transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG0637	Predicted phosphatase/phosphohexomutase	R	General function prediction only
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG1794	Aspartate racemase	M	Cell wall/membrane/envelope biogenesis
COG1414	Transcriptional regulator	K	Transcription
COG1414	Transcriptional regulator	K	Transcription

COG0427	Acetyl-CoA hydrolase	C	Energy production and conversion
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG3832	Uncharacterized conserved protein	S	Function unknown
COG0640	Predicted transcriptional regulators	K	Transcription
COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	C	Energy production and conversion
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG3801	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	E	Amino acid transport and metabolism
COG3823	Glutamine cyclotransferase	O	Posttranslational modification, protein turnover, chaperones
COG2142	Succinate dehydrogenase, hydrophobic anchor subunit	C	Energy production and conversion
COG0421	Spermidine synthase	E	Amino acid transport and metabolism
COG2009	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit	C	Energy production and conversion
COG4882	Predicted aminopeptidase, Iap family	R	General function prediction only
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG1732	Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)	M	Cell wall/membrane/envelope biogenesis
COG4095	Uncharacterized conserved protein	S	Function unknown
COG3509	Poly(3-hydroxybutyrate) depolymerase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2076	Membrane transporters of cations and cationic drugs	P	Inorganic ion transport and metabolism
COG1482	Phosphomannose isomerase	G	Carbohydrate transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG1793	ATP-dependent DNA ligase	L	Replication, recombination and repair
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
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
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
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG1309	Transcriptional regulator	K	Transcription
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG2010	Cytochrome c, mono- and diheme variants	C	Energy production and conversion
COG0835	Chemotaxis signal transduction protein	N	Cell motility
COG1352	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
COG2201	Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain	N	Cell motility
COG3552	Protein containing von Willebrand factor type A (vWA) domain	R	General function prediction only
COG1893	Ketopantoate reductase	H	Coenzyme transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	C	Energy production and conversion
COG0367	Asparagine synthase (glutamine-hydrolyzing)	E	Amino acid transport and metabolism
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1083	CMP-N-acetylneuraminic acid synthetase	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
COG1942	Uncharacterized protein, 4-oxalocrotonate tautomerase homolog	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
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG4957	Predicted transcriptional regulator	K	Transcription
COG1261	Flagellar basal body P-ring biosynthesis protein	N	Cell motility
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
COG1349	Transcriptional regulators of sugar metabolism	K	Transcription
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1813	Predicted transcription factor, homolog of eukaryotic MBF1	K	Transcription
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2110	Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	R	General function prediction only
COG2128	Uncharacterized conserved protein	S	Function unknown
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
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
COG0388	Predicted amidohydrolase	R	General function prediction only
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG2863	Cytochrome c553	C	Energy production and conversion
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1214	Inactive homolog of metal-dependent proteases, putative molecular chaperone	O	Posttranslational modification, protein turnover, chaperones
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain	R	General function prediction only
COG2173	D-alanyl-D-alanine dipeptidase	M	Cell wall/membrane/envelope biogenesis
COG1309	Transcriptional regulator	K	Transcription
COG0707	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase	M	Cell wall/membrane/envelope biogenesis
COG3746	Phosphate-selective porin	P	Inorganic ion transport and metabolism
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon	R	General function prediction only
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG3602	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
COG4275	Uncharacterized conserved protein	S	Function unknown

COG0789	Predicted transcriptional regulators	K	Transcription
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG2421	Predicted acetamidase/formamidase	C	Energy production and conversion
COG1309	Transcriptional regulator	K	Transcription
COG3327	Phenylacetic acid-responsive transcriptional repressor	K	Transcription
COG3293	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG1030	Membrane-bound serine protease (ClpP class)	O	Posttranslational modification, protein turnover, chaperones
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG4857	Predicted kinase	R	General function prediction only
COG1344	Flagellin and related hook-associated proteins	N	Cell motility
COG1256	Flagellar hook-associated protein	N	Cell motility
COG0589	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
COG3798	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1178	ABC-type Fe3+ transport system, permease component	P	Inorganic ion transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1940	Transcriptional regulator/sugar kinase	K	Transcription
COG1562	Phytoene/squalene synthetase	I	Lipid transport and metabolism
COG1826	Sec-independent protein secretion pathway components	U	Intracellular trafficking, secretion, and vesicular transport
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0560	Phosphoserine phosphatase	E	Amino acid transport and metabolism
COG0392	Predicted integral membrane protein	S	Function unknown
COG2261	Predicted membrane protein	S	Function unknown
COG3910	Predicted ATPase	R	General function prediction only
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0406	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG2086	Electron transfer flavoprotein, beta subunit	C	Energy production and conversion
COG1391	Glutamine synthetase adenylyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG2268	Uncharacterized protein conserved in bacteria	S	Function unknown
COG5490	Uncharacterized conserved protein	S	Function unknown
COG0583	Transcriptional regulator	K	Transcription
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG2962	Predicted permeases	R	General function prediction only
COG2365	Protein tyrosine/serine phosphatase	T	Signal transduction mechanisms
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG5006	Predicted permease, DMT superfamily	R	General function prediction only
COG1309	Transcriptional regulator	K	Transcription
COG4122	Predicted O-methyltransferase	R	General function prediction only
COG3492	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
COG0431	Predicted flavoprotein	R	General function prediction only
COG0778	Nitroreductase	C	Energy production and conversion
COG3174	Predicted membrane protein	S	Function unknown
COG1609	Transcriptional regulators	K	Transcription
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0520	Selenocysteine lyase	E	Amino acid transport and metabolism
COG3483	Tryptophan 2,3-dioxygenase (vermilion)	E	Amino acid transport and metabolism
COG1080	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	G	Carbohydrate transport and metabolism
COG1105	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	G	Carbohydrate transport and metabolism
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2153	Predicted acyltransferase	R	General function prediction only
COG3222	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG3239	Fatty acid desaturase	I	Lipid transport and metabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0684	Demethylmenaquinone methyltransferase	H	Coenzyme transport and metabolism
COG0289	Dihydrodipicolinate reductase	E	Amino acid transport and metabolism
COG1392	Phosphate transport regulator (distant homolog of PhoU)	P	Inorganic ion transport and metabolism
COG0071	Molecular chaperone (small heat shock protein)	O	Posttranslational modification, protein turnover, chaperones
COG3393	Predicted acetyltransferase	R	General function prediction only
COG3247	Uncharacterized conserved protein	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3616	Predicted amino acid aldolase or racemase	E	Amino acid transport and metabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG3608	Predicted deacylase	R	General function prediction only
COG0406	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
COG0803	ABC-type metal ion transport system, periplasmic component/surface adhesin	P	Inorganic ion transport and metabolism
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
COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	I	Lipid transport and metabolism
COG1121	ABC-type Mn/Zn transport systems, ATPase component	P	Inorganic ion transport and metabolism
COG2124	Cytochrome P450	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0858	Ribosome-binding factor A	J	Translation, ribosomal structure and biogenesis
COG1291	Flagellar motor component	N	Cell motility
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0684	Demethylmenaquinone methyltransferase	H	Coenzyme transport and metabolism
COG1108	ABC-type Mn2+/Zn2+ transport systems, permease components	P	Inorganic ion 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
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion

COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
COG5605	Predicted small integral membrane protein	S	Function unknown
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0583	Transcriptional regulator	K	Transcription
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	C	Energy production and conversion
COG1846	Transcriptional regulators	K	Transcription
COG5517	Small subunit of phenylpropionate dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1279	Lysine efflux permease	R	General function prediction only
COG1767	Triphosphoribosyl-dephospho-CoA synthetase	H	Coenzyme transport and metabolism
COG0777	Acetyl-CoA carboxylase beta subunit	I	Lipid transport and metabolism
COG4670	Acyl CoA:acetate/3-ketoacid CoA transferase	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1250	3-hydroxyacyl-CoA dehydrogenase	I	Lipid transport and metabolism
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG3063	Tfp pilus assembly protein PilF	N	Cell motility
COG3828	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4123	Predicted O-methyltransferase	R	General function prediction only
COG0620	Methionine synthase II (cobalamin-independent)	E	Amino acid transport and metabolism
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	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
COG0247	Fe-S oxidoreductase	C	Energy production and conversion
COG2243	Precorrin-2 methylase	H	Coenzyme transport and metabolism
COG0007	Uroporphyrinogen-III methylase	H	Coenzyme transport and metabolism
COG2073	Cobalamin biosynthesis protein CbiG	H	Coenzyme transport and metabolism
COG0582	Integrase	L	Replication, recombination and repair
COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	C	Energy production and conversion
COG1309	Transcriptional regulator	K	Transcription
COG1139	Uncharacterized conserved protein containing a ferredoxin-like domain	C	Energy production and conversion
COG4453	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
COG1432	Uncharacterized conserved protein	S	Function unknown
COG1484	DNA replication protein	L	Replication, recombination and repair
COG3328	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG1556	Uncharacterized conserved protein	S	Function unknown
COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG4922	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG3826	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Coenzyme transport and metabolism
COG2840	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1396	Predicted transcriptional regulators	K	Transcription
COG1846	Transcriptional regulators	K	Transcription
COG0038	Chloride channel protein EriC	P	Inorganic ion transport and metabolism
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
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
COG1252	NADH dehydrogenase, FAD-containing subunit	C	Energy production and conversion
COG0409	Hydrogenase maturation factor	O	Posttranslational modification, protein turnover, chaperones
COG2010	Cytochrome c, mono- and diheme variants	C	Energy production and conversion
COG0309	Hydrogenase maturation factor	O	Posttranslational modification, protein turnover, chaperones
COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase	O	Posttranslational modification, protein turnover, chaperones
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0375	Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)	R	General function prediction only
COG0680	Ni,Fe-hydrogenase maturation factor	C	Energy production and conversion
COG1969	Ni,Fe-hydrogenase I cytochrome b subunit	C	Energy production and conversion
COG1740	Ni,Fe-hydrogenase I small subunit	C	Energy production and conversion
COG0488	ATPase components of ABC transporters with duplicated ATPase domains	R	General function prediction only
COG0475	Kef-type K+ transport systems, membrane components	P	Inorganic ion transport and metabolism
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3376	High-affinity nickel permease	P	Inorganic ion transport and metabolism
COG3652	Predicted outer membrane protein	S	Function unknown
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility

COG1704	Uncharacterized conserved protein	S	Function unknown
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle control, cell division, chromosome partitioning
COG1928	Dolichyl-phosphate-mannose--protein O-mannosyl transferase	O	Posttranslational modification, protein turnover, chaperones
COG3607	Predicted lactoylglutathione lyase	R	General function prediction only
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG2807	Cyanate permease	P	Inorganic ion transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3307	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG1894	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	C	Energy production and conversion
COG1910	Periplasmic molybdate-binding protein/domain	P	Inorganic ion transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG2259	Predicted membrane protein	S	Function unknown
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG4454	Uncharacterized copper-binding protein	P	Inorganic ion transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0131	Imidazoleglycerol-phosphate dehydratase	E	Amino acid transport and metabolism
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K	Transcription
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
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG2801	Transposase and inactivated derivatives	L	Replication, recombination and repair
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
COG1605	Chorismate mutase	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
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate 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
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid 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
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG1055	Na+/H+ antiporter NhaD and related arsenite permeases	P	Inorganic ion transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG3239	Fatty acid desaturase	I	Lipid transport and metabolism
COG1541	Coenzyme F390 synthetase	H	Coenzyme transport and metabolism
COG1018	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	C	Energy production and conversion
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
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
COG1546	Uncharacterized protein (competence- and mitomycin-induced)	R	General function prediction only
COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG0681	Signal peptidase I	U	Intracellular trafficking, secretion, and vesicular transport
COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	R	General function prediction only
COG2230	Cyclopropane fatty acid synthase and related methyltransferases	M	Cell wall/membrane/envelope biogenesis
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG4804	Uncharacterized conserved protein	S	Function unknown
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
COG1529	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	C	Energy production and conversion
COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs	C	Energy production and conversion
COG1309	Transcriptional regulator	K	Transcription
COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R	General function prediction only
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG5511	Bacteriophage capsid protein	R	General function prediction only
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
COG0474	Cation transport ATPase	P	Inorganic ion transport and metabolism
COG1396	Predicted transcriptional regulators	K	Transcription
COG1426	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0730	Predicted permeases	R	General function prediction only
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG0836	Mannose-1-phosphate guanylyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3654	Prophage maintenance system killer protein	R	General function prediction only
COG4961	Flp pilus assembly protein TadG	U	Intracellular trafficking, secretion, and vesicular transport

COG4655	Predicted membrane protein	S	Function unknown
COG4988	ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components	C	Energy production and conversion
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG4446	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4178	ABC-type uncharacterized transport system, permease and ATPase components	R	General function prediction only
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG3832	Uncharacterized conserved protein	S	Function unknown
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
COG1215	Glycosyltransferases, probably involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG0398	Uncharacterized conserved protein	S	Function unknown
COG3453	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, g	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	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
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG3510	Cephalosporin hydroxylase	V	Defense mechanisms
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG4430	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3238	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1993	Uncharacterized conserved protein	S	Function unknown
COG1091	dTDP-4-dehydrorhamnose reductase	M	Cell wall/membrane/envelope biogenesis
COG4285	Uncharacterized conserved protein	S	Function unknown
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
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
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
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG2079	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
COG0372	Citrate synthase	C	Energy production and conversion
COG0773	UDP-N-acetylmuramate-alanine ligase	M	Cell wall/membrane/envelope biogenesis
COG1619	Uncharacterized proteins, homologs of microcin C7 resistance protein MccF	V	Defense mechanisms
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
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG0531	Amino acid transporters	E	Amino acid transport and metabolism
COG1246	N-acetylglutamate synthase and related acetyltransferases	E	Amino acid transport and metabolism
COG2121	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0583	Transcriptional regulator	K	Transcription
COG0250	Transcription antiterminator	K	Transcription
COG0772	Bacterial cell division membrane protein	D	Cell cycle control, cell division, chromosome partitioning
COG1017	Hemoglobin-like flavoprotein	C	Energy production and conversion
COG1878	Predicted metal-dependent hydrolase	R	General function prediction only
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG0350	Methylated DNA-protein cysteine methyltransferase	L	Replication, recombination and repair
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG3558	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1309	Transcriptional regulator	K	Transcription
COG0031	Cysteine synthase	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1230	Co/Zn/Cd efflux system component	P	Inorganic ion transport and metabolism
COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G	Carbohydrate transport and metabolism
COG1609	Transcriptional regulators	K	Transcription
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3411	Ferredoxin	C	Energy production and conversion
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG3788	Uncharacterized relative of glutathione S-transferase, MAPEG superfamily	R	General function prediction only
COG4798	Predicted methyltransferase	R	General function prediction only
COG0486	Predicted GTPase	R	General function prediction only
COG1035	Coenzyme F420-reducing hydrogenase, beta subunit	C	Energy production and conversion
COG0655	Multimeric flavodoxin WrbA	R	General function prediction only
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG3959	Transketolase, N-terminal subunit	G	Carbohydrate transport and metabolism
COG3958	Transketolase, C-terminal subunit	G	Carbohydrate transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
COG0025	NhaP-type Na+/H+ and K+/H+ antiporters	P	Inorganic ion transport and metabolism
COG1968	Uncharacterized bacitracin resistance protein	V	Defense mechanisms
COG4244	Predicted membrane protein	S	Function unknown
COG1981	Predicted membrane protein	S	Function unknown
COG3336	Predicted membrane protein	S	Function unknown
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
COG3384	Uncharacterized conserved protein	S	Function unknown
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2859	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1192	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG2234	Predicted aminopeptidases	R	General function prediction only
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
COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	C	Energy production and conversion
COG0165	Argininosuccinate lyase	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG4222	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3951	Rod binding protein	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG1466	DNA polymerase III, delta subunit	L	Replication, recombination and repair
COG3748	Predicted membrane protein	S	Function unknown
COG3677	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG3436	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG3436	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG3547	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG2211	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG1764	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG3954	Phosphoribulokinase	C	Energy production and conversion
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG1348	Nitrogenase subunit NifH (ATPase)	P	Inorganic ion transport and metabolism
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG1233	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
COG5621	Predicted secreted hydrolase	R	General function prediction only
COG0191	Fructose/tagatose bisphosphate aldolase	G	Carbohydrate transport and metabolism
COG1240	Mg-chelatase subunit ChlD	H	Coenzyme transport and metabolism
COG1239	Mg-chelatase subunit ChlI	H	Coenzyme transport and metabolism
COG0644	Dehydrogenases (flavoproteins)	C	Energy production and conversion
COG2211	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	H	Coenzyme transport and metabolism
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG1850	Ribulose 1,5-bisphosphate carboxylase, large subunit	G	Carbohydrate transport and metabolism
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG2227	2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase	H	Coenzyme transport and metabolism
COG0464	ATPases of the AAA+ class	O	Posttranslational modification, protein turnover, chaperones
COG1309	Transcriptional regulator	K	Transcription
COG0402	Cytosine deaminase and related metal-dependent hydrolases	F	Nucleotide transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG2116	Formate/nitrite family of transporters	P	Inorganic ion transport and metabolism
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
COG1794	Aspartate racemase	M	Cell wall/membrane/envelope biogenesis
COG1894	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	C	Energy production and conversion
COG1905	NADH:ubiquinone oxidoreductase 24 kD subunit	C	Energy production and conversion
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
COG1652	Uncharacterized protein containing LysM domain	S	Function unknown
COG0325	Predicted enzyme with a TIM-barrel fold	R	General function prediction only
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG3786	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0721	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit	J	Translation, ribosomal structure and biogenesis
COG3657	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3511	Phospholipase C	M	Cell wall/membrane/envelope biogenesis
COG1450	Type II secretory pathway, component PulD	N	Cell motility
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
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG5360	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4244	Predicted membrane protein	S	Function unknown
COG2133	Glucose/sorbosone dehydrogenases	G	Carbohydrate transport and metabolism
COG1521	Putative transcriptional regulator, homolog of Bvg accessory factor	K	Transcription
COG2509	Uncharacterized FAD-dependent dehydrogenases	R	General function prediction only
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
COG1994	Zn-dependent proteases	R	General function prediction only
COG1354	Uncharacterized conserved protein	S	Function unknown
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
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
COG1235	Metal-dependent hydrolases of the beta-lactamase superfamily I	R	General function prediction only
COG2391	Predicted transporter component	R	General function prediction only
COG0640	Predicted transcriptional regulators	K	Transcription
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1846	Transcriptional regulators	K	Transcription
COG1409	Predicted phosphohydrolases	R	General function prediction only
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG4132	ABC-type uncharacterized transport system, permease component	R	General function prediction only
COG1840	ABC-type Fe3+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
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
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism

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
COG4583	Sarcosine oxidase gamma subunit	E	Amino acid transport and metabolism
COG2086	Electron transfer flavoprotein, beta subunit	C	Energy production and conversion
COG2025	Electron transfer flavoprotein, alpha subunit	C	Energy production and conversion
COG0247	Fe-S oxidoreductase	C	Energy production and conversion
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG1018	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	C	Energy production and conversion
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG3119	Arylsulfatase A and related enzymes	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
COG3942	Surface antigen	R	General function prediction only
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
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
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
COG4671	Predicted glycosyl transferase	R	General function prediction only
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG1247	Sortase and related acyltransferases	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
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG4158	Predicted ABC-type sugar transport system, permease component	R	General function prediction only
COG1850	Ribulose 1,5-bisphosphate carboxylase, large subunit	G	Carbohydrate transport and metabolism
COG3395	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0287	Prephenate dehydrogenase	E	Amino acid transport and metabolism
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG4671	Predicted glycosyl transferase	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
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
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0142	Geranylgeranyl pyrophosphate synthase	H	Coenzyme transport and metabolism
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
COG0843	Heme/copper-type cytochrome/quinol oxidases, subunit 1	C	Energy production and conversion
COG1622	Heme/copper-type cytochrome/quinol oxidases, subunit 2	C	Energy production and conversion
COG3034	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3367	Uncharacterized conserved protein	S	Function unknown
COG0679	Predicted permeases	R	General function prediction only
COG4392	Predicted membrane protein	S	Function unknown
COG0530	Ca2+/Na+ antiporter	P	Inorganic ion transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG5500	Predicted integral membrane protein	S	Function unknown
COG0708	Exonuclease III	L	Replication, recombination and repair
COG1937	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1995	Pyridoxal phosphate biosynthesis protein	H	Coenzyme transport and metabolism
COG3395	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1349	Transcriptional regulators of sugar metabolism	K	Transcription
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG2844	UTP:GlnB (protein PII) uridylyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG3195	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2351	Transthyretin-like protein	R	General function prediction only
COG2820	Uridine phosphorylase	F	Nucleotide transport and metabolism
COG1846	Transcriptional regulators	K	Transcription
COG0583	Transcriptional regulator	K	Transcription
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
COG0583	Transcriptional regulator	K	Transcription
COG2071	Predicted glutamine amidotransferases	R	General function prediction only
COG0582	Integrase	L	Replication, recombination and repair
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG1862	Preprotein translocase subunit YajC	U	Intracellular trafficking, secretion, and vesicular transport
COG1647	Esterase/lipase	R	General function prediction only
COG0141	Histidinol dehydrogenase	E	Amino acid transport and metabolism
COG2607	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	E	Amino acid transport and metabolism
COG0811	Biopolymer transport proteins	U	Intracellular trafficking, secretion, and vesicular transport
COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase	E	Amino acid transport and metabolism
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
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase	R	General function prediction only
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
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG3744	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	R	General function prediction only
COG1309	Transcriptional regulator	K	Transcription
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
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
COG5598	Trimethylamine:corrinoid methyltransferase	H	Coenzyme transport and metabolism
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
COG0778	Nitroreductase	C	Energy production and conversion
COG2831	Hemolysin activation/secretion protein	U	Intracellular trafficking, secretion, and vesicular transport
COG0006	Xaa-Pro aminopeptidase	E	Amino acid 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
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG0415	Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	H	Coenzyme transport and metabolism
COG3239	Fatty acid desaturase	I	Lipid transport and metabolism
COG3238	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2828	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1802	Transcriptional regulators	K	Transcription
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG4989	Predicted oxidoreductase	R	General function prediction only
COG2079	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0473	Isocitrate/isopropylmalate dehydrogenase	C	Energy production and conversion
COG0561	Predicted hydrolases of the HAD superfamily	R	General function prediction only
COG1023	Predicted 6-phosphogluconate dehydrogenase	G	Carbohydrate transport and metabolism
COG0176	Transaldolase	G	Carbohydrate transport and metabolism
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
COG0434	Predicted TIM-barrel enzyme	R	General function prediction only
COG2039	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	O	Posttranslational modification, protein turnover, chaperones
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG1215	Glycosyltransferases, probably involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG2323	Predicted membrane protein	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3307	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG3176	Putative hemolysin	R	General function prediction only
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
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
COG5343	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	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
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG4158	Predicted ABC-type sugar transport system, permease component	R	General function prediction only
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0122	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	L	Replication, recombination and repair
COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase	E	Amino acid transport and metabolism
COG3284	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0459	Chaperonin GroEL (HSP60 family)	O	Posttranslational modification, protein turnover, chaperones
COG2844	UTP:GlnB (protein PII) uridylyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0069	Glutamate synthase domain 2	E	Amino acid transport and metabolism
COG4321	Uncharacterized protein related to arylsulfate sulfotransferase involved in siderophore biosynthesis	R	General function prediction only
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG3118	Thioredoxin domain-containing protein	O	Posttranslational modification, protein turnover, chaperones
COG1252	NADH dehydrogenase, FAD-containing subunit	C	Energy production and conversion
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0841	Cation/multidrug efflux pump	V	Defense mechanisms
COG0651	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	C	Energy production and conversion
COG0650	Formate hydrogenlyase subunit 4	C	Energy production and conversion
COG4237	Hydrogenase 4 membrane component (E)	C	Energy production and conversion
COG3653	N-acyl-D-aspartate/D-glutamate deacylase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3261	Ni,Fe-hydrogenase III large subunit	C	Energy production and conversion
COG3260	Ni,Fe-hydrogenase III small subunit	C	Energy production and conversion
COG1309	Transcriptional regulator	K	Transcription
COG3822	ABC-type sugar transport system, auxiliary component	R	General function prediction only
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis

COG5006	Predicted permease, DMT superfamily	R	General function prediction only
COG3431	Predicted membrane protein	S	Function unknown
COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E	Amino acid transport and metabolism
COG1252	NADH dehydrogenase, FAD-containing subunit	C	Energy production and conversion
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG2421	Predicted acetamidase/formamidase	C	Energy production and conversion
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG4123	Predicted O-methyltransferase	R	General function prediction only
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG0591	Na+/proline symporter	E	Amino acid transport and metabolism
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
COG0863	DNA modification methylase	L	Replication, recombination and repair
COG3893	Inactivated superfamily I helicase	L	Replication, recombination and repair
COG1074	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	L	Replication, recombination and repair
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2936	Predicted acyl esterases	R	General function prediction only
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0558	Phosphatidylglycerophosphate synthase	I	Lipid transport and metabolism
COG2808	Transcriptional regulator	K	Transcription
COG0337	3-dehydroquinate synthetase	E	Amino acid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1419	Flagellar GTP-binding protein	N	Cell motility
COG2128	Uncharacterized conserved protein	S	Function unknown
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
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG4340	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0792	Predicted endonuclease distantly related to archaeal Holliday junction resolvase	L	Replication, recombination and repair
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
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
COG2912	Uncharacterized conserved protein	S	Function unknown
COG1194	A/G-specific DNA glycosylase	L	Replication, recombination and repair
COG4391	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1359	Uncharacterized conserved protein	S	Function unknown
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG3818	Predicted acetyltransferase, GNAT superfamily	R	General function prediction only
COG1733	Predicted transcriptional regulators	K	Transcription
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1345	Flagellar capping protein	N	Cell motility
COG0262	Dihydrofolate reductase	H	Coenzyme transport and metabolism
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG5285	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
COG4091	Predicted homoserine dehydrogenase	E	Amino acid transport and metabolism
COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases	H	Coenzyme transport and metabolism
COG2020	Putative protein-S-isoprenylcysteine methyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG4928	Predicted P-loop ATPase	R	General function prediction only
COG4993	Glucose dehydrogenase	G	Carbohydrate transport and metabolism
COG0127	Xanthosine triphosphate pyrophosphatase	F	Nucleotide transport and metabolism
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG3226	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0689	RNase PH	J	Translation, ribosomal structure and biogenesis
COG2181	Nitrate reductase gamma subunit	C	Energy production and conversion
COG0760	Parvulin-like peptidyl-prolyl isomerase	O	Posttranslational modification, protein turnover, chaperones
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
COG1609	Transcriptional regulators	K	Transcription
COG0607	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG4240	Predicted kinase	R	General function prediction only
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1420	Transcriptional regulator of heat shock gene	K	Transcription
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
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
COG2199	FOG: GGDEF domain	T	Signal transduction mechanisms
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
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
COG1232	Protoporphyrinogen oxidase	H	Coenzyme transport and metabolism
COG2211	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T	Signal transduction mechanisms
COG1294	Cytochrome bd-type quinol oxidase, subunit 2	C	Energy production and conversion
COG1271	Cytochrome bd-type quinol oxidase, subunit 1	C	Energy production and conversion
COG4987	ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components	C	Energy production and conversion
COG1765	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones

COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R	General function prediction only
COG2764	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG5469	Predicted metal-binding protein	S	Function unknown
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
COG2390	Transcriptional regulator, contains sigma factor-related N-terminal domain	K	Transcription
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
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid 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
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG0859	ADP-heptose:LPS heptosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG4547	Cobalamin biosynthesis protein CobT (nicotinate-mononucleotide:5, 6-dimethylbenzimidazole phosphoribosyltransferase)	H	Coenzyme transport and metabolism
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG1446	Asparaginase	E	Amino acid 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
COG1514	2'-5' RNA ligase	J	Translation, ribosomal structure and biogenesis
COG3046	Uncharacterized protein related to deoxyribodipyrimidine photolyase	R	General function prediction only
COG2062	Phosphohistidine phosphatase SixA	T	Signal transduction mechanisms
COG0640	Predicted transcriptional regulators	K	Transcription
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0702	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2188	Transcriptional regulators	K	Transcription
COG0393	Uncharacterized conserved protein	S	Function unknown
COG0347	Nitrogen regulatory protein PII	E	Amino acid transport and metabolism
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG3819	Predicted membrane protein	S	Function unknown
COG3817	Predicted membrane protein	S	Function unknown
COG0558	Phosphatidylglycerophosphate synthase	I	Lipid transport and metabolism
COG1213	Predicted sugar nucleotidyltransferases	M	Cell wall/membrane/envelope biogenesis
COG4585	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
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
COG0330	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification, protein turnover, chaperones
COG0177	Predicted EndoIII-related endonuclease	L	Replication, recombination and repair
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0824	Predicted thioesterase	R	General function prediction only
COG3247	Uncharacterized conserved protein	S	Function unknown
COG1131	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
COG0842	ABC-type multidrug transport system, permease component	V	Defense mechanisms
COG1151	6Fe-6S prismane cluster-containing protein	C	Energy production and conversion
COG4101	Predicted mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG5653	Protein involved in cellulose biosynthesis (CelD)	M	Cell wall/membrane/envelope biogenesis
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
COG0824	Predicted thioesterase	R	General function prediction only
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG3217	Uncharacterized Fe-S protein	R	General function prediction only
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG2854	ABC-type transport system involved in resistance to organic solvents, auxiliary component	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1032	Fe-S oxidoreductase	C	Energy production and conversion
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG3394	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2846	Regulator of cell morphogenesis and NO signaling	D	Cell cycle control, cell division, chromosome partitioning
COG2057	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit	I	Lipid transport and metabolism
COG1788	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit	I	Lipid transport and metabolism
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG3485	Protocatechuate 3,4-dioxygenase beta subunit	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3485	Protocatechuate 3,4-dioxygenase beta subunit	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG3618	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG1312	D-mannonate dehydratase	G	Carbohydrate transport and metabolism

COG0246	Mannitol-1-phosphate/altronate dehydrogenases	G	Carbohydrate transport and metabolism
COG2721	Altronate dehydratase	G	Carbohydrate transport and metabolism
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG2236	Predicted phosphoribosyltransferases	R	General function prediction only
COG1629	Outer membrane receptor proteins, mostly Fe transport	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
COG2095	Multiple antibiotic transporter	U	Intracellular trafficking, secretion, and vesicular transport
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0790	FOG: TPR repeat, SEL1 subfamily	R	General function prediction only
COG1091	dTDP-4-dehydrorhamnose reductase	M	Cell wall/membrane/envelope biogenesis
COG1546	Uncharacterized protein (competence- and mitomycin-induced)	R	General function prediction only
COG2947	Uncharacterized conserved protein	S	Function unknown
COG0308	Aminopeptidase N	E	Amino acid transport and metabolism
COG3788	Uncharacterized relative of glutathione S-transferase, MAPEG superfamily	R	General function prediction only
COG3685	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1748	Saccharopine dehydrogenase and related proteins	E	Amino acid transport and metabolism
COG3714	Predicted membrane protein	S	Function unknown
COG4573	Predicted tagatose 6-phosphate kinase	G	Carbohydrate transport and metabolism
COG3461	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
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG3806	Anti-sigma factor	T	Signal transduction mechanisms
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG4214	ABC-type xylose transport system, permease component	G	Carbohydrate transport and metabolism
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG4213	ABC-type xylose transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	C	Energy production and conversion
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG2944	Predicted transcriptional regulator	K	Transcription
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG3576	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase	R	General function prediction only
COG0714	MoxR-like ATPases	R	General function prediction only
COG2064	Flp pilus assembly protein TadC	N	Cell motility
COG4962	Flp pilus assembly protein, ATPase CpaF	U	Intracellular trafficking, secretion, and vesicular transport
COG4852	Predicted membrane protein	S	Function unknown
COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG5000	Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation	T	Signal transduction mechanisms
COG2366	Protein related to penicillin acylase	R	General function prediction only
COG2224	Isocitrate lyase	C	Energy production and conversion
COG1294	Cytochrome bd-type quinol oxidase, subunit 2	C	Energy production and conversion
COG1271	Cytochrome bd-type quinol oxidase, subunit 1	C	Energy production and conversion
COG1510	Predicted transcriptional regulators	K	Transcription
COG3781	Predicted membrane protein	S	Function unknown
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	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
COG2733	Predicted membrane protein	S	Function unknown
COG1723	Uncharacterized conserved protein	S	Function unknown
COG1926	Predicted phosphoribosyltransferases	R	General function prediction only
COG5502	Uncharacterized conserved protein	S	Function unknown
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
COG0492	Thioredoxin reductase	O	Posttranslational modification, protein turnover, chaperones
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG3628	Phage baseplate assembly protein W	R	General function prediction only
COG3176	Putative hemolysin	R	General function prediction only
COG3522	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2831	Hemolysin activation/secretion protein	U	Intracellular trafficking, secretion, and vesicular transport
COG1848	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG2962	Predicted permeases	R	General function prediction only
COG3173	Predicted aminoglycoside phosphotransferase	R	General function prediction only
COG1113	Gamma-aminobutyrate permease and related permeases	E	Amino acid transport and metabolism
COG5135	Uncharacterized conserved protein	S	Function unknown
COG3173	Predicted aminoglycoside phosphotransferase	R	General function prediction only
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0668	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
COG3898	Uncharacterized membrane-bound protein	S	Function unknown
COG1987	Flagellar biosynthesis pathway, component FliQ	N	Cell motility
COG3279	Response regulator of the LytR/AlgR family	K	Transcription
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG4828	Predicted membrane protein	S	Function unknown
COG4583	Sarcosine oxidase gamma subunit	E	Amino acid transport and metabolism
COG0740	Protease subunit of ATP-dependent Clp proteases	O	Posttranslational modification, protein turnover, chaperones
COG0583	Transcriptional regulator	K	Transcription
COG1802	Transcriptional regulators	K	Transcription
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	I	Lipid transport and metabolism
COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs	C	Energy production and conversion

COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3865	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1309	Transcriptional regulator	K	Transcription
COG5649	Uncharacterized conserved protein	S	Function unknown
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	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), glyoxylate carbolig	E	Amino acid transport and metabolism
COG5483	Uncharacterized conserved protein	S	Function unknown
COG1414	Transcriptional regulator	K	Transcription
COG4553	Poly-beta-hydroxyalkanoate depolymerase	I	Lipid 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
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	E	Amino acid transport and metabolism
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1794	Aspartate racemase	M	Cell wall/membrane/envelope biogenesis
COG1171	Threonine dehydratase	E	Amino acid transport and metabolism
COG1414	Transcriptional regulator	K	Transcription
COG1846	Transcriptional regulators	K	Transcription
COG5394	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3772	Phage-related lysozyme (muraminidase)	R	General function prediction only
COG0730	Predicted permeases	R	General function prediction only
COG3243	Poly(3-hydroxyalkanoate) synthetase	I	Lipid transport and metabolism
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG1788	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit	I	Lipid transport and metabolism
COG2057	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit	I	Lipid transport and metabolism
COG0160	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
COG4269	Predicted membrane protein	S	Function unknown
COG4551	Predicted protein tyrosine phosphatase	R	General function prediction only
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
COG4973	Site-specific recombinase XerC	L	Replication, recombination and repair
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
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG1719	Predicted hydrocarbon binding protein (contains V4R domain)	R	General function prediction only
COG1032	Fe-S oxidoreductase	C	Energy production and conversion
COG3293	Transposase and inactivated derivatives	L	Replication, recombination and repair
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
COG4683	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3718	Uncharacterized enzyme involved in inositol metabolism	G	Carbohydrate transport and metabolism
COG3892	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG4130	Predicted sugar epimerase	G	Carbohydrate transport and metabolism
COG1609	Transcriptional regulators	K	Transcription
COG1858	Cytochrome c peroxidase	P	Inorganic ion transport and metabolism
COG3547	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG1737	Transcriptional regulators	K	Transcription
COG5516	Conserved protein containing a Zn-ribbon-like motif, possibly RNA-binding	R	General function prediction only
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
COG3002	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG5267	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4102	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
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
COG4420	Predicted membrane protein	S	Function unknown
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG0349	Ribonuclease D	J	Translation, ribosomal structure and biogenesis
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG1230	Co/Zn/Cd efflux system component	P	Inorganic ion transport and metabolism
COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	G	Carbohydrate transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG0578	Glycerol-3-phosphate dehydrogenase	C	Energy production and conversion
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG1569	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG0174	Glutamine synthetase	E	Amino acid transport and metabolism
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG4680	Uncharacterized protein conserved in bacteria	S	Function unknown

COG2927	DNA polymerase III, chi subunit	L	Replication, recombination and repair
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG2081	Predicted flavoproteins	R	General function prediction only
COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	M	Cell wall/membrane/envelope biogenesis
COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member	L	Replication, recombination and repair
COG0582	Integrase	L	Replication, recombination and repair
COG3395	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport and metabolism
COG2856	Predicted Zn peptidase	E	Amino acid transport and metabolism
COG4231	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	C	Energy production and conversion
COG3180	Putative ammonia monooxygenase	R	General function prediction only
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG2138	Uncharacterized conserved protein	S	Function unknown
COG4589	Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase	R	General function prediction only
COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	I	Lipid transport and metabolism
COG2863	Cytochrome c553	C	Energy production and conversion
COG3019	Predicted metal-binding protein	R	General function prediction only
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
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG3513	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1518	Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair
COG3512	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1539	Dihydroneopterin aldolase	H	Coenzyme transport and metabolism
COG1914	Mn2+ and Fe2+ transporters of the NRAMP family	P	Inorganic ion transport and metabolism
COG2200	FOG: EAL domain	T	Signal transduction mechanisms
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG0586	Uncharacterized membrane-associated protein	S	Function unknown
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG2890	Methylase of polypeptide chain release factors	J	Translation, ribosomal structure and biogenesis
COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	H	Coenzyme 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
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG0394	Protein-tyrosine-phosphatase	T	Signal transduction mechanisms
COG0586	Uncharacterized membrane-associated protein	S	Function unknown
COG0647	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid 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
COG3839	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
COG1070	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG3347	Uncharacterized conserved protein	S	Function unknown
COG0395	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
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
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG3777	Uncharacterized conserved protein	S	Function unknown
COG2030	Acyl dehydratase	I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1124	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate 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
COG3386	Gluconolactonase	G	Carbohydrate transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate 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
COG3396	Uncharacterized conserved protein	S	Function unknown
COG3460	Uncharacterized enzyme of phenylacetate metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3396	Uncharacterized conserved protein	S	Function unknown
COG2151	Predicted metal-sulfur cluster biosynthetic enzyme	R	General function prediction only
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG3769	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG2129	Predicted phosphoesterases, related to the Icc protein	R	General function prediction only
COG2376	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
COG5010	Flp pilus assembly protein TadD, contains TPR repeats	U	Intracellular trafficking, secretion, and vesicular transport
COG0760	Parvulin-like peptidyl-prolyl isomerase	O	Posttranslational modification, protein turnover, chaperones
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
COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R	General function prediction only
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

COG0647	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
COG3302	DMSO reductase anchor subunit	R	General function prediction only
COG0437	Fe-S-cluster-containing hydrogenase components 1	C	Energy production and conversion
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production and conversion
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG0076	Glutamate decarboxylase and related PLP-dependent proteins	E	Amino acid transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG1189	Predicted rRNA methylase	J	Translation, ribosomal structure and biogenesis
COG2020	Putative protein-S-isoprenylcysteine methyltransferase	O	Posttranslational modification, protein turnover, chaperones
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1734	DnaK suppressor protein	T	Signal transduction mechanisms
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
COG1321	Mn-dependent transcriptional regulator	K	Transcription
COG1652	Uncharacterized protein containing LysM domain	S	Function unknown
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
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG0229	Conserved domain frequently associated with peptide methionine sulfoxide reductase	O	Posttranslational modification, protein turnover, chaperones
COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
COG0141	Histidinol dehydrogenase	E	Amino acid transport and metabolism
COG0040	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1366	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)	T	Signal transduction mechanisms
COG3703	Uncharacterized protein involved in cation transport	P	Inorganic ion transport and metabolism
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
COG3573	Predicted oxidoreductase	R	General function prediction only
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG3455	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG1175	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
COG4770	Acetyl/propionyl-CoA carboxylase, alpha subunit	I	Lipid transport and metabolism
COG3665	Uncharacterized conserved protein	S	Function unknown
COG3665	Uncharacterized conserved protein	S	Function unknown
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG4705	Uncharacterized membrane-anchored protein conserved in bacteria	S	Function unknown
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG0015	Adenylosuccinate lyase	F	Nucleotide transport and metabolism
COG3682	Predicted transcriptional regulator	K	Transcription
COG0073	EMAP domain	R	General function prediction only
COG0535	Predicted Fe-S oxidoreductases	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
COG3970	Fumarylacetoacetate (FAA) hydrolase family protein	R	General function prediction only
COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG0489	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG3246	Uncharacterized conserved protein	S	Function unknown
COG1250	3-hydroxyacyl-CoA dehydrogenase	I	Lipid transport and metabolism
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG4783	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
COG4269	Predicted membrane protein	S	Function unknown
COG1129	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
COG3613	Nucleoside 2-deoxyribosyltransferase	F	Nucleotide transport and metabolism
COG4147	Predicted symporter	R	General function prediction only
COG3791	Uncharacterized conserved protein	S	Function unknown
COG1062	Zn-dependent alcohol dehydrogenases, class III	C	Energy production and conversion
COG4772	Outer membrane receptor for Fe3+-dicitrate	P	Inorganic ion transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG0369	Sulfite reductase, alpha subunit (flavoprotein)	P	Inorganic ion transport and metabolism
COG1522	Transcriptional regulators	K	Transcription
COG3752	Predicted membrane protein	S	Function unknown
COG2230	Cyclopropane fatty acid synthase and related methyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0640	Predicted transcriptional regulators	K	Transcription
COG1055	Na+/H+ antiporter NhaD and related arsenite permeases	P	Inorganic ion transport and metabolism
COG2079	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
COG0655	Multimeric flavodoxin WrbA	R	General function prediction only
COG2919	Septum formation initiator	D	Cell cycle control, cell division, chromosome partitioning
COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
COG2008	Threonine aldolase	E	Amino acid transport and metabolism
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG5309	Exo-beta-1,3-glucanase	G	Carbohydrate transport and metabolism
COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair	L	Replication, recombination and repair
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG0331	(acyl-carrier-protein) S-malonyltransferase	I	Lipid transport and metabolism
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG3185	4-hydroxyphenylpyruvate dioxygenase and related hemolysins	E	Amino acid transport and metabolism

COG2863	Cytochrome c553	C	Energy production and conversion
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
COG5579	Uncharacterized conserved protein	S	Function unknown
COG4154	Fucose dissimilation pathway protein FucU	G	Carbohydrate transport and metabolism
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG3791	Uncharacterized conserved protein	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG3624	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG3625	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG3627	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG4107	ABC-type phosphonate transport system, ATPase component	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
COG3709	Uncharacterized component of phosphonate metabolism	P	Inorganic ion transport and metabolism
COG2188	Transcriptional regulators	K	Transcription
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG3631	Ketosteroid isomerase-related protein	R	General function prediction only
COG2130	Putative NADP-dependent oxidoreductases	R	General function prediction only
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
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
COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	H	Coenzyme transport and metabolism
COG2510	Predicted membrane protein	S	Function unknown
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
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
COG0687	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG0642	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG3307	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1596	Periplasmic protein involved in polysaccharide export	M	Cell wall/membrane/envelope biogenesis
COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG0489	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG3267	Type II secretory pathway, component ExeA (predicted ATPase)	U	Intracellular trafficking, secretion, and vesicular transport
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG5653	Protein involved in cellulose biosynthesis (CelD)	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG4961	Flp pilus assembly protein TadG	U	Intracellular trafficking, secretion, and vesicular transport
COG3254	Uncharacterized conserved protein	S	Function unknown
COG0520	Selenocysteine lyase	E	Amino acid transport and metabolism
COG1002	Type II restriction enzyme, methylase subunits	V	Defense mechanisms
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1349	Transcriptional regulators of sugar metabolism	K	Transcription
COG4952	Predicted sugar isomerase	M	Cell wall/membrane/envelope biogenesis
COG3347	Uncharacterized conserved protein	S	Function unknown
COG2041	Sulfite oxidase and related enzymes	R	General function prediction only
COG4117	Thiosulfate reductase cytochrome B subunit (membrane anchoring protein)	C	Energy production and conversion
COG1225	Peroxiredoxin	O	Posttranslational modification, protein turnover, chaperones
COG0583	Transcriptional regulator	K	Transcription
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG1529	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	C	Energy production and conversion
COG1846	Transcriptional regulators	K	Transcription
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG0160	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG0527	Aspartokinases	E	Amino acid transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0861	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0633	Ferredoxin	C	Energy production and conversion
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG3243	Poly(3-hydroxyalkanoate) synthetase	I	Lipid transport and metabolism
COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
COG1309	Transcriptional regulator	K	Transcription
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
COG2186	Transcriptional regulators	K	Transcription
COG3258	Cytochrome c	C	Energy production and conversion
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG3439	Uncharacterized conserved protein	S	Function unknown
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0039	Malate/lactate dehydrogenases	C	Energy production and conversion
COG2137	Uncharacterized protein conserved in bacteria	R	General function prediction only
COG3157	Hemolysin-coregulated protein (uncharacterized)	S	Function unknown

COG0542	ATPases with chaperone activity, ATP-binding subunit	O	Posttranslational modification, protein turnover, chaperones
COG3515	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3517	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3516	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4455	Protein of avirulence locus involved in temperature-dependent protein secretion	R	General function prediction only
COG3518	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3519	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3520	Uncharacterized protein conserved in bacteria	S	Function unknown
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
COG1309	Transcriptional regulator	K	Transcription
COG2764	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4206	Outer membrane cobalamin receptor protein	H	Coenzyme transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG3531	Predicted protein-disulfide isomerase	O	Posttranslational modification, protein turnover, chaperones
COG0520	Selenocysteine lyase	E	Amino acid transport and metabolism
COG1748	Saccharopine dehydrogenase and related proteins	E	Amino acid transport and metabolism
COG0464	ATPases of the AAA+ class	O	Posttranslational modification, protein turnover, chaperones
COG4372	Uncharacterized protein conserved in bacteria with the myosin-like domain	S	Function unknown
COG2175	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0031	Cysteine synthase	E	Amino acid transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG2453	Predicted protein-tyrosine phosphatase	T	Signal transduction mechanisms
COG3524	Capsule polysaccharide export protein	M	Cell wall/membrane/envelope biogenesis
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
COG5006	Predicted permease, DMT superfamily	R	General function prediction only
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0145	N-methylhydantoinase A/acetone carboxylase, beta subunit	E	Amino acid transport and metabolism
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2144	Selenophosphate synthetase-related proteins	R	General function prediction only
COG2516	Biotin synthase-related enzyme	R	General function prediction only
COG0388	Predicted amidohydrolase	R	General function prediction only
COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	E	Amino acid transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0281	Malic enzyme	C	Energy production and conversion
COG2985	Predicted permease	R	General function prediction only
COG0679	Predicted permeases	R	General function prediction only
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG0583	Transcriptional regulator	K	Transcription
COG0582	Integrase	L	Replication, recombination and repair
COG3448	CBS-domain-containing membrane protein	T	Signal transduction mechanisms
COG3247	Uncharacterized conserved protein	S	Function unknown
COG0406	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
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
COG0076	Glutamate decarboxylase and related PLP-dependent proteins	E	Amino acid transport and metabolism
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG5631	Predicted transcription regulator, contains HTH domain (MarR family)	K	Transcription
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG4123	Predicted O-methyltransferase	R	General function prediction only
COG4773	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	P	Inorganic ion transport and metabolism
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG1737	Transcriptional regulators	K	Transcription
COG0474	Cation transport ATPase	P	Inorganic ion transport and metabolism
COG4191	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)	E	Amino acid transport and metabolism
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG3342	Uncharacterized conserved protein	S	Function unknown
COG0760	Parvulin-like peptidyl-prolyl isomerase	O	Posttranslational modification, protein turnover, chaperones
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism	T	Signal transduction mechanisms
COG1051	ADP-ribose pyrophosphatase	F	Nucleotide transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2199	FOG: GGDEF domain	T	Signal transduction mechanisms
COG1309	Transcriptional regulator	K	Transcription
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG0153	Galactokinase	G	Carbohydrate transport and metabolism
COG1085	Galactose-1-phosphate uridylyltransferase	C	Energy production and conversion
COG0334	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0471	Di- and tricarboxylate transporters	P	Inorganic ion transport and metabolism
COG0666	FOG: Ankyrin repeat	R	General function prediction only
COG2515	1-aminocyclopropane-1-carboxylate deaminase	E	Amino acid transport and metabolism
COG2085	Predicted dinucleotide-binding enzymes	R	General function prediction only
COG0791	Cell wall-associated hydrolases (invasion-associated proteins)	M	Cell wall/membrane/envelope biogenesis
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K	Transcription
COG4150	ABC-type sulfate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG0019	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism

COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG0189	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism
COG4094	Predicted membrane protein	S	Function unknown
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
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
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG0027	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)	F	Nucleotide transport and metabolism
COG1268	Uncharacterized conserved protein	R	General function prediction only
COG3677	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG3121	P pilus assembly protein, chaperone PapD	N	Cell motility
COG5319	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3757	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)	M	Cell wall/membrane/envelope biogenesis
COG1192	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
COG3162	Predicted membrane protein	S	Function unknown
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG4147	Predicted symporter	R	General function prediction only
COG3467	Predicted flavin-nucleotide-binding protein	R	General function prediction only
COG2905	Predicted signal-transduction protein containing cAMP-binding and CBS domains	T	Signal transduction mechanisms
COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R	General function prediction only
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
COG2013	Uncharacterized conserved protein	S	Function unknown
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG1733	Predicted transcriptional regulators	K	Transcription
COG2910	Putative NADH-flavin reductase	R	General function prediction only
COG1664	Integral membrane protein CcmA involved in cell shape determination	M	Cell wall/membrane/envelope biogenesis
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG1846	Transcriptional regulators	K	Transcription
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
COG0520	Selenocysteine lyase	E	Amino acid transport and metabolism
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG3181	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG3588	Fructose-1,6-bisphosphate aldolase	G	Carbohydrate transport and metabolism
COG2085	Predicted dinucleotide-binding enzymes	R	General function prediction only
COG3279	Response regulator of the LytR/AlgR family	K	Transcription
COG5470	Uncharacterized conserved protein	S	Function unknown
COG3644	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4704	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle control, cell division, chromosome partitioning
COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	M	Cell wall/membrane/envelope biogenesis
COG5470	Uncharacterized conserved protein	S	Function unknown
COG2161	Antitoxin of toxin-antitoxin stability system	D	Cell cycle control, cell division, chromosome partitioning
COG3751	Predicted proline hydroxylase	O	Posttranslational modification, protein turnover, chaperones
COG1738	Uncharacterized conserved protein	S	Function unknown
COG0436	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
COG1483	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG1743	Adenine-specific DNA methylase containing a Zn-ribbon	L	Replication, recombination and repair
COG0553	Superfamily II DNA/RNA helicases, SNF2 family	K	Transcription
COG3668	Plasmid stabilization system protein	R	General function prediction only
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1878	Predicted metal-dependent hydrolase	R	General function prediction only
COG0298	Hydrogenase maturation factor	O	Posttranslational modification, protein turnover, chaperones
COG1260	Myo-inositol-1-phosphate synthase	I	Lipid transport and metabolism
COG4286	Uncharacterized conserved protein related to MYG1 family	S	Function unknown
COG3259	Coenzyme F420-reducing hydrogenase, alpha subunit	C	Energy production and conversion
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG2200	FOG: EAL domain	T	Signal transduction mechanisms
COG3143	Chemotaxis protein	N	Cell motility
COG1653	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
COG1203	Predicted helicases	R	General function prediction only
COG3649	Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair
COG1468	RecB family exonuclease	L	Replication, recombination and repair
COG1518	Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair
COG1343	Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair
COG0053	Predicted Co/Zn/Cd cation transporters	P	Inorganic ion transport and metabolism
COG1112	Superfamily I DNA and RNA helicases and helicase subunits	L	Replication, recombination and repair
COG0303	Molybdopterin biosynthesis enzyme	H	Coenzyme transport and metabolism
COG0643	Chemotaxis protein histidine kinase and related kinases	N	Cell motility
COG0835	Chemotaxis signal transduction protein	N	Cell motility
COG0303	Molybdopterin biosynthesis enzyme	H	Coenzyme transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG2855	Predicted membrane protein	S	Function unknown
COG0583	Transcriptional regulator	K	Transcription
COG1017	Hemoglobin-like flavoprotein	C	Energy production and conversion
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG2513	PEP phosphonomutase and related enzymes	G	Carbohydrate transport and metabolism
COG0405	Gamma-glutamyltransferase	E	Amino acid transport and metabolism

COG3728	Phage terminase, small subunit	L	Replication, recombination and repair
COG2837	Predicted iron-dependent peroxidase	P	Inorganic ion transport and metabolism
COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R	General function prediction only
COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
COG0283	Cytidylate kinase	F	Nucleotide transport and metabolism
COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K	Transcription
COG3616	Predicted amino acid aldolase or racemase	E	Amino acid transport and metabolism
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG1846	Transcriptional regulators	K	Transcription
COG1309	Transcriptional regulator	K	Transcription
COG5473	Predicted integral membrane protein	S	Function unknown
COG3907	PAP2 (acid phosphatase) superfamily protein	R	General function prediction only
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG0776	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
COG1414	Transcriptional regulator	K	Transcription
COG0835	Chemotaxis signal transduction protein	N	Cell motility
COG1352	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
COG0643	Chemotaxis protein histidine kinase and related kinases	N	Cell motility
COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG2610	H+/gluconate symporter and related permeases	G	Carbohydrate transport and metabolism
COG1802	Transcriptional regulators	K	Transcription
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG1609	Transcriptional regulators	K	Transcription
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1284	Uncharacterized conserved protein	S	Function unknown
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
COG4608	ABC-type oligopeptide transport system, ATPase component	E	Amino acid transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG1522	Transcriptional regulators	K	Transcription
COG1748	Saccharopine dehydrogenase and related proteins	E	Amino acid transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	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
COG3093	Plasmid maintenance system antidote protein	R	General function prediction only
COG3549	Plasmid maintenance system killer protein	R	General function prediction only
COG1741	Pirin-related protein	R	General function prediction only
COG0725	ABC-type molybdate transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2206	HD-GYP domain	T	Signal transduction mechanisms
COG4251	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	T	Signal transduction mechanisms
COG5611	Predicted nucleic-acid-binding protein, contains PIN domain	R	General function prediction only
COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	I	Lipid transport and metabolism
COG4221	Short-chain alcohol dehydrogenase of unknown specificity	R	General function prediction only
COG0558	Phosphatidylglycerophosphate synthase	I	Lipid transport and metabolism
COG1464	ABC-type metal ion transport system, periplasmic component/surface antigen	P	Inorganic ion transport and metabolism
COG0671	Membrane-associated phospholipid phosphatase	I	Lipid transport and metabolism
COG0714	MoxR-like ATPases	R	General function prediction only
COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG0778	Nitroreductase	C	Energy production and conversion
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
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
COG0583	Transcriptional regulator	K	Transcription
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
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
COG3000	Sterol desaturase	I	Lipid transport and metabolism
COG1273	Uncharacterized conserved protein	S	Function unknown
COG0517	FOG: CBS domain	R	General function prediction only
COG3285	Predicted eukaryotic-type DNA primase	L	Replication, recombination and repair
COG1280	Putative threonine efflux protein	E	Amino acid transport and metabolism
COG0337	3-dehydroquinate synthetase	E	Amino acid transport and metabolism
COG3049	Penicillin V acylase and related amidases	M	Cell wall/membrane/envelope biogenesis
COG0703	Shikimate kinase	E	Amino acid transport and metabolism
COG1974	SOS-response transcriptional repressors (RecA-mediated autopeptidases)	K	Transcription
COG2128	Uncharacterized conserved protein	S	Function unknown
COG3585	Molybdopterin-binding protein	H	Coenzyme transport and metabolism
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
COG0786	Na+/glutamate symporter	E	Amino acid transport and metabolism
COG1289	Predicted membrane protein	S	Function unknown
COG1566	Multidrug resistance efflux pump	V	Defense mechanisms
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
COG0579	Predicted dehydrogenase	R	General function prediction only
COG0523	Putative GTPases (G3E family)	R	General function prediction only
COG3618	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG2188	Transcriptional regulators	K	Transcription
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
COG5448	Uncharacterized conserved protein	S	Function unknown
COG5449	Uncharacterized conserved protein	S	Function unknown
COG5524	Bacteriorhodopsin	R	General function prediction only
COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	M	Cell wall/membrane/envelope biogenesis
COG1666	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0437	Fe-S-cluster-containing hydrogenase components 1	C	Energy production and conversion
COG0709	Selenophosphate synthase	E	Amino acid transport and metabolism
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
COG2851	H+/citrate symporter	C	Energy production and conversion
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG0218	Predicted GTPase	R	General function prediction only
COG0420	DNA repair exonuclease	L	Replication, recombination and repair
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG0759	Uncharacterized conserved protein	S	Function unknown
COG3785	Uncharacterized conserved protein	S	Function unknown
COG2301	Citrate lyase beta subunit	G	Carbohydrate transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1840	ABC-type Fe3+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
COG0594	RNase P protein component	J	Translation, ribosomal structure and biogenesis
COG1034	NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)	C	Energy production and conversion
COG3616	Predicted amino acid aldolase or racemase	E	Amino acid transport and metabolism
COG0456	Acetyltransferases	R	General function prediction only
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
COG0810	Periplasmic protein TonB, links inner and outer membranes	M	Cell wall/membrane/envelope biogenesis
COG0394	Protein-tyrosine-phosphatase	T	Signal transduction mechanisms
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
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
COG2610	H+/gluconate symporter and related permeases	G	Carbohydrate transport and metabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0583	Transcriptional regulator	K	Transcription
COG0510	Predicted choline kinase involved in LPS biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG2212	Multisubunit Na+/H+ antiporter, MnhF subunit	P	Inorganic ion transport and metabolism
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
COG3712	Fe2+-dicitrate sensor, membrane component	P	Inorganic ion transport and metabolism
COG4774	Outer membrane receptor for monomeric catechols	P	Inorganic ion transport and metabolism
COG3576	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase	R	General function prediction only
COG0463	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG1858	Cytochrome c peroxidase	P	Inorganic ion transport and metabolism
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG4977	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
COG0025	NhaP-type Na+/H+ and K+/H+ antiporters	P	Inorganic ion transport and metabolism
COG3619	Predicted membrane protein	S	Function unknown
COG4487	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0121	Predicted glutamine amidotransferase	R	General function prediction only
COG1018	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	C	Energy production and conversion
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
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1846	Transcriptional regulators	K	Transcription
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
COG3280	Maltooligosyl trehalose synthase	G	Carbohydrate transport and metabolism
COG1802	Transcriptional regulators	K	Transcription
COG0402	Cytosine deaminase and related metal-dependent hydrolases	F	Nucleotide transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG3485	Protocatechuate 3,4-dioxygenase beta subunit	Q	Secondary metabolites biosynthesis, transport and catabolism
COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis	M	Cell wall/membrane/envelope biogenesis
COG2223	Nitrate/nitrite transporter	P	Inorganic ion transport and metabolism
COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
COG2180	Nitrate reductase delta subunit	C	Energy production and conversion
COG0247	Fe-S oxidoreductase	C	Energy production and conversion
COG5615	Predicted integral membrane protein	S	Function unknown
COG0559	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG3185	4-hydroxyphenylpyruvate dioxygenase and related hemolysins	E	Amino acid transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2388	Predicted acetyltransferase	R	General function prediction only
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
COG0456	Acetyltransferases	R	General function prediction only
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
COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG1961	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG3652	Predicted outer membrane protein	S	Function unknown
COG3263	NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	P	Inorganic ion transport and metabolism
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
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	C	Energy production and conversion
COG4773	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	P	Inorganic ion transport and metabolism
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
COG5330	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3450	Predicted enzyme of the cupin superfamily	R	General function prediction only
COG2303	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG3713	Outer membrane protein V	M	Cell wall/membrane/envelope 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
COG1720	Uncharacterized conserved protein	S	Function unknown
COG3188	P pilus assembly protein, porin PapC	N	Cell motility
COG5430	Uncharacterized secreted protein	S	Function unknown
COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G	Carbohydrate transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
COG0183	Acetyl-CoA acetyltransferase	I	Lipid transport and metabolism
COG5454	Predicted secreted protein	S	Function unknown
COG2510	Predicted membrane protein	S	Function unknown
COG2370	Hydrogenase/urease accessory protein	O	Posttranslational modification, protein turnover, chaperones
COG0583	Transcriptional regulator	K	Transcription
COG1522	Transcriptional regulators	K	Transcription
COG0840	Methyl-accepting chemotaxis protein	N	Cell motility
COG1376	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4773	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	P	Inorganic ion transport and metabolism
COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
COG2841	Uncharacterized protein conserved in bacteria	S	Function unknown
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
COG1247	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG2005	N-terminal domain of molybdenum-binding protein	R	General function prediction only
COG0146	N-methylhydantoinase B/acetone carboxylase, alpha subunit	E	Amino acid transport and metabolism
COG0684	Demethylmenaquinone methyltransferase	H	Coenzyme transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1764	Predicted redox protein, regulator of disulfide bond formation	O	Posttranslational modification, protein turnover, chaperones
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG1396	Predicted transcriptional regulators	K	Transcription
COG0765	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
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production and conversion
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
COG1051	ADP-ribose pyrophosphatase	F	Nucleotide transport and metabolism
COG0819	Putative transcription activator	K	Transcription
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
COG1359	Uncharacterized conserved protein	S	Function unknown
COG0579	Predicted dehydrogenase	R	General function prediction only
COG4126	Hydantoin racemase	E	Amino acid transport and metabolism
COG1737	Transcriptional regulators	K	Transcription
COG3182	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG3205	Predicted membrane protein	S	Function unknown

COG3284	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0765	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG0583	Transcriptional regulator	K	Transcription
COG3971	2-keto-4-pentenoate hydratase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2072	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0044	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
COG1035	Coenzyme F420-reducing hydrogenase, beta subunit	C	Energy production and conversion
COG5001	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
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
COG1113	Gamma-aminobutyrate permease and related permeases	E	Amino acid transport and metabolism
COG0589	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
COG1396	Predicted transcriptional regulators	K	Transcription
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG1522	Transcriptional regulators	K	Transcription
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Coenzyme transport and metabolism
COG2153	Predicted acyltransferase	R	General function prediction only
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	B	Chromatin structure and dynamics
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG5476	Uncharacterized conserved protein	S	Function unknown
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG3125	Heme/copper-type cytochrome/quinol oxidase, subunit 4	C	Energy production and conversion
COG2188	Transcriptional regulators	K	Transcription
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG3335	Transposase and inactivated derivatives	L	Replication, recombination and repair
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG4388	Mu-like prophage I protein	R	General function prediction only
COG4397	Mu-like prophage major head subunit gpT	R	General function prediction only
COG3948	Phage-related baseplate assembly protein	R	General function prediction only
COG3497	Phage tail sheath protein FI	R	General function prediction only
COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	R	General function prediction only
COG4544	Uncharacterized conserved protein	S	Function unknown
COG3077	DNA-damage-inducible protein J	L	Replication, recombination and repair
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG5350	Predicted protein tyrosine phosphatase	R	General function prediction only
COG0024	Methionine aminopeptidase	J	Translation, ribosomal structure and biogenesis
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
COG3115	Cell division protein	D	Cell cycle control, cell division, chromosome partitioning
COG2128	Uncharacterized conserved protein	S	Function unknown
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG2370	Hydrogenase/urease accessory protein	O	Posttranslational modification, protein turnover, chaperones
COG1807	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	M	Cell wall/membrane/envelope biogenesis
COG0584	Glycerophosphoryl diester phosphodiesterase	C	Energy production and conversion
COG1686	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
COG0563	Adenylate kinase and related kinases	F	Nucleotide transport and metabolism
COG5395	Predicted membrane protein	S	Function unknown
COG0260	Leucyl aminopeptidase	E	Amino acid transport and metabolism
COG0145	N-methylhydantoinase A/acetone carboxylase, beta subunit	E	Amino acid transport and metabolism
COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	H	Coenzyme transport and metabolism
COG0586	Uncharacterized membrane-associated protein	S	Function unknown
COG3908	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG1123	ATPase components of various ABC-type transport systems, contain duplicated ATPase	R	General function prediction only
COG1522	Transcriptional regulators	K	Transcription
COG5573	Predicted nucleic-acid-binding protein, contains PIN domain	R	General function prediction only
COG5345	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3324	Predicted enzyme related to lactoylglutathione lyase	R	General function prediction only
COG3795	Uncharacterized protein conserved in bacteria	S	Function unknown
COG4941	Predicted RNA polymerase sigma factor containing a TPR repeat domain	K	Transcription
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	G	Carbohydrate transport and metabolism
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E	Amino acid transport and metabolism
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
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
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism

COG0847	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	L	Replication, recombination and repair
COG0421	Spermidine synthase	E	Amino acid transport and metabolism
COG1802	Transcriptional regulators	K	Transcription
COG0583	Transcriptional regulator	K	Transcription
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
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	H	Coenzyme transport and metabolism
COG0262	Dihydrofolate reductase	H	Coenzyme transport and metabolism
COG3025	Uncharacterized conserved protein	S	Function unknown
COG1802	Transcriptional regulators	K	Transcription
COG3920	Signal transduction histidine kinase	T	Signal transduction mechanisms
COG2967	Uncharacterized protein affecting Mg2+/Co2+ transport	P	Inorganic ion transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG2836	Uncharacterized conserved protein	S	Function unknown
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG4106	Trans-aconitate methyltransferase	R	General function prediction only
COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
COG1301	Na+/H+-dicarboxylate symporters	C	Energy production and conversion
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
COG1335	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1011	Predicted hydrolase (HAD superfamily)	R	General function prediction only
COG2334	Putative homoserine kinase type II (protein kinase fold)	R	General function prediction only
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2303	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG3535	Uncharacterized conserved protein	S	Function unknown
COG0145	N-methylhydantoinase A/acetone carboxylase, beta subunit	E	Amino acid transport and metabolism
COG0672	High-affinity Fe2+/Pb2+ permease	P	Inorganic ion transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG3177	Uncharacterized conserved protein	S	Function unknown
COG3408	Glycogen debranching enzyme	G	Carbohydrate transport and metabolism
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
COG1359	Uncharacterized conserved protein	S	Function unknown
COG0693	Putative intracellular protease/amidase	R	General function prediction only
COG5361	Uncharacterized conserved protein	S	Function unknown
COG2258	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2122	Uncharacterized conserved protein	S	Function unknown
COG1228	Imidazolonepropionase and related amidohydrolases	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0316	Uncharacterized conserved protein	S	Function unknown
COG0726	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
COG0679	Predicted permeases	R	General function prediction only
COG1262	Uncharacterized conserved protein	S	Function unknown
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG2514	Predicted ring-cleavage extradiol dioxygenase	R	General function prediction only
COG3246	Uncharacterized conserved protein	S	Function unknown
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG1414	Transcriptional regulator	K	Transcription
COG0355	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)	C	Energy production and conversion
COG3737	Uncharacterized conserved protein	S	Function unknown
COG1012	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
COG0146	N-methylhydantoinase B/acetone carboxylase, alpha subunit	E	Amino acid transport and metabolism
COG0793	Periplasmic protease	M	Cell wall/membrane/envelope biogenesis
COG4308	Limonene-1,2-epoxide hydrolase	Q	Secondary metabolites biosynthesis, transport and catabolism
COG5505	Predicted integral membrane protein	S	Function unknown
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
COG0189	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism
COG1785	Alkaline phosphatase	P	Inorganic ion transport and metabolism
COG0799	Uncharacterized homolog of plant Iojap protein	S	Function unknown
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
COG4591	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
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
COG1309	Transcriptional regulator	K	Transcription
COG1228	Imidazolonepropionase and related amidohydrolases	Q	Secondary metabolites biosynthesis, transport and catabolism
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
COG0014	Gamma-glutamyl phosphate reductase	E	Amino acid transport and metabolism
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
COG0260	Leucyl aminopeptidase	E	Amino acid transport and metabolism
COG4277	Predicted DNA-binding protein with the Helix-hairpin-helix motif	R	General function prediction only
COG0451	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
COG2010	Cytochrome c, mono- and diheme variants	C	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG1982	Arginine/lysine/ornithine decarboxylases	E	Amino acid transport and metabolism
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
COG0730	Predicted permeases	R	General function prediction only
COG2021	Homoserine acetyltransferase	E	Amino acid transport and metabolism
COG0637	Predicted phosphatase/phosphohexomutase	R	General function prediction only
COG1414	Transcriptional regulator	K	Transcription
COG0189	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism

COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
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
COG3383	Uncharacterized anaerobic dehydrogenase	R	General function prediction only
COG0598	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
COG3055	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0569	K+ transport systems, NAD-binding component	P	Inorganic ion transport and metabolism
COG0657	Esterase/lipase	I	Lipid transport and metabolism
COG1211	4-diphosphocytidyl-2-methyl-D-erithritol synthase	I	Lipid transport and metabolism
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG4177	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
COG3705	ATP phosphoribosyltransferase involved in histidine biosynthesis	E	Amino acid transport and metabolism
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
COG0603	Predicted PP-loop superfamily ATPase	R	General function prediction only
COG0602	Organic radical activating enzymes	O	Posttranslational modification, protein turnover, chaperones
COG0778	Nitroreductase	C	Energy production and conversion
COG1032	Fe-S oxidoreductase	C	Energy production and conversion
COG1846	Transcriptional regulators	K	Transcription
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport and metabolism
COG0251	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
COG0720	6-pyruvoyl-tetrahydropterin synthase	H	Coenzyme transport and metabolism
COG0824	Predicted thioesterase	R	General function prediction only
COG1960	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production and conversion
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
COG2274	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	V	Defense mechanisms
COG1250	3-hydroxyacyl-CoA dehydrogenase	I	Lipid transport and metabolism
COG0381	UDP-N-acetylglucosamine 2-epimerase	M	Cell wall/membrane/envelope biogenesis
COG1580	Flagellar basal body-associated protein	N	Cell motility
COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
COG1516	Flagellin-specific chaperone FliS	N	Cell motility
COG1815	Flagellar basal body protein	N	Cell motility
COG3618	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG4135	ABC-type uncharacterized transport system, permease component	R	General function prediction only
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
COG2207	AraC-type DNA-binding domain-containing proteins	K	Transcription
COG0428	Predicted divalent heavy-metal cations transporter	P	Inorganic ion transport and metabolism
COG4773	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	P	Inorganic ion transport and metabolism
COG0534	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG2091	Phosphopantetheinyl transferase	H	Coenzyme transport and metabolism
COG3703	Uncharacterized protein involved in cation transport	P	Inorganic ion transport and metabolism
COG1807	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	M	Cell wall/membrane/envelope biogenesis
COG3093	Plasmid maintenance system antidote protein	R	General function prediction only
COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases	T	Signal transduction mechanisms
COG1680	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
COG0583	Transcriptional regulator	K	Transcription
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
COG1309	Transcriptional regulator	K	Transcription
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
COG3193	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	R	General function prediction only
COG0665	Glycine/D-amino acid oxidases (deaminating)	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
COG1305	Transglutaminase-like enzymes, putative cysteine proteases	E	Amino acid transport and metabolism
COG2308	Uncharacterized conserved protein	S	Function unknown
COG1132	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG3717	5-keto 4-deoxyuronate isomerase	G	Carbohydrate transport and metabolism
COG3155	Uncharacterized protein involved in an early stage of isoprenoid biosynthesis	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG3618	Predicted metal-dependent hydrolase of the TIM-barrel fold	R	General function prediction only
COG3961	Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes	G	Carbohydrate transport and metabolism
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport and metabolism
COG0625	Glutathione S-transferase	O	Posttranslational modification, protein turnover, chaperones
COG0008	Glutamyl- and glutaminyl-tRNA synthetases	J	Translation, ribosomal structure and biogenesis
COG1721	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	R	General function prediction only
COG0662	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
COG1835	Predicted acyltransferases	I	Lipid transport and metabolism
COG2146	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases	P	Inorganic ion transport and metabolism
COG5554	Nitrogen fixation protein	Q	Secondary metabolites biosynthesis, transport and catabolism
COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C	Energy production and conversion
COG2346	Truncated hemoglobins	R	General function prediction only
COG0119	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport and metabolism
COG0565	rRNA methylase	J	Translation, ribosomal structure and biogenesis
COG3279	Response regulator of the LytR/AlgR family	K	Transcription
COG5572	Predicted integral membrane protein	S	Function unknown
COG3219	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2259	Predicted membrane protein	S	Function unknown
COG0526	Thiol-disulfide isomerase and thioredoxins	O	Posttranslational modification, protein turnover, chaperones
COG0219	Predicted rRNA methylase (SpoU class)	J	Translation, ribosomal structure and biogenesis
COG3237	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1396	Predicted transcriptional regulators	K	Transcription
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
COG0861	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion transport and metabolism

COG2962	Predicted permeases	R	General function prediction only
COG3333	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2375	Siderophore-interacting protein	P	Inorganic ion transport and metabolism
COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
COG4302	Ethanolamine ammonia-lyase, small subunit	E	Amino acid transport and metabolism
COG0531	Amino acid transporters	E	Amino acid transport and metabolism
COG4974	Site-specific recombinase XerD	L	Replication, recombination and repair
COG3023	Negative regulator of beta-lactamase expression	V	Defense mechanisms
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
COG2271	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG1451	Predicted metal-dependent hydrolase	R	General function prediction only