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	К	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	К	Transcription
COG0300	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
COG0277	FAD/FMN-containing dehydrogenases	С	Energy production and conversion
COG2192	Predicted carbamoyl transferase, NodU family	0	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	0	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
	Type IV secretory pathway, TrbF components	U	Intracellular trafficking, secretion, and vesicular transport
	Type IV secretory pathway, VirB9 components	U	Intracellular trafficking, secretion, and vesicular transport
	Type IV secretory pathway, VirB10 components	U	Intracellular trafficking, secretion, and vesicular transport
	Uncharacterized conserved small protein	S	Function unknown
	Predicted Zn peptidase	E	Amino acid transport and metabolism
	Predicted transcription factor, homolog of eukaryotic MBF1	K	Transcription
	Dihydroorotase	F	Nucleotide transport and metabolism
	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
	Exonuclease VII, large subunit	L	Replication, recombination and repair
	Adenosine deaminase	F	Nucleotide transport and metabolism
	Predicted metal-binding protein	S	Function unknown
	Cobalamin biosynthesis protein CobN and related Mg-chelatases	Н	Coenzyme transport and metabolism
	Precorrin-3B methylase	н	Coenzyme transport and metabolism
	Methionine aminopeptidase	1	Translation, ribosomal structure and biogenesis
	Cobalamin biosynthesis protein CbiD	н	Coenzyme transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted glutathione S-transferase		
			Posttranslational modification, protein turnover, chaperones
	Thiol-disulfide isomerase and thioredoxins	0	Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
COG0526	Thiol-disulfide isomerase and thioredoxins Glycosidases	0	Posttranslational modification, protein turnover, chaperones
COG0526 COG0366	Thiol-disulfide isomerase and thioredoxins Glycosidases ABC-type siderophore export system, fused ATPase and permease components	0	· · · · · · · · · · · · · · · · · · ·
COG0526 COG0366 COG4615	Glycosidases	O O G	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG0526 COG0366 COG4615 COG4591	Glycosidases ABC-type siderophore export system, fused ATPase and permease components	0 0 G Q	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG0526 COG0366 COG4615 COG4591 COG1136	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component	0 0 G Q M	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase	0 0 G Q M V F	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit	0 0 G Q M V F	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase	0 0 G Q M V F I E	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein	O O G Q M V F I E S	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2	O O G Q M V F I E S E	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG2049	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine dearninase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 1	O O G Q M V F I E S E	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0777 COG0405 COG2326 COG1984 COG2049 COG1540	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B	O O G Q M V F I E S E E R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0405 COG2326 COG1984 COG2049 COG1540 COG1075	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 2 Incharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold	O O G Q M V F I E S E	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism
COG0526 COG0366 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG1540 COG1540 COG1540	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein	O O G Q M V F I E S E E R R S	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown
COG0526 COG0366 COG4615 COG4591 COG0777 COG0777 COG0405 COG2326 COG1984 COG2049 COG1540 COG1075 COG4336 COG3911	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase	O O G Q M V F I E S E E R R R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only
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COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0405 COG2326 COG1984 COG1540 COG1540 COG1075 COG3911 COG3900 COG2199 COG0410	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted proteins homologs of lactam utilization protein B Predicted Deriplasmic protein Predicted ATPase Predicted periplasmic protein Procs GOEF domain ABC-type branched-chain amino acid transport systems, ATPase component	O O G Q M V F I E S E E R R S R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG0717 COG0777 COG0405 COG2326 COG1984 COG2049 COG1075 COG4336 COG3911 COG3900 COG2199 COG0410	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted periplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component	O O G Q M V F I E S E E R R S R S R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only
COG0526 COG0366 COG46151 COG4591 COG0717 COG0777 COG0405 COG2326 COG1984 COG1075 COG4366 COG3911 COG3900 COG2199 COG0410	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted Periplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport system, ATPase component Uncharacterized ABC-type transport system, ATPase component ABC-type branched-chain amino acid transport system, permease component	O O Q M V F I E S E R R S T E R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG1540 COG1075 COG4336 COG3911 COG3900 COG2199 COG0410 COG4674 COG4177 COG0642	Glycosidases ABC-type iderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted priplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component Signal transduction histidine kinase	O O G Q M V F I E S E R R S T E R S T E R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only
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COG0526 COG0366 COG4615 COG4591 COG0717 COG0777 COG0405 COG2326 COG1984 COG1075 COG3961 COG3961 COG3961 COG3961 COG436 COG3911 COG3900 COG2199 COG0410 COG4674 COG4177 COG0642 COG3437 COG0643	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted periplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component Signal transduction histidine kinase Response regulator containing a CheY-like receiver domain and an HD-GYP domain Transcriptional regulator	O O G Q M V F I E S E E R R S T E R K K K	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG1540 COG1075 COG4336 COG3911 COG3911 COG3900 COG2199 COG4106 COG4177 COG0642 COG3437 COG0642 COG3437 COG0583 COG0583	Glycosidases ABC-type iderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted Periplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component ABC-type branched-chain amino acid transport system, permease component Signal transduction histidine kinase Response regulator containing a CheY-like receiver domain and an HD-GYP domain Transcriptional regulator Tryptophan synthase alpha chain	O O Q M V F I E S E R R S T E R E T K E E E R	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transport and metabolism Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG1540 COG1075 COG4336 COG3911 COG3900 COG2199 COG0410 COG4674 COG4477 COG0642 COG3437 COG0583 COG0159 COG0655	Glycosidases ABC-type iderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 2 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted Preiplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component Signal transduction histidine kinase Response regulator containing a CheY-like receiver domain and an HD-GYP domain Transcriptional regulator Tryptophan synthase alpha chain Glycine/D-amino acid oxidases (deaminating)	O G Q M V F I E S E R R S T E R E R E R E R E R E R E E R E E E E	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription Amino acid transport and metabolism Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0405 COG2326 COG1984 COG1075 COG436 COG3911 COG3900 COG2199 COG0410 COG4674 COG4177 COG0642 COG3437 COG0583 COG0583 COG0583 COG0159	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted proteins protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component Signal transduction histidine kinase Response regulator containing a CheY-like receiver domain and an HD-GYP domain Transcriptional regulator Tryptophan synthase alpha chain Glycine/D-amino acid oxidases (deaminating) Phosphotransacetylase	O O Q M V F I E S E E R S T E R S T E R C	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription Transcription Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG0526 COG0366 COG4615 COG4591 COG0177 COG0777 COG0405 COG2326 COG1984 COG1075 COG3911 COG3900 COG2199 COG0410 COG4177 COG0417 COG0642 COG3436 COG3911 COG0642 COG1594 COG1075 COG6410 COG6417 COG0642 COG06410 COG0642 COG06410 COG0642 COG0665 COG0280 COG1012	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit G amma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted Periplasmic protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component ABC-type branched-chain amino acid transport system, permease component Signal transduction histidine kinase Response regulator containing a CheV-like receiver domain and an HD-GYP domain Transcriptional regulator Tryptophan synthase alpha chain Glycine/D-amino acid oxidases (deaminating) Phosphotransacetylase NAD-dependent aldehyde dehydrogenases	O O G Q M V F I E S E E R R S T E R E T K K E E C C C C C C C C C C C C C C C C	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Tunction unknown Signal transduction mechanisms General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription Transcription Transcription Transcription Transcription Transport and metabolism Amino acid transport and metabolism Energy production and conversion Energy production and conversion
COG0526 COG0366 COG4615 COG4591 COG1136 COG0717 COG0777 COG0405 COG2326 COG1984 COG1540 COG1075 COG4336 COG3911 COG3910 COG2199 COG0410 COG4674 COG4177 COG0642 COG3437 COG0583 COG0583 COG0583 COG0580 COG0280 COG1012 COG0282	Glycosidases ABC-type siderophore export system, fused ATPase and permease components ABC-type transport system, involved in lipoprotein release, permease component ABC-type antimicrobial peptide transport system, ATPase component Deoxycytidine deaminase Acetyl-CoA carboxylase beta subunit Gamma-glutamyltransferase Uncharacterized conserved protein Allophanate hydrolase subunit 1 Uncharacterized proteins, homologs of lactam utilization protein B Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold Uncharacterized conserved protein Predicted ATPase Predicted ATPase Predicted proteins protein FOG: GGDEF domain ABC-type branched-chain amino acid transport systems, ATPase component Uncharacterized ABC-type transport system, ATPase component Signal transduction histidine kinase Response regulator containing a CheY-like receiver domain and an HD-GYP domain Transcriptional regulator Tryptophan synthase alpha chain Glycine/D-amino acid oxidases (deaminating) Phosphotransacetylase	O O Q M V F I E S E E R S T E R S T E R C	Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Defense mechanisms Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Amino acid transport and metabolism Function unknown Amino acid transport and metabolism General function prediction only General function prediction only Function unknown General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Function unknown Signal transduction mechanisms Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Transcription Transcription Transcription Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism

COG0845			
CO00043	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG3403	Uncharacterized conserved protein	S	Function unknown
	Tryptophan synthase beta chain	E	Amino acid transport and metabolism
COG2055	Malate/L-lactate dehydrogenases	С	Energy production and conversion
COG2050	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	L-lactate permease	С	Energy production and conversion
	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
	Beta-lactamase class A	V	Defense mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Transcriptional regulators	K	Transcription
	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	Lipid transport and metabolism
	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Maleate cis-trans isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
	L-asparaginase/archaeal Glu-tRNAGIn amidotransferase subunit D	E	Amino acid transport and metabolism
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	С	Energy production and conversion
	3-oxoacyl-(acyl-carrier-protein) synthase	l P	Lipid transport and metabolism
	ABC-type Fe3+-siderophore transport system, permease component	P R	Inorganic ion transport and metabolism
	Predicted dinucleotide-utilizing enzyme	к R	General function prediction only
	ATPase components of various ABC-type transport systems, contain duplicated ATPase	K V	General function prediction only
	ABC-type multidrug transport system, permease component	ı	Defense mechanisms
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted 3-hydroxylacyl-(acyl carrier protein) dehydratase	i	Lipid transport and metabolism Lipid transport and metabolism
	3-oxoacyl-(acyl-carrier-protein) synthase	i	Lipid transport and metabolism
	Predicted exporter	R	General function prediction only
	Fe2+-dicitrate sensor, membrane component	P	Inorganic ion transport and metabolism
	Predicted thioesterase	R	General function prediction only
	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	ï	Lipid transport and metabolism
	Acyl carrier protein	i	Lipid transport and metabolism
	FOG: GGDEF domain	Ť	Signal transduction mechanisms
	Acyl carrier protein	i	Lipid transport and metabolism
	1-acyl-sn-glycerol-3-phosphate acyltransferase	i	Lipid transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Plasmid stabilization system protein	R	General function prediction only
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I.	Lipid transport and metabolism
	Coenzyme F390 synthetase	H	Coenzyme transport and metabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	Long-chain acyl-CoA synthetases (AMP-forming)	ı	Lipid transport and metabolism
	Transcriptional regulator	K	Transcription
	Plasmid maintenance system killer protein	R	General function prediction only
	Plasmid maintenance system antidote protein	R	General function prediction only
	GMP synthase - Glutamine amidotransferase domain	 F	Nucleotide transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Permeases	R	General function prediction only
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes		Energy production and conversion
		С	Ellergy production and conversion
COG0438	Glycosyltransferase	M	
	Glycosyltransferase Short-chain dehydrogenases of various substrate specificities		Cell wall/membrane/envelope biogenesis
COG0300	Glycosyltransferase Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	M	
COG0300 COG0764	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	M R	Cell wall/membrane/envelope biogenesis General function prediction only
COG0300 COG0764 COG0304	Short-chain dehydrogenases of various substrate specificities	M R I	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism
COG0300 COG0764 COG0304 COG0526	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase	M R I	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism
COG0300 COG0764 COG0304 COG0526 COG5508	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins	M R I O	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein	M R I O S	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B)	M R I O S R	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins	M R I O S R S	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters	M R I O S R S P	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases	M R I O S R S P R	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG2376	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase	M R I O S R S P R G	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG2376 COG0306	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase	M R I O S R S P R G G P	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription
COG0300 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG2376 COG306 COG5499 COG1622	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2	M R I O S R S P R G G K C	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG2376 COG306 COG5499 COG1622 COG0843	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1	M R I O S R S P R G G C C	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG2376 COG0306 COG5499 COG1622 COG0843 COG3550	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes	M R I O S R S P R G G C C R	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion General function prediction only
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG306 COG5499 COG1622 COG0843 COG3550 COG3842	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-noxacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components	M R I O S R S P R G G P K C C R	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion General function prediction only Amino acid transport and metabolism
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG376 COG6499 COG1622 COG0843 COG3550 COG3842 COG3842	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid	M R I O S R S P R G G C C R E R	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only General function prediction only
COG0300 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG2376 COG0306 COG5499 COG1622 COG0843 COG3550 COG3550 COG3842 COG3842 COG3842 COG3842 COG3842	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	M R I O S R S P R G G P K C C R E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG3376 COG306 COG5499 COG1622 COG0843 COG3550 COG3844 COG5302	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphatef-sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	M R I O S R G G P K C C R E E T	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Franscription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2376 COG306 COG5499 COG1622 COG0843 COG3550 COG3842 COG5302 COG0841	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters	M R I O S R G G P K C C R E T P	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2376 COG306 COG5499 COG1622 COG0843 COG3550 COG3842 COG5302 COG0834 COG5001 COG0598	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN	MRIIOSRSPRGGPKCCREETPS	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown
COG0300 COG0764 COG0526 COG5508 COG2249 COG1357 COG2936 COG2936 COG3936 COG5499 COG1622 COG0843 COG3550 COG3842 COG3842 COG3843 COG3502 COG0884 COG5001 COG0598 COG5902 COG0583 COG5902 COG0598	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator	M R I O S R S P R G G P K C C R E T P S K	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Franscription Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG3376 COG3649 COG3502 COG0843 COG3550 COG3842 COG0884 COG5001 COG0598 COG0598 COG0598	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide transport system, periplasmic component	MRIIOSRRSPRGGPKCCREETPSKEETE	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG376 COG0306 COG5499 COG1622 COG0843 COG3550 COG3842 COG5302 COG0847 COG0501 COG0598 COG2256 COG0584 COG5001 COG0598 COG2250 COG0583	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Uncharacterized low-complexity proteins Uni- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transportes Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide transport system, periplasmic components	MRIIOSSRSPRGGPKCCRRETPSKEEEE	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Function unknown Transcription Amino acid transport and metabolism Amino acid transport and metabolism
COG0300 COG0764 COG0526 COG5508 COG2249 COG1357 COG04913 COG2376 COG0306 COG5499 COG1622 COG0843 COG3550 COG3842 COG3550 COG0501 COG05	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components ABC-type anino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport systems, permease components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	M R I I O S R S P R G G P K C C R E R E T P S K E E E E E E E E E E E E E E E E E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Function unknown Transcription Amino acid transport and metabolism
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG5306 COG5499 COG1622 COG0843 COG3550 COG3842 COG5302 COG0843 COG5001 COG0598 COG5001 COG0598 COG0507 COG0598 COG0508 COG050	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-hoxacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport systems, permease components SGC-type dipeptide/oligopeptide/nickel transport systems, permease components Signal transduction histidine kinase	MRIIOSRSPRGGPKCCREETPSKEEETT	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Signal transduction mechanisms
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG2976 COG0306 COG5499 COG1622 COG0844 COG3550 COG3842 COG05302 COG0834 COG5001 COG0598 COG0598 COG0547 COG0661 COG061173	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transportes Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide transport system, periplasmic components ABC-type dipeptide transport system, periplasmic components ABC-type dipeptide transport system, periplasmic components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ATPase components of various ABC-type transport systems, contain duplicated ATPase	M R I O S R S P R G G P K C C R E E E E E E E E E E E E E E E E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Franscription Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Signal transduction mechanisms General function prediction only
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG4999 COG1622 COG0843 COG3550 COG3844 COG5302 COG0847 COG0501 COG0598 COG2250 COG0583 COG0581 COG0641 COG1173 COG0642 COG1123 COG4948	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transportes Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide/liquepetide/nickel transport systems, permease components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components ABC-type dipeptide/oligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ATPase components of various ABC-type transport systems, contain duplicated ATPase L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M R I I O S R S P R G G P K C C R E T P S K E E E E E E E E E E E E E E E E E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Signal transduction mechanisms General function prediction only Cell wall/membrane/envelope biogenesis
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COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG357 COG0471 COG2936 COG5499 COG5499 COG5499 COG65499 COG65499 COG65499 COG6549 COG6549 COG6549 COG6583 COG0525 COG0583 COG0747 COG0601 COG1173 COG0604 COG1123 COG04944 COG1123 COG04944 COG0520 COG0520 COG0520 COG0540	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ABC-type dipeptide/oligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ATPase components of various ABC-type transport systems, permease components Signal transduction histidine kinase ABC-type dipeptide/logipopetide/nickel transport systems, permease components Signal transduction histidine kinase AFD-type dipeptide transport system, periplasmic component	M R I O S R S P R C C R E R E E E E T R M E E E E T R M E E E E E T R M E E E E E E E E E E E E E E E E E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Franscription Energy production and conversion General function prediction only Amino acid transport and metabolism Signal transduction prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Signal transduction mechanisms General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism
COG0300 COG0764 COG0764 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG2976 COG0306 COG5499 COG1622 COG0844 COG3550 COG3842 COG55001 COG0598 COG5001 COG0598 COG1622 COG0844 COG0501 COG0598 COG0547 COG0642 COG1173 COG0642 COG1123 COG4948 COG5250	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide transport system, periplasmic component ABC-type dipeptide foligopeptide/nickel transport systems, permease components ABC-type dipeptide foligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ATPase components of various ABC-type transport systems, contain duplicated ATPase L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily Selenocysteine lyase ABC-type dipeptide transport system, periplasmic component Glucose/sorbosone dehydrogenases	M R I I O S R S P R G G P K C C R E R E T P S K E E E T R M E E G	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism Amino acid transport and metabolism Signal transduction mechanisms General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Carbohydrate transport and metabolism
COG0300 COG0764 COG0304 COG0526 COG5508 COG2249 COG1357 COG0471 COG2936 COG4993 COG3560 COG5499 COG1622 COG0843 COG3550 COG3842 COG3550 COG0844 COG55001 COG0588 COG05001 COG0588 COG0747 COG0601 COG1123 COG0642 COG0520 COG0548 COG0520 COG0548 COG0520 COG064948 COG0520 COG0747 COG06494 COG052133 COG4953	Short-chain dehydrogenases of various substrate specificities 3-hydroxymyristoryl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases 3-oxoacyl-(acyl-carrier-protein) synthase Thiol-disulfide isomerase and thioredoxins Uncharacterized conserved small protein Putative NADPH-quinone reductase (modulator of drug activity B) Uncharacterized low-complexity proteins Di- and tricarboxylate transporters Predicted acyl esterases Glucose dehydrogenase Dihydroxyacetone kinase Phosphate/sulphate permeases Predicted transcription regulator containing HTH domain Heme/copper-type cytochrome/quinol oxidases, subunit 2 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Uncharacterized protein related to capsule biosynthesis enzymes ABC-type spermidine/putrescine transport systems, ATPase components Post-segregation antitoxin (ccd killing mechanism protein) encoded by the F plasmid ABC-type amino acid transport/signal transduction systems, periplasmic component/domain Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Mg2+ and Co2+ transporters Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN Transcriptional regulator ABC-type dipeptide/nickel transport systems, periplasmic components ABC-type dipeptide/nickel transport systems, permease components ABC-type dipeptide/ligopeptide/nickel transport systems, permease components Signal transduction histidine kinase ATPase components of various ABC-type transport systems, contain duplicated ATPase L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily Selenocysteine lyase ABC-type dipeptide transport system, periplasmic component Glucose/sorbosone dehydrogenases Membrane carboxypeptidase/penicillin-binding protein PbpC	M R I I O S R S P R G G P K C C R E R E T T R M E E G M E E G M E E E E	Cell wall/membrane/envelope biogenesis General function prediction only Lipid transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Energy production and conversion Energy production and conversion General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism Function unknown Transcription Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
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	ABC-type phosphate/phosphonate transport system, periplasmic component	P	Inorganic ion transport and metabolism
	Predicted transcriptional regulator Thioredoxin reductase	К О	Transcription Posttranslational modification, protein turnover, chaperones
	Deoxyhypusine synthase	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized conserved protein	S	Function unknown
COG5381	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
	Mannose-6-phosphate isomerase Phage terminase-like protein, large subunit	G R	Carbohydrate transport and metabolism
	Phage-related protein	S	General function prediction only Function unknown
	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
	Cytochrome P450	Q	Secondary metabolites biosynthesis, transport and catabolism
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	Acetyltransferases Membrane-fusion protein	R M	General function prediction only Cell wall/membrane/envelope biogenesis
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Hydrolases of the alpha/beta superfamily	R	General function prediction only
COG2272	Carboxylesterase type B	1	Lipid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Isopenicillin N synthase and related dioxygenases	R	General function prediction only
	Predicted nucleoside-diphosphate sugar epimerases Sialic acid synthase	M M	Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
	Adenosine deaminase	F	Nucleotide transport and metabolism
COG0515	Serine/threonine protein kinase	R	General function prediction only
	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted Zn-dependent peptidases	R	General function prediction only
	Hydrolases of the alpha/beta superfamily Chemotaxis protein histidine kinase and related kinases	R N	General function prediction only Cell motility
	Predicted transcriptional regulators	K	Transcription
	Orotate phosphoribosyltransferase	F	Nucleotide transport and metabolism
COG0620	Methionine synthase II (cobalamin-independent)	E	Amino acid transport and metabolism
	Beta-xylosidase	G	Carbohydrate transport and metabolism
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Predicted membrane protein Predicted transcriptional regulators	S K	Function unknown Transcription
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Predicted glycosylase	G	Carbohydrate transport and metabolism
COG2201	Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain	N	Cell motility
	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	Dehydrogenases (flavoproteins) Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	С О	Energy production and conversion Posttranslational modification, protein turnover, chaperones
	Predicted phosphotransferase related to Ser/Thr protein kinases	R	General function prediction only
	Predicted membrane protein	S	Function unknown
COG2939	Carboxypeptidase C (cathepsin A)	E	Amino acid transport and metabolism
	Predicted membrane protein	S	Function unknown
	Acetyltransferases, including N-acetylases of ribosomal proteins	J J	Translation, ribosomal structure and biogenesis
	Putative translation initiation inhibitor, yjgF family Outer membrane protein and related peptidoglycan-associated (lipo)proteins	J M	Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis
	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	T	Signal transduction mechanisms
	Uncharacterized conserved protein	S	Function unknown
	Predicted integral membrane protein	S	Function unknown
	Cytosine/adenosine deaminases	F	Nucleotide transport and metabolism
	FOG: CBS domain Phosphoribosyl-AMP cyclohydrolase	R	General function prediction only
	ATP phosphoribosyltransferase	E E	Amino acid transport and metabolism Amino acid transport and metabolism
	Predicted acyl-CoA transferases/carnitine dehydratase	c	Energy production and conversion
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, g	M	Cell wall/membrane/envelope biogenesis
	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein Predicted proteasome-type protease	S O	Function unknown Posttranslational modification, protein turnover, chaperones
	Lignostilbene-alpha, beta-dioxygenase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
	Membrane proteins related to metalloendopeptidases	M	Cell wall/membrane/envelope biogenesis
COG1686	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
	ABC-type tungstate transport system, permease component	н	Coenzyme transport and metabolism
	ABC-type tungstate transport system, periplasmic component	Н	Coenzyme transport and metabolism
	Thymidine phosphorylase Uncharacterized protein required for formate dehydrogenase activity	F	Nucleotide transport and metabolism
	Uncharacterized protein required for formate denyarogenase activity	C S	Energy production and conversion Function unknown
	Molybdopterin-guanine dinucleotide biosynthesis protein A	н	Coenzyme transport and metabolism
	Uncharacterized component of anaerobic dehydrogenases	R	General function prediction only
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Fe-S-cluster-containing hydrogenase components 2 Signal transduction histidine kinase	C T	Energy production and conversion Signal transduction mechanisms
	Glutaredoxin and related proteins	0	Posttranslational modification, protein turnover, chaperones
	Cytochrome b subunit of formate dehydrogenase	c	Energy production and conversion
COG0642	Signal transduction histidine kinase	Т	Signal transduction mechanisms
	Uncharacterized iron-regulated membrane protein	S	Function unknown
	Acyl-CoA hydrolase	l P	Lipid transport and metabolism
	Outer membrane receptor proteins, mostly Fe transport Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	P G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport and metabolism
COG0711	F0F1-type ATP synthase, subunit b	С	Energy production and conversion

COG0711			
	F0F1-type ATP synthase, subunit b	С	Energy production and conversion
	Predicted HD superfamily hydrolase	R	General function prediction only
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C U	Energy production and conversion Intracellular trafficking, secretion, and vesicular transport
	Flp pilus assembly protein TadG Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
	Metal-dependent hydrolase	R	General function prediction only
	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
	Outer membrane receptor for ferrienterochelin and colicins	Р	Inorganic ion transport and metabolism
	Septum formation inhibitor-activating ATPase	D	Cell cycle control, cell division, chromosome partitioning
	Preprotein translocase subunit SecD	U P	Intracellular trafficking, secretion, and vesicular transport
	Carbonic anhydrase Flp pilus assembly protein TadG	U	Inorganic ion transport and metabolism Intracellular trafficking, secretion, and vesicular transport
	L-asparaginase/archaeal Glu-tRNAGIn amidotransferase subunit D	E	Amino acid transport and metabolism
	Predicted dehydrogenases and related proteins	R	General function prediction only
	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0657	Esterase/lipase	1	Lipid transport and metabolism
COG4771	Outer membrane receptor for ferrienterochelin and colicins	P	Inorganic ion transport and metabolism
	Methyl-accepting chemotaxis protein	N	Cell motility
	Glycosyltransferases, probably involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
	Inosine-uridine nucleoside N-ribohydrolase	F P	Nucleotide transport and metabolism
	Uncharacterized protein involved in copper resistance P pilus assembly protein, porin PapC	N N	Inorganic ion transport and metabolism Cell motility
	Pterin-4a-carbinolamine dehydratase	Н	Coenzyme transport and metabolism
	Bacterial lipocalin	M	Cell wall/membrane/envelope biogenesis
	Fucose permease	G	Carbohydrate transport and metabolism
COG0366	Glycosidases	G	Carbohydrate transport and metabolism
	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
	Malate synthase	С	Energy production and conversion
	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member	L	Replication, recombination and repair
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
	Outer membrane protein DNA G:T-mismatch repair endonuclease	M L	Cell wall/membrane/envelope biogenesis Replication, recombination and repair
	Site-specific DNA methylase	L	Replication, recombination and repair
	Site-specific recombinase XerD	Ĺ	Replication, recombination and repair
	Predicted esterase of the alpha-beta hydrolase superfamily	R	General function prediction only
	Ferredoxin-like protein	С	Energy production and conversion
COG5373	Predicted membrane protein	S	Function unknown
COG0644	Dehydrogenases (flavoproteins)	С	Energy production and conversion
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
	Electron transfer flavoprotein, alpha subunit	С	Energy production and conversion
	Transcriptional regulators	K	Transcription
COG1935	Predicted acyltransferases Electron transfer flavoprotein, beta subunit	l C	Lipid transport and metabolism Energy production and conversion
COG2086		C	
	Transcriptional regulator	K	Transcription
COG0583	Transcriptional regulator NAD/NADP transhydrogenase aloha subunit	K C	Transcription Energy production and conversion
COG0583 COG3288	Transcriptional regulator NAD/NADP transhydrogenase alpha subunit Uncharacterized protein conserved in bacteria	K C S	Energy production and conversion Function unknown
COG0583 COG3288 COG3809	NAD/NADP transhydrogenase alpha subunit	С	Energy production and conversion
COG0583 COG3288 COG3809 COG0119	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria	C S	Energy production and conversion Function unknown
COG0583 COG3288 COG3809 COG0119 COG4709	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases	C S E	Energy production and conversion Function unknown Amino acid transport and metabolism
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase	C S E S K R	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins	C S E S K R	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein	C S E S K R P	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoy/glutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C S E S K R P N	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain	C S E S K R P N C S	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a colled-coil domain Short-chain dehydrogenases of various substrate specificities	C S E S K R P N C S R	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only
COG0583 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator	C S E S K R P N C S R K	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription
COG0583 COG3288 COG3289 COG0119 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG2710	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a colled-coil domain Short-chain dehydrogenases of various substrate specificities	C S E S K R P N C S R	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only
COG0583 COG3288 COG3289 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG2710 COG1462	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoy/glutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains	C S E S K R P N C S R K	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Energy production and conversion
COG0583 COG3288 COG3209 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG1462 COG2710	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers	C S E S K R P N C S R K C M	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis
COG0583 COG3288 COG3289 COG0119 COG1695 COG3324 COG4771 COG0840 COG5420 COG0300 COG1309 COG2710 COG1462 COG2710 COG56001 COG5801 COG0840	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoy/glutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein	C S E S K R P N C S R K C M C T N	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility
COG0583 COG3288 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG2710 COG1462 COG2710 COG5001 COG5001 COG6840 COG2971	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-accepting chemotaxis protein	C S E S K R P N C S R K C M C T N G	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism
COG0583 COG3288 COG3289 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG1309 COG2710 COG5001 COG5001 COG5001 COG0840 COG2971 COG62971 COG1252	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-acetylglucosamine kinase NADH dehydrogenase, FAD-containing subunit	C S E S K R P N C S R K C M C T N G C	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion
COG0583 COG3288 COG3288 COG6119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG2710 COG0840 COG2710 COG0840 COG2710 COG0840 COG2971 COG0840 COG2971 COG1252 COG1959	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-acetylglucosamine kinase NADH dehydrogenase, FAD-containing subunit Predicted transcriptional regulator	C S E S K R P N C S R K C M C T N G C K	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion Transcription
COG0583 COG3288 COG3288 COG3099 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG2710 COG5001 COG0840 COG2971 COG5901 COG0840 COG2971 COG1252 COG1959 COG2710	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoy/glutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-accetylglucosamine kinase NADH dehydrogenase, FAD-containing subunit Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains	C S E S K R P N C S R K C M C T N G C K C	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion Transcription Energy production and conversion Transcription Energy production and conversion
COG0583 COG3288 COG3288 COG3809 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG1462 COG2710 COG0840 COG2971 COG1252 COG1959 COG2710 COG35031	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-accepting chemotaxis protein Predicted N-accepting chemotaxis protein Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains	C S E S K R P N C S R K C M C T N G C K C S	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion Transcription Energy production and conversion Transcription Energy production and conversion Function unknown
COG0583 COG3288 COG3288 COG3209 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG0300 COG1309 COG1710 COG5001 COG5001 COG5001 COG92710 COG9840 COG2971 COG2971 COG1252 COG1959 COG2710 COG3503 COG2710	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-acetylglucosamine kinase NADH dehydrogenase, FAD-containing subunit Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted dembrane protein Nitrogenase molybdenum-iron protein, alpha and beta chains	C S E S K R P N C S R K C M C T N G C K C	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion Transcription Energy production and conversion Function unknown Energy production and conversion Function unknown Energy production and conversion
COG0583 COG3288 COG3288 COG309 COG0119 COG4709 COG1695 COG3324 COG4771 COG0840 COG1143 COG5420 COG2710 COG0840 COG2710 COG0840 COG2710 COG0840 COG2710 COG0840 COG2710 COG0840 COG2711 COG1252 COG1959 COG2710 COG3503 COG2710 COG3503 COG2710 COG3503	NAD/NADP transinydrogenase alpha subunit Uncharacterized protein conserved in bacteria Isopropylmalate/homocitrate/citramalate synthases Predicted membrane protein Predicted transcriptional regulators Predicted enzyme related to lactoylglutathione lyase Outer membrane receptor for ferrienterochelin and colicins Methyl-accepting chemotaxis protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Uncharacterized conserved small protein containing a coiled-coil domain Short-chain dehydrogenases of various substrate specificities Transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Uncharacterized protein involved in formation of curli polymers Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Methyl-accepting chemotaxis protein Predicted N-accepting chemotaxis protein Predicted N-accepting chemotaxis protein Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains Predicted transcriptional regulator Nitrogenase molybdenum-iron protein, alpha and beta chains	C S E S K R P N C S R K C M C T N G C K C S C	Energy production and conversion Function unknown Amino acid transport and metabolism Function unknown Transcription General function prediction only Inorganic ion transport and metabolism Cell motility Energy production and conversion Function unknown General function prediction only Transcription Energy production and conversion Cell wall/membrane/envelope biogenesis Energy production and conversion Signal transduction mechanisms Cell motility Carbohydrate transport and metabolism Energy production and conversion Transcription Energy production and conversion Transcription Energy production and conversion Function unknown
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COG2721	Altronate dehydratase	G	Carbohydrate transport and metabolism
	Galactose mutarotase and related enzymes	G	Carbohydrate transport and metabolism
	Gluconolactonase	G	Carbohydrate transport and metabolism
	Serine proteases of the peptidase family S9A	E	Amino acid transport and metabolism
	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) ABC-type molybdate transport system, ATPase component	C P	Energy production and conversion Inorganic ion transport and metabolism
	Predicted Fe-S oxidoreductases	R	General function prediction only
	Predicted transcriptional regulators	К	Transcription
	Nucleoside phosphorylase	F	Nucleotide transport and metabolism
	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	1	Lipid transport and metabolism
	NADH:ubiquinone oxidoreductase subunit 6 (chain J)	С	Energy production and conversion
	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Energy production and conversion
	Queuine/archaeosine tRNA-ribosyltransferase	J	Translation, ribosomal structure and biogenesis
	Pseudouridylate synthase Phosphoribosylaminoimidazole (AIR) synthetase	J F	Translation, ribosomal structure and biogenesis Nucleotide transport and metabolism
	Multisubunit Na+/H+ antiporter, MnhC subunit	P P	Inorganic ion transport and metabolism
	Multisubunit Na+/H+ antiporter, MnhB subunit	P	Inorganic ion transport and metabolism
	Predicted subunit of the Multisubunit Na+/H+ antiporter	P	Inorganic ion transport and metabolism
	Multisubunit Na+/H+ antiporter, MnhG subunit	P	Inorganic ion transport and metabolism
COG1385	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0196	FAD synthase	Н	Coenzyme transport and metabolism
	ABC-type protease/lipase transport system, ATPase and permease components	R	General function prediction only
	Enoyl-[acyl-carrier-protein] reductase (NADH)	Ţ	Lipid transport and metabolism
	Sulfur transfer protein involved in thiamine biosynthesis	H	Coenzyme transport and metabolism
	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	R	General function prediction only
	Arginyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	Integral membrane protein, interacts with FtsH NADH:ubiquinone oxidoreductase subunit 1 (chain H)	R C	General function prediction only Energy production and conversion
	Predicted periplasmic or secreted lipoprotein	R	General function prediction only
	Ribosomal protein S15P/S13E	ï.	Translation, ribosomal structure and biogenesis
	Adenylosuccinate lyase	F	Nucleotide transport and metabolism
	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
	Predicted ATPase with chaperone activity	0	Posttranslational modification, protein turnover, chaperones
	Cytosine/adenosine deaminases	F	Nucleotide transport and metabolism
	Methionyl-tRNA formyltransferase	J J	Translation, ribosomal structure and biogenesis
	Pseudouridine synthase Ribonucleases G and E	J	Translation, ribosomal structure and biogenesis Translation, ribosomal structure and biogenesis
	Nicotinate-nucleotide pyrophosphorylase	Н	Coenzyme transport and metabolism
	Ribosomal protein S16	 J	Translation, ribosomal structure and biogenesis
	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
	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)	С	Energy production and conversion
	5-formyltetrahydrofolate cyclo-ligase	Н	Coenzyme transport and metabolism
	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G L	Carbohydrate transport and metabolism
	Site-specific recombinase XerD Pseudouridylate synthases, 23S RNA-specific	ı.	Replication, recombination and repair Translation, ribosomal structure and biogenesis
	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
	Na+/alanine symporter	E	Amino acid transport and metabolism
	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
	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	0	Posttranslational modification, protein turnover, chaperones
	Membrane protease subunits, stomatin/prohibitin homologs	0	Posttranslational modification, protein turnover, chaperones
	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	0	Posttranslational modification, protein turnover, chaperones
	DNA polymerase sliding clamp subunit (PCNA homolog)	L	Replication, recombination and repair
	Isocitrate/isopropylmalate dehydrogenase	С	Energy production and conversion
	Predicted Zn-dependent peptidases ATP dependent protects of HelVII (ClayO), poptidase subunit	R O	General function prediction only
	ATP-dependent protease HsIVU (ClpYQ), peptidase subunit Dihydroorotate dehydrogenase	F	Posttranslational modification, protein turnover, chaperones Nucleotide transport and metabolism
	5-enolpyruvylshikimate-3-phosphate synthase	E E	Amino acid transport and metabolism
	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)	F	Nucleotide transport and metabolism
	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
	Cation/multidrug efflux pump	V	Defense mechanisms
	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)	J	Translation, ribosomal structure and biogenesis
	Recombinational DNA repair ATPase (RecF pathway)	L	Replication, recombination and repair
	N6-adenine-specific methylase Stress induced members (activity unknown)	L T	Replication, recombination and repair
	Stress-induced morphogen (activity unknown)	T 0	Signal transduction mechanisms
	Glutaredoxin-related protein ABC-type phosphate transport system, permease component	O P	Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism
	Primosomal protein N' (replication factor Y) - superfamily II helicase	Ĺ	Replication, recombination and repair
	Uncharacterized ABC-type transport system, permease components	R	General function prediction only
	Type IV secretory pathway, VirB9 components	Ü	Intracellular trafficking, secretion, and vesicular transport
	Molecular chaperone GrpE (heat shock protein)	0	Posttranslational modification, protein turnover, chaperones
COG0180	Tryptophanyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	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
	Ribose 5-phosphate isomerase RpiB	G 	Carbohydrate transport and metabolism
	Thiamine monophosphate synthase Carbamoylphosphate synthase large subunit (split gene in MJ)	H E	Coenzyme transport and metabolism Amino acid transport and metabolism
	Predicted Zn-dependent proteases and their inactivated homologs	R	General function prediction only
	Adenylosuccinate synthase	F	Nucleotide transport and metabolism
COG0240	Glycerol-3-phosphate dehydrogenase	С	Energy production and conversion
	Predicted transcriptional regulators	K	Transcription
	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Ţ	Signal transduction mechanisms
	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase Metal-dependent proteases with possible chaperone activity	F O	Nucleotide transport and metabolism Posttranslational modification, protein turnover, chaperones
	TRAP-type uncharacterized transport system, periplasmic component	R	General function prediction only
	Geranylgeranyl pyrophosphate synthase	Н	Coenzyme transport and metabolism
	Predicted permeases	R	General function prediction only
COG0769	UDP-N-acetylmuramyl tripeptide synthase	M	Cell wall/membrane/envelope biogenesis
	Predicted EndoIII-related endonuclease	L	Replication, recombination and repair
	Phosphatidylserine synthase	!	Lipid transport and metabolism
	Phosphatidylserine decarboxylase Predicted metal-dependent hydrolase	r R	Lipid transport and metabolism General function prediction only
	Succinyl-CoA synthetase, alpha subunit	C	Energy production and conversion
	Succinyl-CoA synthetase, beta subunit	c	Energy production and conversion
	Thiamine monophosphate kinase	Н	Coenzyme transport and metabolism
COG0149	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
	Predicted sulfurtransferase	R	General function prediction only
	Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L33 Cytochrome oxidase assembly factor	0	Translation, ribosomal structure and biogenesis Posttranslational modification, protein turnover, chaperones
	ATPase involved in DNA replication initiation	L	Replication, recombination and repair
	Aspartate-semialdehyde dehydrogenase	Ē	Amino acid transport and metabolism
	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
	Ribosomal protein L23	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L2	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L22	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein S3 Ribosomal protein L16/L10E	,	Translation, ribosomal structure and biogenesis Translation, ribosomal structure and biogenesis
	Ribosomal protein S17	j	Translation, ribosomal structure and biogenesis
	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
	Ribosomal protein S8	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L6P/L9E	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L18 Ribosomal protein S5	J	Translation, ribosomal structure and biogenesis Translation, ribosomal structure and biogenesis
	Ribosomal protein L15	ı	Translation, ribosomal structure and biogenesis
	Preprotein translocase subunit SecY	Ü	Intracellular trafficking, secretion, and vesicular transport
	Adenylate kinase and related kinases	F	Nucleotide transport and metabolism
COG0099	Ribosomal protein S13	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein S11	J	Translation, ribosomal structure and biogenesis
	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	K	Transcription
	Ribosomal protein L17 Transcriptional regulator containing CAE AAA time ATRace, and DNA hinding domains	J K	Translation, ribosomal structure and biogenesis
	Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains Predicted transcriptional regulators	K	Transcription Transcription
	Phosphatidylglycerophosphatase A and related proteins	ì	Lipid transport and metabolism
	Translation initiation factor 3 (IF-3)	J	Translation, ribosomal structure and biogenesis
COG0633	Ferredoxin	С	Energy production and conversion
COG0316	Uncharacterized conserved protein	S	Function unknown
	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	E	Amino acid transport and metabolism
	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes ABC-type Fe3+ transport system, permease component	E P	Amino acid transport and metabolism
	Ribosomal protein L25 (general stress protein Ctc)	,	Inorganic ion transport and metabolism Translation, ribosomal structure and biogenesis
	Peptidyl-tRNA hydrolase	j	Translation, ribosomal structure and biogenesis
	Dephospho-CoA kinase	Н	Coenzyme transport and metabolism
COG0061	Predicted sugar kinase	G	Carbohydrate transport and metabolism
	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	K	Transcription
	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
	Predicted membrane metal-binding protein Predicted aminomethyltransferase related to GcvT	R R	General function prediction only General function prediction only
	Pyridoxal phosphate biosynthesis protein	Н	Coenzyme transport and metabolism
	Ribosomal protein L28	j.	Translation, ribosomal structure and biogenesis
	Lipoate synthase	Н	Coenzyme transport and metabolism
COG2867	Oligoketide cyclase/lipid transport protein	1	Lipid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Hemolysins and related proteins containing CBS domains	R	General function prediction only
	Ferredoxin	С	Energy production and conversion
	Cysteinyl-tRNA synthetase Pentose-5-phosphate-3-epimerase	G G	Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism
	Methionine aminopeptidase	J	Translation, ribosomal structure and biogenesis
	Ubiquinone biosynthesis protein COQ7	н	Coenzyme transport and metabolism
	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	K	Transcription
	Cell division GTPase	D	Cell cycle control, cell division, chromosome partitioning
	Ribosome-associated protein Y (PSrp-1)	J	Translation, ribosomal structure and biogenesis
	Tyrosyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	Bacterioferritin (cytochrome b1) Thisming management cytothese	P	Inorganic ion transport and metabolism
	Thiamine monophosphate synthase Predicted membrane protein	H S	Coenzyme transport and metabolism Function unknown
	Glutamine synthetase	E E	Amino acid transport and metabolism
	Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains	K	Transcription
	Superfamily I DNA and RNA helicases	L	Replication, recombination and repair

	Mg-dependent DNase	L	Replication, recombination and repair
	Preprotein translocase subunit SecB	U	Intracellular trafficking, secretion, and vesicular transport
	Uncharacterized protein conserved in bacteria Dimethyladenosine transferase (rRNA methylation)	S	Function unknown
	Prolyl-tRNA synthetase	j	Translation, ribosomal structure and biogenesis Translation, ribosomal structure and biogenesis
	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	G	Carbohydrate transport and metabolism
	Pyridoxamine-phosphate oxidase	Н	Coenzyme transport and metabolism
	tRNA-dihydrouridine synthase	J	Translation, ribosomal structure and biogenesis
COG0496	Predicted acid phosphatase	R	General function prediction only
COG0029	Aspartate oxidase	Н	Coenzyme transport and metabolism
	ATPase involved in DNA replication	L	Replication, recombination and repair
	NADPH:quinone reductase and related Zn-dependent oxidoreductases	С	Energy production and conversion
	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	H	Coenzyme transport and metabolism
	Porphobilinogen deaminase Predicted nucleoside-diphosphate-sugar epimerases	H M	Coenzyme transport and metabolism
	Predicted Notice significations and a second	L	Cell wall/membrane/envelope biogenesis Replication, recombination and repair
	N-formylmethionyl-tRNA deformylase	j	Translation, ribosomal structure and biogenesis
	Delta-aminolevulinic acid dehydratase	Н	Coenzyme transport and metabolism
COG1295	Predicted membrane protein	S	Function unknown
COG0356	F0F1-type ATP synthase, subunit a	С	Energy production and conversion
COG0054	Riboflavin synthase beta-chain	Н	Coenzyme transport and metabolism
	Preprotein translocase subunit YidC	U	Intracellular trafficking, secretion, and vesicular transport
	Hemolysins and related proteins containing CBS domains	R	General function prediction only
	Protein chain release factor A	J	Translation, ribosomal structure and biogenesis
	1-acyl-sn-glycerol-3-phosphate acyltransferase	I .	Lipid transport and metabolism
	Ribosomal protein S1 Periology is proteoned (Clap class)) J	Translation, ribosomal structure and biogenesis
	Periplasmic serine proteases (CIpP class) ABC-type multidrug transport system, ATPase and permease components	V	Posttranslational modification, protein turnover, chaperones Defense mechanisms
	Ribonucleotide reductase, alpha subunit	F	Nucleotide transport and metabolism
	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	F	Nucleotide transport and metabolism
	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
	ATP-dependent Zn proteases	0	Posttranslational modification, protein turnover, chaperones
	Phenylalanyl-tRNA synthetase beta subunit	J	Translation, ribosomal structure and biogenesis
	Actin-like ATPase involved in cell division	D	Cell cycle control, cell division, chromosome partitioning
	NADH:ubiquinone oxidoreductase subunit 3 (chain A)	С	Energy production and conversion
	NADH: ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases	C C	Energy production and conversion
	NADH:ubiquinone oxidoreductase 27 kD subunit Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	G	Energy production and conversion Carbohydrate transport and metabolism
	3-phosphoglycerate kinase	G	Carbohydrate transport and metabolism
	Penicillin tolerance protein	Ī	Lipid transport and metabolism
	Uroporphyrinogen-III synthase	Н	Coenzyme transport and metabolism
COG0743	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1	Lipid transport and metabolism
COG0536	Predicted GTPase	R	General function prediction only
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Site-specific recombinase XerC	L	Replication, recombination and repair
	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain	F .	Nucleotide transport and metabolism
	3-oxoacyl-(acyl-carrier-protein) synthase	1	Lipid transport and metabolism
	Coproporphyrinogen III oxidase Predicted aspartyl protease	H R	Coenzyme transport and metabolism General function prediction only
	dGTP triphosphohydrolase	F	Nucleotide transport and metabolism
	Recombinational DNA repair protein (RecF pathway)	į.	Replication, recombination and repair
	Uncharacterized protein conserved in bacteria	S	Function unknown
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	С	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
	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	L	Replication, recombination and repair
	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
	Predicted hydrolase of the alpha/beta superfamily	R	General function prediction only
	Cytochrome c2 Folate-dependent phosphoribosylglycinamide formyltransferase PurN	C F	Energy production and conversion
	Leucyl aminopeptidase	E	Nucleotide transport and metabolism Amino acid transport and metabolism
	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
	Uncharacterized enzyme of thiazole biosynthesis	Н	Coenzyme transport and metabolism
	Dihydropteroate synthase and related enzymes	Н	Coenzyme transport and metabolism
COG0801	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	Н	Coenzyme transport and metabolism
	S-adenosylmethionine synthetase	Н	Coenzyme transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	DNA polymerase III, gamma/tau subunits	L	Replication, recombination and repair
	Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C	H M	Coenzyme transport and metabolism
	Apolipoprotein N-acyltransferase Pyrimidine deaminase	H	Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism
	Carbamoylphosphate synthase small subunit	E	Amino acid transport and metabolism
	Ribosomal protein L31	j	Translation, ribosomal structure and biogenesis
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ABC-type transport system involved in cytochrome c biogenesis, permease component	0	Posttranslational modification, protein turnover, chaperones
	Aspartate carbamoyltransferase, catalytic chain	F	Nucleotide transport and metabolism
	Response regulator containing a CheY-like receiver domain and a GGDEF domain	T	Signal transduction mechanisms
	Ribonucleotide reductase, beta subunit	F	Nucleotide transport and metabolism
	Transcription elongation factor	K	Transcription
	Predicted hydrolase of the alpha/beta-hydrolase fold	R	General function prediction only
	IMP dehydrogenase/GMP reductase ARC type transport system involved in resistance to organic solvents, periplasmic component	F	Nucleotide transport and metabolism
	ABC-type transport system involved in resistance to organic solvents, periplasmic component Ribonuclease D	Q J	Secondary metabolites biosynthesis, transport and catabolism Translation, ribosomal structure and biogenesis
	RecA/RadA recombinase	L	Replication, recombination and repair
COG0408	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	C	Energy production and conversion
	DnaJ-class molecular chaperone with C-terminal Zn finger domain	0	Posttranslational modification, protein turnover, chaperones
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COG1160	Predicted GTPases	R	General function prediction only
	Orotate phosphoribosyltransferase	F	Nucleotide transport and metabolism
	Signal recognition particle GTPase	U	Intracellular trafficking, secretion, and vesicular transport
	Dioxygenases related to 2-nitropropane dioxygenase	R	General function prediction only
	Signal recognition particle GTPase 23S rRNA methylase	U J	Intracellular trafficking, secretion, and vesicular transport
	Thymidylate kinase	J F	Translation, ribosomal structure and biogenesis
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	C	Nucleotide transport and metabolism Energy production and conversion
	Predicted Zn-dependent proteases and their inactivated homologs	R	General function prediction only
	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems	R	General function prediction only
	Replicative DNA helicase	L	Replication, recombination and repair
	Phage head maturation protease	R	General function prediction only
	Pseudouridylate synthases, 23S RNA-specific	J	Translation, ribosomal structure and biogenesis
	Thioredoxin reductase	0	Posttranslational modification, protein turnover, chaperones
COG0450	Peroxiredoxin	0	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	С	Energy production and conversion
	Seryl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	tRNA delta(2)-isopentenylpyrophosphate transferase	J	Translation, ribosomal structure and biogenesis
	Cytochrome c biogenesis factor	0	Posttranslational modification, protein turnover, chaperones
	Holliday junction resolvasome, DNA-binding subunit	L	Replication, recombination and repair
	Holliday junction resolvasome, helicase subunit	L	Replication, recombination and repair
	Metal-dependent hydrolases of the beta-lactamase superfamily I	R	General function prediction only
	Ribosomal protein S4 and related proteins GTP cyclohydrolase I	J H	Translation, ribosomal structure and biogenesis
	F0F1-type ATP synthase, gamma subunit	C	Coenzyme transport and metabolism Energy production and conversion
	UDP-N-acetylmuramate dehydrogenase	М	Cell wall/membrane/envelope biogenesis
	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase and related proteins	G	Carbohydrate transport and metabolism
	Predicted O-methyltransferase	R	General function prediction only
	Aconitase A	C	Energy production and conversion
COG1565	Uncharacterized conserved protein	S	Function unknown
	Valyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	Protein chain release factor B	J	Translation, ribosomal structure and biogenesis
	DNA mismatch repair enzyme (predicted ATPase)	L	Replication, recombination and repair
COG0502	Biotin synthase and related enzymes	Н	Coenzyme transport and metabolism
COG0156	7-keto-8-aminopelargonate synthetase and related enzymes	Н	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	н	Coenzyme transport and metabolism
COG0132	Dethiobiotin synthetase	н	Coenzyme transport and metabolism
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Н	Coenzyme transport and metabolism
COG1622	Heme/copper-type cytochrome/quinol oxidases, subunit 2	С	Energy production and conversion
	Heme/copper-type cytochrome/quinol oxidases, subunit 1	С	Energy production and conversion
	Polyprenyltransferase (cytochrome oxidase assembly factor)	0	Posttranslational modification, protein turnover, chaperones
	Rieske Fe-S protein	С	Energy production and conversion
	Cytochrome b subunit of the bc complex	С	Energy production and conversion
	Cytochrome c1	C	Energy production and conversion
	Preprotein translocase subunit SecD	U	Intracellular trafficking, secretion, and vesicular transport
	2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase	н	Coenzyme transport and metabolism
	3-oxoacyl-[acyl-carrier-protein] synthase III	!	Lipid transport and metabolism
	Fatty acid/phospholipid biosynthesis enzyme Ribosomal protein L32	j	Lipid transport and metabolism Translation, ribosomal structure and biogenesis
	NADH:ubiquinone oxidoreductase 24 kD subunit	c	Energy production and conversion
	Predicted unusual protein kinase	R	General function prediction only
	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
	Uncharacterized conserved protein	S	Function unknown
	Chaperonin GroEL (HSP60 family)	0	Posttranslational modification, protein turnover, chaperones
	Co-chaperonin GroES (HSP10)	0	Posttranslational modification, protein turnover, chaperones
COG0760	Parvulin-like peptidyl-prolyl isomerase	0	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	1	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	Lipid transport and metabolism
COG0328	Ribonuclease HI	L	Replication, recombination and repair
	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Transcription elongation factor	K	Transcription
	DNA polymerase I - 3'-5' exonuclease and polymerase domains	L	Replication, recombination and repair
	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
	Ribosomal protein L1	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L11	J	Translation, ribosomal structure and biogenesis
	Transcription antiterminator	K J	Transcription Translation, ribosomal structure and biogenesis
	Ribosomal protein S7 Ribosomal protein S12	J	Translation, ribosomal structure and biogenesis Translation, ribosomal structure and biogenesis
	NADH:ubiquinone oxidoreductase subunit 4 (chain M)	C	Energy production and conversion
	NADH:ubiquinone oxidoreductase subunit 4 (chain N)	C	Energy production and conversion
	Biotin-(acetyl-CoA carboxylase) ligase	н	Coenzyme transport and metabolism
	Geranylgeranyl pyrophosphate synthase	н	Coenzyme transport and metabolism
	ABC-type transport system involved in resistance to organic solvents, permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
	ABC-type transport system involved in resistance to organic solvents, ATPase component	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted ATPase or kinase	R	General function prediction only
	Ribonuclease HII	Ĺ	Replication, recombination and repair
	Transketolase	G	Carbohydrate transport and metabolism
	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	С	Energy production and conversion
	Outer membrane lipoprotein-sorting protein	M	Cell wall/membrane/envelope biogenesis
	Single-stranded DNA-specific exonuclease	L	Replication, recombination and repair
	Folylpolyglutamate synthase	Н	Coenzyme transport and metabolism
	Outer membrane protein/protective antigen OMA87	M	Cell wall/membrane/envelope biogenesis
	Predicted membrane-associated Zn-dependent proteases 1	M	Cell wall/membrane/envelope biogenesis
	Glucoamylase and related glycosyl hydrolases	G	Carbohydrate transport and metabolism
	Transcriptional regulator	K	Transcription
COG 1947	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase	1	Lipid transport and metabolism

COG1225	Peroxiredoxin	0	Posttranslational modification, protein turnover, chaperones
	Na+/proline symporter	E	Amino acid transport and metabolism
COG0194	Guanylate kinase	F	Nucleotide transport and metabolism
	Citrate synthase	С	Energy production and conversion
COG0148		G	Carbohydrate transport and metabolism
	Inorganic pyrophosphatase	C	Energy production and conversion
	Glutamyl- and glutaminyl-tRNA synthetases	J S	Translation, ribosomal structure and biogenesis
	Predicted membrane protein Flp pilus assembly protein, ATPase CpaF	S U	Function unknown Intracellular trafficking, secretion, and vesicular transport
	Type IV secretory pathway, component VirB8	U	Intracellular trafficking, secretion, and vesicular transport
	GTP cyclohydrolase II	н	Coenzyme transport and metabolism
	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	c	Energy production and conversion
	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	0	Posttranslational modification, protein turnover, chaperones
	Protease subunit of ATP-dependent Clp proteases	0	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
	Transaldolase	G	Carbohydrate transport and metabolism
	Lysyl-tRNA synthetase (class I)	J	Translation, ribosomal structure and biogenesis
	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	Н	Coenzyme transport and metabolism
	Thioredoxin reductase	0	Posttranslational modification, protein turnover, chaperones
	Histidyl-tRNA synthetase	T	Translation, ribosomal structure and biogenesis
	Stress-induced morphogen (activity unknown) Nitrate/nitrite transporter	I P	Signal transduction mechanisms
	Signal peptidase I	U	Inorganic ion transport and metabolism Intracellular trafficking, secretion, and vesicular transport
	2-methylthioadenine synthetase	J	Translation, ribosomal structure and biogenesis
	Protoheme ferro-lyase (ferrochelatase)	H	Coenzyme transport and metabolism
	Ribosomal protein S20	 J	Translation, ribosomal structure and biogenesis
	Orotidine-5'-phosphate decarboxylase	F	Nucleotide transport and metabolism
	Membrane protein TerC, possibly involved in tellurium resistance	Р	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	1	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	С	Energy production and conversion
COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	Н	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	Р	Inorganic ion transport and metabolism
	tmRNA-binding protein	0	Posttranslational modification, protein turnover, chaperones
	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	F	Nucleotide transport and metabolism
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Phosphoribosylpyrophosphate synthetase	F	Nucleotide transport and metabolism
	Thioredoxin-like proteins and domains	0	Posttranslational modification, protein turnover, chaperones
	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	C	Energy production and conversion
	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase 7-keto-8-aminopelargonate synthetase and related enzymes	H H	Coenzyme transport and metabolism
	Cytochrome c-type biogenesis protein CcmE	0	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones
	Predicted hydrolase of the metallo-beta-lactamase superfamily	R	General function prediction only
	2-methylthioadenine synthetase	 J	Translation, ribosomal structure and biogenesis
	Multidrug resistance efflux pump	V	Defense mechanisms
	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
	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport and metabolism
	Ornithine/acetylornithine aminotransferase	E	Amino acid transport and metabolism
	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	0	Posttranslational modification, protein turnover, chaperones
	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	F	Nucleotide transport and metabolism
	Riboflavin synthase alpha chain	H	Coenzyme transport and metabolism
	Prolipoprotein diacylglyceryltransferase Uncharacterized protein required for cytochrome oxidase assembly	М О	Cell wall/membrane/envelope biogenesis Posttranslational modification, protein turnover, chaperones
	Type IV secretory pathway, VirB4 components	U	Intracellular trafficking, secretion, and vesicular transport
	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Nucleotide-binding protein implicated in inhibition of septum formation	D	Cell cycle control, cell division, chromosome partitioning
	Translation initiation factor 1 (IF-1)	J	Translation, ribosomal structure and biogenesis
COG1225	Peroxiredoxin	0	Posttranslational modification, protein turnover, chaperones
COG0475	Kef-type K+ transport systems, membrane components	Р	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
	Phosphoglyceromutase	G	Carbohydrate transport and metabolism
	Predicted hydrolase of the alpha/beta superfamily	R	General function prediction only
	Methionyl-tRNA synthetase	J	Translation, ribosomal structure and biogenesis
	Thioredoxin domain-containing protein	0	Posttranslational modification, protein turnover, chaperones
	Ribosomal protein L19	J	Translation, ribosomal structure and biogenesis
	tRNA-(guanine-N1)-methyltransferase	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L27	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L21 Recombinational DNA repair protein (RecF pathway)	L	Translation, ribosomal structure and biogenesis Replication, recombination and repair
	Protein-disulfide isomerase	0	Posttranslational modification, protein turnover, chaperones
	Protein-disulfide isomerase	0	Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
	Predicted GTPase, probable translation factor	0	Translation, ribosomal structure and biogenesis
	Predicted Zn-dependent peptidases	R	General function prediction only
	Predicted Zn-dependent peptidases	R	General function prediction only
	Lipoprotein signal peptidase	M	Cell wall/membrane/envelope biogenesis
	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

COG4105			
COG4105	Predicted S-adenosylmethionine-dependent methyltransferase	R	General function prediction only
COG0151	DNA uptake lipoprotein	R	General function prediction only
	Phosphoribosylamine-glycine ligase	F	Nucleotide transport and metabolism
	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
COG3038	Cytochrome B561	С	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
	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG0371	Glycerol dehydrogenase and related enzymes	С	Energy production and conversion
COG2938	Uncharacterized conserved protein	S	Function unknown
COG0575	CDP-diglyceride synthetase	1	Lipid transport and metabolism
	Undecaprenyl pyrophosphate synthase	1	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	н	Coenzyme transport and metabolism
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	С	Energy production and conversion
COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	Н	Coenzyme transport and metabolism
COG0817	Holliday junction resolvasome, endonuclease subunit	L	Replication, recombination and repair
COG0039	Malate/lactate dehydrogenases	С	Energy production and conversion
COG0756	dUTPase	F	Nucleotide transport and metabolism
COG1159	GTPase	R	General function prediction only
COG0331	(acyl-carrier-protein) S-malonyltransferase	1	Lipid transport and metabolism
COG0358	DNA primase (bacterial type)	L	Replication, recombination and repair
COG0736	Phosphopantetheinyl transferase (holo-ACP synthase)	1	Lipid transport and metabolism
COG0717	Deoxycytidine deaminase	F	Nucleotide transport and metabolism
COG0026	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)	F	Nucleotide transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	Lipid transport and metabolism
COG5410	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uroporphyrinogen-III decarboxylase	н	Coenzyme transport and metabolism
	Quinolinate synthase	н	Coenzyme transport and metabolism
	Phosphopantetheine adenylyltransferase	н	Coenzyme transport and metabolism
	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
COG4638	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	Р	Inorganic ion transport and metabolism
	Antirestriction protein	L	Replication, recombination and repair
	Multimeric flavodoxin WrbA	R	General function prediction only
	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
	FAD/FMN-containing dehydrogenases	С	Energy production and conversion
	FAD/FMN-containing dehydrogenases	С	Energy production and conversion
	2-keto-4-pentenoate hydratase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Endopolygalacturonase	M	Cell wall/membrane/envelope biogenesis
	Fe-S oxidoreductase	С	Energy production and conversion
	Beta-galactosidase/beta-glucuronidase	G	Carbohydrate transport and metabolism
	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
	CMP-N-acetylneuraminic acid synthetase	M	Cell wall/membrane/envelope biogenesis
COG1083			
	Uncharacterized protein related to capsule biosynthesis enzymes	R	
COG3550	Uncharacterized protein related to capsule biosynthesis enzymes Pterin-4a-carbinolamine dehydratase	R	General function prediction only
COG3550 COG2154	Pterin-4a-carbinolamine dehydratase		General function prediction only Coenzyme transport and metabolism
COG3550 COG2154 COG1960	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases	R H I	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism
COG3550 COG2154 COG1960 COG1070	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases	R H	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases	R H I G I	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases	R H I G	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS)	R H I G I C	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase	R H I G I C J	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase	R H I G I C J M	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438 COG1192	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning	R H I G I C J M M	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438 COG1192 COG0157	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase	R H I G I C J M M D H	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438 COG1192 COG0157 COG0665	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating)	R H G I C J M D H E	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438 COG1192 COG0157 COG0665 COG2605	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase	R H I G I C J M D H E R	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase	R H I G I C J M D H E R	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942 COG2377	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases	R H I G I C J M D H E R G O	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG01192 COG0157 COG0665 COG2605 COG2942 COG2977 COG0545	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase Glycosyltransferase Glycosyltransferase Glyconed in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1	R H I G I C J M D H E R	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942 COG2377 COG0545 COG1045	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosyhorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase	R H I G I C J M D H E R G O O	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942 COG2377 COG0545 COG1045 COG1959	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase Predicted transcriptional regulator	R H I G I C J M D H E R G O O E K	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG01192 COG0157 COG0665 COG2605 COG2942 COG2377 COG0545 COG1045 COG1045 COG1045 COG1045	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUA5) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase Predicted transcriptional regulator DnaJ-domain-containing proteins 1	R H I G I C J M D H E R G O E	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942 COG0157 COG0545 COG1045 COG1959 COG1076 COG0598	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase Predicted transcriptional regulator DnaJ-domain-containing proteins 1 Mg2+ and Co2+ transporters	R H I G I C J M D H E R G O E K O P	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism
COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG1192 COG0157 COG0665 COG2605 COG2942 COG377 COG0545 COG1045 COG10598 COG2588	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acytransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosyhorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase Predicted transcriptional regulator DnaJ-domain-containing proteins 1 Mg2+ and Co2+ transporters Predicted acetyltransferase	R H I G I C J M D H E R G O E K O P R	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism General function prediction only
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COG3550 COG2154 COG1960 COG1070 COG1835 COG0277 COG0009 COG0438 COG0438 COG0157 COG0665 COG2605 COG2942 COG0197 COG0598 COG1959 COG2388 COG5066 COG2197 COG3916 COG2197 COG0599 COG2175 COG0599 COG2175 COG0599 COG2175 COG02223	Pterin-4a-carbinolamine dehydratase Acyl-CoA dehydrogenases Sugar (pentulose and hexulose) kinases Predicted acyltransferases FAD/FMN-containing dehydrogenases Putative translation factor (SUAS) Glycosyltransferase Glycosyltransferase Glycosyltransferase Glycosyltransferase ATPases involved in chromosome partitioning Nicotinate-nucleotide pyrophosphorylase Glycine/D-amino acid oxidases (deaminating) Predicted kinase related to galactokinase and mevalonate kinase N-acyl-D-glucosamine 2-epimerase Predicted molecular chaperone distantly related to HSP70-fold metalloproteases FKBP-type peptidyl-prolyl cis-trans isomerases 1 Serine acetyltransferase Predicted transcriptional regulator DnaJ-domain-containing proteins 1 Mg2+ and Co2+ transporters Predicted acetyltransferase Predicted acetyltransferase Predicted metal-dependent hydrolase of the TIM-barrel fold Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain N-acyl-L-homoserine lactone synthetase Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit Probable taurine catabolism dioxygenase Nitrate/nitrite transporter Predicted cateamidase/formamidase Short-chain dehydrogenases of various substrate specificities	RHIGICJM MDHERGOOEKOPRRTTMSQPCR	General function prediction only Coenzyme transport and metabolism Lipid transport and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Translation, ribosomal structure and biogenesis Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning Coenzyme transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism General function prediction only General function prediction only General function prediction only Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms Sell wall/membrane/envelope biogenesis Function unknown Secondary metabolites biosynthesis, transport and catabolism Inorganic ion transport and metabolism Energy production and conversion General function prediction only
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COG0793	Periplasmic protease	M	Cell wall/membrane/envelope biogenesis
COG4771	Outer membrane receptor for ferrienterochelin and colicins	Р	Inorganic ion transport and metabolism
	Uncharacterized protein involved in copper resistance	P	Inorganic ion transport and metabolism
	Predicted methyltransferase (contains TPR repeat)	R	General function prediction only
	Predicted membrane protein	S	Function unknown
	Integral membrane protein CcmA involved in cell shape determination	М	Cell wall/membrane/envelope biogenesis
	Short-chain alcohol dehydrogenase of unknown specificity Transcriptional regulator	R K	General function prediction only Transcription
	Peroxiredoxin	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized conserved protein	S	Function unknown
	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
	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
	Membrane-bound lytic murein transglycosylase B	M	Cell wall/membrane/envelope biogenesis
	Predicted phosphatases	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	Predicted membrane protein Uncharacterized conserved protein	S S	Function unknown Function unknown
	Alcohol dehydrogenase, class IV	C	Energy production and conversion
	Predicted permeases	R	General function prediction only
	ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism
COG4675	Microcystin-dependent protein	S	Function unknown
COG0438	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ATPases involved in chromosome partitioning	D	Cell cycle control, cell division, chromosome partitioning
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	Predicted membrane protein	S	Function unknown
	ABC-type arginine transport system, permease component	E L	Amino acid transport and metabolism
	Uracil DNA glycosylase Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Replication, recombination and repair Amino acid transport and metabolism
	Glutathione peroxidase	0	Posttranslational modification, protein turnover, chaperones
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
	Predicted ring-cleavage extradiol dioxygenase	R	General function prediction only
	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
	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure and biogenesis
	Beta-galactosidase	G	Carbohydrate transport and metabolism
	Prephenate dehydrogenase	E H	Amino acid transport and metabolism
	3-polyprenyl-4-hydroxybenzoate decarboxylase Transcriptional regulator	K	Coenzyme transport and metabolism Transcription
	NADPH:quinone reductase and related Zn-dependent oxidoreductases	Č	Energy production and conversion
	Predicted membrane protein/domain	S	Function unknown
	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
	FOG: EAL domain	Т	Signal transduction mechanisms
	Uncharacterized MobA-related protein	R	General function prediction only
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Ţ	Signal transduction mechanisms
	Homogentisate 1,2-dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted metal-dependent hydrolase with the TIM-barrel fold Enterochelin esterase and related enzymes	R P	General function prediction only
	Methyl-accepting chemotaxis protein	N N	Inorganic ion transport and metabolism Cell motility
	FOG: CheY-like receiver	T	Signal transduction mechanisms
	Beta-glucanase/Beta-glucan synthetase	G	Carbohydrate transport and metabolism
	Pyrroline-5-carboxylate reductase	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	1	Lipid transport and metabolism
COG3011	Uncharacterized protein conserved in bacteria	S	Function unknown
	Proline racemase	E	Amino acid transport and metabolism
	Multidrug resistance efflux pump	V	Defense mechanisms
	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
	Esterase/lipase	I M	Lipid transport and metabolism
	ADP-heptose:LPS heptosyltransferase Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
	G:T/U mismatch-specific DNA glycosylase	L	Replication, recombination and repair
	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)	j	Translation, ribosomal structure and biogenesis
	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
	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	1	Lipid transport and metabolism
	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	K	Transcription
	Cellulase M and related proteins	G	Carbohydrate transport and metabolism
	D-alanine-D-alanine ligase and related ATP-grasp enzymes	M	Cell wall/membrane/envelope biogenesis
	ABC-type transport system involved in cytochrome c biogenesis, ATPase component	0	Posttranslational modification, protein turnover, chaperones
	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits Membrane protease subunits, stomatin/prohibitin homologs	C 0	Energy production and conversion Posttranslational modification, protein turnover, chaperones
	Anthranilate/para-aminobenzoate synthases component I	E	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	NAD/NADP transhydrogenase alpha subunit	C	Energy production and conversion
	NAD/NADP transhydrogenase alpha subunit	С	Energy production and conversion
	NAD/NADP transhydrogenase beta subunit	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
COG0665	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism

COG0413	Ketopantoate hydroxymethyltransferase	Н	Coenzyme transport and metabolism
	Ribosomal protein S21	J	Translation, ribosomal structure and biogenesis
	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	C	Energy production and conversion
	Regulator of competence-specific genes	K	Transcription
	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family ABC-type uncharacterized transport system, periplasmic component	O R	Posttranslational modification, protein turnover, chaperones General function prediction only
	ABC-type uncharacterized transport system, permassinc component ABC-type uncharacterized transport system, permasse component	R	General function prediction only
	ABC-type uncharacterized transport system, ATPase component	R	General function prediction only
	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	E	Amino acid transport and metabolism
	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
	Ketol-acid reductoisomerase	E	Amino acid transport and metabolism
	Actin-like ATPase involved in cell morphogenesis	D	Cell cycle control, cell division, chromosome partitioning
	Cell shape-determining protein	M	Cell wall/membrane/envelope biogenesis
	Cell division protein FtsI/penicillin-binding protein 2	M E	Cell wall/membrane/envelope biogenesis
	Putative threonine efflux protein ABC-type uncharacterized transport systems, ATPase components	R	Amino acid transport and metabolism General function prediction only
	ABC-type uncharacterized transport system, permease component	R	General function prediction only
	Purine nucleoside phosphorylase	F	Nucleotide transport and metabolism
	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
	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
	Glycosidases	G	Carbohydrate transport and metabolism
	FOG: EAL domain	T	Signal transduction mechanisms
	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	С	Energy production and conversion
	Multisubunit Na+/H+ antiporter, MnhE subunit	P	Inorganic ion transport and metabolism Function unknown
	Uncharacterized conserved protein Micrococcal nuclease (thermonuclease) homologs	S L	Replication, recombination and repair
	Predicted membrane protein	S	Function unknown
	N-terminal domain of molybdenum-binding protein	R	General function prediction only
	NADPH:quinone reductase and related Zn-dependent oxidoreductases	c	Energy production and conversion
	Predicted transcriptional regulators	K	Transcription
COG0526	Thiol-disulfide isomerase and thioredoxins	0	Posttranslational modification, protein turnover, chaperones
COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	1	Lipid transport and metabolism
COG1171	Threonine dehydratase	E	Amino acid transport and metabolism
COG0546	Predicted phosphatases	R	General function prediction only
	Uncharacterized protein involved in biosynthesis of c-type cytochromes	0	Posttranslational modification, protein turnover, chaperones
	Molybdopterin biosynthesis enzymes	н	Coenzyme transport and metabolism
	Predicted membrane protein	S	Function unknown
	Pyruvate kinase Predicted membrane protein	G S	Carbohydrate transport and metabolism
	Integral membrane protein possibly involved in chromosome condensation	D D	Function unknown Cell cycle control, cell division, chromosome partitioning
	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
	Holliday junction resolvase	Ĺ	Replication, recombination and repair
	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
	Periplasmic glucans biosynthesis protein	Р	Inorganic ion transport and metabolism
	Gluconolactonase	G	Carbohydrate transport and metabolism
	Transcription elongation factor	K	Transcription
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
	ABC-type uncharacterized transport system, permease component	R R	General function prediction only
	Uncharacterized ABC-type transport system, permease component Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein	R	General function prediction only General function prediction only
	Predicted transcriptional regulator	K	Transcription
	Response regulator containing a CheY-like receiver domain and a GGDEF domain	T	Signal transduction mechanisms
	Predicted exonuclease of the beta-lactamase fold involved in RNA processing	j	Translation, ribosomal structure and biogenesis
	Rhodanese-related sulfurtransferase	Р	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	0	Posttranslational modification, protein turnover, chaperones
	ADP-ribose pyrophosphatase	F	Nucleotide transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Phosphomannomutase	G	Carbohydrate transport and metabolism
	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	K E	Transcription Amino acid transport and metabolism
	Lactoylglutathione lyase and related lyases Multidrug resistance efflux pump	V	Defense mechanisms
	Predicted epimerase, PhzC/PhzF homolog	v R	General function prediction only
	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
	Predicted sugar phosphate isomerase	R	General function prediction only
	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
	Thiol-disulfide isomerase and thioredoxins	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized conserved protein	S	Function unknown
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Argininosuccinate synthase	E P	Amino acid transport and metabolism
	NhaP-type Na+/H+ and K+/H+ antiporters Outer membrane recentor proteins, mostly Fe transport	P P	Inorganic ion transport and metabolism
	Outer membrane receptor proteins, mostly Fe transport Nicotinamide mononucleotide transporter	Р Н	Inorganic ion transport and metabolism Coenzyme transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Ī	Lipid transport and metabolism
	Metal-dependent hydrolase	R	General function prediction only
	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)	С	Energy production and conversion
COG0863	DNA modification methylase	L	Replication, recombination and repair
	Nitroreductase	C	Energy production and conversion
		C R	

	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
	Predicted transcriptional regulators	K	Transcription
	Zn-dependent alcohol dehydrogenases Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	R T	General function prediction only Signal transduction mechanisms
	Cation/multidrug efflux pump	v	Defense mechanisms
	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
	Acyl-[acyl carrier protein]UDP-N-acetylglucosamine O-acyltransferase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Lipid A disaccharide synthetase DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	M K	Cell wall/membrane/envelope biogenesis Transcription
	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	Т	Signal transduction mechanisms
COG0346	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	C	Energy production and conversion
	Acetyltransferases Clutathione S transferase	R O	General function prediction only Posttranslational modification, protein turnover, chaperones
	Glutathione S-transferase Anti-sigma factor	Т	Signal transduction mechanisms
	Predicted enzyme of the cupin superfamily	R	General function prediction only
COG2706	3-carboxymuconate cyclase	G	Carbohydrate transport and metabolism
	SOS-response transcriptional repressors (RecA-mediated autopeptidases)	K	Transcription
	Molybdopterin biosynthesis enzyme	Н	Coenzyme transport and metabolism
	Molybdenum cofactor biosynthesis enzyme Acetyltransferases	H R	Coenzyme transport and metabolism General function prediction only
	Indole-3-glycerol phosphate synthase	E	Amino acid transport and metabolism
	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
	Uncharacterized conserved protein	S	Function unknown
	Anthranilate/para-aminobenzoate synthases component II	E E	Amino acid transport and metabolism
	Anthranilate/para-aminobenzoate synthases component I Predicted small integral membrane protein	S	Amino acid transport and metabolism Function unknown
	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
	Transcriptional regulator	K	Transcription
	3-deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase	M	Cell wall/membrane/envelope biogenesis
	Predicted Fe-S oxidoreductases	R	General function prediction only
	Transcriptional regulator	K S	Transcription Function unknown
	Uncharacterized protein conserved in bacteria Biopolymer transport proteins	S U	Intracellular trafficking, secretion, and vesicular transport
	Metal-dependent hydrolases of the beta-lactamase superfamily I	R	General function prediction only
	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Superfamily I DNA and RNA helicases and helicase subunits	L	Replication, recombination and repair
	Sugar phosphate permease rRNA methylases	G	Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis
	Nitroreductase	C	Energy production and conversion
	Predicted metal-dependent hydrolase	R	General function prediction only
COG0705	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	R	General function prediction only
	Predicted membrane protein	S	Function unknown
	Uncharacterized iron-regulated membrane protein	S	Function unknown
	Peroxiredoxin NADPH-dependent glutamate synthase beta chain and related oxidoreductases	O E	Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	Predicted membrane protein	S	Function unknown
	NhaP-type Na+/H+ and K+/H+ antiporters	P	Inorganic ion transport and metabolism
	Purine nucleoside permease	F	Nucleotide transport and metabolism
	Predicted O-methyltransferase	R E	General function prediction only
	L-asparaginase II Predicted transcriptional regulators	K	Amino acid transport and metabolism Transcription
	Fe-S oxidoreductase	C	Energy production and conversion
	Acyl-CoA dehydrogenases	Ī	Lipid transport and metabolism
COG0583	Transcriptional regulator	K	Transcription
	Serine kinase of the HPr protein, regulates carbohydrate metabolism	Т	Signal transduction mechanisms
	Sugar phosphate permease	G R	Carbohydrate transport and metabolism
	Acetyltransferase (isoleucine patch superfamily) Rhodanese-related sulfurtransferase	R P	General function prediction only Inorganic ion transport and metabolism
	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC	M	Cell wall/membrane/envelope biogenesis
COG0236	Acyl carrier protein	1	Lipid transport and metabolism
	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	1	Lipid transport and metabolism
	GTP:adenosylcobinamide-phosphate guanylyltransferase	Н	Coenzyme transport and metabolism
	Threonine dehydratase DNA gyrase inhibitor	E L	Amino acid transport and metabolism Replication, recombination and repair
	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
	Phosphoenolpyruvate carboxylase	С	Energy production and conversion
	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
	Gluconolactonase	G	Carbohydrate transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P H	Inorganic ion transport and metabolism
	Methylase involved in ubiquinone/menaquinone biosynthesis Sulfate permease and related transporters (MFS superfamily)	P	Coenzyme transport and metabolism Inorganic ion transport and metabolism
	UDP-galactopyranose mutase	M	Cell wall/membrane/envelope biogenesis
COG2267	Lysophospholipase	1	Lipid transport and metabolism
	dTDP-glucose pyrophosphorylase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
	Uncharacterized protein conserved in bacteria Ammonia permease	S P	Function unknown Inorganic ion transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted membrane protein	S	Function unknown
	Uncharacterized NAD(FAD)-dependent dehydrogenases	R	General function prediction only
	Uncharacterized protein involved in tolerance to divalent cations	P	Inorganic ion transport and metabolism
	Esterase/lipase Uncharacterized conserved protein	l S	Lipid transport and metabolism Function unknown
	Cystathionine beta-lyases/cystathionine gamma-synthases	S E	Amino acid transport and metabolism
		-	

COG1832			
	Predicted CoA-binding protein	R	General function prediction only
COG1024	Enoyl-CoA hydratase/carnithine racemase	1	Lipid transport and metabolism
COG1739	Uncharacterized conserved protein	S	Function unknown
COG3667	Uncharacterized protein involved in copper resistance	Р	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
	Transcriptional regulators	K	Transcription
	Site-specific recombinase XerC	L	Replication, recombination and repair
	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
	ADP-glucose pyrophosphorylase	G	Carbohydrate transport and metabolism
	FAD/FMN-containing dehydrogenases	С	Energy production and conversion
	Homoserine dehydrogenase	E	Amino acid transport and metabolism
	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	R	General function prediction only
	Biotin carboxyl carrier protein	!	Lipid transport and metabolism
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Outer membrane receptor for ferrienterochelin and colicins	P 	Inorganic ion transport and metabolism
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
	Glycogen synthase	G P	Carbohydrate transport and metabolism
	Predicted iron-dependent peroxidase	R	Inorganic ion transport and metabolism
	Aldo/keto reductases, related to diketogulonate reductase Cytosine/uracil/thiamine/allantoin permeases	F	General function prediction only Nucleotide transport and metabolism
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Transcriptional regulators	K	Transcription
	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
	Acyl-CoA dehydrogenases	,	Lipid transport and metabolism
	NAD-dependent aldehyde dehydrogenases	c	Energy production and conversion
	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	В	Chromatin structure and dynamics
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Ketopantoate reductase	н	Coenzyme transport and metabolism
	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
	Gluconate kinase	G	Carbohydrate transport and metabolism
	ABC-type Fe3+-hydroxamate transport system, periplasmic component	P	Inorganic ion transport and metabolism
	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	i	Lipid transport and metabolism
	Predicted transcriptional regulators	K	Transcription
	Sulfate permease and related transporters (MFS superfamily)	Р	Inorganic ion transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
	Transposase and inactivated derivatives	L	Replication, recombination and repair
	Transcriptional regulators	K	Transcription
	Uncharacterized protein probably involved in high-affinity Fe2+ transport	Р	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	0	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		Carbabudata transport and matabalism
COG0673		G	Carbohydrate transport and metabolism
0000075	Predicted dehydrogenases and related proteins	G R	General function prediction only
	·		
COG0463	Predicted dehydrogenases and related proteins	R	General function prediction only
COG0463 COG1396	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis	R M K R	General function prediction only Cell wall/membrane/envelope biogenesis
COG0463 COG1396 COG3577 COG1803	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase	R M K R G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase	R M K R G R	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component	R M K R G R	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639 COG0456	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases	R M K R G R P R	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639 COG0456 COG0463	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis	R M K R G R P R M	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639 COG0456 COG0463	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein	R M K R G R P R M E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639 COG0456 COG0463 COG1280 COG3952	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein	R M K G R P R M E S	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown
COG0463 COG1396 COG3577 COG1803 COG0388 COG3639 COG0456 COG0463 COG1280 COG3952 COG0559	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease components	R M K R G R P R M E S E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG0456 COG0456 COG0463 COG1280 COG3952 COG0559	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport system, permease components	R M K R G R P R M E S E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG0456 COG0463 COG1280 COG3952 COG0559 COG4177 COG0411	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component	R M K G R P R M E S E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG0456 COG0463 COG1280 COG3952 COG0559 COG4177 COG0411 COG1125	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase component	R M K G R P R M E S E E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG0388 COG0465 COG0463 COG1280 COG3952 COG0559 COG4177 COG0411 COG1125 COG1732	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type pranched-chain amino acid transport system, APase component ABC-type proline/glycine betaine transport systems, ATPase components Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)	R M K R G R M E S E E E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis
COG0463 COG1396 COG3577 COG1803 COG0388 COG0456 COG0456 COG0463 COG1280 COG0559 COG4177 COG0411 COG1125 COG1732 COG0683	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase components ABC-type proline/glycine betaine transport systems, ATPase components ABC-type pronched-chain amino acid transport systems, ATPase components ABC-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic components	R M K G R P R M E S E E E E E M E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
C0G0463 C0G1396 C0G3577 C0G1803 C0G0456 C0G0456 C0G0463 C0G1280 C0G3952 C0G0595 C0G4177 C0G0411 C0G1125 C0G173 C0G0683 C0G0683 C0G1047	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type pranched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type pranched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2	R M K G R P R M E S E E E E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones
C0G0463 C0G3796 C0G3797 C0G1803 C0G0388 C0G03639 C0G0463 C0G1280 C0G3952 C0G0577 C0G0417 C0G0411 C0G1732 C0G0633 C0G1732 C0G0637 C0G0477	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC	R M K R G R M E S E E E M E O L	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair
COG0463 COG1396 COG3577 COG1803 COG0388 COG0388 COG0456 COG0456 COG0459 COG0459 COG0417 COG0417 COG0417 COG0417 COG0683 COG1047 COG0683 COG0497 COG0683	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type pranched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria	R M K R G R M E S E E E E M E O L S	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown
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C0G0463 C0G1396 C0G3577 C0G1803 C0G0468 C0G0466 C0G0463 C0G1280 C0G3952 C0G0595 C0G4177 C0G0411 C0G1125 C0G1047 C0G0683 C0G1047 C0G493 C0G494	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type pranched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes	R M K G R P R M E S E E E E O L S R L	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair
COG0463 COG1396 COG1397 COG1803 COG0388 COG0463 COG0456 COG0412 COG0552 COG0552 COG0552 COG1732 COG0683 COG1073 COG04973 COG04973 COG04973 COG04974 COG1373	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Metyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase components Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins	R M K R G R M E S E E E M E O L S R M	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis
COG0463 COG1396 COG3577 COG1803 COG03563 COG0456 COG0456 COG0456 COG0417 COG0411 COG0172 COG053 COG0473 COG0473 COG0473 COG0473 COG0473 COG0473 COG0474 COG047	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine transport systems, ATPase components Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators	R M K G R P R M E S E E E E O L S R L M K	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription
COG0463 COG1396 COG3577 COG1803 COG03639 COG0466 COG0463 COG1280 COG0599 COG4177 COG0411 COG1722 COG0599 COG1732 COG0599 COG1737 COG0494 COG1922 COG1653	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase component ABC-type proline/glycine betaine transport systems, periplasmic components FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport system, periplasmic component	R M K R G R P R M E S E E E E E E O L S R L M K G G R D C I S R D L S R D C I S R D C I S R D C I S R D C I S R D C I S R D C I S R D C I S R D C I S R D C I S I S R D C I S I S R D I S I S I S I S I S I S I S I S I S I	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism
COG0463 COG1396 COG357 COG1803 COG0368 COG0466 COG04663 COG1280 COG0456 COG0467 COG0417 COG0411 COG1125 COG0763 COG0563 COG1047 COG0494 COG1922 COG1653 COG175	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type pentidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport system, periplasmic component ABC-type sugar transport system, periplasmic component	R M K R G R M E S E E E E M E O L S R L M K G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG0463 COG1396 COG1397 COG1803 COG0388 COG0395 COG0456 COG0417 COG0417 COG0412 COG1280 COG1323 COG0583 COG1073 COG0583 COG1073 COG0583 COG1073 COG0583 COG1075 COG0595 COG1373 COG0583 COG0697 COG0595 COG1575 COG0995	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Metyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease components ABC-type sugar transport system, permease components	R M K G R P R M E S E E E E M E O L S R L M K G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Transcription recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG0463 COG1396 COG3577 COG1803 COG3639 COG0466 COG0463 COG1280 COG0456 COG0417 COG0411 COG1125 COG053 COG0437 COG0438 COG175 COG0338	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase components Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease components ABC-type sugar transport systems, permease components	R M K G R P R M E S E E E E M E O L S R L M K G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism
COG0463 COG1396 COG3577 COG388 COG3639 COG0466 COG0463 COG1280 COG0456 COG0463 COG1280 COG0559 COG4177 COG0411 COG1125 COG0539 COG1732 COG0539 COG1737 COG0494 COG1732 COG0590 COG1733 COG0494 COG175 COG0738 COG175 COG0738 COG175 COG0787	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport systems, permease component ABC-type branched-chain amino acid transport systems, ATPase component ABC-type proline/glycine betaine transport systems, ATPase components ABC-type proline/glycine betaine transport systems, periplasmic components FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease components	R M K R G R P R M E S E E E E M E O L S R L M K G G G G M	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism
C0G0463 C0G1396 C0G357 C0G1803 C0G0368 C0G0463 C0G1280 C0G0456 C0G0463 C0G1280 C0G0456 C0G0463 C0G1280 C0G0457 C0G0411 C0G1125 C0G0723 C0G0683 C0G1047 C0G494 C0G1922 C0G1069 C0G1653 C0G1175 C0G0395 C0G0387 C0G0387 C0G2330	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyi clis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport system, permease component ABC-type sugar transport systems, permease components ABC-type sugar transport systems, permease components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components Cyclopropane fatty acid synthase and related methyltransferases	R M K G R P R M E S E E E E M E O L S R L M K G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Transcription General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism Call wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
COG0463 COG1396 COG1397 COG1803 COG0388 COG0398 COG0463 COG1280 COG0455 COG0417 COG0411 COG125 COG1732 COG0683 COG10732 COG0683 COG10732 COG0683 COG10732 COG0683 COG10732 COG0683 COG10732 COG0683 COG10732 COG0683 COG0732 COG08330 COG0732 COG0230 COG0732	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted transcriptional regulators Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase Methylglyoxal synthase Predicted amidohydrolase Metcytpe phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Putative threonine efflux protein Predicted membrane protein Branched-chain amino acid ABC-type transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type branched-chain amino acid transport system, permease component ABC-type proline/glycine betaine transport systems, ATPase component Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type proline/glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) ABC-type branched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease component ABC-type sugar transport systems, permease components Alanine racemase Cyclopropane fatty acid synthase and related methyltransferases Ribosomal protein S18	R M K R G R M E S E E E E M E O L S R L M K G G G M M M M E S B E E E E E E E E E E E E E E E E E	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Trunction unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism Call wall/membrane/envelope biogenesis Translation, ribosomal structure and biogenesis
COG0463 COG1396 COG3577 COG1803 COG0358 COG03659 COG0456 COG0463 COG1280 COG0456 COG0417 COG0411 COG1125 COG057 COG047 CO	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Predicted membrane protein Branched-chain amino acid transport system, permease component BBC-type branched-chain amino acid transport system, permease component BBC-type branched-chain amino acid transport systems, permease component BBC-type proline/glycine betaine transport systems, ATPase component BBC-type proline/glycine betaine transport systems, ATPase component BBC-type pranched-chain amino acid transport systems, permease component BBC-type proline/glycine betaine/choline-binding (lipol)protein of an ABC-type transport system (osmoprotectant binding protein) BBC-type perbanched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport system, permease component ABC-type sugar transport system, permease component ABC-type sugar transport system, permease components ABC-type sugar transport systems, permease components ABC-type sugar transport systems, permease components ABC-type sugar transport systems, ATPase components Alanine racemase Cyclopropane fatty acid synthase and related methyltransferases Ribosomal protein 518 Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	R M K R G R M E S E E E E M E O L S R L M K G G G M M E S G M M E S G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Replication, recombination and repair Function unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism
COG0463 COG1396 COG1397 COG1803 COG0388 COG03639 COG0463 COG1280 COG0463 COG1280 COG0463 COG1280 COG0417 COG0411 COG1125 COG0683 COG1047 COG0494 COG1047 COG0494 COG1692 COG1693 COG1693 COG1693 COG1693 COG1693 COG175 COG0383 COG0383 COG0230 COG0236	Predicted dehydrogenases and related proteins Glycosyltransferases involved in cell wall biogenesis Predicted aspartyl protease Methylglyoxal synthase Predicted amidohydrolase ABC-type phosphate/phosphonate transport system, permease component Acetyltransferases Glycosyltransferases involved in cell wall biogenesis Predicted membrane protein Branched-chain amino acid transport system, permease component BBC-type branched-chain amino acid transport system, permease component BBC-type branched-chain amino acid transport systems, permease component BBC-type proline/glycine betaine transport systems, ATPase component BBC-type proline/glycine betaine transport systems, ATPase component BBC-type pranched-chain amino acid transport systems, permease component BBC-type proline/glycine betaine/choline-binding (lipol)protein of an ABC-type transport system (osmoprotectant binding protein) BBC-type perbanched-chain amino acid transport systems, periplasmic component FKBP-type peptidyl-prolyl cis-trans isomerases 2 Site-specific recombinase XerC Uncharacterized protein conserved in bacteria Predicted ATPase (AAA+ superfamily) NTP pyrophosphohydrolases including oxidative damage repair enzymes Teichoic acid biosynthesis proteins Transcriptional regulators ABC-type sugar transport system, permease component ABC-type sugar transport system, permease component ABC-type sugar transport system, permease components ABC-type sugar transport systems, permease components ABC-type sugar transport systems, permease components ABC-type sugar transport systems, ATPase components Alanine racemase Cyclopropane fatty acid synthase and related methyltransferases Ribosomal protein 518 Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	R M K R G R M E S E E E E M E O L S R L M K G G G M M E S G M M E S G G G G G G G G G G G G G G G G G G	General function prediction only Cell wall/membrane/envelope biogenesis Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Trunction unknown General function prediction only Replication, recombination and repair Cell wall/membrane/envelope biogenesis Transcription Carbohydrate transport and metabolism Call wall/membrane/envelope biogenesis Translation, ribosomal structure and biogenesis

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
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Beta-lactamase class D	V	Defense mechanisms
	Putative threonine efflux protein	E K	Amino acid transport and metabolism
	Predicted transcriptional regulators Uncharacterized conserved protein	S	Transcription Function unknown
	Phospholipid-binding protein	R	General function prediction only
	Transcriptional regulator	K	Transcription
	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	1	Lipid transport and metabolism
	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S	Function unknown
COG0038	Chloride channel protein EriC	Р	Inorganic ion transport and metabolism
COG1487	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
	Predicted membrane-associated, metal-dependent hydrolase	R	General function prediction only
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized protein conserved in bacteria	S E	Function unknown
	ABC-type branched-chain amino acid transport systems, ATPase component Signal transduction histidine kinase	T	Amino acid transport and metabolism Signal transduction mechanisms
	ABC-type branched-chain amino acid transport systems, ATPase component	Ë	Amino acid transport and metabolism
	Methyl-accepting chemotaxis protein	N	Cell motility
	ABC-type Fe3+-hydroxamate transport system, periplasmic component	Р	Inorganic ion transport and metabolism
COG4737	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2944	Predicted transcriptional regulator	K	Transcription
	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
	DnaK suppressor protein	Т	Signal transduction mechanisms
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Multisubunit Na+/H+ antiporter, MnhG subunit Multisubunit Na+/H+ antiporter, MnhC subunit	P P	Inorganic ion transport and metabolism
	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	C	Inorganic ion transport and metabolism Energy production and conversion
	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
	Alanine dehydrogenase	E	Amino acid transport and metabolism
	GMP synthase - Glutamine amidotransferase domain	F	Nucleotide transport and metabolism
	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	0	Posttranslational modification, protein turnover, chaperones
COG1975	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	0	Posttranslational modification, protein turnover, chaperones
	Putative ammonia monooxygenase	R	General function prediction only
	Protein containing von Willebrand factor type A (vWA) domain	R	General function prediction only
	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
	MoxR-like ATPases	R C	General function prediction only
	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs	C	Energy production and conversion Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	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
	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
	Orotidine-5'-phosphate decarboxylase	F E	Nucleotide transport and metabolism
	ABC-type amino acid transport system, permease component ABC-type amino acid transport system, permease component	E	Amino acid transport and metabolism
		E	Amino acid transport and metabolism
		E F	Amino acid transport and metabolism Amino acid transport and metabolism
COG1126	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG1126 COG0079	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	=	Amino acid transport and metabolism Amino acid transport and metabolism
COG1126 COG0079 COG0623	ABC-type polar amino acid transport system, ATPase component	E	Amino acid transport and metabolism
COG1126 COG0079 COG0623 COG0456	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH)	E E I	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism
COG1126 COG0079 COG0623 COG0456 COG2897	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases	E E I R	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase	E E I R P R E	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG2195 COG0659	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily)	E E I R P R E P	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG2195 COG0659 COG0031	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase	E E I R P R E P	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG2195 COG0659 COG0031 COG0265	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	E E I R P R E P E O	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones
COG1126 COG0079 COG0623 COG0456 COG2897 COG2195 COG0659 COG0031 COG0265 COG1476	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators	E E I R P R E P E O K	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription
COG1126 COG0079 COG0623 COG0456 COG2872 COG2195 COG0659 COG0031 COG0265 COG1476 COG0818	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase	E E I R P R E P E O K M	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis
COG1126 COG0079 COG0623 COG0456 COG2897 COG2195 COG0659 COG0031 COG0265 COG1476 COG0818 COG02835	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein	E E I R P R E P E O K	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG0195 COG0031 COG0265 COG1476 COG0818 COG2835 COG3293	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase	E I R P R E O K M S	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG2195 COG0659 COG0031 COG0265 COG1476 COG0818 COG2835 COG3293 COG2518	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives	E I R P R E O K M S L	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown
COG1126 COG0079 COG0029 COG0456 COG2872 COG2195 COG0659 COG0031 COG0265 COG1476 COG0818 COG2835 COG3293 COG2518 COG2518	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives Protein-L-isoaspartate carboxylmethyltransferase	E E I R P R E O K M S L	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair Posttranslational modification, protein turnover, chaperones
COG1126 COG0079 COG0623 COG0456 COG2897 COG2872 COG0659 COG0659 COG0659 COG0818 COG2835 COG3293 COG2518 COG2755 COG0563	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives Protein-L-isoaspartate carboxylmethyltransferase Lysophospholipase L1 and related esterases	E I R P R E O K M S L O E	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism
COG1126 COG0079 COG0623 COG0456 COG2897 COG2195 COG0031 COG0659 COG0031 COG0658 COG1476 COG0818 COG2835 COG22518 COG2755 COG0563 COG1434 COG4222	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives Protein-L-isoaspartate carboxylmethyltransferase Lysophospholipase L1 and related esterases Adenylate kinase and related kinases Uncharacterized conserved protein Uncharacterized protein conserved in bacteria	E E I R P R E O K M S L O E F S S	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Nucleotide transport and metabolism Function unknown Function unknown
COG1126 COG0079 COG0027 COG0456 COG2872 COG2195 COG0059 COG0031 COG0265 COG1476 COG0818 COG2835 COG2518 COG2518 COG2518 COG2755 COG0563 COG1434 COG4222 COG4134	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives Protein-L-isoaspartate carboxylmethyltransferase Lysophospholipase L1 and related esterases Adenylate kinase and related kinases Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved in bacteria ABC-type uncharacterized transport system, periplasmic component	E I R P R E O K M S L O E F S R	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Nucleotide transport and metabolism Function unknown Function unknown General function prediction only
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COG1126 COG0079 COG00623 COG0456 COG2872 COG2195 COG0659 COG0031 COG0659 COG01476 COG2835 COG2518 COG5511	ABC-type polar amino acid transport system, ATPase component Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase Enoyl-[acyl-carrier-protein] reductase (NADH) Acetyltransferases Rhodanese-related sulfurtransferase Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain Di- and tripeptidases Sulfate permease and related transporters (MFS superfamily) Cysteine synthase Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain Predicted transcriptional regulators Diacylglycerol kinase Uncharacterized conserved protein Transposase and inactivated derivatives Protein-L-isoaspartate carboxylmethyltransferase Lysophospholipase L1 and related esterases Adenylate kinase and related kinases Uncharacterized conserved protein Uncharacterized onserved protein Uncharacterized protein conserved in bacteria ABC-type uncharacterized transport system, periplasmic component D-alanyl-D-alanine carboxypeptidase Uncharacterized protein conserved in bacteria Arginase/agmatinase/formimionoglutamate hydrolase, arginase family Uncharacterized protein conserved in bacteria Serine/threonine protein phosphatase	E I R P R E O K M S L O E F S S R M S E S T R	Amino acid transport and metabolism Amino acid transport and metabolism Lipid transport and metabolism General function prediction only Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Cell wall/membrane/envelope biogenesis Function unknown Replication, recombination and repair Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Nucleotide transport and metabolism Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Amino acid transport and metabolism Function unknown Amino acid transport and metabolism Function unknown Signal transduction mechanisms
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	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
	Predicted dehydrogenases and related proteins Glutamine synthetase	R E	General function prediction only Amino acid transport and metabolism
	Glycine/D-amino acid oxidases (deaminating)	F	Amino acid transport and metabolism Amino acid transport and metabolism
	Transcriptional regulators, similar to M. xanthus CarD	K	Transcription
	Predicted ferric reductase	P	Inorganic ion transport and metabolism
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	С	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
	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
	Methyl-accepting chemotaxis protein	N	Cell motility
	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport system, permease component	E E	Amino acid transport and metabolism Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport system, ATPase component Putative protein-S-isoprenylcysteine methyltransferase	0	Posttranslational modification, protein turnover, chaperones
	Precorrin-3B methylase	Н	Coenzyme transport and metabolism
	Putative threonine efflux protein	E	Amino acid transport and metabolism
	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain	K	Transcription
COG0314	Molybdopterin converting factor, large subunit	Н	Coenzyme transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	Molybdopterin-guanine dinucleotide biosynthesis protein	H	Coenzyme transport and metabolism
	Nuclease subunit of the excinuclease complex	L	Replication, recombination and repair
	Glycine cleavage system T protein (aminomethyltransferase)	E R	Amino acid transport and metabolism
	Predicted Fe-S-cluster oxidoreductase Predicted branched-chain amino acid permease (azaleucine resistance)	F F	General function prediction only Amino acid transport and metabolism
	Monoamine oxidase	F	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	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
	Predicted thioesterase	R	General function prediction only
	Biopolymer transport proteins	U	Intracellular trafficking, secretion, and vesicular transport
	Biopolymer transport protein	U	Intracellular trafficking, secretion, and vesicular transport
	Periplasmic component of the Tol biopolymer transport system	U	Intracellular trafficking, secretion, and vesicular transport
	Outer membrane protein and related peptidoglycan-associated (lipo)proteins Predicted transcriptional regulator	M K	Cell wall/membrane/envelope biogenesis Transcription
	Predicted nucleoside-diphosphate sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T	Signal transduction mechanisms
	Metal-dependent amidase/aminoacylase/carboxypeptidase	R	General function prediction only
	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
	Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	UDP-N-acetylglucosamine enolpyruvyl transferase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized protein conserved in bacteria	S S	Function unknown Function unknown
	Uncharacterized protein conserved in bacteria Outer membrane receptor for ferrienterochelin and colicins	5 P	Inorganic ion transport and metabolism
	Galactose mutarotase and related enzymes	G	Carbohydrate transport and metabolism
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Membrane transporters of cations and cationic drugs	Р	Inorganic ion transport and metabolism
COG1133	ABC-type long-chain fatty acid transport system, fused permease and ATPase components	1	Lipid transport and metabolism
COG2337	Growth inhibitor	Т	Signal transduction mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	Uncharacterized protein, similar to the N-terminal domain of Lon protease		
COG0697		R	General function prediction only
6064046	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
	Transcriptional regulators	G K	Carbohydrate transport and metabolism Transcription
COG2852	Transcriptional regulators Uncharacterized protein conserved in bacteria	G K S	Carbohydrate transport and metabolism Transcription Function unknown
COG2852 COG3755	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria	G K	Carbohydrate transport and metabolism Transcription Function unknown Function unknown
COG2852 COG3755 COG0529	Transcriptional regulators Uncharacterized protein conserved in bacteria	G K S	Carbohydrate transport and metabolism Transcription Function unknown
COG2852 COG3755 COG0529 COG4520	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases	G K S S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component	G K S P M E P	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases	G K S P M E P C	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein	G K S P M E P C N	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria	G K S P M E P C	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase	G K S P M E P C N S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins	G K S P M E P C N S I P	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases	G K S P M E P C N S I P R	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only
COG2852 COG3755 COG0529 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735 COG0730 COG0730	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria	G K S P M E P C N S I P R S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735 COG0730 COG4427	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylylsulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases	G K S P M E P C N S I P R	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735 COG0730 COG4427 COG0451	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nuchearacterized protein conserved in bacteria	G K S P M E P C N S I P R S M	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG3730 COG0735 COG0730 COG4764 COG64581 COG4581	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase	G K S P M E P C N S I P R S M L	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair
COG2852 COG3755 COG0526 COG04520 COG0665 COG1230 COG0277 COG0840 COG0735 COG0730 COG0451 COG0451 COG05607 COG05607	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins	G K S P M E P C N S I P R S M L S G R	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only
COG2852 COG3755 COG0529 COG4520 COG0655 COG1230 COG0277 COG0840 COG4764 COG0735 COG0730 COG4427 COG4551 COG4551 COG4567 COG2723 COG2723 COG0673 COG0730	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases	G K S S P M E P C N S I P R S M L S G R G G G G G G G G G G G G G G G G G	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG4652 COG1230 COG0735 COG0735 COG0735 COG0735 COG0451 COG5607 COG5723 COG673 COG673 COG673 COG673 COG673 COG673 COG673	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase	G K S P M E P C N S I P R S M L S G R G G G G G G G G G G G G G G G G G	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0775 COG0840 COG0735 COG0730 COG4427 COG0451 COG5650 COG2723 COG073 COG2723 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase F2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel	G K S P M E P C N S I P R S G R G G M M	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis
COG2852 COG3755 COG0529 COG0652 COG0665 COG1230 COG0277 COG0840 COG4764 COG3000 COG0735 COG0430 COG4427 COG0451 COG5607 COG2723 COG073 COG1082 COG0736 COG1082 COG0673 COG1082 COG0668 COG0668 COG0668	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysluffate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Sugar phosphate sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators	G K S S P M E P C N S I P R S M L S G R G G M K K S M K S S M K S M K S M K S M K S M K S M K S M K S M K S M K S S M K S S M K S S C S N S C S C S C S C S C S C S C S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carlowlymembrane/envelope biogenesis Transcription
COG2852 COG3755 COG0529 COG4529 COG4520 COG0665 COG1230 COG0777 COG0840 COG0735 COG0730 COG451 COG451 COG5607 COG2723 COG062723 COG062723 COG0668 COG0668 COG0668 COG2789	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transcriptional regulators Uncharacterized conserved protein	G K S S P M E P C N S I P R S M L S G R G G M K S S S M K S S G M K S S G M K S S S S S M K S S S S S S S S S S S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG665 COG1230 COG6764 COG3000 COG4764 COG3000 COG4754 COG0451 COG5607 COG5723 COG673 COG	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators Uncharacterized conserved protein Type IV secretory pathway, Virl component	G K S S P M E P C N S I P R S M L S G R G G M K S U	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Transcription Function unknown Intracellular trafficking, secretion, and vesicular transport
COG2852 COG3755 COG0529 COG4520 COG0665 COG1230 COG0277 COG0840 COG0735 COG0730 COG4427 COG0451 COG5607 COG2723 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG073 COG074 CO	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysluffate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators Uncharacterized conserved protein Type IV secretory pathway, Virl component Methyl-accepting chemotaxis protein	G K S S P M E P C N S I P R S M L S G R G G M K S U N	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carlomydrate transport and metabolism
COG2852 COG3755 COG0529 COG4520 COG665 COG1230 COG0277 COG0840 COG0735 COG0730 COG4751 COG4581 COG5607 COG0723 COG0673	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators Uncharacterized conserved protein Type IV secretory pathway, Virl component	G K S S P M E P C N S I P R S M L S G R G G M K S U	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Transcription Function unknown Intracellular trafficking, secretion, and vesicular transport
COG2852 COG3755 COG6529 COG4520 COG665 COG1230 COG6077 COG0840 COG4764 COG30035 COG0730 COG4427 COG6481 COG5607 COG2723 COG0682 COG0176 COG0686 COG282 COG0176 COG282 COG282 COG282 COG282 COG282 COG282 COG282 COG282	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysulfate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Transcriptional regulators Uncharacterized conserved protein Type IV secretory pathway, Virl component Methyl-accepting chemotaxis protein Predicted permeases	G K S S P M E P C N S I P R S M L S G R G G M K S U N R	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Transcription Function unknown Intracellular trafficking, secretion, and vesicular transport Cell motility General function prediction only
COG2852 COG3755 COG0529 COG64520 COG6655 COG1230 COG6464 COG3000 COG4764 COG3000 COG4764 COG0730 COG4581 COG5607 COG2723 COG0673 COG6082 COG0176 COG6088 COG2188 COG288 COG3946 COG688 COG2186	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylysluffate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators Uncharacterized conserved protein Vye IV secretory pathway, Virl component Methyl-accepting chemotaxis protein Predicted permeases Adenylate cyclase, family 3 (some proteins contain HAMP domain)	G K S S P M E P C N S I P R S M L S G R G G M K S U N R T	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carlowhydrate transport and metabolism Carlowhydrate transport and metabolism Call wall/membrane/envelope biogenesis Transcription Function unknown Intracellular trafficking, secretion, and vesicular transport Cell motility General function prediction only Signal transduction mechanisms
COG2852 COG3755 COG0529 COG64520 COG6655 COG1230 COG0777 COG08840 COG4764 COG3000 COG0735 COG04427 COG0451 COG56507 COG2723 COG0673 COG1076 COG0668 COG2186 COG2186 COG2860 COG2962 COG0840 COG2962 COG0126 COG2962 COG0664	Transcriptional regulators Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Adenylyslufate kinase and related kinases Surface antigen Glycine/D-amino acid oxidases (deaminating) Co/Zn/Cd efflux system component FAD/FMN-containing dehydrogenases Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Sterol desaturase Fe2+/Zn2+ uptake regulation proteins Predicted permeases Uncharacterized protein conserved in bacteria Nucleoside-diphosphate-sugar epimerases Superfamily II RNA helicase Uncharacterized conserved protein Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase Predicted dehydrogenases and related proteins Sugar phosphate isomerases/epimerases Transaldolase Small-conductance mechanosensitive channel Transcriptional regulators Uncharacterized conserved protein Type IV secretory pathway, Virl component Methyl-accepting chemotaxis protein Predicted permeases Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein	G K S S P M E P C N S I P R S M L S G R G G M K S U N R T S	Carbohydrate transport and metabolism Transcription Function unknown Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Cell motility Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Replication, recombination and repair Function unknown Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism General function prediction only Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Transcription Function unknown Intracellular trafficking, secretion, and vesicular transport Cell motility General function prediction only Signal transduction mechanisms Function unknown

COG3173	Predicted aminoglycoside phosphotransferase	R	General function prediction only
	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	Н	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
	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
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	Transglutaminase-like enzymes, putative cysteine proteases	E	Amino acid transport and metabolism
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Universal stress protein UspA and related nucleotide-binding proteins	Т	Signal transduction mechanisms
	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
	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
	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
	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
	Transcriptional regulator	K	Transcription
COG0644	Dehydrogenases (flavoproteins)	С	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
	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
	Response regulator	T	Signal transduction mechanisms
	Transcriptional regulators	K	Transcription
	Glutathionylspermidine synthase	E	Amino acid transport and metabolism
	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
	Formate/nitrite family of transporters	P	Inorganic ion transport and metabolism
	Predicted thiamine-pyrophosphate-binding protein	R	General function prediction only
	Transcriptional regulators	K	Transcription
	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
	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
COG1207	, , , , , , , , , , , , , , , , , , , ,	M	Cell wall/membrane/envelope biogenesis
	Predicted phosphatases	R	General function prediction only
	Response regulator of citrate/malate metabolism	K	Transcription
	Predicted GTPases	R	General function prediction only
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
	Panthothenate synthetase	Н	Coenzyme transport and metabolism
	RecA-superfamily ATPases implicated in signal transduction	Т	Signal transduction mechanisms
	Transcriptional regulator	K	Transcription
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
	Nicotinic acid phosphoribosyltransferase	н	Coenzyme transport and metabolism
	Ferredoxin	С	Energy production and conversion
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Riboflavin synthase beta-chain	Н	Coenzyme transport and metabolism
	Enoyl-CoA hydratase/carnithine racemase	1	Lipid transport and metabolism
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
	Alpha-galactosidase	G	Carbohydrate transport and metabolism
	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis	Q	Secondary metabolites biosynthesis, transport and catabolism
		-	Analysis and Assessment and Assets 19
COG0685	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport and metabolism

	Biotin carboxyl carrier protein	I	Lipid transport and metabolism
	Allophanate hydrolase subunit 1	E	Amino acid transport and metabolism
	Poly(3-hydroxybutyrate) depolymerase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
	Predicted glycosyltransferases	R	General function prediction only
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized protein conserved in bacteria	S H	Function unknown
	Panthothenate kinase Transcriptional resultant (super kinase	н К	Coenzyme transport and metabolism
	Transcriptional regulator/sugar kinase	K	Transcription
	Transcriptional regulators	S	Transcription Function unknown
	Uncharacterized homolog of Blt101	S E	Function unknown
	4-aminobutyrate aminotransferase and related aminotransferases Uncharacterized conserved protein	S	Amino acid transport and metabolism Function unknown
	Predicted naringenin-chalcone synthase	Q	Secondary metabolites biosynthesis, transport and catabolism
	ABC-type hemin transport system, ATPase component	P	Inorganic ion transport and metabolism
	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	, F	Nucleotide transport and metabolism
	Arsenite efflux pump ACR3 and related permeases	Р	Inorganic ion transport and metabolism
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Т	Signal transduction mechanisms
	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	c C	Energy production and conversion
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
	ABC-type Fe3+ transport system, periplasmic component	Р	Inorganic ion transport and metabolism
	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
	Exo-beta-1,3-glucanase	G	Carbohydrate transport and metabolism
	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	F	Nucleotide transport and metabolism
	Predicted redox protein, regulator of disulfide bond formation	0	Posttranslational modification, protein turnover, chaperones
	Predicted transmembrane transcriptional regulator (anti-sigma factor)	K	Transcription
	Predicted dehydrogenases and related proteins	R	General function prediction only
	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
	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
	ABC-type Mn2+/Zn2+ transport systems, permease components	P	Inorganic ion transport and metabolism
	3-methyladenine DNA glycosylase	L	Replication, recombination and repair
	Predicted acyltransferase	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Cold shock proteins	K	Transcription
	Thioredoxin domain-containing protein	0	Posttranslational modification, protein turnover, chaperones
	ABC-type proline/glycine betaine transport systems, permease component	E	Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport systems, permease component	E	Amino acid transport and metabolism
	3,4-dihydroxy-2-butanone 4-phosphate synthase	н	Coenzyme transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Glutamate dehydrogenase/leucine dehydrogenase	E	Amino acid transport and metabolism
	Transcription termination factor	K	Transcription
	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)	Н	Coenzyme transport and metabolism
COG2895	GTPases - Sulfate adenylate transferase subunit 1	Р	Inorganic ion transport and metabolism
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Р	Inorganic ion transport and metabolism
COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	Р	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
	Putative sterol carrier protein	1	Lipid transport and metabolism
	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
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Phosphopantothenoylcysteine synthetase/decarboxylase	Н	Coenzyme transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ATPases of the AAA+ class	0	Posttranslational modification, protein turnover, chaperones
	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
	FOG: WD40-like repeat	S	Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Non-ribosomal peptide synthetase modules and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted membrane protein	S	Function unknown
	Uncharacterized protein encoded in hypervariable junctions of pilus gene clusters	S	Function unknown
	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Predicted permeases	R	General function prediction only
	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C	Energy production and conversion
	Flagellar motor protein	N	Cell motility
	Predicted integral membrane protein	S	Function unknown
	Glycine cleavage system H protein (lipoate-binding)	E	Amino acid transport and metabolism
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted extracellular nuclease	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	Putative homoserine kinase type II (protein kinase fold)	R	General function prediction only
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	ı	Lipid transport and metabolism

COG0678	Peroxiredoxin	0	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
	Uncharacterized conserved protein	S	Function unknown
	ABC-type oligopeptide transport system, ATPase component	E	Amino acid transport and metabolism
COG5349	Uncharacterized protein conserved in bacteria	S	Function unknown
	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
	Phosphate uptake regulator	P	Inorganic ion transport and metabolism
	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
	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	Transcriptional regulators	K	Transcription
	Threonine aldolase	E	Amino acid transport and metabolism
	Uncharacterized conserved small protein	S	Function unknown
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
	Trk-type K+ transport systems, membrane components	Р	Inorganic ion transport and metabolism
	Phosphoserine aminotransferase	Н	Coenzyme transport and metabolism
	Predicted membrane protein	S	Function unknown
	Chorismate synthase	E	Amino acid transport and metabolism
	ABC-type phosphate transport system, permease component	P	Inorganic ion transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Enoyl-CoA hydratase/carnithine racemase	1	Lipid transport and metabolism
	Methylase of chemotaxis methyl-accepting proteins	N	Cell motility
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Signal transduction histidine kinase	T _	Signal transduction mechanisms
	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms
	Tfp pilus assembly protein PilF	N T	Cell motility
	Signal transduction histidine kinase	· ·	Signal transduction mechanisms
	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	C	Energy production and conversion
	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
	Uncharacterized conserved protein	S	Function unknown
	Demethylmenaquinone methyltransferase	H	Coenzyme transport and metabolism
	N-acyl-L-homoserine lactone synthetase	T	Signal transduction mechanisms
	Uncharacterized protein containing SIS (Sugar ISomerase) phosphosugar binding domain	R	General function prediction only
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Arsenate reductase and related proteins, glutaredoxin family	P	Inorganic ion transport and metabolism
	Triosephosphate isomerase	G	Carbohydrate transport and metabolism
	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases	V	Defense mechanisms
	Restriction endonuclease S subunits	V	Defense mechanisms
	Type I restriction-modification system methyltransferase subunit	V	Defense mechanisms
	Predicted Rossmann fold nucleotide-binding protein	R	General function prediction only
	Isocitrate dehydrogenases	C	Energy production and conversion
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ABC-type Fe3+ transport system, permease component	P	Inorganic ion transport and metabolism
	Predicted transmembrane transcriptional regulator (anti-sigma factor)	K	Transcription
	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides	R	General function prediction only
	Methyl-accepting chemotaxis protein	N	Cell motility
	Guanosine polyphosphate pyrophosphohydrolases/synthetases	T	Signal transduction mechanisms
	Predicted membrane protein	S	Function unknown
	Cation transport ATPase	P	Inorganic ion transport and metabolism
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	C	Energy production and conversion
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	C	Energy production and conversion
	Transcriptional regulator	K	Transcription
	Polyferredoxin	C	Energy production and conversion
	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhIB	S	Function unknown
	ABC-type spermidine/putrescine transport system, permease component I Collagenase and related proteases	E 0	Amino acid transport and metabolism
	·		Posttranslational modification, protein turnover, chaperones
	Collagenase and related proteases	0	Posttranslational modification, protein turnover, chaperones
	Plastocyanin Membrana associated linearetein involved in thirming biocyathesis	С	Energy production and conversion
	Membrane-associated lipoprotein involved in thiamine biosynthesis	Н С	Coenzyme transport and metabolism Energy production and conversion
	Predicted lipoprotein involved in nitrous oxide reduction ABC-type transport system involved in multi-copper enzyme maturation, permease component	R	General function prediction only
	ABC-type transport system involved in multi-copper enzyme maturation, permease component ABC-type multidrug transport system, ATPase component	K V	Defense mechanisms
	ABC-type multidrug transport system, ATPase component Nitrous oxidase accessory protein	V P	
	Nitrous oxidase accessory protein Nitrous oxide reductase	C P	Inorganic ion transport and metabolism
	Nitrous oxide reductase Putative multicopper oxidases	Q	Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism
		Q P	· · · · · · · · · · · · · · · · · · ·
	Nitric oxide reductase activation protein	R	Inorganic ion transport and metabolism General function prediction only
	MoxR-like ATPases Nitric oxide reductase large subunit	R P	· · · · · · · · · · · · · · · · · · ·
	<u> </u>	· ·	Inorganic ion transport and metabolism
	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C	Energy production and conversion
	Chemotaxis protein	N	Cell motility
	NAD-dependent aldehyde dehydrogenases Prodicted enderwelesse sentriping a UPI demain.	C L	Energy production and conversion
	Predicted endonuclease containing a URI domain	=	Replication, recombination and repair
	Flagellar basal body-associated protein	N	Cell motility
	Protein related to penicillin acylase	R	General function prediction only
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
	5-carboxymethyl-2-hydroxymuconate isomerase	E	Amino acid transport and metabolism
	Transcriptional regulators	K	Transcription
	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
	Predicted hydrolase (HAD superfamily)	R M	General function prediction only
		IV/I	Cell wall/membrane/envelope biogenesis
	Predicted nucleoside-diphosphate-sugar epimerases		
COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG0596 COG2030	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Acyl dehydratase	R I	General function prediction only Lipid transport and metabolism
COG0596 COG2030	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only

COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	0	Posttranslational modification, protein turnover, chaperones
COG0071	Molecular chaperone (small heat shock protein)	0	Posttranslational modification, protein turnover, chaperones
	DNA repair exonuclease	L	Replication, recombination and repair
	Uncharacterized conserved protein	S	Function unknown
	Fructosamine-3-kinase	G	Carbohydrate transport and metabolism
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Metal-dependent hydrolases of the beta-lactamase superfamily II Uncharacterized conserved protein	R S	General function prediction only Function unknown
	Predicted permeases	R	General function prediction only
	Transcriptional regulators	K	Transcription
	Ribosomal protein L30/L7E	J	Translation, ribosomal structure and biogenesis
	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
	Putative multicopper oxidases	Q	Secondary metabolites biosynthesis, transport and catabolism
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Plastocyanin Pud Mad ATRACA	C R	Energy production and conversion
	Predicted ATPase Ribosomal protein L24	K.	General function prediction only Translation, ribosomal structure and biogenesis
	Ribosomal protein L29	j	Translation, ribosomal structure and biogenesis
	Ribosomal protein S19	J	Translation, ribosomal structure and biogenesis
	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
	Zn-dependent proteases	R	General function prediction only
	NAD(P)H-nitrite reductase	C	Energy production and conversion
	Ribosomal protein L7/L12	J	Translation, ribosomal structure and biogenesis
	Ribosomal protein L10	J R	Translation, ribosomal structure and biogenesis
	Short-chain dehydrogenases of various substrate specificities Preprotein translocase subunit SecE	K U	General function prediction only
	Site-specific recombinase XerC	L	Intracellular trafficking, secretion, and vesicular transport Replication, recombination and repair
	Putative multicopper oxidases	Q	Secondary metabolites biosynthesis, transport and catabolism
	Bacteriophage protein gp37	S	Function unknown
	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
	Methyl-accepting chemotaxis protein	N	Cell motility
	Uncharacterized ABC-type transport system, ATPase component	R	General function prediction only
	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	H E	Coenzyme transport and metabolism
	Histidinol phosphatase and related phosphatases ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism Amino acid transport and metabolism
	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	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
	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Cell wall/membrane/envelope biogenesis
	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	Р	Inorganic ion transport and metabolism
	Transcriptional regulator	K	Transcription
	Anthranilate/para-aminobenzoate synthases component II	E M	Amino acid transport and metabolism
	Outer membrane protein and related peptidoglycan-associated (lipo)proteins ABC-type spermidine/putrescine transport system, permease component II	E E	Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Predicted membrane protein	S	Function unknown
	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
	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
	Predicted membrane protein involved in D-alanine export	M	Cell wall/membrane/envelope biogenesis
	Homoserine acetyltransferase	E	Amino acid transport and metabolism
	Lactoylglutathione lyase and related lyases	E T	Amino acid transport and metabolism
	Signal transduction histidine kinase Predicted hydrolase (HAD superfamily)	R	Signal transduction mechanisms General function prediction only
	Putative Zn-dependent protease, contains TPR repeats	R	General function prediction only
	Predicted transcriptional regulator	K	Transcription
	Predicted transcriptional regulators	K	Transcription
COG3572	Gamma-glutamylcysteine synthetase	н	Coenzyme transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG3631	Ketosteroid isomerase-related protein	R	General function prediction only
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases	н	Coenzyme transport and metabolism
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Predicted membrane protein	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
	Predicted Zn peptidase Uncharacterized protein conserved in hacteria	E S	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria AraC-type DNA-binding domain-containing proteins	S K	Function unknown Transcription
COG2207	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	I I	Lipid transport and metabolism
COG2908	Uncharacterized protein conserved in bacteria	S	Function unknown
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Tfp pilus assembly protein PilN	N	Cell motility
	3-deoxy-D-manno-octulosonic-acid transferase	M	Cell wall/membrane/envelope biogenesis
COG1663	Tetraacyldisaccharide-1-P 4'-kinase	М	Cell wall/membrane/envelope biogenesis
COG1560	Lauroyl/myristoyl acyltransferase	M	Cell wall/membrane/envelope biogenesis

COG4549	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	NADH:ubiquinone oxidoreductase 17.2 kD subunit	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Biotin carboxylase	1	Lipid transport and metabolism
	Biotin carboxyl carrier protein	ĺ	Lipid transport and metabolism
	3-dehydroquinate dehydratase II	Е	Amino acid transport and metabolism
	Putative copper export protein	P	Inorganic ion transport and metabolism
	ABC-type spermidine/putrescine transport systems, ATPase components	E	Amino acid transport and metabolism
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Ribosome-associated protein Y (PSrp-1)	j.	Translation, ribosomal structure and biogenesis
	1,4-alpha-glucan branching enzyme	G	Carbohydrate transport and metabolism
	Spermidine/putrescine-binding periplasmic protein	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	N-Dimethylarginine dimethylaminohydrolase	E	Amino acid transport and metabolism
	Putative effector of murein hydrolase LrgA	R	General function prediction only
	Putative effector of murein hydrolase Putative effector of murein hydrolase	M	Cell wall/membrane/envelope biogenesis
	Beta-fructosidases (levanase/invertase)	G	Carbohydrate transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P	Inorganic ion transport and metabolism
	Predicted exporters of the RND superfamily	R	General function prediction only
	Periplasmic serine proteases (ClpP class)	0	Posttranslational modification, protein turnover, chaperones
		R	
	Predicted O-methyltransferase		General function prediction only
	Uncharacterized conserved protein	S C	Function unknown
	FAD/FMN-containing dehydrogenases	0	Energy production and conversion
	DnaJ-domain-containing proteins 1		Posttranslational modification, protein turnover, chaperones General function prediction only
	ATPase components of ABC transporters with duplicated ATPase domains Permeases of the drug/metabolite transporter (DMT) superfamily	R G	•
		G	Carbohydrate transport and metabolism
	Beta-glucosidase-related glycosidases		Carbohydrate transport and metabolism
	Negative regulator of beta-lactamase expression	V	Defense mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Cell division protein Ftsl/penicillin-binding protein 2	M	Cell wall/membrane/envelope biogenesis
	UDP-N-acetylmuramyl pentapeptide synthase	M	Cell wall/membrane/envelope biogenesis
	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	M	Cell wall/membrane/envelope biogenesis
	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	С	Energy production and conversion
COG3000	Sterol desaturase	1	Lipid transport and metabolism
COG0206	Cell division GTPase	D	Cell cycle control, cell division, chromosome partitioning
	Na+/phosphate symporter	Р	Inorganic ion transport and metabolism
COG0774	UDP-3-O-acyl-N-acetylglucosamine deacetylase	M	Cell wall/membrane/envelope biogenesis
	Superoxide dismutase	P	Inorganic ion transport and metabolism
COG0266	Formamidopyrimidine-DNA glycosylase	L	Replication, recombination and repair
COG0266 COG0304	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase	L I	Replication, recombination and repair Lipid transport and metabolism
COG0266 COG0304 COG0596	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	L I R	Replication, recombination and repair Lipid transport and metabolism General function prediction only
COG0266 COG0304 COG0596 COG0497	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair	L I R L	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair
COG0266 COG0304 COG0596 COG0497 COG4753	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	L I R L T	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein	L I R L T N	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein	L I R L T N S	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria	L I R L T N S S	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607	Formamidopyrimidine-DNA glycosylase 3-oxoaçı-[acçı-carrier-protein] synthase Predicted hydrolases or acçıttransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase	L I R L T N S S	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis	L I R L T N S S P H	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1524 COG1598 COG4103 COG0607 COG2226 COG5622	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells	L I R L T N S S P H N	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Cenzyme transport and metabolism Cell motility
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239	Formamidopyrimidine-DNA glycosylase 3-oxoaçı-[acçı-carrier-protein] synthase Predicted hydrolases or acyttransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase	L I R L T N S S P H N	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component	L I R L T N S S P H N I G	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase	L I R L T N S S P H N I G	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis
COG0266 COG0304 COG0596 COG0497 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917	Formamidopyrimidine-DNA glycosylase 3-oxoacyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain	L I R L T N S S P H N I G M S	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Cenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown
COG0266 COG0304 COG0596 COG0497 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein	L I R L T N S S P H N I G M S S	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG4992	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase	L I R L T N S P H N G M S E	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280	Formamidopyrimidine-DNA glycosylase 3-oxoqv-I (acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase	L I R L T N S S P H N I G M S S E C	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2520	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase	L I R L T N S P H N I G M S S E C R	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG64103 COG0607 COG2226 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG280 COG2520 COG2520 COG2271	Formamidopyrimidine-DNA glycosylase 3-oxoqv-I (acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease	L I R L T N S S P H N I G M S C R G	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2271 COG4771	Formamidopyrimidine-DNA glycosylase 3-oxoqv-[acqv]-carrier-protein] synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane erceptor for ferrienterochelin and colicins	L I R L T N S P H N G M S E C R G P	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG32304 COG1879 COG0859 COG1917 COG3304 COG4992 COG0226 COG2520 COG2271 COG4771 COG5285	Formamidopyrimidine-DNA glycosylase 3-oxoqv-I (acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	L I R L T N S S P H N I G M S S C R G P	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1729 COG4007 COG226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2520 COG2271 COG4771 COG5285 COG1309	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator	L I R L T N S S P H N I G M S C R G P Q K	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Fenergy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG280 COG2271 COG4771 COG5285 COG1309 COG1247	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases	L I R L T N S S P H N I G M S S E C R G P Q K M	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown General function prediction only Carbohydrate transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane erceptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme	L I R L T N S S P H N G M S E C R G P Q K M H	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2571 COG2771 COG5285 COG1309 COG1247 COG2806 COG1247 COG2896 COG2896 COG3899 COG1247	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferase Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase	L I R L T N S S P H N I G M S S E C R G P Q K M H R	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1729 COG4703 COG0607 COG2266 COG5622 COG3239 COG1879 COG3304 COG4992 COG2520 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG1247 COG2896 COG1247 COG2896 COG1247 COG3890 COG1247 COG3890	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase	L I R L T N S S P H N I G M S S E C R G P Q K M H R T	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Function unknown Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG64103 COG0607 COG2226 COG5222 COG52239 COG1879 COG3859 COG1917 COG3304 COG4992 COG280 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG1247 COG2896 COG31800 COG1247 COG2896 COG33920 COG0330	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs	L I R L T N S S P H N I G M S S E C R G P Q K M H R T	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown Function prediction only Carbohydrate transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG3180 COG3920 COG3300 COG1216	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases	L I R L T N S S P H N I G M S S E C R G P Q K M H R T O R	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG2271 COG5285 COG1309 COG1247 COG5285 COG1309 COG1247 COG5286 COG3380 COG1247 COG3896 COG390 COG1247 COG5896 COG390 COG1247 COG3896 COG390 COG1246 COG390 COG390 COG390 COG390 COG390 COG4216 COG4986	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component	LIRLTNSSPHNIGGMSSECRGPQKMHRTORP	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Enell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG2271 COG5285 COG1309 COG1247 COG5285 COG1309 COG1247 COG5286 COG3380 COG1247 COG3896 COG390 COG1247 COG5896 COG390 COG1247 COG3896 COG390 COG1246 COG390 COG390 COG390 COG390 COG390 COG4216 COG4986	Formamidopyrimidine-DNA glycosylase 3-oxocyl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases	L I R L T N S S P H N I G M S S E C R G P Q K M H R T O R	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG3304 COG4992 COG02806 COG2520 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG390 COG1247 COG390 COG1246 COG3920 COG3920 COG3920 COG0330 COG1216 COG4986 COG5507	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component	LIRLTNSSPHNIGGMSSECRGPQKMHRTTORPSK	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Enell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG64103 COG0607 COG2226 COG5622 COG5622 COG3239 COG1917 COG3304 COG4992 COG280 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG1247 COG2896 COG3180 COG1247 COG2896 COG3920 COG0330 COG1216 COG4986 COG5507 COG1733	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein	LIRLTNSSPHNIGMSSECRGPQKMHRTORPSKT	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carlohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function in metabolism Ceneral function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Ceneral function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG0859 COG1971 COG3304 COG226 COG2521 COG271 COG280 COG271 COG280 COG271 COG380 COG1247 COG380 COG1247 COG380 COG390 COG1247 COG380 COG390 COG390 COG1247 COG380 COG390 COG390 COG1247 COG380 COG390 COG1247 COG2896 COG390 COG1247 COG2896 COG390 COG1216 COG4986 COG4986 COG4986 COG5507	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane erceptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators	LIRLTNSSPHNIGGMSSECRGPQKMHRTTORPSK	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown Function unknown Ceneral function prediction only Carbohydrate transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG226 COG5522 COG3239 COG1879 COG3304 COG4992 COG2271 COG5285 COG1309 COG1247 COG5286 COG3290 COG1247 COG5286 COG3290 COG1247 COG5585 COG1309 COG1266 COG390 COG1267 COG5585 COG1309 COG1267 COG5585 COG1309 COG1266 COG390 COG127 COG5285 COG1309 COG1267 COG5380 COG1216 COG4986 COG5507 COG1733 COG2114 COG2718	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferase Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain)	LIRLTNSSPHNIGMSSECRGPQKMHRTORPSKT	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Call wall/membrane/envelope biogenesis Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2226 COG3239 COG1879 COG3304 COG4992 COG3290 COG2271 COG4771 COG5285 COG1309 COG1247 COG3869 COG1247 COG3869 COG1247 COG3869 COG1246 COG3860 COG1246 COG3860 COG1247 COG3860 COG1247 COG3860 COG1247 COG3860 COG1246 COG3800 COG1246 COG3800 COG1246 COG5507 COG1733 COG1146 COG4986 COG5507 COG1733 COG2114 COG2718 COG0642	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein	LIRLTNSSPHNIGGMSSECRGPQKMHRTORPSKTS	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Fosttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Function unknown Function unknown
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG64103 COG0607 COG2226 COG5229 COG1879 COG0859 COG1917 COG3304 COG4992 COG0280 COG2271 COG4771 COG5285 COG1309 COG1247 COG2896 COG1247 COG2896 COG3180 COG1247 COG2896 COG3380 COG1214 COG0380 COG1214 COG0745	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein Signal transduction histidine kinase	L I R L T N S S P H N I G M S S E C R G P Q K M H R T O R P S K T S T	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carlohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown Function in transport and metabolism Ceneral function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Franscription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Function unknown Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG4103 COG0607 COG2266 COG5622 COG3239 COG1879 COG0859 COG1917 COG3304 COG4992 COG2271 COG4771 COG5285 COG1207 COG1247 COG2806 COG320 COG12416 COG4986 COG3920 COG12414 COG2718 COG2711 COG2718 COG2714 COG2718 COG0642	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized grotein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein Signal transduction histidine kinase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	LIRLTNSSPHNIGMSSECRGPQKMHRTORPSKTSTT	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Function unknown Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1729 COG0607 COG2266 COG0607 COG3239 COG1879 COG3304 COG4992 COG2250 COG2271 COG4771 COG5285 COG1309 COG1247 COG3304 COG4992 COG0330 COG1216 COG4986 COG5507 COG1247 COG5285 COG12114 COG2718 COG0330 COG1216 COG4986 COG5507 COG1733 COG2114 COG2718 COG0642 COG0745 COG0642 COG0745	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized conserved in bacteria Rhodanses-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:IPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Orrithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monoxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulator Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein Signal transduction histidine kinase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Predicted metal-dependent hydrolase	LIRLTNSSPHNIGGMSSECRGPQKMHRTORPSKTSTR	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Amino acid transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Function unknown Signal transduction mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG6403 COG0607 COG2226 COG3239 COG1879 COG3304 COG4992 COG2896 COG2520 COG2271 COG4771 COG3804 COG4992 COG3809 COG1247 COG3806 COG1247 COG3806 COG3800 COG1246 COG3800 COG1246 COG63800 COG1246 COG6486 COG5507 COG1733 COG1403 COG1403 COG1403 COG1403 COG1403	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized grotein conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiguinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:IPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted glycosyltransferases ABC-type anion transport system, duplicated permease component Uncharacterized conserved protein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein Signal transduction histidine kinase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Predicted metal-dependent hydrolase Restriction endonuclease	LIRLTNSSPHNIGMSSECRGPQKMHRTORPSKTSTTRVOS	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Function unknown Function unknown Function unknown Function unknown Function and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Transcription Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Function unknown Signal transduction mechanisms General function prediction only Defense mechanisms
COG0266 COG0304 COG0596 COG0497 COG4753 COG1724 COG1598 COG64103 COG0607 COG2226 COG5229 COG1917 COG3304 COG4992 COG0280 COG2271 COG4771 COG5285 COG1271 COG3809 COG1247 COG2806 COG1247 COG2896 COG1247 COG1247 COG1247 COG1247 COG1247 COG1495 COG1495 COG1495 COG1495 COG1495 COG1495	Formamidopyrimidine-DNA glycosylase 3-oxoayl-(acyl-carrier-protein) synthase Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) ATPase involved in DNA repair Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain Predicted periplasmic or secreted lipoprotein Uncharacterized conserved protein Uncharacterized conserved in bacteria Rhodanese-related sulfurtransferase Methylase involved in ubiquinone/menaquinone biosynthesis Protein required for attachment to host cells Fatty acid desaturase ABC-type sugar transport system, periplasmic component ADP-heptose:LPS heptosyltransferase Uncharacterized conserved protein, contains double-stranded beta-helix domain Predicted membrane protein Ornithine/acetylornithine aminotransferase Phosphotransacetylase Predicted methyltransferase Sugar phosphate permease Outer membrane receptor for ferrienterochelin and colicins Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Transcriptional regulator Sortase and related acyltransferases Molybdenum cofactor biosynthesis enzyme Putative ammonia monooxygenase Signal transduction histidine kinase Membrane protease subunits, stomatin/prohibitin homologs Predicted meta-deprotein Predicted transcriptional regulators Adenylate cyclase, family 3 (some proteins contain HAMP domain) Uncharacterized conserved protein Signal transduction histidine kinase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Predicted metal-dependent hydrolase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Predicted metal-dependent hydrolase Restriction endonuclease Disulfide bond formation protein DsbB	LIRLTNSSPHNIGGMSSECRGPQKMHRTORPSKTSTTRVO	Replication, recombination and repair Lipid transport and metabolism General function prediction only Replication, recombination and repair Signal transduction mechanisms Cell motility Function unknown Inorganic ion transport and metabolism Coenzyme transport and metabolism Cell motility Lipid transport and metabolism Carbohydrate transport and metabolism Carlohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Function unknown Function unknown Function unknown Function unknown Function in transport and metabolism Energy production and conversion General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function in transport and metabolism General function prediction only Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones General function prediction only Inorganic ion transport and metabolism Function unknown Transcription Signal transduction mechanisms Posttranslational modification, protein turnover, chaperones

COC071E			
COG0713	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Р	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
	Predicted secreted protein	S	Function unknown
	Short chain fatty acids transporter	1	Lipid transport and metabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
	Signal transduction histidine kinase	Т	Signal transduction mechanisms
	Transposase and inactivated derivatives	L	Replication, recombination and repair
	Lactate dehydrogenase and related dehydrogenases	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized protein conserved in bacteria	S K	Function unknown
	Predicted transcriptional regulators		Transcription
	Uncharacterized conserved protein	S K	Function unknown
	Predicted transcriptional regulators Exonuclease I	K L	Transcription
	Cytochrome c2	C	Replication, recombination and repair Energy production and conversion
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Gentisate 1,2-dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Ketopantoate reductase	н	Coenzyme transport and metabolism
	Peptide methionine sulfoxide reductase	0	Posttranslational modification, protein turnover, chaperones
	Acyl-CoA dehydrogenases	ı	Lipid transport and metabolism
	Acyl-CoA dehydrogenases	i	Lipid transport and metabolism
	Citrate synthase	c c	Energy production and conversion
	Uncharacterized membrane protein	S	Function unknown
	Nitric oxide reductase large subunit	P	Inorganic ion transport and metabolism
	Transcriptional regulators	K	Transcription
	Methylase involved in ubiquinone/menaquinone biosynthesis	н	Coenzyme transport and metabolism
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Rubrerythrin	c	Energy production and conversion
	Micrococcal nuclease (thermonuclease) homologs	Ĺ	Replication, recombination and repair
	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted nucleoside-diphosphate-sugar epimerase	M	Cell wall/membrane/envelope biogenesis
	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	н	Coenzyme transport and metabolism
	3-isopropylmalate dehydratase small subunit	E	Amino acid transport and metabolism
	3-isopropylmalate dehydratase large subunit	E	Amino acid transport and metabolism
	Predicted membrane protein	S	Function unknown
	DNA-binding ferritin-like protein (oxidative damage protectant)	Р	Inorganic ion transport and metabolism
COG0735	Fe2+/Zn2+ uptake regulation proteins	P	Inorganic ion transport and metabolism
	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	С	Energy production and conversion
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport and metabolism
	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains		
COG2204		T	Signal transduction mechanisms
	Uncharacterized protein conserved in bacteria	T S	Signal transduction mechanisms Function unknown
COG3011			=
COG3011 COG0702	Uncharacterized protein conserved in bacteria	S M I	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism
COG3011 COG0702 COG1024 COG3832	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein	S M I S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump	S M I S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases	S M I S V M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor	S M I S V M S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase	S M I S V M S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator	S M I S V M S I K	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein	S M I S V M S I K	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component	S M I S V M S I K S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136 COG4591	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, involved in lipoprotein release, permease component	S M I S V M S I K S V M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG3791 COG1136 COG4591 COG1262	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein	S M I S V M S I K S V	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity	S M I S V M S I K S V M S O O	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones
COG3011 COG0702 COG1024 COG3832 COG0534 COG0455 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, envolved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity	S M I S V M S I K S V M S O O	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Poetense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG41309 COG3791 COG1136 COG4591 COG1262 COG6066 COG0606 COG0730	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, eremease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted premeases	S M I S V M S I K S V M S O O R	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones General function prediction only
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG3791 COG1136 COG4591 COG1262 COG0606 COG0606 COG0730	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases	S M I S V M S I K S V M S O O R M M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG11309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0606 COG0730 COG0730	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases	S M I S V M S I K S V M S O O R M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification only Cell wall/membrane/envelope biogenesis General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1162 COG0606 COG0606 COG0730 COG0730 COG0730	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, erease, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit	S M I S V M S I K S V M S O O R M C	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posternslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Predicted permeases	S M I S V M S I K S V M S O O R M R C G	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG0730 COG0730 COG0730 COG1144 COG2814 COG0715	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	S M I S V M S I K S V M S O O R M R C G P	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0554 COG1024 COG1309 COG3791 COG1136 COG4591 COG1666 COG0606 COG0730 COG0730 COG1144 COG2814 COG2814 COG2816 COG0715 COG0715	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permeases ABC-type intrate/sulfonate/bicarbonate transport systems, periplasmic components ACJ-CoA synthetases (AMP-forming)/AMP-acid ligases II	S M I S V M S I K S V M S O O R M R C G P I	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Lipid transport and metabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0554 COG1024 COG1309 COG1309 COG1136 COG4591 COG1262 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814 COG2814 COG0715 COG0318 COG0584	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Previouted permeases Pyruvate-ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase	S M I S V M S I K S V M S O O R M R C G P I I C	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1309 COG3791 COG1262 COG0606 COG0730 COG073	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Lnoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, eremase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Predicted permeases ABC-type intrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin	S M I S V M S I K S V M S O O R M R C G P I C C	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Energy production and conversion Energy production and conversion
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG073	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase	S M I S V M S I K S V M S O O R M R C G P I C C Q	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion
COG3011 COG0702 COG1024 COG3832 COG0534 COG0554 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814 COG2814 COG2814 COG0584 COG0584 COG0584 COG0584 COG1146 COG3917 COG2852	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria	S M I S V M S I K S V M S O O R M R C G P I C C	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Energy production and conversion Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown
COG3011 COG0702 COG1024 COG3832 COG0534 COG0554 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814 COG0715 COG0715 COG0736 COG0730 COG1144 COG2814 COG0715 COG0318 COG0318	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase	S M I S V M S I K S V M S O O R M R C G P I C C Q S	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Postranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inergy production and conversion Energy production and conversion Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG073	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Lnoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	S M I S V M S I K S V M S O O R M R C G P I C C Q S I	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Replication, recombination and repair
COG3011 COG0702 COG1024 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136 COG64591 COG1262 COG0606 COG0730 COG0730 COG0730 COG0730 COG0730 COG1144 COG2814 COG0584 COG146 COG3917 COG2852 COG0318 COG2818 COG0318 COG2818 COG0318	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Lnoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases ABC-type intrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-Coa synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-Coa Synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Postranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism
COG3011 COG0702 COG1024 COG3832 COG0534 COG0554 COG1024 COG1309 COG1309 COG1136 COG4591 COG1262 COG0606 COG0606 COG0730 COG0730 COG1144 COG2814 COG2814 COG0318 COG0584 COG1146 COG3917 COG2852 COG0318 COG0318 COG0715 COG0318 COG0715 COG1960	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Lnoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L P	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posternslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Seneral function prediction only Finergy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism
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COG3011 COG0702 COG1024 COG3832 COG0534 COG0534 COG0451 COG1309 COG3791 COG1136 COG4591 COG1606 COG0606 COG0730 COG0730 COG1144 COG2814 COG2814 COG0584 COG0584 COG0381 COG0584 COG0311 COG0584 COG0311 COG0584 COG0311 COG0584 COG0715 COG0318 COG0584 COG0715 COG1960 COG1960 COG1902 COG3181	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ARC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA dehydrogenases Coeazyme F42O-dependent N5,N1O-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductase, Acyl-CoA dehydrogenases Coeazyme F42O-dependent N5,N1O-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductase, NDH:flavin oxidoreductases, Old Yellow Enzyme family	S M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism
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COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1262 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814 COG3917 COG2852 COG0318 COG2818 COG0715 COG2814 COG2814 COG2814 COG2814 COG2814 COG3917 COG2852 COG0318 COG2818 COG0715 COG3181 COG2818 COG0715 COG3181 COG2818 COG0715 COG3181 COG3960 COG1144 COG3917 COG387 COG3181 COG3960 COG3181 COG3960 COG3181 COG3961	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimeraes Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimeraes Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate-ferredoxin oxidoreductase and related 2-oxoacid-ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA dehydrogenases Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducts NADH-flavin oxidoreductases, Dld Yellow Enzyme family Uncharacterized protein conserved in bacteria Predicted flavoprotein involved in K-transport	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L P I C C S P	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Function unknown Inorganic ion transport and metabolism
COG3011 COG0702 COG1024 COG1024 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0730 COG1144 COG2812 COG0715 COG3181 COG0715 COG1960 COG2141 COG1902 COG3181 COG2072 COG3764 COG2304	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Nar-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Previate permeases Pyruvate-ferredoxin oxidoreductase and related 2-oxoacid-ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA dehydrogenases Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductar NADH-flavin oxidoreductases, Old Yellow Enzyme family Uncharacterized protein conserved in bacteria Predicted flavoprotein involved in K+ transport Sortase (surface protein transpeptidase)	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L P I C C S P M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posternaslational modification, protein turnover, chaperones Function unknown Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism Replication, recombination and repair Inorganic jon transport and metabolism Energy production and conversion Energy production by the size of the second sec
COG3011 COG0702 COG1024 COG3832 COG0534 COG0534 COG0451 COG1309 COG3791 COG1136 COG4591 COG1262 COG0606 COG0606 COG0730 COG0730 COG1144 COG2814 COG2814 COG2814 COG0584 COG0715 COG0318 COG0584 COG0715 COG1146 COG2818 COG0318 COG0715 COG1902 COG3181 COG2141 COG2904 COG2104 COG2904 COG2904 COG0491	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Membrane proteins related to metalloendopeptidases Predicted permeases Predicted permeases ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA dehydrogenases Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta: ANDH-flavin oxidoreductases, Old Vellow Enzyme family Uncharacterized protein conserved in bacteria Predicted flavoprotein involved in K+ transport Sortase (surface protein transpeptidase) Uncharacterized protein containing a von Willebrand factor type A (vWA) domain	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L P I C C S P M R	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Function unknown Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis General function prediction only
COG3011 COG0702 COG1024 COG3832 COG0534 COG0534 COG1024 COG1309 COG1136 COG4591 COG1262 COG0606 COG0730 COG0730 COG1144 COG2814 COG2814 COG2818 COG0930 COG1144 COG2814 COG2818 COG10606 COG0730 COG1144 COG2818 COG1146 COG3917 COG2852 COG0318 COG2141 COG1900 COG2141 COG1900 COG3181 COG277 COG3764 COG2704 COG3764 COG2941 COG0491 COG0491	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, involved in lipoprotein release, permease component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted premeases Membrane proteins related to metalloendopeptidases Predicted permeases Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit Arabinose efflux permease ABC-type intrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ACyl-CoA synthetases (AMP-forming)/AMP-acid ligases II 3-methyladenine DNA glycosylase Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta NADH-flavin oxidoreductases, Old Vellow Enzyme family Uncharacterized protein conserved in bacteria Predicted flavoprotein involved in K+ transport Sortase (surface protein transpeptidase) Uncharacterized protein containing a von Willebrand factor type A (wWA) domain Zn-dependent hydrolases, including glyoxylases	S M	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion
COG3011 COG0702 COG1024 COG3832 COG0534 COG0451 COG4458 COG1024 COG1309 COG3791 COG1262 COG0606 COG0730 COG0730 COG0730 COG1144 COG2814 COG3917 COG2852 COG0715 COG0715 COG0716 COG2072 COG3188 COG2141 COG1960 COG2141 COG1962 COG3188 COG2072 COG3764 COG2304 COG0491 COG2514 COG0318	Uncharacterized protein conserved in bacteria Predicted nucleoside-diphosphate-sugar epimerases Enoyl-CoA hydratase/carnithine racemase Uncharacterized conserved protein Na+-driven multidrug efflux pump Nucleoside-diphosphate-sugar epimerases Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized protein conserved in bacteria, putative virulence factor Enoyl-CoA hydratase/carnithine racemase Transcriptional regulator Uncharacterized conserved protein ABC-type antimicrobial peptide transport system, ATPase component ABC-type antimicrobial peptide transport system, ATPase component Uncharacterized conserved protein Predicted ATPase with chaperone activity Predicted ATPase with chaperone activity Predicted permeases Predicted permeases Predicted permeases Predicted permeases Predicted permeases ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-formingl)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 2-hydroxychromene-2-carboxylate isomerase Uncharacterized protein conserved in bacteria Acyl-CoA synthetases (AMP-formingl)/AMP-acid ligases II 3-methyladenine DNA glycosylase BaC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Acyl-CoA synthetases (AMP-formingl)/AMP-acid ligases II Glycerophosphoryl diester phosphodiesterase Ferredoxin 3-methyladenine DNA glycosylase Concayme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductase, Old Yellow Enzyme family Uncharacterized protein conserved in bacteria Predicted flavoprotein involved in K+ transport Sortase (surface protein conserved in bacteria Predicted flavoprotein involved in K+ transport Sortase (surface protein containing a von Willebrand factor type A (wWA) domain Zn-dependent hydrolases, including glyoxylases Predicted ring-cleavage extradiol dioxygenase	S M I S V M S I K S V M S O O R M R C G P I C C Q S I L P I C C S P M R R R R	Function unknown Cell wall/membrane/envelope biogenesis Lipid transport and metabolism Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Lipid transport and metabolism Transcription Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Defense mechanisms Cell wall/membrane/envelope biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Energy production and conversion Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Function unknown Lipid transport and metabolism Replication, recombination and repair Inorganic ion transport and metabolism Lipid transport and metabolism Energy production and conversion Function unknown Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis General function prediction only General function prediction only

COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	Е	Amino acid transport and metabolism
COG0703	Shikimate kinase	E	Amino acid transport and metabolism
COG1024	Enoyl-CoA hydratase/carnithine racemase	1	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	Н	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	С	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	0	Posttranslational modification, protein turnover, chaperones
COG1309	Transcriptional regulator	K	Transcription
COG1024	Enoyl-CoA hydratase/carnithine racemase	1	Lipid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	С	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	1	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	1	Lipid transport and metabolism
COG1309	Transcriptional regulator	K	Transcription
COG1024	Enoyl-CoA hydratase/carnithine racemase	1	Lipid transport and metabolism
	Acyl-CoA dehydrogenases	1	Lipid transport and metabolism
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	Predicted integral membrane protein	S	Function unknown
	Predicted nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein	S	Function unknown
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
	Monoamine oxidase	E	Amino acid transport and metabolism
	Alkylated DNA repair protein	L	Replication, recombination and repair
	DNA modification methylase	L	Replication, recombination and repair
	Phage shock protein A (IM30), suppresses sigma54-dependent transcription	K	Transcription
	Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
	Site-specific recombinases, DNA invertase Pin homologs	Ĺ	Replication, recombination and repair
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
	D-alanine-D-alanine ligase and related ATP-grasp enzymes	M	Cell wall/membrane/envelope biogenesis
	Dienelactone hydrolase and related enzymes	Q	Secondary metabolites biosynthesis, transport and catabolism
COG0412			Function unknown
		S	
COG3502	Uncharacterized protein conserved in bacteria	S R	
COG3502 COG0730	Uncharacterized protein conserved in bacteria Predicted permeases	R	General function prediction only
COG3502 COG0730 COG4297	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain	R S	General function prediction only Function unknown
COG3502 COG0730 COG4297 COG0596	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R S R	General function prediction only Function unknown General function prediction only
COG3502 COG0730 COG4297 COG0596 COG0596	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R S R R	General function prediction only Function unknown General function prediction only General function prediction only
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators	R S R R K	General function prediction only Function unknown General function prediction only General function prediction only Transcription
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein	R S R R K E	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase	R S R R K E	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	R S R R K E L	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204 COG2159	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold	R S R R K E L T	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204 COG2159 COG3653	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase	R S R R K E L	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204 COG2159 COG3653 COG1960	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold	R S R K E L T R	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2004 COG2159 COG3653 COG1960 COG1024	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase	R S R K E L T R Q I	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG1804	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase	R S R K E L T R Q I I	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion
COG3502 COG0730 COG04297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2204 COG2159 COG3653 COG1064 COG1024 COG1804 COG1804	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities	R S R K E L T R Q I I C R	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Energy production and conversion General function prediction only
COG3502 COG0730 COG04297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204 COG2159 COG3653 COG1960 COG1024 COG1804 COG3000 COG0779	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-apartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratases/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria	R S R K E L T R Q I I C R S	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG1804 COG3000 COG0779 COG2124	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450	R S R K E L T R Q I I C R S Q	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism
COG3502 COG0730 COG04297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG3804 COG0300 COG0779 COG2124 COG4783	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats	R S R K E L T R Q I I C R S Q R	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG300 COG0779 COG2124 COG3783 COG4783 COG3795	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria	R S R K E L T R Q I I C R S Q R S S S S S S S S S S S S S S S S	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG3795	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria	R S R K E L T R Q I I C R S Q R S S S S S S S S S S S S S S S S	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Function unknown
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG1024 COG3000 COG0779 COG2124 COG4783 COG3795 COG1359 COG01359	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases	R S R K E L T R Q I I C R S Q R S S H H	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Coenzyme transport and metabolism
COG3502 COG0730 COG04297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG1280 COG3795 COG2124 COG4783 COG3795 COG1359 COG1359 COG1359	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized conserved protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase	R S R K E L T R Q I I C R S Q R S S S S S S S S S S S S S S S S	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Function unknown Function unknown Foenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones
COG3502 COG0730 COG04297 COG0596 COG0696 COG0696 COG1280 COG2159 COG3653 COG1960 COG1024 COG300 COG0779 COG21284 COG3795 COG3795 COG1359 COG1359 COG1359 COG1111 COG0225 COG1733	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Untcharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Predicted transcriptional regulators	R S R K E L T R Q I I C R S Q R S S S H O K S S H O K S S S S S S S S S S S S S S S S S S	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG1024 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1359 COG0111 COG0225 COG1733 COG0277	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases	RSRRKELTRQIICRSQRSSHOKC	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG1024 COG1024 COG3000 COG0779 COG2124 COG4783 COG3795 COG1359 COG1111 COG0225 COG1733 COG0277 COG2124	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Cytochrome P450	R S R K E L T R Q I I C R S Q R S S S H O K C Q Q R S S D K C Q D K D K D K D K D K D K D K D K D K D	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0596 COG0596 COG1280 COG4119 COG2204 COG2159 COG3653 COG1960 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1359 COG1359 COG1733 COG0277 COG2124 COG1731	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein	R S R K E L T R Q I I C R S Q R S S H O K C Q N C Q N O N C Q N O N C N O N O N O N O N O N O N O N O	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility
COG3502 COG0730 COG04297 COG0596 COG0596 COG06497 COG0596 COG06401 COG1280 COG4119 COG2204 COG1024 COG1024 COG1024 COG1024 COG300 COG0779 COG2124 COG4783 COG03795 COG1359 COG0111 COG0225 COG1733 COG0277 COG2124 COG1317 COG1212	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-apartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type Ill secretory pathway protein Predicted redox protein, regulator of disulfide bond formation	RSRRKELTRQIICRSQRSSHOKCQNO	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Foeneral function prediction only Function unknown Function unknown Foeneral function prediction, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones
COG3502 COG0730 COG04297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG1024 COG1024 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1111 COG0225 COG1733 COG0277 COG2124 COG1317 COG1214 COG1653	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component	RSRRKELTRQIICRSQRSSHOKCQNOG	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG2159 COG3653 COG1960 COG1024 COG1024 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1359 COG111 COG0225 COG13359 COG0111 COG0225 COG13359 COG0171 COG025 COG1359 COG01553 COG0277 COG2124 COG1359 COG16553 COG0395	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport system, periplasmic component	R S R K E L T R Q I I C R S Q R S S H O K C Q N O O G G O G O G O G O G O G O G O G O	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0596 COG0596 COG1280 COG4119 COG2204 COG1259 COG3653 COG1960 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1359 COG0277 COG2124 COG1373 COG0277 COG2124 COG1373 COG0275 COG1559 COG0177 COG2124 COG1387 COG1765 COG1653 COG0395 COG03839	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted thydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved dehydrogenases Predicted transcriptional regulators Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type Ill secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, peripasmic component ABC-type sugar transport system, peripasmic component ABC-type sugar transport system, permease component	R S R R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG3502 COG0730 COG04297 COG0596 COG0596 COG06480 COG4119 COG2204 COG1159 COG3653 COG1960 COG1024 COG1024 COG3795 COG3795 COG1359 COG0111 COG0225 COG1733 COG0277 COG2124 COG1733 COG0277 COG2124 COG3895 COG1359 COG1889	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnithine racemase Predicted acyl-CoA transferases/carnithine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized dehydrogenase and related dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components	R S R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG2159 COG3653 COG1960 COG1024 COG1024 COG1024 COG1024 COG1025 COG0779 COG2124 COG4783 COG0779 COG2124 COG1317 COG1765 COG11733 COG0277 COG2124 COG1317 COG1765 COG13839 COG3839 COG3839 COG1880	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted transcriptional regulator of disulfide bond formation ABC-type sugar transport system, permease component ABC-type sugar transport system, permease components ABC-type sugar transport system, permease components ABC-type sugar transport systems, ATPase components Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	R S R R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG3502 COG0730 COG0730 COG0737 COG0596 COG0596 COG0596 COG0596 COG1280 COG2119 COG2204 COG2159 COG3653 COG1960 COG1024 COG3795 COG0779 COG2124 COG4783 COG3795 COG1359 COG0111 COG0225 COG1733 COG0277 COG2124 COG1359 COG1653 COG0395 COG3839 COG3839 COG3839 COG3839 COG3839 COG1080 COG0683	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted thydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheV-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type branched-chain amino acid transport systems, periplasmic component	R S R R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG3502 COG0730 COG04297 COG0596 COG0696 COG0696 COG1280 COG4119 COG2204 COG1596 COG1024 COG1024 COG1024 COG1030 COG0779 COG2124 COG4783 COG3795 COG1359 COG1181 COG025 COG1733 COG0277 COG2124 COG1733 COG0277 COG2124 COG1804 COG1804 COG18083 COG18083 COG18839 COG3839 COG3839 COG3839 COG3839 COG3839 COG1080 COG0683 COG1652	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphotydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Predicted acyl-CoA transferases/carnithine racemase Predicted acyl-CoA transferases/carnithine racemase Predicted acyl-CoA transferases/carnithine edhydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Plagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport system, periplasmic components ABC-type sugar transport systems, AFPase components ABC-type sugar transport systems, AFPase components Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) ABC-type branched-chain amino acid transport systems, periplasmic component Outer membrane receptor proteins, mostly fe transport	R S R R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G E P	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Function unknown Foottranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1640 COG124 COG1159 COG3653 COG1960 COG1024 COG1024 COG1024 COG3795 COG1359 COG1353 COG0215 COG1653 COG0277 COG2124 COG1373 COG0275 COG11655 COG1653 COG3895 COG1653 COG3895 COG1880 COG38839 COG38839 COG1880 COG0683	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Predicted transcriptional regulators Predicted TATP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, peripasmic component ABC-type sugar transport systems, ATPase components Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) ABC-type branched-chain amino acid transport systems, periplasmic component Predicted phosphatase/phosphohexomutase	R S R R K E L T R Q I I C R S S B H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Carbonydrate transport and metabolism
COG3502 COG0730 COG4297 COG0596 COG0596 COG0640 COG1280 COG4119 COG2204 COG2159 COG3653 COG1960 COG1024 COG1024 COG300 COG0779 COG2124 COG4783 COG3795 COG1111 COG0225 COG1733 COG0277 COG2124 COG1317 COG1653 COG0395 COG1653 COG0395 COG13839 COG3839 COG1880 COG0683 COG0683 COG0683 COG0683 COG06637 COG1177	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted Transcriptional regulators Putative threonine efflux protein Predicted MTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA dehydrogenases Predicted acyl-CoA transferases/carnitine dehydratase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, in Pase components ABC-type sugar transport systems, beriplasmic component in bacteria) ABC-type branched-chain amino acid transport systems, periplasmic component Outer membrane receptor proteins, mostly fe transport Predicted phosphatase/plosphohexomulase ABC-type spermidine/putrescine transport system, permease component II	R S R R K E L T R Q I I C R S S H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Carbohydrate function prediction only Amino acid transport and metabolism
COG3502 COG0730 COG04297 COG0596 COG0596 COG0596 COG0596 COG0596 COG1280 COG1280 COG1280 COG1960 COG1024 COG1020 COG1024 COG1359 COG1359 COG1359 COG1359 COG1733 COG0277 COG2124 COG1373 COG0275 COG1733 COG0277 COG2124 COG1359 COG1653 COG0395 COG3839 COG1880 COG08839 COG1883 COG1683 COG1683 COG1683 COG1680 COG0683 COG1629 COG0687 COG1177 COG1794	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted thydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted NTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases Enotyl-CoA end hydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Peptide methionine sulfoxide reductase Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) ABC-type sugar transport systems, permease component Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) ABC-type sugar transport systems, permease component Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) ABC-type sugar transport systems, permease component II ABC-type sugar transport systems, permease component II	R S R R K E L T R Q I I C R S S B H O K C Q N O G G G G G G G G G G G G G G G G G G	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis
COG3502 COG0730 COG04297 COG0596 COG0696 COG0696 COG0596 COG0596 COG1280 COG1119 COG2204 COG1196 COG1024 COG1024 COG1024 COG1030 COG0779 COG2124 COG4783 COG025 COG1359 COG1653 COG0252 COG1359 COG1653 COG0395 COG3839 COG3839 COG3839 COG1080 COG0683 COG1629 COG0683 COG1629 COG0637 COG1794 COG1414	Uncharacterized protein conserved in bacteria Predicted permeases Uncharacterized protein containing double-stranded beta helix domain Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Predicted transcriptional regulators Putative threonine efflux protein Predicted Transcriptional regulators Putative threonine efflux protein Predicted MTP pyrophosphohydrolase Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted metal-dependent hydrolase of the TIM-barrel fold N-acyl-D-aspartate/D-glutamate deacylase Acyl-CoA dehydrogenases Enoyl-CoA dehydrogenases Predicted acyl-CoA transferases/carnitine dehydratase Predicted acyl-CoA transferases/carnitine dehydratase Short-chain dehydrogenases of various substrate specificities Uncharacterized protein conserved in bacteria Cytochrome P450 Putative Zn-dependent protease, contains TPR repeats Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved protein Phosphoglycerate dehydrogenase and related dehydrogenases Predicted transcriptional regulators FAD/FMN-containing dehydrogenases Cytochrome P450 Flagellar biosynthesis/type III secretory pathway protein Predicted redox protein, regulator of disulfide bond formation ABC-type sugar transport system, periplasmic component ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, ATPase components ABC-type sugar transport systems, in Pase components ABC-type sugar transport systems, beriplasmic component in bacteria) ABC-type branched-chain amino acid transport systems, periplasmic component Outer membrane receptor proteins, mostly fe transport Predicted phosphatase/plosphohexomulase ABC-type spermidine/putrescine transport system, permease component II	R S R R K E L T R Q I I C R S Q R S S H O K C Q N O G G G G E P R E M	General function prediction only Function unknown General function prediction only General function prediction only Transcription Amino acid transport and metabolism Replication, recombination and repair Signal transduction mechanisms General function prediction only Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion General function prediction only Function unknown Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Function unknown Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Energy production and conversion Secondary metabolites biosynthesis, transport and catabolism Cell motility Posttranslational modification, protein turnover, chaperones Carbohydrate transport and metabolism Carbohydrate function prediction only Amino acid transport and metabolism

	Acetyl-CoA hydrolase	С	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	С	Energy production and conversion
	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	E	Amino acid transport and metabolism
	Glutamine cyclotransferase	0	Posttranslational modification, protein turnover, chaperones
	Succinate dehydrogenase, hydrophobic anchor subunit	С	Energy production and conversion
	Spermidine synthase	E	Amino acid transport and metabolism
	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit	С	Energy production and conversion
	Predicted aminopeptidase, lap family	R	General function prediction only
	Sortase and related acyltransferases	М	Cell wall/membrane/envelope biogenesis
	Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)	M S	Cell wall/membrane/envelope biogenesis Function unknown
	Uncharacterized conserved protein Poly(3-hydroxybutyrate) depolymerase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Membrane transporters of cations and cationic drugs	Q P	Inorganic ion transport and metabolism
	Phosphomannose isomerase	G	Carbohydrate transport and metabolism
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	ATP-dependent DNA ligase	Ĺ	Replication, recombination and repair
	Predicted ATPase	R	General function prediction only
	Pyridoxal/pyridoxamine kinase	н	Coenzyme transport and metabolism
	Citrate lyase beta subunit	G	Carbohydrate transport and metabolism
	Isocitrate/isopropylmalate dehydrogenase	c	Energy production and conversion
	3-isopropylmalate dehydratase small subunit	E	Amino acid transport and metabolism
	Glycosyltransferases involved in cell wall biogenesis	М	Cell wall/membrane/envelope biogenesis
COG1225	Peroxiredoxin	0	Posttranslational modification, protein turnover, chaperones
	Diaminopimelate epimerase	E	Amino acid transport and metabolism
	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
	Transcriptional regulator	K	Transcription
COG0491	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
COG2010	Cytochrome c, mono- and diheme variants	С	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	Н	Coenzyme transport and metabolism
COG0277	FAD/FMN-containing dehydrogenases	С	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
	Superfamily II DNA and RNA helicases	L	Replication, recombination and repair
	Putative hemolysin	R	General function prediction only
	Uncharacterized protein, 4-oxalocrotonate tautomerase homolog	R	General function prediction only
	Predicted dioxygenase of extradiol dioxygenase family	R	General function prediction only
	Predicted esterase	R	General function prediction only
COG0183	Acetyl-CoA acetyltransferase		Lipid transport and metabolism
		1	
COG1250	3-hydroxyacyl-CoA dehydrogenase	i	Lipid transport and metabolism
COG1250 COG2271	Sugar phosphate permease	I G	Lipid transport and metabolism Carbohydrate transport and metabolism
COG1250 COG2271 COG5001	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	I G T	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms
COG1250 COG2271 COG5001 COG4957	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator	I G T K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription
COG1250 COG2271 COG5001 COG4957 COG1261	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein	I G T K N	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog)	G T K N T	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components	I G T K N	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component	G T K N T U	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840 COG1414	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components	G T K N T	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840 COG1414 COG1349	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-fring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator	G T K N T U P K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840 COG1414 COG1349 COG1653	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulators of sugar metabolism ABC-type sugar transport system, periplasmic component	G T K N T U P K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840 COG1414 COG1349 COG1653 COG1813	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulators of sugar metabolism	G T K N T U P K K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1414 COG1349 COG1653 COG1813 COG0697	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1	G T K N T U P K K K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1840 COG1414 COG1349 COG1653 COG1813 COG0697	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulators of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily	G T K N T U P K K G K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism
COG1250 COG2271 COG5001 COG4957 COG1261 COG3476 COG1826 COG1414 COG1349 COG1653 COG1813 COG0697 COG2110 COG2128	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	G T K N T U P K K G K	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only
COG1250 COG2271 COG5001 COG4957 COG1261 COG13476 COG1826 COG1840 COG1414 COG1653 COG1813 COG0697 COG2110 COG2128 COG0604	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Ityptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulators of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein	G T K N T U P K K G K G R S	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown
C0G1250 C0G2271 C0G5001 C0G4957 C0G1261 C0G3476 C0G1840 C0G16144 C0G1349 C0G1633 C0G1813 C0G0697 C0G2110 C0G2128 C0G0694 C0G0456	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-fing biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein NADPH:quinone reductase and related Zn-dependent oxidoreductases	G T K N T U P K K G K G R S	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown Energy production and conversion
COG1250 COG2271 COG5001 COG49957 COG1261 COG3476 COG1840 COG1414 COG1349 COG1653 COG1813 COG1813 COG2128 COG0604 COG2128 COG0604 COG456 COG1807	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein NADPH-iquinone reductase and related Zn-dependent oxidoreductases Acetyltransferases	G T K N T U P K K G R S C R	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown Energy production and conversion General function prediction only
C0G1250 C0G2271 C0G50011 C0G50011 C0G4957 C0G1261 C0G1826 C0G1840 C0G1414 C0G1453 C0G1653 C0G1813 C0G0697 C0G2128 C0G0604 C0G0456 C0G0604 C0G0456 C0G1088 C0G1088 C0G1088 C0G1088 C0G1088 C0G1088 C0G1088 C0G1088 C0G1088	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulators of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein NADPH:quinone reductase and related Zn-dependent oxidoreductases Acetyltransferases 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family Predicticed amidohydrolase Mannose-6-phosphate isomerase	G T K N T U P K K G K G R S C R M G R	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown Energy production and conversion General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Carbohydrate transport and metabolism
COG1250 COG2271 COG5001 COG4957 COG1261 COG1840 COG1840 COG1840 COG16349 COG16349 COG1631 COG2110 COG2110 COG2110 COG2164 COG0604 COG0604 COG0604 COG0604 COG06062 COG06062 COG06062 COG2863	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein NADPH-iquinone reductase and related Zn-dependent oxidoreductases Acetyltransferases 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family Predicted amidohydrolase Mannose-6-phosphate isomerase Cytochrome c553	. I G T K N T U P K K G K G R S C R M R G C	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown Energy production and conversion General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Carbohydrate transport and metabolism Energy production and conversion
COG1250 COG2271 COG5001 COG4097 COG1261 COG3476 COG1262 COG1840 COG1414 COG1349 COG1653 COG0697 COG2110 COG2128 COG0645 COG1807 COG0388 COG0664 COG06863 COG0604	Sugar phosphate permease Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain Predicted transcriptional regulator Flagellar basal body P-ring biosynthesis protein Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog) Sec-independent protein secretion pathway components ABC-type Fe3+ transport system, periplasmic component Transcriptional regulator Transcriptional regulator of sugar metabolism ABC-type sugar transport system, periplasmic component Predicted transcription factor, homolog of eukaryotic MBF1 Permeases of the drug/metabolite transporter (DMT) superfamily Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Uncharacterized conserved protein NADPH:quinone reductase and related Zn-dependent oxidoreductases Acetyltransferases 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family Predicted amidohydrolase Mannose-6-phosphate isomerase Cytochrome c553 NADPH:quinone reductase and related Zn-dependent oxidoreductases	GTKNTUPKKGGRSCRMRGCCC	Lipid transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Transcription Cell motility Signal transduction mechanisms Intracellular trafficking, secretion, and vesicular transport Inorganic ion transport and metabolism Transcription Carbohydrate transport and metabolism Transcription Carbohydrate transport and metabolism General function prediction only Function unknown Energy production and conversion General function prediction only Cell wall/membrane/envelope biogenesis General function prediction only Carbohydrate transport and metabolism Energy production and conversion Energy production and conversion Energy production and conversion Energy production and conversion
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COG0789	Predicted transcriptional regulators	K	Transcription
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
COG0845	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
	Predicted acetamidase/formamidase	С	Energy production and conversion
	Transcriptional regulator	K	Transcription
	Phenylacetic acid-responsive transcriptional repressor	K	Transcription
	Transposase and inactivated derivatives	L O	Replication, recombination and repair
	Membrane-bound serine protease (CIpP class) Sortase and related acyltransferases	M	Posttranslational modification, protein turnover, chaperones Cell wall/membrane/envelope biogenesis
	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	P	Inorganic ion transport and metabolism
	Aspartate/tyrosine/aromatic aminotransferase	r E	Amino acid transport and metabolism
	Predicted kinase	R	General function prediction only
	Flagellin and related hook-associated proteins	N	Cell motility
	Flagellar hook-associated protein	N	Cell motility
	Universal stress protein UspA and related nucleotide-binding proteins	Т	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	1	Lipid transport and metabolism
	Sec-independent protein secretion pathway components	U	Intracellular trafficking, secretion, and vesicular transport
	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Phosphoserine phosphatase	E	Amino acid transport and metabolism
	Predicted integral membrane protein	S	Function unknown Function unknown
	Predicted membrane protein Predicted ATPase	S R	General function prediction only
	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
	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	0	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
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Predicted permeases	R	General function prediction only
	Protein tyrosine/serine phosphatase	Т	Signal transduction mechanisms
	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
	Predicted permease, DMT superfamily	R	General function prediction only
	Transcriptional regulator		
		K	Transcription Constal function prediction only
COG4122	Predicted O-methyltransferase	R	General function prediction only
COG4122 COG3492	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria	R S	General function prediction only Function unknown
COG4122 COG3492 COG0473	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase	R S C	General function prediction only Function unknown Energy production and conversion
COG4122 COG3492 COG0473 COG0431	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein	R S C R	General function prediction only Function unknown Energy production and conversion General function prediction only
COG4122 COG3492 COG0473 COG0431 COG0778	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase	R S C	General function prediction only Function unknown Energy production and conversion
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein	R S C R C	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein	R S C R C S	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609 COG2050	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators	R S C R C S K	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609 COG2050 COG0520	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism	R S C R C S K Q	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609 COG2050 COG0520 COG3483	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase	R S C R C S K Q E E G	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609 COG2050 COG0520 COG3483 COG1080	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion)	R S C R C S K Q E E G G	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG4122 COG3492 COG0473 COG0431 COG0778 COG3174 COG1609 COG2050 COG0520 COG3483 COG1080 COG1105 COG2050	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (Pf&B) Uncharacterized protein, possibly involved in aromatic compounds catabolism	R S C R C S K Q E E G G	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG4122 COG3492 COG0473 COG0778 COG3174 COG1609 COG2050 COG0520 COG3483 COG1080 COG1105 COG2050 COG2050	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase	R S C R C S K Q E E G G Q R	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only
COG4122 COG3492 COG0473 COG0473 COG3174 COG1609 COG2050 COG0520 COG3483 COG1105 COG2050 COG2050 COG2050	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyttransferase Uncharacterized protein conserved in bacteria	R S C R C S K Q E E G G Q R S	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown
COG4122 COG3492 COG0473 COG0473 COG0178 COG3174 COG1609 COG2050 COG0520 COG3483 COG1105 COG2050 COG2050 COG2153 COG3222 COG2271	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine Iyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease	R S C R C S K Q E E G G Q R S G	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0178 COG3174 COG1609 COG2050 COG3282 COG1105 COG2050 COG2153 COG2271 COG3239	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfRB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase	R S C S K Q E E G Q R S G I	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG61609 COG2050 COG0520 COG3483 COG1080 COG2153 COG2251 COG3222 COG3222 COG3223 COG3239 COG1012	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases	R S C R C S K Q E E G G Q R S G I C	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion
COG4122 COG3492 COG0473 COG0473 COG0778 COG1609 COG2050 COG0520 COG3483 COG1105 COG2050 COG2250 COG2251 COG3222 COG3223 COG3221 COG3239 COG10112 COG0684	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase	R S C R C S K Q E E G G Q R S G I C H	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0178 COG3174 COG1609 COG2050 COG0520 COG1080 COG1105 COG2050 COG2153 COG3222 COG2271 COG3239 COG1012 COG0684 COG0884	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermillion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase	R S C R C S K Q E E G G Q R S G I C	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0473 COG3174 COG1609 COG2050 COG3250 COG3483 COG1105 COG2153 COG2271 COG3222 COG3227 COG3239 COG1012 COG0684 COG1089 COG1392	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfRB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU)	R S C S K Q E E G G Q R S G I C H E P	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG61609 COG2050 COG2050 COG3250 COG1105 COG2153 COG2251 COG3222 COG2271 COG3239 COG1012 COG0684 COG1392 COG1392 COG1392 COG071	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein)	R S C R C S K Q E E G Q R S G I C H E P	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones
COG4122 COG3492 COG0473 COG0473 COG0178 COG1609 COG2050 COG0520 COG0520 COG1080 COG2153 COG2222 COG2271 COG3222 COG2271 COG3289 COG1012 COG0684 COG1392 COG0389 COG0393	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfRB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU)	R S C S K Q E E G G Q R S G I C H E P	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG01609 COG2050 COG0520 COG0520 COG1105 COG2050 COG2153 COG2222 COG2271 COG3239 COG1012 COG0684 COG1392 COG0379 COG3393 COG0379 COG3247	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted accyltransferase	R S C R C S K Q E E G G Q R S G I C H E P O R	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Inergy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only
COG4122 COG3492 COG3493 COG0431 COG0778 COG3174 COG1609 COG2050 COG3250 COG3483 COG1105 COG2153 COG2271 COG3229 COG3227 COG3292 COG0684 COG1092 COG0684 COG1092 COG0392 COG0392 COG0392 COG0392 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG034 COG043 COG043	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfRB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acetyltransferase Uncharacterized conserved protein	R S C R C S K Q E E G G Q R S G I C H E P O R S S S S S S S S S S S S S S S S S S	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown
COG4122 COG3492 COG0473 COG0473 COG0778 COG1609 COG2050 COG0520 COG0520 COG2050 COG2050 COG2253 COG2271 COG3229 COG2271 COG0684 COG0289 COG0392 COG0392 COG0393 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0394 COG0438 COG0438 COG0438	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acctyltransferase Uncharacterized conserved protein Glycosyltransferase	R S C S K Q E E G G Q R S G I C H E P O R S M	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Acribohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Inergy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG01778 COG3174 COG1609 COG2050 COG0520 COG0520 COG3483 COG1105 COG2050 COG2153 COG3222 COG2271 COG3239 COG1012 COG0684 COG0289 COG1392 COG0371 COG3393 COG3247 COG0438 COG3247 COG0438 COG3616 COG0765	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selencysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acetyltransferase Uncharacterized conserved protein Glycosyltransferase Predicted amino acid aldolase or racemase	RSCRCSKQEEGGQRSGICHEPORSME	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0473 COG0174 COG1609 COG2050 COG0520 COG3483 COG1105 COG2050 COG2153 COG2271 COG3227 COG3289 COG1012 COG0684 COG0071 COG3393 COG3192 COG0071 COG3393 COG3247 COG048 COG0684 COG0466 COG3608 COG0406	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acetyltransferase Uncharacterized conserved protein Glycosyltransferase Predicted amino acid aldolase or racemase ABC-type amino acid transport system, permease component Predicted deacylase Fructose-2,6-bisphosphatase	R S C R C S K Q E E G G Q R S G I C H E P O R S M E E R G G G S M E E R G S M E E R S M E E R S M E E R S M E E R S M E E R S M E E R S M E E R S M E E R S B E E R S B E E E R S B E E E E E E E E E E E E E E E E E E	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism
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COG4122 COG3492 COG0473 COG0473 COG0473 COG0174 COG1609 COG2050 COG0520 COG3483 COG1080 COG1105 COG2050 COG2153 COG2271 COG3239 COG1012 COG0684 COG0406 COG0680 COG0406 COG0803 COG1028 COG1012 COG4799 COG11012 COG4799 COG1121 COG6388 COG12124 COG0888 COG12124 COG0888 COG12124 COG0888 COG1128 COG1121 COG2124 COG0858 COG1291 COG06684 COG06684 COG1008	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfRB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acetyltransferase Uncharacterized conserved protein Glycosyltransferase Predicted amino acid transport system, permease component Predicted deacylse Fructose-2,6-bisphosphatase RABC-type metal ion transport system, periplasmic component/surface adhesin Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) NAD-dependent aldehyde dehydrogenases ABC-type metal ion transport systems, ATPase component Cytochrome P450 Ribosome-binding factor A Hagellar motor component Short-chain dehydrogenases of various substrate specificities Short-chain dehydrogenases of various substrate specificities Short-chain dehydrogenases of various substrate specificities	R S C R C S K Q E E G G Q R S G I C H E P O R S M E E R G P I C I P Q J N R H	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Garbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Ipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Lipid transport and metabolism Energy production and conversion Lipid transport and metabolism Energy production and conversion Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Translation, ribosomal structure and biogenesis Cell motility General function prediction only Coenzyme transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0473 COG0778 COG1609 COG0520 COG0520 COG0520 COG2050 COG2153 COG2251 COG2271 COG3229 COG2271 COG3239 COG1012 COG0684 COG0289 COG071 COG3393 COG1012 COG0684 COG0765 COG0803 COG1012 COG0684 COG0765 COG0803 COG1012 COG406 COG0803 COG1012 COG4799 COG1121 COG2124 COG0828 COG1012 COG4799 COG1121 COG2124 COG0828 COG1012 COG61028 COG01012 COG61012 COG61012 COG61012 COG61012 COG61012 COG61012 COG61012 COG61012 COG06084	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/isopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermillon) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted acetyltransferase Uncharacterized conserved protein Glycosyltransferase Uncharacterized conserved protein Predicted acetyltransferase Uncharacterized conserved protein Predicted acetyltransferase Uncharacterized conserved protein Predicted deacylase Predicted deacylase Predicted deacylase Predicted deacylase Predicted deacylase ABC-type maino acid transport system, periplasmic component/surface adhesin Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) NAD-dependent aldehyde dehydrogenases ABC-type metal ion transport systems, periplasmic component (subunits alpha and beta) ABC-type Mn/Zn transport systems, ATPase component Cytochrome P450 Ribosome-binding factor A Flagellar motor component Short-chain dehydrogenases of various substrate specificities Demethylmenaquinone methyltransferase ABC-type Mn/2+transport systems, permease components	R S C R C S K Q E E G G Q R S G I C H E P O R S M E E R G P I C I P Q J N R H P	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion Lipid transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Translation, ribosomal structure and biogenesis Cell motility General function prediction only Coenzyme transport and metabolism Inorganic ion transport and metabolism
COG4122 COG3492 COG0473 COG0473 COG0473 COG01609 COG0520 COG0520 COG0520 COG0520 COG0520 COG2050 COG2050 COG2050 COG2050 COG2153 COG3222 COG2271 COG3239 COG1012 COG0684 COG0803 COG36166 COG0765 COG3608 COG0803 COG1012 COG0408 COG0803 COG1012 COG2153 COG1012 COG2153 COG36161 COG0765 COG3608 COG0406 COG0803 COG1012 COG4799 COG1121 COG2124 COG0858 COG1012 COG4799 COG1121 COG2124 COG0858 COG10684 COG1012 COG06844 COG161622 COG0843	Predicted O-methyltransferase Uncharacterized protein conserved in bacteria Isocitrate/Sopropylmalate dehydrogenase Predicted flavoprotein Nitroreductase Predicted membrane protein Transcriptional regulators Uncharacterized protein, possibly involved in aromatic compounds catabolism Selenocysteine lyase Tryptophan 2,3-dioxygenase (vermilion) Phosphoenolpyruvate-protein kinase (PTS system El component in bacteria) Pructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB) Uncharacterized protein, possibly involved in aromatic compounds catabolism Predicted acyltransferase Uncharacterized protein conserved in bacteria Sugar phosphate permease Fatty acid desaturase NAD-dependent aldehyde dehydrogenases Demethylmenaquinone methyltransferase Dihydrodipicolinate reductase Phosphate transport regulator (distant homolog of PhoU) Molecular chaperone (small heat shock protein) Predicted aceyltransferase Uncharacterized conserved protein Glycosyltransferase Predicted danno acid transport system, permease component Predicted daexplase Fructose-2,6-bisphosphatase ABC-type maino acid transport system, periplasmic component/surface adhesin Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) NAD-dependent aldehyde dehydrogenases Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta) ABC-type maino acid stransport systems, ATPase component Cytochrome P450 Ribosome-binding factor A Riagellar motor component Short-chain dehydrogenases of various substrate specificities Demethylmenaquinone methyltransferase components Heme/copper-type cytochrome/quinol oxidases, subunit 2	RSCRCSKQEEGGQRSGICHEPORSMEERGPICIPQJNRHPC	General function prediction only Function unknown Energy production and conversion General function prediction only Energy production and conversion Function unknown Transcription Secondary metabolites biosynthesis, transport and catabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Garbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism General function prediction only Function unknown Carbohydrate transport and metabolism Lipid transport and metabolism Energy production and conversion Coenzyme transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Amino acid transport and metabolism General function prediction only Carbohydrate transport and metabolism Inorganic ion transport and metabolism

COG1845			
	Heme/copper-type cytochrome/quinol oxidase, subunit 3	С	Energy production and conversion
	Predicted small integral membrane protein	S	Function unknown
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Small-conductance mechanosensitive channel Signal transduction histidine kinase	M T	Cell wall/membrane/envelope biogenesis Signal transduction mechanisms
	Transcriptional regulator	K	Transcription
	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
	Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	j	Translation, ribosomal structure and biogenesis
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	С	Energy production and conversion
	Transcriptional regulators	K	Transcription
	Small subunit of phenylpropionate dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Lysine efflux permease	R	General function prediction only
	Triphosphoribosyl-dephospho-CoA synthetase Acetyl-CoA carboxylase beta subunit	Н	Coenzyme transport and metabolism
	Acetyl-CoA:acetate/3-ketoacid CoA transferase	- 1	Lipid transport and metabolism Lipid transport and metabolism
	Acyl-CoA dehydrogenases	i	Lipid transport and metabolism
	Acyl-CoA dehydrogenases	i	Lipid transport and metabolism
	3-hydroxyacyl-CoA dehydrogenase	1	Lipid transport and metabolism
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	1	Lipid transport and metabolism
COG2148	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Tfp pilus assembly protein PilF	N	Cell motility
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Predicted O-methyltransferase	R E	General function prediction only
	Methionine synthase II (cobalamin-independent) ADP-heptose:LPS heptosyltransferase	M	Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Asparagine synthase (glutamine-hydrolyzing)	E	Amino acid transport and metabolism
	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
	Fe-S oxidoreductase	С	Energy production and conversion
COG2243	Precorrin-2 methylase	Н	Coenzyme transport and metabolism
COG0007	Uroporphyrinogen-III methylase	н	Coenzyme transport and metabolism
	Cobalamin biosynthesis protein CbiG	Н	Coenzyme transport and metabolism
COG0582		L	Replication, recombination and repair
	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	С	Energy production and conversion
	Transcriptional regulator	K	Transcription
	Uncharacterized conserved protein containing a ferredoxin-like domain	С	Energy production and conversion
	Uncharacterized protein conserved in bacteria Thisming pure phosphate requiring payment facetalactate purphase, purphase debudrageness (cutesbrown), glyanylate carbolic	S E	Function unknown
	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Acetyltransferases	R	Amino acid transport and metabolism General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	DNA replication protein	Ĺ	Replication, recombination and repair
	Transposase and inactivated derivatives	L	Replication, recombination and repair
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
COG0625	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized conserved protein	S	Function unknown
	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	М	Cell wall/membrane/envelope biogenesis
	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
COG4922	Uncharacterized protein conserved in bacteria	S	Function unknown
6063307	AraC-type DNA-binding domain-containing proteins		
	Multidrug resistance efflux numn	K	Transcription Defense mechanisms
COG1566	Multidrug resistance efflux pump ABC-type transport system involved in lipoprotein release, permease component	K V	Defense mechanisms
COG1566 COG4591	ABC-type transport system, involved in lipoprotein release, permease component	K V M	Defense mechanisms Cell wall/membrane/envelope biogenesis
COG1566 COG4591 COG0028		K V	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
COG1566 COG4591 COG0028 COG3826	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria	K V M E	Defense mechanisms Cell wall/membrane/envelope biogenesis
COG1566 COG4591 COG0028 COG3826 COG1028	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	K V M E	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	K V M E S	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	K V M E S	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028 COG1960	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	K V M E S I I I	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028 COG1960 COG2072	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport	K V M E S	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028 COG1960 COG2072 COG0183	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase	K V M E S I I I I	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028 COG1960 COG2072 COG0183 COG1136	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component	K V M E S I I I I V	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Defense mechanisms
COG1566 COG4591 COG0028 COG3826 COG1028 COG1024 COG1028 COG1960 COG2072 COG0183 COG1136	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	K V M E S I I I I V H	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Defense mechanisms Coenzyme transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1960 COG1024 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria	K V M E S I I I I V	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Coenzyme transport and metabolism Coenzyme transport and metabolism Function unknown
COG1566 COG4591 COG0288 COG3826 COG1028 COG1024 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	K V M E S I I I I P I V H S	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Defense mechanisms Coenzyme transport and metabolism
COG1566 COG4591 COG0282 COG1960 COG1028 COG1028 COG1028 COG1028 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840 COG1396 COG1846	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators	K V M E S I I I I V H S K	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Corenzyme transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription
COG1566 COG4591 COG0282 COG1960 COG1960 COG1028 COG1960 COG2072 COG01843 COG1366 COG2840 COG1396 COG1396	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators	K V M E S I I I V H S K K	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Lipid transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription
COG1566 COG4591 COG0288 COG1960 COG1960 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840 COG1396 COG1846 COG0384 COG10846 COG0038 COG1063	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Chloride channel protein EriC	K V M E S I I I V H S K K	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Loganic ion transport and metabolism Lipid transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism
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COG1566 COG4591 COG0282 COG1960 COG1960 COG1028 COG1960 COG2072 COG1863 COG1136 COG1136 COG1366 COG2840 COG1396 COG1396 COG1366 COG0654 COG0654 COG1638	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component	K V M E S I I I V H S K K P E G H G	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Soenzyme transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1566 COG4591 COG028 COG1960 COG1960 COG1028 COG1960 COG2072 COG1136 COG1136 COG1136 COG1396 COG1396 COG1396 COG1396 COG16386 COG0662 COG0662 COG0662 COG0654 COG1638 COG1638	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit	K V M E S I I I P I V H S K K P E G H G G G G G G G G G G G G G G G G G	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Sefense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism
COG1566 COG4591 COG0028 COG1960 COG1024 COG1024 COG1028 COG1960 COG1024 COG1061 COG0161 COG2840 COG1396 COG1396 COG1396 COG161 COG0662 COG0654 COG1663 COG16252 COG0409	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Transcriptional regulators Transcriptional protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor	K V M E S I I I I V H S K K F E G H G C O O	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism
COG1566 COG4591 COG0282 COG1960 COG1028 COG1960 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840 COG1396 COG1068 COG1068 COG1068 COG0662 COG0662 COG0654 COG1638 COG1659 COG1659 COG1659 COG0660 COG0650 COG0600 COG2010	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase Predicted flavoprotein involved in K+ transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants	K V M E S I I I I V H S K K P E G H G C O C O C	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbostranslational modification, protein turnover, chaperones Energy production and conversion
COG1566 COG4591 COG0282 COG1960 COG1928 COG1960 COG2072 COG01846 COG01846 COG0654 COG1638 COG1638 COG1638 COG1638 COG1638 COG1638 COG1638 COG06654 COG0654 COG0654 COG0659 COG0409 COG2010 COG0309	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor	K V M E S I I I I P I V H S K K P E G C O C O C O C O C O C O C O C O C O C	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Energy production and conversion Posttranslational modification, protein turnover, chaperones
COG1566 COG4591 COG0028 COG3826 COG1028 COG1024 COG1028 COG1960 COG2072 COG0183 COG1136 COG16184 COG1396 COG1638 COG1662 COG0654 COG1638 COG1752 COG0409 COG0309 COG0378	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase	K V M E S I I I I V H S K K P E G H G C O C O C	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and meta
COG1566 COG4591 COG0282 COG1960 COG1024 COG1028 COG1960 COG1024 COG1960 COG1024 COG1038 COG1136 COG0161 COG0384 COG1396 COG1396 COG1846 COG0038 COG1662 COG0654 COG1638 COG1638 COG1638 COG1638 COG0662 COG0654 COG0378 COG0378 COG0642	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dethydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Signal transduction histidine kinase	K V M E S I I I V H S K K F E G H G C O C O O O O O O O O O O O O O O O O	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms
COG1566 COG4591 COG02826 COG1960 COG1028 COG1960 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840 COG1396 COG1396 COG1646 COG0388 COG1662 COG0662 COG0654 COG1638 COG1654 COG1654 COG0378 COG0378	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase Predicted flavoprotein involved in K+ transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Signal transduction histidine kinase	K V M E S I I I I V H S K K P E G H G C O C O O C O O C O O C O O C O O C O O C O O C O O C O O C O O C O O C O O C O O C O O O C O O O O C O	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Energy production and conversion Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism
COG1566 COG4591 COG0282 COG1960 COG1928 COG1960 COG2072 COG01846 COG0654 COG1638 COG1654 COG0654 COG0654 COG0654 COG0657 COG037	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dethydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Signal transduction histidine kinase	K V M E S I I I I I P I V H S K K P E G H G C O C T G	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms
COG1566 COG4591 COG0028 COG3826 COG1024 COG1024 COG1028 COG1960 COG1024 COG1038 COG1136 COG1136 COG1136 COG1636 COG1396 COG1846 COG1396 COG1638 COG1252 COG0009 COG0378 COG0662 COG0654 COG0654 COG0654 COG0654 COG0658 COG0667 COG0667 COG0680	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-G-phosphate isomerase 2-polyprenyl-G-methoxylphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Sugar phosphate permease Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)	K V M E S I I I P I V H S K K P E G H G C O O O T G O O O O O O O O O O O O O O O	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Energy production and conversion Posttranslational modification, protein turnover, chaperones Fenergy production and conversion Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism Garbohydrate transport and metabolism
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COG1566 COG4591 COG0028 COG3826 COG1028 COG1028 COG1960 COG1960 COG2072 COG0183 COG1136 COG16163 COG1662 COG0654 COG1638	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein Fric Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Sugar phosphate permease Zn finger protein HypA/HybF (possibly regulating hydrogenase expression) Ni,Fe-hydrogenase maturation factor Ni,Fe-hydrogenase maturation factor Ni,Fe-hydrogenase and I cytochrome b subunit Ni,Fe-hydrogenase I small subunit ATPase components of ABC transporters with duplicated ATPase domains	K V M E S I I I I P I V H S K K P E G H G C O C O O T G R C C C R	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Carbohydrate transport and metabolism Energy production and conversion Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism General function prediction only Energy production and conversion Energy production and conversion Energy production and conversion General function prediction only
COG1566 COG4591 COG0028 COG3826 COG1024 COG1024 COG1028 COG1960 COG1024 COG1038 COG1136 COG0161 COG2840 COG1396 COG1396 COG1396 COG1638 COG1740 COG0375 COG0680 COG1740 COG0488 COG1458	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transport system and related protein from the protein from the protein for the protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Nij-E-indring GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Sugar phosphate permease In finger protein HypA/HybF (possibly regulating hydrogenase expression) Ni,Fe-hydrogenase maturation factor Ni,Fe-hydrogenase samal subunit Ni,Fe-hydrogenase is mall subunit Kef-type K+ transport systems, membrane components Kef-type K+ transport systems, membrane components	K V M E S I I I I V H S K K P E G H G C O C C C C R P	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Poefense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism General function prediction only Energy production and conversion
COG1566 COG4591 COG0282 COG1028 COG1061 COG0161 COG0380 COG1662 COG0662 COG0654 COG1638 COG1252 COG0409 COG2071 COG0378 COG0642 COG2271 COG0378 COG0662 COG0475 COG0488 COG1969 COG1740 COG0488 COG1740 COG0488 COG0475 COG0682	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyl-GoA acetyl-transferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Sugar phosphate permease Zn finger protein HypA/HybF (possibly regulating hydrogenase expression) Ni,Fe-hydrogenase I small subunit Ni,Fe-hydrogenase I small subunit Ni,Fe-hydrogenase I small subunit ATPase components of ABC transporters with duplicated ATPase domains Kef-type K+ transport systems, membrane components Signal transduction histidine kinase	K V M E S I I I I P I V H S K K P E G H G C O C O O T G R C C C R P T	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism General function prediction only Energy production and conversion Energy production and conversion Energy production and conversion Energy production and conversion General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms
COG1566 COG4591 COG04891 COG03826 COG1960 COG1960 COG1028 COG1960 COG2072 COG0183 COG1136 COG0161 COG2840 COG1396 COG1640 COG0642 COG0375 COG0682 COG0684 COG1969 COG1740 COG0488 COG1486 COG0488 COG1486 COG0475 COG06482 COG0475 COG06482 COG0475 COG06482 COG0475 COG06484 COG0475 COG06442 COG0475 COG06442 COG0475 COG06442 COG0475 COG06442 COG0475 COG06442 COG0475 COG06442 COG0475	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Enoyl-CoA hydratase/carnithine racemase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavogrotein involved in K+ transport Acetyl-CoA acetyltransferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related 2n-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C4-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor NI,Fe-hydrogenase s membrane components Signal transduction histidine kinase High-affinity nickel permease	K V M E S I I I I P I V H S K K P E G H G C O C O O T G R C C C R P T P	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Coenzyme transport and metabolism Function unknown Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism General function prediction only Energy production and conversion Energy production and metabolism Signal transduction mechanisms Inorganic ion transport and metabolism
COG1566 COG4591 COG0028 COG3826 COG1028 COG1028 COG1028 COG1960 COG1024 COG1960 COG2072 COG0183 COG1136 COG1636 COG1636 COG1638 COG1652 COG0642 COG0675 COG0680 COG1740 COG0488 COG0475 COG0642 COG0645	ABC-type transport system, involved in lipoprotein release, permease component Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Acyl-CoA dehydrogenases Predicted flavoprotein involved in K+ transport Acetyl-CoA acetyl-GoA acetyl-transferase ABC-type antimicrobial peptide transport system, ATPase component Adenosylmethionine-8-amino-7-oxononanoate aminotransferase Uncharacterized protein conserved in bacteria Predicted transcriptional regulators Chloride channel protein EriC Threonine dehydrogenase and related Zn-dependent dehydrogenases Mannose-6-phosphate isomerase 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases TRAP-type C-dicarboxylate transport system, periplasmic component NADH dehydrogenase, FAD-containing subunit Hydrogenase maturation factor Cytochrome c, mono- and diheme variants Hydrogenase maturation factor Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase Signal transduction histidine kinase Sugar phosphate permease Zn finger protein HypA/HybF (possibly regulating hydrogenase expression) Ni,Fe-hydrogenase I small subunit Ni,Fe-hydrogenase I small subunit Ni,Fe-hydrogenase I small subunit ATPase components of ABC transporters with duplicated ATPase domains Kef-type K+ transport systems, membrane components Signal transduction histidine kinase	K V M E S I I I I P I V H S K K P E G H G C O C O O T G R C C C R P T	Defense mechanisms Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Function unknown Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Coenzyme transport and metabolism Function unknown Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Posttranslational modification, protein turnover, chaperones Energy production and conversion Posttranslational modification, protein turnover, chaperones Signal transduction mechanisms Carbohydrate transport and metabolism General function prediction only Energy production and conversion Energy production and conversion Energy production and conversion Energy production and conversion General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms

	Uncharacterized conserved protein	S	Function unknown
	Glycosyltransferases involved in cell wall biogenesis	М	Cell wall/membrane/envelope biogenesis
	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle control, cell division, chromosome partitioning
	Dolichyl-phosphate-mannoseprotein O-mannosyl transferase	0	Posttranslational modification, protein turnover, chaperones
	Predicted lactoy/glutathione lyase	R	General function prediction only
	Enoyl-CoA hydratase/carnithine racemase	P	Lipid transport and metabolism
	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit Predicted acyltransferases	r	Inorganic ion transport and metabolism Lipid transport and metabolism
	Cyanate permease	P	Inorganic ion transport and metabolism
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Lipid A core - O-antigen ligase and related enzymes	M	Cell wall/membrane/envelope biogenesis
	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	I	Lipid transport and metabolism
	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	Ċ	Energy production and conversion
	Periplasmic molybdate-binding protein/domain	P	Inorganic ion transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Predicted membrane protein	S	Function unknown
	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
	Predicted dehydrogenases and related proteins	R	General function prediction only
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Uncharacterized copper-binding protein	Р	Inorganic ion transport and metabolism
	Signal transduction histidine kinase	Т	Signal transduction mechanisms
	Imidazoleglycerol-phosphate dehydratase	E	Amino acid transport and metabolism
	Predicted acyltransferases	1	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	С	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	Н	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)	1	Lipid transport and metabolism
	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Na+/H+ antiporter NhaD and related arsenite permeases	P	Inorganic ion transport and metabolism
	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport and metabolism
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Fatty acid desaturase	1	Lipid transport and metabolism
	Coenzyme F390 synthetase	Н	Coenzyme transport and metabolism
	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	C	Energy production and conversion
	Uncharacterized protein, possibly involved in aromatic compounds catabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	ABC-type branched-chain amino acid transport system, permease component	E D	Amino acid transport and metabolism
	Uncharacterized protein (competence- and mitomycin-induced)	R	General function prediction only
	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T T	Signal transduction mechanisms
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain		Signal transduction mechanisms
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K U	Transcription Intracellular trafficking, secretion, and vesicular transport
	Signal peptidase I Predicted esterase of the alpha-beta hydrolase superfamily	R	General function prediction only
	Cyclopropane fatty acid synthase and related methyltransferases	M	Cell wall/membrane/envelope biogenesis
COG2230			
COG1070	Sugar (nentulose and hexulose) kinases	G	Carbobydrate transport and metabolism
	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
COG4804	Uncharacterized conserved protein	S	Function unknown
COG4804 COG3030	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid	S R	Function unknown General function prediction only
COG4804 COG3030 COG1172	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	S R G	Function unknown General function prediction only Carbohydrate transport and metabolism
COG4804 COG3030 COG1172 COG1089	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase	S R G M	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis
COG4804 COG3030 COG1172 COG1089 COG1089	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase	S R G M M	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs	S R G M M	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1319	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs	S R G M M C C	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator	S R G M M C C	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1319 COG1309 COG1853	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	S R G M C C C K R	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein	S R G M M C C C K R	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5511	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	S R G M C C C K R	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5511 COG1573	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein	S R G M C C K R N R	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1853 COG0840 COG5511 COG1573 COG1758	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase	S R G M C C K R N L	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5511 COG1573 COG1758 COG0317	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega	S R G M C C K R N R L	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5511 COG1573 COG1758 COG0317	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases	S R G M C C K R N R L K	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms
COG4804 COG3030 COG1172 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5511 COG1573 COG1758 COG0317 COG0119	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases	S R G M C C K R N R L K T E	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1319 COG1309 COG1853 COG0840 COG5517 COG1758 COG0317 COG0174 COG1396	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase	S R G M C C K R N E L K T E P	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1309 COG1309 COG1373 COG0840 COG5511 COG1573 COG0175 COG0179 COG0474 COG1366 COG1426	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase Predicted transcriptional regulators	S R G M C C K R N R L K T E K	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism Transcription
COG4804 COG3030 COG1172 COG1089 COG1089 COG1319 COG1319 COG1309 COG6183 COG0851 COG1573 COG1758 COG0175 COG0179 COG0142 COG0730	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase Predicted transcriptional regulators Uncharacterized protein conserved in bacteria	S R M M C C K R N R L K T E P K S	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism Transcription Function unknown
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1309 COG1309 COG1311 COG1573 COG1758 COG0171 COG0119 COG0474 COG1396 COG1396 COG0530 COG0530 COG0730	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase Predicted transcriptional regulators Uncharacterized protein conserved in bacteria Predicted permeases	S R G M C C K R N E L K T E P K S R	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism Transcription Function unknown General function prediction only
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1319 COG1309 COG1317 COG1130 COG5157 COG1758 COG0317 COG0119 COG0474 COG1396 COG1426 COG0704 COG06174 COG0836	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase Predicted transcriptional regulators Uncharacterized protein conserved in bacteria Predicted permeases Glutamine synthetase	S R G M C C K R N R L K T E P K S R E	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism Transcription Function unknown General function prediction only Amino acid transport and metabolism
COG4804 COG3030 COG1172 COG1089 COG1089 COG1529 COG1309 COG1309 COG1373 COG0840 COG5511 COG0737 COG0174 COG0474	Uncharacterized conserved protein Protein affecting phage T7 exclusion by the F plasmid Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components GDP-D-mannose dehydratase GDP-D-mannose dehydratase GDP-D-mannose dehydratase Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Transcriptional regulator Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family Methyl-accepting chemotaxis protein Bacteriophage capsid protein Uracil-DNA glycosylase DNA-directed RNA polymerase, subunit K/omega Guanosine polyphosphate pyrophosphohydrolases/synthetases Isopropylmalate/homocitrate/citramalate synthases Cation transport ATPase Predicted transcriptional regulators Uncharacterized protein conserved in bacteria Predicted permeases Glutamine synthetase Mannose-1-phosphate guanylyltransferase	S R G M M C C K R N R L K T E F K S R E	Function unknown General function prediction only Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis Energy production and conversion Energy production and conversion Transcription General function prediction only Cell motility General function prediction only Replication, recombination and repair Transcription Signal transduction mechanisms Amino acid transport and metabolism Inorganic ion transport and metabolism Transcription Function unknown General function prediction only Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis

	Predicted membrane protein ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components	S C	Function unknown Energy production and conversion
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ABC-type uncharacterized transport system, permease and ATPase components	R	General function prediction only
	Multidrug resistance efflux pump	V	Defense mechanisms
	Uncharacterized conserved protein	Š	Function unknown
COG1538	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
COG1472	Beta-glucosidase-related glycosidases	G	Carbohydrate transport and metabolism
	Glycosyltransferases, probably involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T	Signal transduction mechanisms
	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	T	Signal transduction mechanisms
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, g	M	Cell wall/membrane/envelope biogenesis
	Nucleoside-diphosphate-sugar epimerases dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	M M	Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
	Permeases of the major facilitator superfamily	R	General function prediction only
	Methylase involved in ubiquinone/menaquinone biosynthesis	н	Coenzyme transport and metabolism
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Cephalosporin hydroxylase	٧	Defense mechanisms
	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
	dTDP-4-dehydrorhamnose reductase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein	S	Function unknown
	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	M	Cell wall/membrane/envelope biogenesis
	dTDP-glucose pyrophosphorylase	M	Cell wall/membrane/envelope biogenesis
	Signal transduction histidine kinase	T	Signal transduction mechanisms
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Predicted ATPase Nucleotide hinding protein implicated in inhibition of contum formation	R D	General function prediction only Cell cycle control, cell division, chromosome partitioning
	Nucleotide-binding protein implicated in inhibition of septum formation Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	ī	Lipid transport and metabolism
	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
	Citrate synthase	C	Energy production and conversion
	UDP-N-acetylmuramate-alanine ligase	M	Cell wall/membrane/envelope biogenesis
	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	1	Lipid transport and metabolism
COG0169	Shikimate 5-dehydrogenase	E	Amino acid transport and metabolism
COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	1	Lipid transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
	Amino acid transporters	E	Amino acid transport and metabolism
	N-acetylglutamate synthase and related acetyltransferases	E	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria Transcriptional regulator	S K	Function unknown
	Transcriptional regulator Transcription antiterminator	K	Transcription Transcription
	Bacterial cell division membrane protein	D	Cell cycle control, cell division, chromosome partitioning
	Hemoglobin-like flavoprotein	c	Energy production and conversion
	Predicted metal-dependent hydrolase	R	General function prediction only
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	1	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	1	Lipid transport and metabolism
COG3558	Uncharacterized protein conserved in bacteria	S	Function unknown
	Transcriptional regulator	K	Transcription
	Cysteine synthase	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	Co/Zn/Cd efflux system component		
		P	Inorganic ion transport and metabolism
COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism
COG1830 COG1609	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators	G K	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription
COG1830 COG1609 COG0438	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase	G K M	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis
COG1830 COG1609 COG0438 COG3411	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin	G K M C	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion
COG1830 COG1609 COG0438 COG3411 COG3839	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components	G K M C G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin	G K M C	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily	G K M C G R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase	G K M C G R R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798 COG0486 COG1035 COG0655	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA	G K M C G R R R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only General function prediction only
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028	DinA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	G K M C G R R C R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism
COG1830 COG1609 COG0438 COG3411 COG3839 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit	G K M C G R R C R C R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit	G K M C G R R C R I G G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958	DinA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator	G K M C G R R C R I G K	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription
COG1830 COG1609 COG0438 COG3411 COG3839 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3959 COG1309 COG2223	DinA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter	G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism
COG1830 COG1609 COG0438 COG34811 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958 COG3958 COG3025	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters	G K M C G R R C R I G K P P	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958 COG1309 COG2223 COG0025 COG1968	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein	G K M C G R R C R G K P V	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Defense mechanisms
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG0486 COG1035 COG0655 COG1028 COG3959 COG3959 COG2223 COG0225 COG1968 COG4244	DinA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein	G K M C G R R R C G K P P V S	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Function unknown
COG1830 COG1609 COG0438 COG3481 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958 COG3959 COG3959 COG3959 COG3959 COG1309 COG2223 COG0025 COG1968	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein	G K M C G R R C R G K P V	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Defense mechanisms
COG1830 COG1609 COG0438 COG34811 COG3788 COG4798 COG0486 COG1035 COG1028 COG3959 COG3958 COG3958 COG1309 COG2223 COG025 COG1968 COG4244 COG1981 COG3336	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein	G K M C G R R C G K C F V S S	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Function unknown Function unknown
COG1830 COG1609 COG0438 COG3491 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958 COG1309 COG2223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein	G K M C G R R C R C R V S S S	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Function unknown Function unknown Function unknown
COG1830 COG1609 COG0438 COG3481 COG3788 COG04798 COG0486 COG1035 COG0655 COG1028 COG3958 COG3958 COG1309 COG2223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166 COG0357	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin Wrba Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted s-adenosylmethionine-dependent methyltransferase involved in bacterial cell division Uncharacterized conserved protein	G K M C G R R C R C R C R C R M S S S R M S	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Function unknown Function unknown General function prediction only
COG1830 COG1609 COG0438 COG34811 COG3839 COG3788 COG0496 COG1035 COG0655 COG1028 COG3959 COG3958 COG1309 COG2223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166 COG357 COG3384 COG0697	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted membrane protein SufE protein probably involved in Fe-S center assembly Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division Uncharacterized conserved protein Permeases of the drug/metabolite transporter (DMT) superfamily	G K M C G R R C R C R V S S S R M S G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Function unknown Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism
COG1830 COG1609 COG0438 COG3491 COG3788 COG4798 COG0486 COG1035 COG0655 COG1028 COG3959 COG3958 COG1309 COG223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166 COG357 COG3386 COG2386 COG6387 COG697 COG2859	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted membrane protein SufE protein probably involved in Fe-S center assembly Predicted 5-adenosylmethionine-dependent methyltransferase involved in bacterial cell division Uncharacterized conserved protein Permeases of the drug/metabbolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria	G K M C G R R C R C R V S S S R M S G S	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown
COG1830 COG1609 COG0438 COG3411 COG3839 COG3788 COG0498 COG1035 COG0655 COG1028 COG3958 COG1309 COG2223 COG0025 COG1968 COG4244 COG1981 COG3366 COG62166 COG0357 COG3884 COG06957 COG3884 COG06957 COG3884 COG0697	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division Uncharacterized conserved protein Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria ATPases involved in chromosome partitioning	G K M C G R R C R C R V S S S S R M S G D	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown Centeral function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown Carbohydrate transport and metabolism Function unknown Carbohydrate transport and metabolism Function unknown Cell cycle control, cell division, chromosome partitioning
COG1830 COG1609 COG0438 COG3481 COG3788 COG4798 COG0498 COG1035 COG0655 COG1028 COG3958 COG3958 COG1029 COG2223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166 COG0357 COG384 COG0697 COG2859 COG1992 COG2859	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin Wrba Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted conserved protein Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria ATPases involved in chromosome partitioning Predicted aminopeptidases	G K M C G R R C R C R C R C R C R C R C R C R	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Defense mechanisms Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown Carbohydrate transport and metabolism Function unknown Call cycle control, cell division, chromosome partitioning General function prediction only
COG1830 COG1609 COG0438 COG3481 COG3788 COG4798 COG0456 COG1035 COG0655 COG1028 COG3959 COG3958 COG1309 COG2223 COG0025 COG1968 COG4244 COG1981 COG3336 COG2166 COG357 COG3844 COG0697 COG2859 COG2234 COG1682	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes Transcriptional regulators Glycosyltransferase Ferredoxin ABC-type sugar transport systems, ATPase components Uncharacterized relative of glutathione S-transferase, MAPEG superfamily Predicted methyltransferase Predicted GTPase Coenzyme F420-reducing hydrogenase, beta subunit Multimeric flavodoxin WrbA Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transketolase, N-terminal subunit Transketolase, C-terminal subunit Transcriptional regulator Nitrate/nitrite transporter NhaP-type Na+/H+ and K+/H+ antiporters Uncharacterized bacitracin resistance protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division Uncharacterized conserved protein Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria ATPases involved in chromosome partitioning	G K M C G R R C R C R V S S S S R M S G D	Inorganic ion transport and metabolism Carbohydrate transport and metabolism Transcription Cell wall/membrane/envelope biogenesis Energy production and conversion Carbohydrate transport and metabolism General function prediction only General function prediction only Energy production and conversion General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Inorganic ion transport and metabolism Inorganic ion transport and metabolism Pefense mechanisms Function unknown Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown Centeral function prediction only Cell wall/membrane/envelope biogenesis Function unknown Carbohydrate transport and metabolism Function unknown Carbohydrate transport and metabolism Function unknown Carbohydrate transport and metabolism Function unknown Cell cycle control, cell division, chromosome partitioning

COG0019	Diaminopimelate decarboxylase	E	Amino acid transport and metabolism
	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	С	Energy production and conversion
	Argininosuccinate lyase	E	Amino acid transport and metabolism
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Rod binding protein Glycosyltransferase	M M	Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
	DNA polymerase III, delta subunit	Ĺ	Replication, recombination and repair
	Predicted membrane protein	S	Function unknown
	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	Ĺ	Replication, recombination and repair
	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
	Esterase/lipase	I	Lipid transport and metabolism
	Deacetylases, including yeast histone deacetylase and acetoin utilization protein Predicted redox protein, regulator of disulfide bond formation	В О	Chromatin structure and dynamics Posttranslational modification, protein turnover, chaperones
	Lactoylglutathione lyase and related lyases	E	Amino acid transport and metabolism
	Phosphoribulokinase	C	Energy production and conversion
	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	С	Energy production and conversion
COG1348	Nitrogenase subunit NifH (ATPase)	P	Inorganic ion transport and metabolism
	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
	Phytoene dehydrogenase and related proteins	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted secreted hydrolase	R	General function prediction only
	Fructose/tagatose bisphosphate aldolase Mg-chelatase subunit ChID	G H	Carbohydrate transport and metabolism
	Mg-chelatase subunit Chil	Н	Coenzyme transport and metabolism Coenzyme transport and metabolism
	Dehydrogenases (flavoproteins)	C	Energy production and conversion
	Na+/melibiose symporter and related transporters	G	Carbohydrate transport and metabolism
	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	н	Coenzyme transport and metabolism
	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	С	Energy production and conversion
	Nitrogenase molybdenum-iron protein, alpha and beta chains	C	Energy production and conversion
	2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase	Н	Coenzyme transport and metabolism
	ATPases of the AAA+ class	0	Posttranslational modification, protein turnover, chaperones
	Transcriptional regulator	K	Transcription
	Cytosine deaminase and related metal-dependent hydrolases	F P	Nucleotide transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Formate/nitrite family of transporters	P	Inorganic ion transport and metabolism Inorganic ion transport and metabolism
	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	r E	Amino acid transport and metabolism
	Aspartate racemase	M	Cell wall/membrane/envelope biogenesis
	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	C	Energy production and conversion
	NADH:ubiquinone oxidoreductase 24 kD subunit	Ċ	Energy production and conversion
COG0583	Transcriptional regulator	K	Transcription
COG0225	Peptide methionine sulfoxide reductase	0	Posttranslational modification, protein turnover, chaperones
	UDP-N-acetylglucosamine 2-epimerase	M	Cell wall/membrane/envelope biogenesis
	Transcriptional regulators	K	Transcription
	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Ţ	Signal transduction mechanisms
	Signal transduction histidine kinase Uncharacterized protein containing LysM domain	T S	Signal transduction mechanisms Function unknown
	Predicted enzyme with a TIM-barrel fold	R	General function prediction only
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	т	Signal transduction mechanisms
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Asp-tRNAAsn/Glu-tRNAGIn 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 PuID	N	Cell motility
	Type II secretory pathway, component PulF	N	Cell motility
	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB	N	Cell motility
	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases		Cell motility
	Outer membrane recentor proteins, mostly be transport	N	· · · · · · · · · · · · · · · · · · ·
COG1629	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
COG1629 COG5360	Uncharacterized protein conserved in bacteria	P S	Inorganic ion transport and metabolism Function unknown
COG1629 COG5360 COG4244	Uncharacterized protein conserved in bacteria Predicted membrane protein	P S S	Inorganic ion transport and metabolism Function unknown Function unknown
COG1629 COG5360 COG4244 COG2133	Uncharacterized protein conserved in bacteria	P S	Inorganic ion transport and metabolism Function unknown
COG1629 COG5360 COG4244 COG2133 COG1521	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases	P S S G	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor	P S S G K	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases	P S S G K R	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein	P S G K R G R S	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component	P S G K R G R S E	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177 COG1386	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain	P S G K R G R S E K	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177 COG1386 COG0491	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases	P S G K R G R S E K R	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177 COG1386 COG0491 COG2391	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component	PSSSGKRGRSEKRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only
COG1629 COG5360 COG4244 COG1521 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177 COG1386 COG0491 COG2391 COG1235	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I	P S G K R G R S E K R	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG4177 COG1386 COG0491 COG2391 COG2391	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component	PSSGKRGGRSEKRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only
COG1629 COG5360 COG4244 COG2133 COG1521 COG1994 COG1354 COG4177 COG1386 COG0491 COG2391 COG2391 COG2391 COG0640	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I	PSSGKRGGRSEKRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG4177 COG1368 COG0491 COG2391 COG2391 COG0666	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter component	PSSGKRGRSEKRRKK	Inorganic ion transport and metabolism Function unknown Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only Transcription
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG4197 COG4197 COG2391 COG2391 COG2391 COG0665 COG0665 COG0665	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter component Glycine/D-amino acid oxidases (deaminating)	PSSGKRGRSEKRRRKE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription General function prediction only General function prediction only Transcription Amino acid transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1354 COG1354 COG0491 COG2391 COG0640 COG0665 COG1440 COG1440 COG1440 COG1440	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases T-n-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Z-n-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter component Predicted transcriptional regulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Predicted phosphohydrolases ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	PSSGKRGRSEKRRKEKREKRE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism Transcription Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism
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COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG4197 COG2391 COG2391 COG2391 COG2391 COG6409 COG1409 COG1409 COG1409 COG1409 COG1409	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter peulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Predicted phosphohydrolases ABC-type dipeptide/oligopeptide/nickel transport systems, permease components ABC-type purcharacterized transport system, permease component	PSSGKRGRSEKRRKEKRERP	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only Transcription Amino acid transport and metabolism Transcription General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only
COG1629 COG5360 COG2444 COG2133 COG1521 COG16472 COG1994 COG1354 COG4177 COG1366 COG0491 COG2391 COG0640 COG0665 COG1846 COG14409 COG1173 COG1344 COG1173 COG1344	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transcriptional regulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Predicted phosphohydrolases ABC-type dippeptide/oligopeptide/nickel transport systems, permease components ABC-type uncharacterized transport system, periplasmic component ABC-type Fe3+ transport system, periplasmic component	PSSGKRGRSEKRRKEKRRRERPE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Inorganic ion transport and metabolism Amino acid transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1994 COG1354 COG391 COG2391 COG0640 COG0665 COG1440 COG1440 COG1173 COG137 COG1317 COG1412 COG1413 COG1413 COG1413 COG1413 COG14113	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter component Predicted transcriptional regulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Fredicted phosphohydrolases ABC-type dipeptide/oligopeptide/nickel transport systems, permease component ABC-type Fe3+ transport system, periplasmic component ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic component	PSSGKRGRSEKRRKEKRERPEE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism Transcription General function prediction only General function prediction only Transcription Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Inorganic ion transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG2509 COG1472 COG1394 COG4177 COG1366 COG0491 COG2391 COG0665 COG1846 COG0665 COG1846 COG107 COG1840 COG0665 COG1840 COG0666 COG1840 COG067 COG4175	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transcriptional regulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Predicted phosphohydrolases Predicted phosphohydrolases ABC-type dipeptide/oligopeptide/nickel transport systems, permease component ABC-type purcharacterized transport system, periplasmic component ABC-type proline/glycine betaine transport systems, periplasmic component ABC-type proline/glycine betaine transport system, perplasmic component ABC-type proline/glycine betaine transport system, perpease component ABC-type proline/glycine betaine transport system, perpease component ABC-type proline/glycine betaine transport system, perpease component	PSSGKRGRSEKRRKEKRERPEEE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only Inorganic ion transport and metabolism Amino acid transport and metabolism
COG1629 COG5360 COG4244 COG2133 COG1521 COG209 COG1472 COG1994 COG1354 COG4177 COG1366 COG0491 COG2391 COG2391 COG0640 COG1625 COG1846 COG1409 COG123 COG123 COG123 COG123 COG127 COG1340 COG127 COG1340 COG173 COG4175 COG1340 COG2113 COG4175 COG175 COG175 COG1012	Uncharacterized protein conserved in bacteria Predicted membrane protein Glucose/sorbosone dehydrogenases Putative transcriptional regulator, homolog of Bvg accessory factor Uncharacterized FAD-dependent dehydrogenases Beta-glucosidase-related glycosidases Zn-dependent proteases Uncharacterized conserved protein ABC-type branched-chain amino acid transport system, permease component Predicted transcriptional regulator containing the HTH domain Zn-dependent hydrolases, including glyoxylases Predicted transporter component Metal-dependent hydrolases of the beta-lactamase superfamily I Predicted transporter component Predicted transporter component Predicted transcriptional regulators Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators Fredicted phosphohydrolases ABC-type dipeptide/oligopeptide/nickel transport systems, permease component ABC-type Fe3+ transport system, periplasmic component ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic components ABC-type proline/glycine betaine transport systems, periplasmic component	PSSGKRGRSEKRRKEKRERPEE	Inorganic ion transport and metabolism Function unknown Carbohydrate transport and metabolism Transcription General function prediction only Carbohydrate transport and metabolism General function prediction only Function unknown Amino acid transport and metabolism Transcription General function prediction only General function prediction only General function prediction only General function prediction only Transcription Amino acid transport and metabolism Transcription General function prediction only General function prediction only Transcription Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Inorganic ion transport and metabolism Amino acid transport and metabolism 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	С	Energy production and conversion
	Electron transfer flavoprotein, alpha subunit	С	Energy production and conversion
	Fe-S oxidoreductase	С	Energy production and conversion
	NADH:flavin oxidoreductases, Old Yellow Enzyme family	С	Energy production and conversion
	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	С	Energy production and conversion
	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	Р	Inorganic ion transport and metabolism
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
	Arylsulfatase A and related enzymes	P	Inorganic ion transport and metabolism
	Aspartokinases	E	Amino acid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
	Surface antigen	R	General function prediction only
	Pyrroline-5-carboxylate reductase	E	Amino acid transport and metabolism
	Phosphomannomutase USD all constructions for the second se	G	Carbohydrate transport and metabolism
	UDP-glucose pyrophosphorylase	М	Cell wall/membrane/envelope biogenesis
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Galactose mutarotase and related enzymes	G M	Carbohydrate transport and metabolism
	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	R	Cell wall/membrane/envelope biogenesis
	Predicted glycosyl transferase ABC-type branched-chain amino acid transport systems, ATPase component	E E	General function prediction only Amino acid transport and metabolism
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	Dehydrogenases (flavoproteins)	C	Energy production and conversion
	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	M	Cell wall/membrane/envelope biogenesis
	Predicted dehydrogenases and related proteins	R	General function prediction only
	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
	Predicted ABC-type sugar transport system, permease component	R	General function prediction only
	Ribulose 1,5-bisphosphate carboxylase, large subunit	G	Carbohydrate transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Prephenate dehydrogenase	E	Amino acid transport and metabolism
	Putative threonine efflux protein	E	Amino acid transport and metabolism
	Predicted glycosyl transferase	R	General function prediction only
	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
	Hydrogenase/urease accessory protein	ō	Posttranslational modification, protein turnover, chaperones
	ABC-type Co2+ transport system, periplasmic component	P	Inorganic ion transport and metabolism
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	Geranylgeranyl pyrophosphate synthase	н	Coenzyme transport and metabolism
	Predicted flavoprotein involved in K+ transport	Р	Inorganic ion transport and metabolism
	Transcriptional regulator		Transcription
COG1309		K	Haliscription
	Heme/copper-type cytochrome/quinol oxidase, subunit 3	K C	Energy production and conversion
COG1845			· · · · · · · · · · · · · · · · · · ·
COG1845 COG0843	Heme/copper-type cytochrome/quinol oxidase, subunit 3	С	Energy production and conversion
COG1845 COG0843 COG1622	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1	C C	Energy production and conversion Energy production and conversion
COG1845 COG0843 COG1622 COG3034	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2	C C C	Energy production and conversion Energy production and conversion Energy production and conversion
COG1845 COG0843 COG1622 COG3034 COG1961	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria	C C C S	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs	C C C S L	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase	C C C S L	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein	C C S L M S	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679 COG4392	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases	C C S L M S R	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679 COG4392 COG0530 COG0673	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins	C C S L M S R S P R	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679 COG4392 COG0530 COG0673	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter	C C S L M S R S	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679 COG4392 COG0530 COG0673	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins	C C S L M S R S P R S L	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG6590 COG0530 COG0673 COG6500 COG0708 COG1937	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria	C C S L M S R S P R S L	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG679 COG64392 COG05500 COG0708 COG1937 COG1835	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases	C C C S L M S R S P R S L S	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0679 COG4392 COG0530 COG0673 COG0708 COG1937 COG1835	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted ehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	C C S L M S R S P R S L S	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Replication, recombination and repair Function unknown Amino acid transport and metabolism
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0530 COG0530 COG0673 COG5500 COG1937 COG1835 COG0834 COG0179	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	C C S L M S R S P R S L S L	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG1845 COG0843 COG1622 COG3034 COG1961 COG0679 COG0679 COG0530 COG0673 COG5500 COG0708 COG1835 COG0834 COG0179 COG10179	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases	C C C S L M S R S P R S L S I E Q C	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0530 COG0673 COG5500 COG0708 COG1937 COG1835 COG0834 COG0179 COG1815 COG01712	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	C C S L M S R S P R S L S I E Q C G	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG367 COG0679 COG4392 COG0530 COG0673 COG5500 COG0708 COG1937 COG1835 COG0834 COG0179 COG1012 COG1172 COG1879	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/kylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component	C C S L M S R S P R S L S C G G	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism
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COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3679 COG4392 COG0530 COG0708 COG1937 COG1835 COG0179 COG1172 COG1172 COG1879 COG1995	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component Pyridoxal phosphate biosynthesis protein Uncharacterized protein conserved in bacteria Transcriptional regulators of sugar metabolism	C C S L M S R S P R S L G G H S K	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism Coenzyme transport and metabolism Coenzyme transport and metabolism Function unknown Transcription
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COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3367 COG0530 COG0530 COG0708 COG1937 COG1835 COG0834 COG1172 COG1172 COG1172 COG1879 COG1995 COG3395 COG1349 COG4977 COG2844 COG3195	Heme/copper-type cytochrome/quinol oxidases, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component Pyridoxal phosphate biosynthesis protein Uncharacterized protein conserved in bacteria Transcriptional regulators of sugar metabolism Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain UTP-GIBB (protein PII) uridylyltransferase Uncharacterized protein conserved in bacteria	C C S L M S R S P R S L S I E Q C G G H S K K	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism Caronyme transport and metabolism Caronyme transport and metabolism Function unknown Transcription Transcription Transcription Transcription Fosttranslational modification, protein turnover, chaperones
COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG367 COG6392 COG0530 COG0708 COG1937 COG1835 COG0179 COG1172 COG1172 COG1172 COG1975 COG1995 COG3995 COG1997 COG1995 COG3995 COG1997 COG1995 COG3995	Heme/copper-type cytochrome/quinol oxidase, subunit 3 Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted membrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted integral membrane protein Exonuclease III Uncharacterized protein conserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component Pyridoxal phosphate biosynthesis protein Uncharacterized protein conserved in bacteria Transcriptional regulators of sugar metabolism Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain UTP-GlnB (protein PII) uridylyltransferase Uncharacterized protein conserved in bacteria Transthyretin-like protein	CCCSLMSRSPRSLSIEQCGGHSKKOSR	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Coenzyme transport and metabolism Function unknown Transcription Transcription Transcription Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only
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COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3679 COG4392 COG0530 COG0673 COG1937 COG1835 COG0834 COG1799 COG1879 COG1879 COG1879 COG1879 COG1879 COG1879 COG1975 COG1975 COG1975 COG1975 COG1975 COG1879 COG1886 COG0624 COG0583 COG16862	Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted permeases Predicted dehydrogenases and related proteins Predicted graph and protein conserved in bacteria Predicted graph and protein conserved in bacteria Predicted permeases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component Pyridoxal phosphate biosynthesis protein Uncharacterized protein conserved in bacteria Transcriptional regulators of sugar metabolism Transcriptional regulators of sugar metabolism Transcriptional regulators or containing an amidase domain and an AraC-type DNA-binding HTH domain UTP-GinB (protein Pil) uridylyltransferase Uncharacterized protein conserved in bacteria Transcriptional regulators Transcriptional regulators Transcriptional regulator Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases Transcriptional regulator Predicted dyltorenia es subunit YajC Esterase/Deacetylases, including yeast histone deacetylase and acetoin utilization protein Preprotein translocase subunit YajC Esterase/Ipase Predicted ATPase (AAA+ superfamily)	CCCSLMSRSPRSLSIEQCGGHSKKOSRFKKEEKRLBURER	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Replication, recombination and repair Function unknown Lipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Transcription Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Nucleotide transport and metabolism Transcription Transcription Transcription Transcription Transcription Transcription Transcription General function prediction only Replication, recombination and repair Chromatin structure and dynamics Intracellular trafficking, secretion, and vesicular transport General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism
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COG1845 COG0843 COG1622 COG3034 COG1961 COG0438 COG3679 COG0530 COG0673 COG5500 COG0708 COG1937 COG1835 COG01172 COG1172 COG1879 COG1937 COG1844 COG4977 COG2844 COG4977 COG2844 COG0624 COG0681 COG0582 COG0624 COG0583 COG0154 COG0583 COG0155 COG01867 COG0115 COG0811 COG0811 COG0811	Heme/copper-type cytochrome/quinol oxidases, subunit 1 Heme/copper-type cytochrome/quinol oxidases, subunit 2 Uncharacterized protein conserved in bacteria Site-specific recombinases, DNA invertase Pin homologs Glycosyltransferase Uncharacterized conserved protein Predicted permeases Predicted permeases Predicted dembrane protein Ca2+/Na+ antiporter Predicted dehydrogenases and related proteins Predicted dehydrogenases and related proteins Predicted acyltransferase Uncharacterized croserved in bacteria Predicted acyltransferases ABC-type amino acid transport/signal transduction systems, periplasmic component/domain 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) NAD-dependent aldehyde dehydrogenases Ribose/nylose/arabinose/galactoside ABC-type transport systems, permease components ABC-type sugar transport system, periplasmic component Pyridoxal phosphate biosynthesis protein Uncharacterized protein conserved in bacteria Transcriptional regulators of sugar metabolism Transcriptional regulators of sugar metabolism Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain UTP-Gin8 (protein PII) uridyhytransferase Uncharacterized protein conserved in bacteria Transcriptional regulator Transcripti	C C C S L M S R S P R S L S I E Q C G G H S K K O S R F K K E E K R L B U R E R E U	Energy production and conversion Energy production and conversion Energy production and conversion Function unknown Replication, recombination and repair Cell wall/membrane/envelope biogenesis Function unknown General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Inorganic ion transport and metabolism General function prediction only Function unknown Ilipid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion Carbohydrate transport and metabolism Carbohydrate transport and metabolism Coenzyme transport and metabolism Coenzyme transport and metabolism Function unknown Transcription Transcription Posttranslational modification, protein turnover, chaperones Function unknown General function prediction only Nucleotide transport and metabolism Transcription Transcription Transcription Transcription Transcription Amino acid transport and metabolism Transcription General function prediction only Replication, recombination and repair Chromatin structure and dynamics Intracellular trafficking, secretion, and vesicular transport General function prediction only Amino acid transport and metabolism General function prediction only Amino acid transport and metabolism Intracellular trafficking, secretion, and vesicular transport

	Predicted redox protein, regulator of disulfide bond formation	0	Posttranslational modification, protein turnover, chaperones
	Amidases related to nicotinamidase Short-chain dehydrogenases of various substrate specificities	Q R	Secondary metabolites biosynthesis, transport and catabolism General function prediction only
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Metal-dependent amidase/aminoacylase/carboxypeptidase	R	General function prediction only
COG0141	Histidinol dehydrogenase	E	Amino acid transport and metabolism
	Uncharacterized enzyme involved in inositol metabolism	G	Carbohydrate transport and metabolism
	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q I	Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Glycosyltransferases involved in cell wall biogenesis	M	Cell wall/membrane/envelope biogenesis
COG1082	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport and metabolism
	Putative NADPH-quinone reductase (modulator of drug activity B)	R	General function prediction only
	Transcriptional regulator	K	Transcription
	Site-specific recombinase XerC Putative threonine efflux protein	L E	Replication, recombination and repair Amino acid transport and metabolism
	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	Ī	Lipid transport and metabolism
COG5598	Trimethylamine:corrinoid methyltransferase	н	Coenzyme transport and metabolism
COG0110	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
	Nitroreductase	С	Energy production and conversion
	Hemolysin activation/secretion protein	U E	Intracellular trafficking, secretion, and vesicular transport
	Xaa-Pro aminopeptidase Xaa-Pro aminopeptidase	E	Amino acid transport and metabolism Amino acid transport and metabolism
	Maleate cis-trans isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Acetyl-CoA acetyltransferase	Ĩ	Lipid transport and metabolism
	Acyl-CoA dehydrogenases	I	Lipid transport and metabolism
	Deoxyribodipyrimidine photolyase	L	Replication, recombination and repair
	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	H	Coenzyme transport and metabolism
	Fatty acid desaturase Uncharacterized protein conserved in bacteria	S	Lipid transport and metabolism Function unknown
	Uncharacterized protein conserved in bacteria	s	Function unknown
	Transcriptional regulators	K	Transcription
COG0673	Predicted dehydrogenases and related proteins	R	General function prediction only
	Predicted oxidoreductase	R	General function prediction only
	Uncharacterized protein involved in propionate catabolism	R E	General function prediction only
	Aspartate/tyrosine/aromatic aminotransferase Sugar phosphate permease	G	Amino acid transport and metabolism Carbohydrate transport and metabolism
	Isocitrate/isopropylmalate dehydrogenase	c	Energy production and conversion
	Predicted hydrolases of the HAD superfamily	R	General function prediction only
COG1023	Predicted 6-phosphogluconate dehydrogenase	G	Carbohydrate transport and metabolism
	Transaldolase	G	Carbohydrate transport and metabolism
	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q S	Secondary metabolites biosynthesis, transport and catabolism
	Uncharacterized protein conserved in bacteria Predicted TIM-barrel enzyme	S R	Function unknown General function prediction only
	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	0	Posttranslational modification, protein turnover, chaperones
	ABC-type branched-chain amino acid transport system, permease component	E	Amino acid transport and metabolism
	Glycosyltransferases, probably involved in cell wall biogenesis	М	Cell wall/membrane/envelope biogenesis
	Predicted membrane protein	S	Function unknown
	Glycosyltransferase Lipid A core - O-antigen ligase and related enzymes	M M	Cell wall/membrane/envelope biogenesis Cell wall/membrane/envelope biogenesis
	Putative hemolysin	R	General function prediction only
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	Pirin-related protein	R	General function prediction only
	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Predicted esterase Uncharacterized protein conserved in bacteria	R S	General function prediction only Function unknown
	Lactoylglutathione lyase and related lyases	E E	Amino acid transport and metabolism
	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
	Ribonucleases G and E	J	Translation, ribosomal structure and biogenesis
	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
	ABC-type sugar transport system, ATPase component Predicted ABC-type sugar transport system, permease component	G R	Carbohydrate transport and metabolism General function prediction only
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	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
	Transcriptional activator of acetoin/glycerol metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	Chaperonin GroEL (HSP60 family)	0	Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
	UTP:GlnB (protein PII) uridylyltransferase ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	O P	Inorganic ion transport and metabolism
	Glutamate synthase domain 2	E E	Amino acid transport and metabolism
	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
	Thioredoxin domain-containing protein	0	Posttranslational modification, protein turnover, chaperones
	NADH dehydrogenase, FAD-containing subunit	С	Energy production and conversion
	Rhodanese-related sulfurtransferase Membrane-fusion protein	P M	Inorganic ion transport and metabolism Cell wall/membrane/envelope biogenesis
	Cation/multidrug efflux pump	V	Defense mechanisms
	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit	c	Energy production and conversion
	Formate hydrogenlyase subunit 4	С	Energy production and conversion
	Hydrogenase 4 membrane component (E)	С	Energy production and conversion
	N-acyl-D-aspartate/D-glutamate deacylase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Ni,Fe-hydrogenase III large subunit Ni,Fe-hydrogenase III small subunit	C C	Energy production and conversion Energy production and conversion
	Transcriptional regulator	K	Transcription
	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-tRNAGIn amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis

COG5006			
	Predicted permease, DMT superfamily	R	General function prediction only
	Predicted membrane protein	S	Function unknown
	Zn-dependent dipeptidase, microsomal dipeptidase homolog NADH dehydrogenase, FAD-containing subunit	E C	Amino acid transport and metabolism Energy production and conversion
	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Ï	Lipid transport and metabolism
COG2421	Predicted acetamidase/formamidase	С	Energy production and conversion
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Predicted O-methyltransferase	R	General function prediction only
	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component Transcriptional regulators	P K	Inorganic ion transport and metabolism
	Transcriptional regulator Small-conductance mechanosensitive channel	M	Transcription Cell wall/membrane/envelope biogenesis
	Na+/proline symporter	E	Amino acid transport and metabolism
	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
	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	L	Replication, recombination and repair
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	Predicted acyl esterases Arabinose efflux permease	R G	General function prediction only Carbohydrate transport and metabolism
	Phosphatidylglycerophosphate synthase	ı	Lipid transport and metabolism
	Transcriptional regulator	ĸ	Transcription
COG0337	3-dehydroquinate synthetase	E	Amino acid transport and metabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	Flagellar GTP-binding protein	N	Cell motility
	Uncharacterized conserved protein	S .	Function unknown
	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases Predicted methyltransferases	J R	Translation, ribosomal structure and biogenesis General function prediction only
	Protein involved in catabolism of external DNA	R	General function prediction only
	Predicted hydrolase (HAD superfamily)	R	General function prediction only
	Uncharacterized protein conserved in bacteria	S	Function unknown
COG0792	Predicted endonuclease distantly related to archaeal Holliday junction resolvase	L	Replication, recombination and repair
	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
	Rhodanese-related sulfurtransferase	P	Inorganic ion transport and metabolism
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	T S	Signal transduction mechanisms
	Uncharacterized conserved protein A/G-specific DNA glycosylase	S L	Function unknown Replication, recombination and repair
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
COG1216	Predicted glycosyltransferases	R	General function prediction only
COG3818	Predicted acetyltransferase, GNAT superfamily	R	General function prediction only
	Predicted transcriptional regulators	К	Transcription
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	Lipid transport and metabolism
	Flagellar capping protein	N	Cell motility
	Dihydrofolate reductase Acetyltransferase (isoleucine patch superfamily)	H R	Coenzyme transport and metabolism General function prediction only
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Methyl-accepting chemotaxis protein	N	Cell motility
	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q	Secondary metabolites biosynthesis, transport and catabolism
	Predicted homoserine dehydrogenase	Ē	Amino acid transport and metabolism
COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases	E H	Coenzyme transport and metabolism
COG0635 COG2020	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase	Е Н О	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones
COG0635 COG2020 COG0300	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities	E H O R	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only
COG0635 COG2020 COG0300 COG4928	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase	E H O R R	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only
COG0635 COG2020 COG0300 COG4928 COG4993	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase	E H O R	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase	E H O R R G	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase	E H O R R G F	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria	E H O R R G F I I S	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226 COG0667	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	E H O R R G F I S C	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226 COG0667 COG1629	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport	E H O R G F I I S C P	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG197 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator	E H O R G F I I S C P K	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription
COG0635 COG2020 COG0300 COG4928 COG0127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator	E H O R G F I I S C P	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1689 COG0688 COG2181	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA Synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH	E H O R G F I S C P K J	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis
COG0635 COG2020 COG0300 COG4928 COG0127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG2181 COG0760	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases IUncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit	E H O R R G I I S C P K J C	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion
COG0635 COG2020 COG0300 COG4928 COG0127 COG1960 COG0318 COG3226 COG1629 COG1309 COG0689 COG2181 COG760 COG2223 COG1609	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA Synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators	E H O R G F I S C P K J C O P K	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription
COG0635 COG2020 COG0300 COG4928 COG4928 COG0127 COG0667 COG0318 COG3226 COG1629 COG1309 COG0689 COG2181 COG0760 COG2223 COG1609 COG0607	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase	E H O R R G F I J C O P K J C P	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG22181 COG2223 COG16009 COG0607 COG1663	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases	E H O R G F I I S C P K J C O P K P E	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Transcription Transcription Amino acid transport and metabolism Amino acid transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226 COG1629 COG1629 COG1629 COG1669 COG0687 COG1669 COG02223 COG1609 COG0667 COG16066 COG0607	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase	E H O R R G F I J C O P K J C P	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only
COG0635 COG2020 COG0300 COG4928 COG4928 COG9127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG2181 COG2223 COG1609 COG0607 COG1063 COG4240 COG1028	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA Synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	E H O R G F I I S C P K J C O P K P E	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4928 COG1960 COG0318 COG3226 COG0667 COG1629 COG0689 COG2223 COG1609 COG0607 COG1063 COG4240 COG1028 COG1420	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene	E H O R R G F I S C P K J C O P K P E R I	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Transcription
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1629 COG0689 COG0689 COG2223 COG16009 COG06607 COG1063 COG4240 COG1028	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA Synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	E H O R R G F I S C P K J C O P K P E R I	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4928 COG9127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG2181 COG2223 COG1609 COG0607 COG1063 COG4240 COG1028 COG1420 COG1028 COG1420 COG2084 COG1879 COG1172	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	E H O R R G F I I S C P K J C O P K P E R I K I I G G G G G G G G G G G G G G G G	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG2223 COG1009 COG0607 COG1063 COG4240 COG1028 COG1028 COG1028 COG1029 COG1084 COG1879	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain	E H O R R G F I I S C P K J C O P K P E R I I G G T I I G G T I I G G G T I I G G G T I I G G G T I I I I	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1609 COG0689 COG0607 COG1063 COG4240 COG1028 COG1084 COG1028 COG1889 COG1089	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	E H O R G F I I S C P K J C O P K P E R I K I G G T T T T T T T T T T T T T T T T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG0689 COG0680 COG061060 COG2223 COG1609 COG1063 COG4240 COG1028 COG1420 COG1028 COG1420 COG2084 COG1420 COG2181 COG2199 COG2181	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	E H O R R G F I S C P K J C O P K P E R I K I G G T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms
COG0635 COG2020 COG0300 COG4928 COG4928 COG9127 COG1960 COG0318 COG3226 COG0667 COG1629 COG1629 COG1629 COG1609 COG0607 COG1063 COG2223 COG1609 COG0607 COG1063 COG4240 COG1028 COG1420 COG1028 COG1420 COG2084 COG2199 COG2199 COG2199 COG2204 COG2204	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein	E H O R R G F I I S C P K J C O P K P E R I K I G G T T T T T T T T T T T T T T T T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG22181 COG2223 COG1609 COG0607 COG1068 COG4240 COG1028 COG1028 COG1028 COG1028 COG1020 COG204 COG204 COG204 COG204 COG2204 COG2204 COG2204 COG2907 COG3496	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/kylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein Uncharacterized conserved protein	E H O R R G F I I S C P K J C O P K P E R I K I G G T T T T T T T T T T T T T T T T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms
COG0635 COG2020 COG0300 COG4928 COG4993 COG0127 COG1960 COG3226 COG667 COG1629 COG0689 COG0689 COG0667 COG1609 COG0607 COG1063 COG4240 COG1028 COG1172 COG1172 COG2199 COG2204 COG2204 COG2204 COG2204 COG2204 COG2204 COG2204 COG2309	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein	E H O R R G F I I S C P K J C O P K P E R I K I G G T T T T T T T T T T T T T T T T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only
COG0635 COG2020 COG0300 COG0300 COG4928 COG4928 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG0689 COG0689 COG1811 COG0760 COG2223 COG1069 COG1063 COG4240 COG1028 COG1420 COG2084 COG1420 COG2084 COG2181 COG2199 COG2204 COG2203 COG1232	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein Uncharacterized conserved protein Cyclopropane fatty acid synthase and related methyltransferases	E H O R R G F I I S C P K P E R I K I G G T T T R S M M M M M M M M M M M M M M M M M M	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only Function unknown Cell wall/membrane/envelope biogenesis
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1609 COG0689 COG0689 COG1609 COG0667 COG1660 COG2223 COG1060 COG2044 COG1028 COG1420 COG204 COG204 COG204 COG2004 COG2007 COG3496 COG2211 COG0639	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein Uncharacterized conserved protein Cyclopropane fatty acid synthase and related transporters Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	EHORRGFIISCPKJCOPKPERIKIGGTTTRSMHGT	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Transcription Inorganic ion transport and metabolism Amino acid transport and metabolism General function prediction only Lipid transport and metabolism Transcription Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
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COG0635 COG2020 COG0300 COG4928 COG4928 COG1960 COG0318 COG3226 COG06627 COG1629 COG1629 COG1629 COG1629 COG1629 COG1629 COG16294 COG2204 COG204 COG2204 COG2204 COG2204 COG2204 COG2204 COG2204 COG2204 COG22	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Cyclopropane fatty acid synthase and related methyltransferases Protoporphyrinogen oxidase Na+/melibiose symporter and related transporters Diadenosine tetraphosphatase and related serine/threonine protein phosphatases Cytochrome bd-type quinol oxidase, subunit 1	E H O R R G F I I S C P K J C O P K P E R I K I G G T T T T R S M H G G T T T T T T T T T T T T T T T T T	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Function unknown Energy production and conversion Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms Ceneral function prediction only Function unknown Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion
COG0635 COG2020 COG0300 COG4928 COG4993 COG1960 COG0318 COG3226 COG0667 COG1629 COG1309 COG0689 COG2223 COG1009 COG0607 COG1063 COG4240 COG204 COG207 COG3496 COG2201 COG2907 COG3496 COG2211 COG0639 COG1271 COG64987	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases Putative protein-S-isoprenylcysteine methyltransferase Short-chain dehydrogenases of various substrate specificities Predicted P-loop ATPase Glucose dehydrogenase Xanthosine triphosphate pyrophosphatase Acyl-CoA dehydrogenases Acyl-CoA dehydrogenases Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Uncharacterized protein conserved in bacteria Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) Outer membrane receptor proteins, mostly Fe transport Transcriptional regulator RNase PH Nitrate reductase gamma subunit Parvulin-like peptidyl-prolyl isomerase Nitrate/nitrite transporter Transcriptional regulators Rhodanese-related sulfurtransferase Threonine dehydrogenase and related Zn-dependent dehydrogenases Predicted kinase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator of heat shock gene 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases ABC-type sugar transport system, periplasmic component Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components FOG: GGDEF domain Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains Predicted NAD/FAD-binding protein Uncharacterized conserved protein Cyclopropane fatty acid synthase and related methyltransferases Protoporphyrinogen oxidase Na+/melibiose symporter and related transporters Diadenosine tetraphosphatase and related serine/threonine protein phosphatases Cytochrome bd-type quinol oxidase, subunit 2	EHORRGFIISCPKJCOPKPERIKIGGTTTRSMHGTC	Coenzyme transport and metabolism Posttranslational modification, protein turnover, chaperones General function prediction only General function prediction only Carbohydrate transport and metabolism Nucleotide transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Inorganic ion transport and metabolism Transcription Translation, ribosomal structure and biogenesis Energy production and conversion Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism General function prediction only Lipid transport and metabolism General function prediction only Lipid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Signal transduction mechanisms Signal transduction mechanisms General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms General function prediction only Function unknown Cell wall/membrane/envelope biogenesis Coenzyme transport and metabolism Carbohydrate transport and metabolism Signal transduction mechanisms Energy production and conversion

COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R	General function prediction only
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	Lipid transport and metabolism
	Predicted metal-binding protein ARC true quark represent system parmassa companies.	S G	Function unknown
	ABC-type sugar transport system, permease component ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism Carbohydrate transport and metabolism
	ABC-type sugar transport systems, perinease component	G	Carbohydrate transport and metabolism
	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
	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
	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
	Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, permease component	Q	Secondary metabolites biosynthesis, transport and catabolism
	Sterol desaturase	1	Lipid transport and metabolism
	TRAP-type C4-dicarboxylate transport system, periplasmic component Enoyl-CoA hydratase/carnithine racemase	G I	Carbohydrate transport and metabolism Lipid transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	i	Lipid transport and metabolism
	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
	Uncharacterized conserved protein	S	Function unknown
COG2755	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
	Membrane-fusion protein	M	Cell wall/membrane/envelope biogenesis
	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
	ABC-type antimicrobial peptide transport system, ATPase component	V	Defense mechanisms
	ADP-heptose:LPS heptosyltransferase	М	Cell wall/membrane/envelope biogenesis
	Cobalamin biosynthesis protein CobT (nicotinate-mononucleotide:5, 6-dimethylbenzimidazole phosphoribosyltransferase) ABC-type sugar transport system, permease component	H G	Coenzyme transport and metabolism Carbohydrate transport and metabolism
	Asparaginase	E	Amino acid transport and metabolism
	Multiple antibiotic transporter	Ū	Intracellular trafficking, secretion, and vesicular transport
	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
	Phosphohistidine phosphatase SixA	Ţ	Signal transduction mechanisms
	Predicted transcriptional regulators	K	Transcription
	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
	Uncharacterized iron-regulated membrane protein	S	Function unknown
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)		Lipid transport and metabolism Lipid transport and metabolism
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	NAD-dependent aldehyde dehydrogenases	C	Energy production and conversion
	Outer membrane protein	M	Cell wall/membrane/envelope biogenesis
	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
	Uncharacterized conserved protein	S	Function unknown
	Nitrogen regulatory protein PII	E	Amino acid transport and metabolism
	Sulfite oxidase and related enzymes	R	General function prediction only
	Predicted membrane protein	S	Function unknown
	Predicted membrane protein Phosphatidylglycerophosphate synthase	S I	Function unknown Lipid transport and metabolism
	Predicted sugar nucleotidyltransferases	M	Cell wall/membrane/envelope biogenesis
	Signal transduction histidine kinase	т	Signal transduction mechanisms
	Uncharacterized iron-regulated membrane protein	S	Function unknown
COG1674	DNA segregation ATPase FtsK/SpolIIE and related proteins	D	Cell cycle control, cell division, chromosome partitioning
COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	Н	Coenzyme transport and metabolism
	Zn-dependent hydrolases, including glyoxylases	R	General function prediction only
	Predicted HD phosphohydrolase	R	General function prediction only
	Membrane protease subunits, stomatin/prohibitin homologs	0	Posttranslational modification, protein turnover, chaperones
	Predicted EndoIII-related endonuclease	L C	Replication, recombination and repair Energy production and conversion
	NAD-dependent aldehyde dehydrogenases Predicted thioesterase	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
	ABC-type multidrug transport system, permease component	V	Defense mechanisms
	6Fe-6S prismane cluster-containing protein	С	Energy production and conversion
	Predicted mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Protein involved in cellulose biosynthesis (CelD)	M	Cell wall/membrane/envelope biogenesis
	Glycosyltransferase	М	Cell wall/membrane/envelope biogenesis
	Predicted HD phosphohydrolase	R R	General function prediction only General function prediction only
	Predicted phosphatase/phosphohexomutase Predicted thioesterase	R R	General function prediction only
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Uncharacterized Fe-S protein	R	General function prediction only
	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	ABC-type transport system involved in resistance to organic solvents, auxiliary component	Q	Secondary metabolites biosynthesis, transport and catabolism
	Fe-S oxidoreductase	C	Energy production and conversion
	Thiol-disulfide isomerase and thioredoxins	0	Posttranslational modification, protein turnover, chaperones
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Regulator of cell morphogenesis and NO signaling	D	Cell cycle control, cell division, chromosome partitioning
	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit	!	Lipid transport and metabolism
	Acoul CoA acoust/transferace	1	Lipid transport and metabolism
	Acetyl-CoA acetyltransferase Protocatechuate 3,4-dioxygenase beta subunit	Q Q	Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
	Protocatechuate 3,4-dioxygenase beta subunit Protocatechuate 3,4-dioxygenase beta subunit	Q	Secondary metabolites biosynthesis, transport and catabolism
	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	Н	Coenzyme transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	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
	Altronate dehydratase	G	Carbohydrate transport and metabolism
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Predicted phosphoribosyltransferases	R	General function prediction only
	Outer membrane receptor proteins, mostly Fe transport	P T	Inorganic ion transport and metabolism
	Signal transduction histidine kinase Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	T	Signal transduction mechanisms Signal transduction mechanisms
	Multiple antibiotic transporter	U	Intracellular trafficking, secretion, and vesicular transport
	Multidrug resistance efflux pump	V	Defense mechanisms
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	FOG: TPR repeat, SEL1 subfamily	R	General function prediction only
	dTDP-4-dehydrorhamnose reductase	M	Cell wall/membrane/envelope biogenesis
COG1546	Uncharacterized protein (competence- and mitomycin-induced)	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	Aminopeptidase N	E	Amino acid transport and metabolism
	Uncharacterized relative of glutathione S-transferase, MAPEG superfamily	R S	General function prediction only
	Uncharacterized protein conserved in bacteria Saccharopine dehydrogenase and related proteins	5 E	Function unknown Amino acid transport and metabolism
	Predicted membrane protein	S	Function unknown
	Predicted tagatose 6-phosphate kinase	G	Carbohydrate transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	С	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
	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Н	Coenzyme transport and metabolism
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	Anti-sigma factor	T	Signal transduction mechanisms
	NADH:flavin oxidoreductases, Old Yellow Enzyme family	С	Energy production and conversion
	ABC-type xylose transport system, permease component ABC-type sugar transport system, ATPase component	G G	Carbohydrate transport and metabolism Carbohydrate transport and metabolism
	ABC-type sign transport system, Arrase component ABC-type sylose transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Transcriptional regulator	К	Transcription
	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	C	Energy production and conversion
	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
	Sulfite oxidase and related enzymes	R	General function prediction only
	Predicted dehydrogenases and related proteins	R	General function prediction only
	Lysophospholipase L1 and related esterases	E	Amino acid transport and metabolism
	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase	R	General function prediction only
	MoxR-like ATPases	R	General function prediction only
	Flp pilus assembly protein TadC Flp pilus assembly protein, ATPase CpaF	N U	Cell motility Intracellular trafficking, secretion, and vesicular transport
	Predicted membrane protein	S	Function unknown
	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
	Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation	T	Signal transduction mechanisms
	Protein related to penicillin acylase	R	General function prediction only
COG2224	Isocitrate lyase	С	Energy production and conversion
	Cytochrome bd-type quinol oxidase, subunit 2	С	Energy production and conversion
	Cytochrome bd-type quinol oxidase, subunit 1	С	Energy production and conversion
	Predicted transcriptional regulators	K	Transcription
	Predicted membrane protein	S	Function unknown
	Anaerobic dehydrogenases, typically selenocysteine-containing Predicted transcriptional regulator	C R	Energy production and conversion General function prediction only
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
	Predicted membrane protein	 S	Function unknown
	Uncharacterized conserved protein		
		S	Function unknown
COG1926	Predicted phosphoribosyltransferases		Function unknown General function prediction only
	•	S	
COG5502	Predicted phosphoribosyltransferases	S R	General function prediction only
COG5502 COG2814 COG2271	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease	S R S G G	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG5502 COG2814 COG2271 COG0626	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases	S R S G G	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase	S R S G G E O	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating)	S R S G G E O E	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator	S R S G E O E K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	S R S G E O E K E	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sygar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W	S R S G E O E K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	S R S G E O E K E R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin	S R S G E O E K E R R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria	S R S G E O E K E R S S	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2226	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis	S R S G E O E K E R S S U	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2848 COG1848 COG2266	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases	S R S G E O E K E R R S U R H R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase	S R S G G E O E K E R R S U R H R R R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only General function prediction only General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2226 COG2962 COG2962	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases	SRSGGEOEKERRSURHRRE	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only General function prediction only General function prediction only Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG226 COG2962 COG2962 COG2963 COG3173	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein	S R S G G E O E K E R R S U R H R R E S	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only General function prediction only Amino acid transport and metabolism Function unknown Function unknown
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG3176 COG3522 COG2831 COG1848 COG226 COG2962 COG3173 COG3173 COG5135 COG3173	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase	S R S G G E O E K E R R S U R H R R E S R E B E S R E B E B E B E B E B E B E B E B E B E	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only General function prediction only Amino acid transport and metabolism Function unknown General function prediction only General function prediction only Amino acid transport and metabolism Function unknown General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962 COG2962 COG3173 COG1113 COG3173 COG3173	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities	S R S G G E O E K E R R S U R H R R E S R R R R E S R R R R R R R R R R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG2226 COG2831 COG1848 COG2226 COG2962 COG3173 COG1113 COG5135 COG3173 COG3000 COG0668	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel	SRSGGEOEKERRSURHRRESRRM	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962 COG3173 COG3113 COG3173 COG3173 COG3173 COG3868 COG3888	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein	S R S G G E O E K E R R S U R H R R E S R R R R E S R R R R R R R R R R	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962 COG3173 COG5135 COG3173 COG61113 COG61888 COG06688 COG06688 COG06688	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel	S R S G G E O E K E R R S U R H R R E S R R M S	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG3173 COG1113 COG5135 COG3173 COG3173 COG0666 COG3898 COG0688 COG3898 COG1987 COG1987	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ	S R S G G E O E K E R R S U R H R R E S R R M S N	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only General function prediction only Amino acid transport and metabolism Function unknown General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2226 COG3173 COG1113 COG5135 COG3173 COG0300 COG0668 COG3898 COG3279 COG0840	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family	S R S G G E O E K E R R S U R H R R E S R R M S N K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility Transcription
COG5502 COG2814 COG2271 COG0626 COG0492 COG06656 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962 COG3173 COG1113 COG61153 COG6187 COG3279 COG66688 COG3279 COG3279 COG3279 COG3279 COG4828 COG4583	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AIgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility Transcription Cell motility Function unknown Amino acid transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2262 COG3173 COG1113 COG3173 COG3173 COG3173 COG3173 COG0300 COG0668 COG3898 COG1987 COG3279 COG0840 COG4828 COG44828 COG4740	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted permeases Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit Protease subunit of ATP-dependent Clp proteases	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E O	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility Transcription Cell motility Function unknown Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2226 COG3173 COG1113 COG5135 COG3173 COG0300 COG0668 COG3898 COG3898 COG3279 COG0840 COG4828 COG4828 COG4583 COG0740	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit Proteases subunit of ATP-dependent Clp proteases Transcriptional regulator	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E O K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility Transcription Cell motility Function unknown Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription
COG5502 COG2814 COG2271 COG0626 COG0492 COG06685 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG2962 COG3173 COG3173 COG3173 COG3173 COG3000 COG0668 COG3898 COG1987 COG3279 COG0840 COG4828 COG4883 COG0583 COG1880	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit Protease subunit of ATP-dependent Clp proteases Transcriptional regulators	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E O K K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell multility Transcription Cell motility Function unknown Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Transcription
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2831 COG1848 COG2266 COG3173 COG1113 COG3173 COG3173 COG3173 COG0668 COG3898	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit Protease subunit of ATP-dependent Clp proteases Transcriptional regulators Methylase involved in ubiquinone/menaquinone biosynthesis	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E O K K H	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Function unknown Cell motility Transcription Cell motility Franscription Tenscription Transcription Transcription Transcription Transcription Transcription Coenzyme transport and metabolism
COG5502 COG2814 COG2271 COG0626 COG0492 COG0665 COG0583 COG0444 COG3628 COG3176 COG3522 COG2226 COG3173 COG1113 COG5135 COG3173 COG1113 COG5135 COG3173 COG1068 COG3680 COG3680 COG3680 COG3680 COG376 COG06881 COG0740 COG0583 COG0740 COG0583 COG1802 COG2226 COG1502	Predicted phosphoribosyltransferases Uncharacterized conserved protein Arabinose efflux permease Sugar phosphate permease Cystathionine beta-lyases/cystathionine gamma-synthases Thioredoxin reductase Glycine/D-amino acid oxidases (deaminating) Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component Phage baseplate assembly protein W Putative hemolysin Uncharacterized protein conserved in bacteria Hemolysin activation/secretion protein Predicted nucleic acid-binding protein, contains PIN domain Methylase involved in ubiquinone/menaquinone biosynthesis Predicted aminoglycoside phosphotransferase Gamma-aminobutyrate permease and related permeases Uncharacterized conserved protein Predicted aminoglycoside phosphotransferase Short-chain dehydrogenases of various substrate specificities Small-conductance mechanosensitive channel Uncharacterized membrane-bound protein Flagellar biosynthesis pathway, component FliQ Response regulator of the LytR/AlgR family Methyl-accepting chemotaxis protein Predicted membrane protein Sarcosine oxidase gamma subunit Protease subunit of ATP-dependent Clp proteases Transcriptional regulators	S R S G G E O E K E R R S U R H R R E S R R M S N K N S E O K K	General function prediction only Function unknown Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Amino acid transport and metabolism Transcription Amino acid transport and metabolism General function prediction only General function prediction only Function unknown Intracellular trafficking, secretion, and vesicular transport General function prediction only Coenzyme transport and metabolism General function prediction only Cell multility Transcription Cell motility Function unknown Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones Transcription Transcription

	Signal transduction histidine kinase	T	Signal transduction mechanisms
	Uncharacterized protein conserved in bacteria Transcriptional regulator	S K	Function unknown Transcription
	Uncharacterized conserved protein	S	Function unknown
	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	K	Transcription
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	i i	Lipid transport and metabolism
	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
	Poly-beta-hydroxyalkanoate depolymerase	1	Lipid transport and metabolism
	ABC-type branched-chain amino acid transport systems, ATPase component	E	Amino acid transport and metabolism
	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
	Methionine synthase II (cobalamin-independent)	E G	Amino acid transport and metabolism
	Arabinose efflux permease Dihydroxyacid dehydratase/phosphogluconate dehydratase	E	Carbohydrate transport and metabolism Amino acid transport and metabolism
	Predicted glycosyltransferases	R	General function prediction only
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	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
	Transcriptional regulator	K	Transcription
	Transcriptional regulators	K	Transcription
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Phage-related lysozyme (muraminidase) Predicted permeases	R R	General function prediction only General function prediction only
	Poly(3-hydroxyalkanoate) synthetase	K I	Lipid transport and metabolism
	Acetyl-CoA acetyltransferase	i	Lipid transport and metabolism
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit	i	Lipid transport and metabolism
COG2057	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit	1	Lipid transport and metabolism
COG0160	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
COG4269	Predicted membrane protein	S	Function unknown
	Predicted protein tyrosine phosphatase	R	General function prediction only
	Predicted metal-sulfur cluster biosynthetic enzyme	R	General function prediction only
	NifU homolog involved in Fe-S cluster formation	С	Energy production and conversion
	ABC-type transport system involved in Fe-S cluster assembly, permease component	0	Posttranslational modification, protein turnover, chaperones
	Site-specific recombinase XerC ARC three transport system involved in Eq.S. sluctor assembly. ATRasa company	L O	Replication, recombination and repair
	ABC-type transport system involved in Fe-S cluster assembly, ATPase component ABC-type transport system involved in Fe-S cluster assembly, permease component	0	Posttranslational modification, protein turnover, chaperones Posttranslational modification, protein turnover, chaperones
	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	Т	Signal transduction mechanisms
	Predicted hydrocarbon binding protein (contains V4R domain)	R	General function prediction only
	Fe-S oxidoreductase	C	Energy production and conversion
	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	Н	Coenzyme transport and metabolism
COG4683	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized enzyme involved in inositol metabolism	G	Carbohydrate transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G J	Carbohydrate transport and metabolism
	Acetyltransferases, including N-acetylases of ribosomal proteins ABC-type sugar transport system, periplasmic component	G	Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism
	Predicted sugar epimerase	G	Carbohydrate transport and metabolism
	Transcriptional regulators	K	Transcription
	Cytochrome c peroxidase	Р	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
	Transcriptional regulators	K	Transcription
	Conserved protein containing a Zn-ribbon-like motif, possibly RNA-binding	R	General function prediction only
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
	Predicted dehydrogenases and related proteins	R	General function prediction only
	Predicted dehydrogenases and related proteins Uncharacterized protein conserved in bacteria	R S	General function prediction only Function unknown
	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit	c	Energy production and conversion
	Transcriptional regulator	К	Transcription
	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
	Truncated hemoglobins	R	General function prediction only
	Phosphoheptose isomerase	G	Carbohydrate transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
	Predicted membrane protein	S	Function unknown
	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II Ribonuclease D	l J	Lipid transport and metabolism
	Enoyl-CoA hydratase/carnithine racemase	J	Translation, ribosomal structure and biogenesis Lipid transport and metabolism
	Co/Zn/Cd efflux system component	I P	Inorganic ion transport and metabolism
	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	G	Carbohydrate transport and metabolism
	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
	Glycerol-3-phosphate dehydrogenase	c	Energy production and conversion
	Methyl-accepting chemotaxis protein	N	Cell motility
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	Predicted nucleic acid-binding protein, contains PIN domain	R	General function prediction only
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Glutamine synthetase Acatul CoA acatultransforace	E	Amino acid transport and metabolism
	Acetyl-CoA acetyltransferase Nucleoside-diphosphate-sugar epimerases	I M	Lipid transport and metabolism Cell wall/membrane/envelope biogenesis
	Uncharacterized protein conserved in bacteria	S S	Function unknown
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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	1	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	С	Energy production and conversion
COG3180	Putative ammonia monooxygenase	R	General function prediction only
COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family	С	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	1	Lipid transport and metabolism
COG2863	Cytochrome c553	С	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 I	Lipid transport and metabolism
COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	1	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	Н	Coenzyme transport and metabolism
COG1914	Mn2+ and Fe2+ transporters of the NRAMP family	P	Inorganic ion transport and metabolism
COG2200	FOG: EAL domain	Т	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	Н	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	Т	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
	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
	ABC-type sugar transport systems, ATPase components	G	Carbohydrate transport and metabolism
	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport and metabolism
	Phosphoglycerate dehydrogenase and related dehydrogenases	н	Coenzyme transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	ABC-type sugar transport system, permease component	G	Carbohydrate transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport system, permease component	E	Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
	Predicted acyl-CoA transferases/carnitine dehydratase	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Acyl dehydratase	Ī	Lipid transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	i	Lipid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	Ē	Amino acid transport and metabolism
	Gluconolactonase	G	Carbohydrate transport and metabolism
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Gluconolactonase	G	Carbohydrate transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	I	Lipid transport and metabolism
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Predicted Fe-S oxidoreductases	R	General function prediction only
COG1879	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	Predicted membrane protein	S	Function unknown
	ABC-type sugar transport system, ATPase component	G	Carbohydrate transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized enzyme of phenylacetate metabolism	Q	Secondary metabolites biosynthesis, transport and catabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted metal-sulfur cluster biosynthetic enzyme	R	General function prediction only
	Putative threonine efflux protein	E	Amino acid transport and metabolism
	Predicted hydrolase (HAD superfamily)	R	General function prediction only
	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
	Predicted phosphoesterases, related to the Icc protein	R	General function prediction only
	Dihydroxyacetone kinase	G	Carbohydrate transport and metabolism
	Flp pilus assembly protein TadD, contains TPR repeats	U	Intracellular trafficking, secretion, and vesicular transport
	Parvulin-like peptidyl-prolyl isomerase	0	Posttranslational modification, protein turnover, chaperones
		M	Cell wall/membrane/envelope biogenesis
(.()(-)//5/	Organic solvent tolerance protein OstA		
	Organic solvent tolerance protein OstA Predicted permeases		
COG0795	Predicted permeases	R	General function prediction only
COG0795 COG0795	Predicted permeases Predicted permeases	R R	General function prediction only General function prediction only
COG0795 COG0795 COG1995	Predicted permeases Predicted permeases Pyridoxal phosphate biosynthesis protein	R R H	General function prediction only General function prediction only Coenzyme transport and metabolism
COG0795 COG0795 COG1995 COG1853	Predicted permeases Predicted permeases Pyridoxal phosphate biosynthesis protein Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R R	General function prediction only General function prediction only Coenzyme transport and metabolism General function prediction only
COG0795 COG0795 COG1995 COG1853 COG0122	Predicted permeases Predicted permeases Pyridoxal phosphate biosynthesis protein	R R H R	General function prediction only General function prediction only Coenzyme transport and metabolism

COG0647	Predicted sugar phosphatases of the HAD superfamily	G	Carbohydrate transport and metabolism
	DMSO reductase anchor subunit	R	General function prediction only
	Fe-S-cluster-containing hydrogenase components 1	C	Energy production and conversion
	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production and conversion
	Spermidine/putrescine-binding periplasmic protein Glutamate decarboxylase and related PLP-dependent proteins	E E	Amino acid transport and metabolism Amino acid transport and metabolism
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
	Predicted rRNA methylase	 J	Translation, ribosomal structure and biogenesis
	Putative protein-S-isoprenylcysteine methyltransferase	0	Posttranslational modification, protein turnover, chaperones
	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
	Uncharacterized protein containing LysM domain	S	Function unknown
	Acylphosphatases	C	Energy production and conversion
	Succinyl-CoA synthetase, beta subunit	С	Energy production and conversion
	Succinyl-CoA synthetase, alpha subunit Predicted acyl-CoA transferases/carnitine dehydratase	C C	Energy production and conversion Energy production and conversion
	Conserved domain frequently associated with peptide methionine sulfoxide reductase	0	Posttranslational modification, protein turnover, chaperones
	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	c	Energy production and conversion
	Histidinol dehydrogenase	E	Amino acid transport and metabolism
	ATP phosphoribosyltransferase	E	Amino acid transport and metabolism
COG1804	Predicted acyl-CoA transferases/carnitine dehydratase	С	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
	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)	Т	Signal transduction mechanisms
	Uncharacterized protein involved in cation transport	P	Inorganic ion transport and metabolism
	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
	Predicted oxidoreductase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	R J	General function prediction only
	Uncharacterized protein conserved in bacteria	S	Translation, ribosomal structure and biogenesis Function unknown
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	ABC-type sugar transport systems, permease components	G	Carbohydrate transport and metabolism
	Acetyl/propionyl-CoA carboxylase, alpha subunit	Ĭ	Lipid transport and metabolism
	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
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Р	Inorganic ion transport and metabolism
	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
	Uncharacterized membrane-anchored protein conserved in bacteria	S	Function unknown
	ABC-type polar amino acid transport system, ATPase component	E F	Amino acid transport and metabolism
	Adenylosuccinate lyase Predicted transcriptional regulator	K	Nucleotide transport and metabolism Transcription
	EMAP domain	R	General function prediction only
	Predicted Fe-S oxidoreductases	R	General function prediction only
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Ï	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
	2-hydroxychromene-2-carboxylate isomerase	Q	Secondary metabolites biosynthesis, transport and catabolism
	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family	E	Amino acid transport and metabolism
	Fumarylacetoacetate (FAA) hydrolase family protein	R	General function prediction only
	Uncharacterized protein involved in exopolysaccharide biosynthesis ATPases involved in chromosome partitioning	M D	Cell wall/membrane/envelope biogenesis Cell cycle control, cell division, chromosome partitioning
	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	3-hydroxyacyl-CoA dehydrogenase	i	Lipid transport and metabolism
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	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
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	G	Carbohydrate transport and metabolism
	Nucleoside 2-deoxyribosyltransferase	F R	Nucleotide transport and metabolism
	Predicted symporter Uncharacterized conserved protein	K S	General function prediction only Function unknown
	Zn-dependent alcohol dehydrogenases, class III	C	Energy production and conversion
	Outer membrane receptor for Fe3+-dicitrate	P	Inorganic ion transport and metabolism
	Permeases of the drug/metabolite transporter (DMT) superfamily	G	Carbohydrate transport and metabolism
	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
	Predicted transcriptional regulators	K	Transcription
	Na+/H+ antiporter NhaD and related arsenite permeases	Р	Inorganic ion transport and metabolism
	Uncharacterized protein involved in propionate catabolism	R	General function prediction only
	Multimeric flavodoxin WrbA Septum formation initiator	R D	General function prediction only
		C	Cell cycle control, cell division, chromosome partitioning
	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit Threonine aldolase	E	Energy production and conversion Amino acid transport and metabolism
	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production and conversion
	Transcriptional regulator	K	Transcription
	Exo-beta-1,3-glucanase	G	Carbohydrate transport and metabolism
	Nucleotidyltransferase/DNA polymerase involved in DNA repair	L	Replication, recombination and repair
	Sterol desaturase	1	Lipid transport and metabolism
	Sterol desaturase	1	Lipid transport and metabolism
COG0331	(acyl-carrier-protein) S-malonyltransferase	1	Lipid transport and metabolism
	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig 4-hydroxyphenylpyruvate dioxygenase and related hemolysins	E E	Amino acid transport and metabolism Amino acid transport and metabolism

	Cytochrome c553	C	Energy production and conversion
	ABC-type branched-chain amino acid transport systems, periplasmic component	E	Amino acid transport and metabolism
	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs Uncharacterized conserved protein	C S	Energy production and conversion Function unknown
	Fucose dissimilation pathway protein FucU	G	Carbohydrate transport and metabolism
	Predicted glycosyltransferases	R	General function prediction only
	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	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized enzyme of phosphonate metabolism	P P	Inorganic ion transport and metabolism
	Uncharacterized enzyme of phosphonate metabolism Site-specific recombinases, DNA invertase Pin homologs	P I	Inorganic ion transport and metabolism Replication, recombination and repair
	Uncharacterized enzyme of phosphonate metabolism	P	Inorganic ion transport and metabolism
	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	Р	Inorganic ion transport and metabolism
	Transcriptional regulators	K	Transcription
	Predicted glycosyltransferases	R	General function prediction only
	Ketosteroid isomerase-related protein Putative NADP-dependent oxidoreductases	R R	General function prediction only General function prediction only
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
	Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
	ABC-type proline/glycine betaine transport systems, periplasmic components	E	Amino acid transport and metabolism
	ABC-type proline/glycine betaine transport system, permease component	E	Amino acid transport and metabolism
	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	Н	Coenzyme transport and metabolism
	Predicted membrane protein	S	Function unknown
	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	T	Signal transduction mechanisms
	Ammonia permease	P C	Inorganic ion transport and metabolism
	NADPH:quinone reductase and related Zn-dependent oxidoreductases L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M	Energy production and conversion Cell wall/membrane/envelope biogenesis
	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
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	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
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Periplasmic protein involved in polysaccharide export	М	Cell wall/membrane/envelope biogenesis
	Uncharacterized protein involved in exopolysaccharide biosynthesis	М	Cell wall/membrane/envelope biogenesis
	ATPases involved in chromosome partitioning Type II correctory pathyray component EyeA (predicted ATPase)	D U	Cell cycle control, cell division, chromosome partitioning
	Type II secretory pathway, component ExeA (predicted ATPase) Predicted xylanase/chitin deacetylase	G	Intracellular trafficking, secretion, and vesicular transport Carbohydrate transport and metabolism
	Protein involved in cellulose biosynthesis (CelD)	M	Cell wall/membrane/envelope biogenesis
	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	Р	Inorganic ion transport and metabolism
	Flp pilus assembly protein TadG	U	Intracellular trafficking, secretion, and vesicular transport
	Uncharacterized conserved protein	S	Function unknown
	Selenocysteine lyase	E V	Amino acid transport and metabolism
	Type II restriction enzyme, methylase subunits ABC-type sugar transport system, periplasmic component	V G	Defense mechanisms Carbohydrate transport and metabolism
	Transcriptional regulators of sugar metabolism	K	Transcription
	Predicted sugar isomerase	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein	S	Function unknown
	Sulfite oxidase and related enzymes	R	General function prediction only
COG4117	Thiosulfate reductase cytochrome B subunit (membrane anchoring protein)	С	Energy production and conversion
	Peroxiredoxin	0	Posttranslational modification, protein turnover, chaperones
	Transcriptional regulator	K	Transcription
	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Function unknown
	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs Transcriptional regulators	C K	Energy production and conversion Transcription
	Sortase and related acyltransferases	M	Cell wall/membrane/envelope biogenesis
	4-aminobutyrate aminotransferase and related aminotransferases	E	Amino acid transport and metabolism
	Mannose-6-phosphate isomerase	G	Carbohydrate transport and metabolism
	Aspartokinases	E	Amino acid transport and metabolism
COG2814	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Membrane protein TerC, possibly involved in tellurium resistance	P	Inorganic ion transport and metabolism
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Ferredoxin	C	Energy production and conversion
	Putative threonine efflux protein	E	Amino acid transport and metabolism
	Poly(3-hydroxyalkanoate) synthetase Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	S	Lipid transport and metabolism Function unknown
	Transcriptional regulator	K	Transcription
	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
	TRAP-type C4-dicarboxylate transport system, large permease component	G	Carbohydrate transport and metabolism
	Transcriptional regulators	K	Transcription
	Cytochrome c	С	Energy production and conversion
	TRAP-type C4-dicarboxylate transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Predicted permeases	R	General function prediction only
	Uncharacterized conserved protein	S	Function unknown
	Methylase involved in ubiquinone/menaquinone biosynthesis Membrane-fusion protein	H M	Coenzyme transport and metabolism
	Malate/lactate dehydrogenases	C	Cell wall/membrane/envelope biogenesis Energy production and conversion
	Uncharacterized protein conserved in bacteria	R	General function prediction only
	Hemolysin-coregulated protein (uncharacterized)	S	Function unknown

COG0542			
COG0342	ATPases with chaperone activity, ATP-binding subunit	0	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
	Uncharacterized protein conserved in bacteria	S	Function unknown
COG3520	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E	Amino acid transport and metabolism
	Branched-chain amino acid ABC-type transport system, permease components	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Outer membrane cobalamin receptor protein	Н	Coenzyme transport and metabolism
	Predicted hydrolase (HAD superfamily)	R	General function prediction only
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Predicted protein-disulfide isomerase	O E	Posttranslational modification, protein turnover, chaperones
	Selenocysteine lyase	E	Amino acid transport and metabolism
	Saccharopine dehydrogenase and related proteins ATPases of the AAA+ class	0	Amino acid transport and metabolism Posttranslational modification, protein turnover, chaperones
	Uncharacterized protein conserved in bacteria with the myosin-like domain	S	Function unknown
	Probable taurine catabolism dioxygenase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Cysteine synthase	E E	Amino acid transport and metabolism
	NADPH:quinone reductase and related Zn-dependent oxidoreductases	c	Energy production and conversion
	Glutathione S-transferase	Ö	Posttranslational modification, protein turnover, chaperones
	Predicted protein-tyrosine phosphatase	T	Signal transduction mechanisms
	Capsule polysaccharide export protein	M	Cell wall/membrane/envelope biogenesis
	ABC-type polysaccharide/polyol phosphate export systems, permease component	G	Carbohydrate transport and metabolism
	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	С	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	Т	Signal transduction mechanisms
COG0583	Transcriptional regulator	K	Transcription
	Integrase	L	Replication, recombination and repair
	CBS-domain-containing membrane protein	Т	Signal transduction mechanisms
	Uncharacterized conserved protein	S	Function unknown
	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
	Fructose-2,6-bisphosphatase	G	Carbohydrate transport and metabolism
	TRAP-type C4-dicarboxylate transport system, small permease component	G	Carbohydrate transport and metabolism
	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
COG0076 COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	E G	Amino acid transport and metabolism Carbohydrate transport and metabolism
COG0076 COG1638 COG2814	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease	E G G	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG0076 COG1638 COG2814 COG5631	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family)	E G G K	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription
COG0076 COG1638 COG2814 COG5631 COG0494	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes	E G K L	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) MTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase	E G G K L	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	E G K L R	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport	E G K L R P	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators	E G K L R P P K	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport	E G K L R P	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase	E G K L R P K P	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system	E G K L R P P K P	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family	E G K L R P P K P T	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase)	E G K L R P K P T E	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342 COG0760	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein	E G K L R P K P T E J S	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG474 COG4191 COG1364 COG0251 COG3342 COG0760 COG1028	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase	E G K L R P K P T E J S	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342 COG0760 COG1028 COG1493	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yigF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	E G K L R P K P T E J S O I	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG3342 COG0760 COG1028 COG1028 COG1028	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism	E G K L R P K P T E J S O I T	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3424 COG0760 COG1028 COG1051 COG0438	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yigf family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase	E G K L R P K P T E J S O I T	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG474 COG4191 COG1364 COG0251 COG3342 COG1051 COG1088 COG1051 COG0454 COG1051	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase	E G K L R P F K F O I T F M	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342 COG0760 COG1028 COG1028 COG1028 COG1028 COG1028 COG10309	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain	E G K L R P K P T E J S O I T F M T K J	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Signal transduction mechanisms Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG4791 COG36491 COG0251 COG0251 COG0488 COG1051 COG0488 COG2199 COG1309 COG1309 COG1051 COG0251 COG0153	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase	E G K L R P K P T E J S O I T F M T K J G	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG1629 COG1737 COG1629 COG1737 COG191 COG1364 COG0251 COG0342 COG1051 COG0438 COG2199 COG1309 COG1309 COG0251 COG0251	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase Galactose-1-phosphate uridylyltransferase	E G K L R P K P T E J S O I T F M T K J G G G G G G G G G G G G G G G G G G	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Cerl souli/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342 COG1028 COG1028 COG1028 COG1028 COG10309 COG0251 COG0354 COG0251 COG0354 COG0153 COG0155 COG0155 COG0155 COG0155	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yigF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDF domain Transcriptional regulator Putative translation initiation inhibitor, yigF family Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase	E G K L R P K P T E J S O I T F M T K J G C E E G I E E I E I E I E I E I E I E I E	Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Transcription Inorganic ion transport and metabolism Iranscription Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG3342 COG0760 COG1028 COG1093 COG1091 COG0309 COG0251 COG01309 COG01053 COG01085 COG01085 COG01085 COG01834 COG1682	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase ABC-type polysaccharide/polyol phosphate export systems, permease component	E G K L R P P K P T E J S O I T F M T K J G G G G G G G G G G G G G G G G G G	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Carbohydrate transport and metabolism
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COG0076 COG1638 COG2814 COG65631 COG0474 COG1629 COG1737 COG0474 COG0479 COG1364 COG0551 COG0760 COG1028 COG1038 COG1038 COG1038 COG0551 COG0560 COG05	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDFF domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase ABC-type polysaccharide/polyol phosphate export systems, permease component Transcriptional regulator Uracil-DNA glycosylase Methyl-accepting chemotaxis protein Di- and tricarboxylate transporters FOG: Ankyrin repeat 1-aminocyclopropane-1-carboxylate deaminase	E G K L R P K P T E J S O I T F M T K J G C E G K L N P P K P T E I S O I S O I S O I S O I S O I S O I S O I S O I S D R D P I S D I S D R D E I S D R D R D E I S D E I S D R D E I S D R D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I S D E I I S D E I B D E I B D E I I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B D E I B E I B E I B D E I B E I E I	Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair Cell motility Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism
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COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG1629 COG1737 COG04791 COG1364 COG0251 COG0342 COG1028 COG1038 COG00314 COG0666 COG2515 COG00391 COG06991 COG0791	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase Glalactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase ABC-type polysaccharide/polyol phosphate export systems, permease component Transcriptional regulator Uracil-DNA glycosylase Methyl-accepting chemotaxis protein Di- and tricarboxylate transporters FOG: Ankyrin repeat 1-aminocyclopropane-1-carboxylate deaminase Predicted dinucleotide-binding enzymes Ell wall-associated hydrolases (invasion-associated proteins) Enoyl-CoA hydratase/carnithine racemase	E G G K L R P P K P T E J S O I T F M T K J G C E G K L N P R R E R E R S D R E R E R E R E R E R E R E R E R E R	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Transcription Replication, recombination and repair Cell motility Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Lipid transport and metabolism
COG0076 COG1638 COG2814 COG2814 COG2814 COG2814 COG2814 COG0479 COG1737 COG0474 COG0151 COG03342 COG1028 COG1028 COG1038 COG1038 COG0531 COG05	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotrulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yigF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yigF family Galactokinase Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase ABC-type polysaccharide/polyol phosphate export systems, permease component Transcriptional regulator Uracil-DNA glycosylase Methyl-accepting chemotaxis protein Di- and tricarboxylate transporters FOG: Ankyrin repeat 1-aminocyclopropane-1-carboxylate deaminase Predicted dinucleotide-binding enzymes Cell wall-associated hydrolases (invasion-associated proteins) Enoyl-CoA hydratase/carnithine racemase Predicted permeases	E G K L R P K P T E J S O I T F M T K J G C E G K L N P R E R E R E R E R E R E R E R E R E R	Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair Cell motility Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Lipid transport and metabolism General function prediction only
COG0076 COG1638 COG2814 COG5631 COG0494 COG4123 COG4773 COG1629 COG1737 COG1629 COG1737 COG0474 COG4191 COG1364 COG0251 COG0334 COG1051 COG0351 COG0351 COG0348 COG1093 COG1085 COG0551 COG06840 COG0751 COG06840 COG0751 COG0730 COG0730 COG1167	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yjgF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPP protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDFE domain Transcriptional regulator Putative translation initiation inhibitor, yjgF family Galactokinase Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase BABC-type polysaccharide/polyol phosphate export systems, permease component Transcriptional regulator Uracil-DNA glycosylase Methyl-accepting chemotaxis protein Di- and tricarboxylate transporters FOG: Ankyrin repeat 1-aminocyclopropane-1-carboxylate deaminase Predicted dinucleotide-binding enzymes Cell wall-associated hydrolases (invasion-associated proteins) Enoyl-CoA hydratase/carnithine racemase Predicted foundeotide-binding enzymes Cell wall-associated hydrolases (invasion-associated proteins) Enoyl-CoA hydratase/carnithine racemase Predicted demicana aminotransferase domain (MocR family) and their euk	E G G K L R P P K P T E J S O I T F M T K J G C E G K L N P R R E R E R M I S D R E R M B M I S B B M B B B B B B B B B B B B B B B B	Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair Cell motility Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Lipid transport and metabolism General function prediction only Transcription
COG0076 COG1638 COG2814 COG5531 COG0494 COG4123 COG1629 COG1737 COG074 COG4791 COG1629 COG1028 COG0047 COG0047 COG0666 COG251 COG0048 COG0047 COG0666 COG251 COG0047 COG0666 COG2515 COG0085 COG0071 COG0666 COG2515 COG0085 COG071 COG1024 COG0761 COG1024 COG0761 COG1167 CO	TRAP-type C4-dicarboxylate transport system, periplasmic component Arabinose efflux permease Predicted transcription regulator, contains HTH domain (MarR family) NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted O-methyltransferase Outer membrane receptor for ferric coprogen and ferric-rhodotrulic acid Outer membrane receptor proteins, mostly Fe transport Transcriptional regulators Cation transport ATPase Signal transduction histidine kinase regulating C4-dicarboxylate transport system N-acetylglutamate synthase (N-acetylornithine aminotransferase) Putative translation initiation inhibitor, yigF family Uncharacterized conserved protein Parvulin-like peptidyl-prolyl isomerase Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Serine kinase of the HPr protein, regulates carbohydrate metabolism ADP-ribose pyrophosphatase Glycosyltransferase FOG: GGDEF domain Transcriptional regulator Putative translation initiation inhibitor, yigF family Galactokinase Galactose-1-phosphate uridylyltransferase Glutamate dehydrogenase/leucine dehydrogenase ABC-type polysaccharide/polyol phosphate export systems, permease component Transcriptional regulator Uracil-DNA glycosylase Methyl-accepting chemotaxis protein Di- and tricarboxylate transporters FOG: Ankyrin repeat 1-aminocyclopropane-1-carboxylate deaminase Predicted dinucleotide-binding enzymes Cell wall-associated hydrolases (invasion-associated proteins) Enoyl-CoA hydratase/carnithine racemase Predicted permeases	E G K L R P K P T E J S O I T F M T K J G C E G K L N P R E R E R E R E R E R E R E R E R E R	Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair General function prediction only Inorganic ion transport and metabolism Signal transduction mechanisms Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Function unknown Posttranslational modification, protein turnover, chaperones Lipid transport and metabolism Signal transduction mechanisms Nucleotide transport and metabolism Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Transcription Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Energy production and conversion Amino acid transport and metabolism Carbohydrate transport and metabolism Transcription Replication, recombination and repair Cell motility Inorganic ion transport and metabolism General function prediction only Amino acid transport and metabolism General function prediction only Cell wall/membrane/envelope biogenesis Lipid transport and metabolism General function prediction only

	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Transcriptional regulator	I K	Lipid transport and metabolism Transcription
	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism
	Predicted membrane protein	S	Function unknown
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Predicted NAD/FAD-dependent oxidoreductase	R	General function prediction only
	Glutaredoxin and related proteins Predicted amidohydrolase	O R	Posttranslational modification, protein turnover, chaperones General function prediction only
	ABC-type multidrug transport system, ATPase and permease components	V	Defense mechanisms
	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
	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)	F	Nucleotide transport and metabolism
	Uncharacterized conserved protein	R	General function prediction only
	Transposase and inactivated derivatives P pilus assembly protein, chaperone PapD	L N	Replication, recombination and repair Cell motility
	Uncharacterized protein conserved in bacteria	S	Function unknown
	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
	Predicted membrane protein	S	Function unknown
	Na+-driven multidrug efflux pump DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	V K	Defense mechanisms Transcription
	Predicted symporter	R	General function prediction only
	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
	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R	General function prediction only
	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Energy production and conversion
	Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components	S V	Function unknown Defense mechanisms
	Predicted transcriptional regulators	K	Transcription
	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
	Acetyltransferase (isoleucine patch superfamily)	R	General function prediction only
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	Transcriptional regulators Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	K J	Transcription Translation, ribosomal structure and biogenesis
	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	Ĺ	Replication, recombination and repair
	Selenocysteine lyase	E	Amino acid transport and metabolism
COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	L	Replication, recombination and repair
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Thiamine pyrophosphate-requiring enzymes (acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E C	Amino acid transport and metabolism
	Predicted acyl-CoA transferases/carnitine dehydratase ABC-type branched-chain amino acid transport systems, periplasmic component	E	Energy production and conversion Amino acid transport and metabolism
	Predicted acyltransferases	Ī	Lipid transport and metabolism
	Fructose-1,6-bisphosphate aldolase	G	Carbohydrate transport and metabolism
COG2085	Predicted dinucleotide-binding enzymes	R	General function prediction only
	Response regulator of the LytR/AlgR family	K	Transcription
	Uncharacterized conserved protein	S S	Function unknown Function unknown
	Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria	S	Function unknown
	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle control, cell division, chromosome partitioning
	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	M	Cell wall/membrane/envelope biogenesis
	Uncharacterized conserved protein	S	Function unknown
	Antitoxin of toxin-antitoxin stability system	D	Cell cycle control, cell division, chromosome partitioning
	Predicted proline hydroxylase Uncharacterized conserved protein	O S	Posttranslational modification, protein turnover, chaperones Function unknown
	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport and metabolism
	Predicted ATPase (AAA+ superfamily)	R	General function prediction only
COG1743	Adenine-specific DNA methylase containing a Zn-ribbon	L	Replication, recombination and repair
	Superfamily II DNA/RNA helicases, SNF2 family	K	Transcription
	Plasmid stabilization system protein	R	General function prediction only
	Glycosyltransferases involved in cell wall biogenesis Predicted metal-dependent hydrolase	M R	Cell wall/membrane/envelope biogenesis General function prediction only
	Hydrogenase maturation factor	0	Posttranslational modification, protein turnover, chaperones
	Myo-inositol-1-phosphate synthase	1	Lipid transport and metabolism
COG4286	Uncharacterized conserved protein related to MYG1 family	S	Function unknown
	Coenzyme F420-reducing hydrogenase, alpha subunit	C -	Energy production and conversion
	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains FOG: EAL domain	T T	Signal transduction mechanisms Signal transduction mechanisms
	Chemotaxis protein	N	Cell motility
	ABC-type sugar transport system, periplasmic component	G	Carbohydrate transport and metabolism
	Predicted helicases	R	General function prediction only
	Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair
	RecB family exonuclease	L	Replication, recombination and repair
	Uncharacterized protein predicted to be involved in DNA repair Uncharacterized protein predicted to be involved in DNA repair	L	Replication, recombination and repair Replication, recombination and repair
	Predicted Co/Zn/Cd cation transporters	P	Inorganic ion transport and metabolism
	Superfamily I DNA and RNA helicases and helicase subunits	L	Replication, recombination and repair
COG0303	Molybdopterin biosynthesis enzyme	н	Coenzyme transport and metabolism
	Chemotaxis protein histidine kinase and related kinases	N	Cell motility
	Chemotaxis signal transduction protein	N	Cell motility
	Molybdopterin biosynthesis enzyme AraC-type DNA-binding domain-containing proteins	H K	Coenzyme transport and metabolism Transcription
	Predicted membrane protein	S	Function unknown
	Transcriptional regulator	K	Transcription
COG1017	Hemoglobin-like flavoprotein	С	Energy production and conversion
	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	Inorganic ion transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	P P	Inorganic ion transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components PEP phosphonomutase and related enzymes	G G	Inorganic ion transport and metabolism Carbohydrate transport and metabolism
	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
	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R	General function prediction only
	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolig	E	Amino acid transport and metabolism
	Cytidylate kinase Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their euk	F	Nucleotide transport and metabolism
	Predicted amino acid aldolase or racemase	K E	Transcription Amino acid transport and metabolism
	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	Н	Amino acid transport and metabolism Coenzyme transport and metabolism
	Transcriptional regulators	K	Transcription
	Transcriptional regulator	K	Transcription
	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
	Bacterial nucleoid DNA-binding protein	L	Replication, recombination and repair
	Transcriptional regulator	K	Transcription
	Chemotaxis signal transduction protein	N	Cell motility
	Methylase of chemotaxis methyl-accepting proteins Chemotaxis protein histidine kinase and related kinases	N N	Cell motility Cell motility
	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
	Glycosyltransferase	M	Cell wall/membrane/envelope biogenesis
	H+/gluconate symporter and related permeases	G	Carbohydrate transport and metabolism
COG1802	Transcriptional regulators	K	Transcription
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	Transcriptional regulators	K	Transcription
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E E	Amino acid transport and metabolism
	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases ABC-type oligopeptide transport system, ATPase component	E	Amino acid transport and metabolism Amino acid transport and metabolism
	ABC-type digopeptide/nickel transport system, ATPase component ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism Amino acid transport and metabolism
	Transcriptional regulators	K	Transcription
	Saccharopine dehydrogenase and related proteins	E	Amino acid transport and metabolism
	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	С	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
	Pirin-related protein	R	General function prediction only
	ABC-type molybdate transport system, periplasmic component	P	Inorganic ion transport and metabolism
	Arabinose efflux permease	G	Carbohydrate transport and metabolism
	Permeases of the drug/metabolite transporter (DMT) superfamily HD-GYP domain	G T	Carbohydrate transport and metabolism Signal transduction mechanisms
	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	Ť	Signal transduction mechanisms
	Predicted nucleic-acid-binding protein, contains PIN domain	R	General function prediction only
	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	ï	Lipid transport and metabolism
	Short-chain alcohol dehydrogenase of unknown specificity	R	General function prediction only
COG0558	Phosphatidylglycerophosphate synthase	1	Lipid transport and metabolism
	ABC-type metal ion transport system, periplasmic component/surface antigen	P	Inorganic ion transport and metabolism
	Membrane-associated phospholipid phosphatase	1	Lipid transport and metabolism
	MoxR-like ATPases	R	General function prediction only
	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	E	Amino acid transport and metabolism
	Nitroreductase Zn-dependent hydrolases, including glyoxylases	C R	Energy production and conversion General function prediction only
	DnaJ-class molecular chaperone with C-terminal Zn finger domain	0	Posttranslational modification, protein turnover, chaperones
	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Т	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
	Sterol desaturase		
		1	Lipid transport and metabolism
	Uncharacterized conserved protein	S	Lipid transport and metabolism Function unknown
COG0517	FOG: CBS domain	S R	Lipid transport and metabolism Function unknown General function prediction only
COG0517 COG3285	FOG: CBS domain Predicted eukaryotic-type DNA primase	S R L	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair
COG0517 COG3285 COG1280	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein	S R L E	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism
COG0517 COG3285 COG1280 COG0337	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase	S R L E	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases	S R L E	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase	S R L E E	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase	S R L E E M	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases)	S R L E E M E K	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component	R L E E M E K	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component	S R L E E M E K S H P	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG1974 COG2128 COG3585 COG3639 COG3639	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component	S R L E E M E K S H P P	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3639 COG3221 COG2364	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein	S R L E E M E K S H P P S	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown
COG0517 COG3285 COG1280 COG3049 COG0703 COG1974 COG2128 COG3685 COG3639 COG3639 COG3221 COG2364 COG3638	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component	S R L E M E K S H P P S P	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG3128 COG3585 COG3639 COG3264 COG3638 COG3638 COG3638	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphatase	SRLEEM EKSHPPSPG	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG01974 COG2128 COG36385 COG36363 COG3221 COG2364 COG3638 COG0406 COG0154	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein	SRLEEMMEKSHPPSPGJ	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Translation, ribosomal structure and biogenesis
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3639 COG3634 COG3644 COG3644 COG0164	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphataes Glucose-6-phosphate isomerase	SRLEEMMEKSHPPSPGJG	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3639 COG3639 COG3639 COG3639 COG3638 COG0406 COG0154 COG0166 COG0156	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, perplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphatase Asp-tRNAAsn/Glu-tRNAGin amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter	SRLEEMMEKSHPPSPGJ	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Translation, ribosomal structure and biogenesis
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3621 COG2364 COG0166 COG0166 COG0166 COG0766 COG0766 COG0786	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphataes Glucose-6-phosphate isomerase	SRLEEMEKSHPPSPGJGE	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function inknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3639 COG3639 COG3639 COG3639 COG3640 COG0154 COG0156 COG0156 COG1289 COG1566	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphatase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein	SRLEEMEKSHPPSGJGES	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3639 COG3639 COG3634 COG066 COG0154 COG0166 COG0786 COG0786 COG03333	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, perplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, at Plase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, at Plase component Predicted membrane protein Multidrug resistance efflux pump	SRLEEMEKSHPPSPGJGESVSI	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Function in transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3221 COG2364 COG0156 COG0156 COG0156 COG0768 COG1589 COG1589 COG1589 COG1589 COG1580 COG158	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, at Plase component Predicted membrane protein ABC-type phosphate isomerase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Debydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted membrane protein	SRLEEMEKSHPPSPGJGESVSIS	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Lipid transport and metabolism Function unknown
COG0517 COG3285 COG1282 COG0327 COG3049 COG0703 COG1744 COG2128 COG3639 COG3639 COG3639 COG3639 COG3634 COG0166 COG0154 COG0166 COG0158 COG1086 COG03333 COG1028 COG0359 COG359	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, at Pase component Predicted membrane protein ABC-type phosphate isomerase Asp-tRNAAsn/Glu-tRNAGin amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted membrane protein Predicted membrane protein	S R L E E M E K S H P P P S P G J G E S V S I I S R I S R S R S S R S S R S S R S S R S R	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Transport ion transport and metabolism Transport ion transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Lipid transport and metabolism Function unknown General function prediction only
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3639 COG3634 COG0464 COG0166 COG0186 COG0166 COG0186 COG0186 COG03333 COG1028 COG3152 COG0527 COG0527	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphataes Asy-tRNAAsn/Glu-tRNAGin amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted membrane protein Predicted dehydrogenase Putative GTPases (G3E family)	S R L E E M E K S H P P P S P G J G E S V S I I S R R R R R R S R S R R R R R R R	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Transport ion transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Function unknown Defense mechanisms Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Function unknown Ceneral function prediction only General function prediction only
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3639 COG3639 COG3639 COG3639 COG3640 COG0154 COG0156 COG015	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphate Fructose-2,6-bisphosphatase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted dembrane protein Predicted dembrane protein Predicted dembrane protein Predicted dembrane protein Predicted dental-dependent hydrolase of the TIM-barrel fold	SRLEEMEKSHPPSPGJGESVSISRRRRRR	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Surcarbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Function unknown General function prediction only General function prediction only
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3585 COG3639 COG3221 COG2364 COG0154 COG0156 COG0156 COG1289 COG1566 COG1289 COG1566 COG1289 COG1566 COG0186 COG0188	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Predicted membrane protein ABC-type phosphate isomerase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Debydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted membrane protein Predicted membrane protein Predicted membrane protein Predicted metal-dependent hydrolase of the TIM-barrel fold Transcriptional regulators	SRLEEMEKSHPPSPGJGESVSISRRKK	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Function unknown Defense mechanisms Function unknown Upid transport and metabolism Function unknown General function prediction only General function prediction only General function prediction only Transcription
COG0517 COG3285 COG1280 COG0337 COG3049 COG0703 COG1974 COG2128 COG3639 COG3639 COG3639 COG3639 COG3639 COG3639 COG3638 COG0406 COG0154 COG0166 COG0786 COG0158 COG1028 COG128 COG128 COG0579 COG0523 COG0523 COG0523 COG0528	FOG: CBS domain Predicted eukaryotic-type DNA primase Putative threonine efflux protein 3-dehydroquinate synthetase Penicillin V acylase and related amidases Shikimate kinase SOS-response transcriptional repressors (RecA-mediated autopeptidases) Uncharacterized conserved protein Molybdopterin-binding protein ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, permease component ABC-type phosphate/phosphonate transport system, periplasmic component Predicted membrane protein ABC-type phosphate/phosphonate transport system, ATPase component Fructose-2,6-bisphosphate Fructose-2,6-bisphosphatase Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases Glucose-6-phosphate isomerase Na+/glutamate symporter Predicted membrane protein Multidrug resistance efflux pump Uncharacterized protein conserved in bacteria Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted dembrane protein Predicted dembrane protein Predicted dembrane protein Predicted dembrane protein Predicted dental-dependent hydrolase of the TIM-barrel fold	SRLEEMEKSHPPSPGJGESVSISRRRRRR	Lipid transport and metabolism Function unknown General function prediction only Replication, recombination and repair Amino acid transport and metabolism Amino acid transport and metabolism Cell wall/membrane/envelope biogenesis Amino acid transport and metabolism Transcription Function unknown Coenzyme transport and metabolism Inorganic ion transport and metabolism Function unknown Inorganic ion transport and metabolism Surcarbohydrate transport and metabolism Translation, ribosomal structure and biogenesis Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Lipid transport and metabolism Function unknown Lipid transport and metabolism Function unknown General function prediction only General function prediction only

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	С	Energy production and conversion
	Selenophosphate synthase	E	Amino acid transport and metabolism
	Small-conductance mechanosensitive channel	M	Cell wall/membrane/envelope biogenesis
	Predicted membrane protein	S	Function unknown
	Acetylglutamate kinase	E	Amino acid transport and metabolism
	H+/citrate symporter	С	Energy production and conversion
	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production and conversion
	Predicted GTPase	R	General function prediction only
	DNA repair exonuclease	L	Replication, recombination and repair
	Methyl-accepting chemotaxis protein	N	Cell motility
	Uncharacterized conserved protein	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
	Citrate lyase beta subunit	G K	Carbohydrate transport and metabolism
	Transcriptional regulator ARC type Fo2 transport system periplasmic component	R P	Transcription
	ABC-type Fe3+ transport system, periplasmic component RNase P protein component	í	Inorganic ion transport and metabolism Translation, ribosomal structure and biogenesis
		C	Energy production and conversion
	NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G) Predicted amino acid aldolase or racemase	E	Amino acid transport and metabolism
	Acetyltransferases	R	General function prediction only
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	Phosphoglycerate dehydrogenase and related dehydrogenases	н	Coenzyme transport and metabolism
	ABC-type uncharacterized transport system involved in gliding motility, auxiliary component	N.	Cell motility
	ABC-type transport system involved in multi-copper enzyme maturation, permease component	R	General function prediction only
	Periplasmic protein TonB, links inner and outer membranes	M	Cell wall/membrane/envelope biogenesis
	Protein-tyrosine-phosphatase	т	Signal transduction mechanisms
	Short-chain dehydrogenases of various substrate specificities	R	General function prediction only
	AraC-type DNA-binding domain-containing proteins	K	Transcription
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	ï	Lipid transport and metabolism
	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E E	Amino acid transport and metabolism
	ABC-type spermidine/putrescine transport system, permease component I	E	Amino acid transport and metabolism
	ABC-type spermidine/putrescine transport system, permease component II	E	Amino acid transport and metabolism
	H+/gluconate symporter and related permeases	G	Carbohydrate transport and metabolism
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Transcriptional regulator	K	Transcription
	Predicted choline kinase involved in LPS biosynthesis	M	Cell wall/membrane/envelope biogenesis
	Outer membrane receptor proteins, mostly Fe transport	P	Inorganic ion transport and metabolism
	Multisubunit Na+/H+ antiporter, MnhF subunit	P	Inorganic ion transport and metabolism
	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	К	Transcription
	Fe2+-dicitrate sensor, membrane component	P	Inorganic ion transport and metabolism
	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	К	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	С	Energy production and conversion
	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport and metabolism
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Glycine cleavage system T protein (aminomethyltransferase)	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
		K	Transcription
COG1846	Transcriptional regulators		
COG1846 COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
COG1846 COG0596 COG0451	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases	R M	Cell wall/membrane/envelope biogenesis
COG1846 COG0596 COG0451 COG0397	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein	R M S	Cell wall/membrane/envelope biogenesis Function unknown
COG1846 COG0596 COG0451 COG0397 COG0677	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase	R M S M	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UPP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein	R M S M T	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase	R M S M T G	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators	R M S M T G K	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases	R M S M T G	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402 COG2084	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UPP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	R M S M T G K F	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402 COG2084 COG3485	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxylsobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit	R M S M T G K F I Q	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402 COG2084 COG3485 COG3206	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis	R M S M T G K F I Q M	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402 COG2084 COG3485 COG3206 COG2223	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter	R M S M T G K F I Q M P	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism
COG1846 COG0596 COG0451 COG0677 COG3448 COG3280 COG0402 COG0402 COG2084 COG3485 COG3206 COG2223 COG0664	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UpP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	R M T G K F I Q M P T	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms
COG1846 COG0596 COG0451 COG0397 COG0677 COG3280 COG0402 COG2084 COG3206 COG2223 COG0664 COG2180	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxylsobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - Catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit	R M T G K F I Q M P T C	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG1802 COG0402 COG2084 COG3485 COG3206 COG2223 COG0664 COG2180	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxylsobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase	R M S M T G K F I Q M P T C	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion
COG1846 COG0596 COG0451 COG0397 COG3448 COG3280 COG1802 COG2084 COG3485 COG3286 COG2223 COG0664 COG2180	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein	R M T G K F I Q M P T C C S	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown
COG1846 COG0596 COG0451 COG0397 COG3448 COG1802 COG0402 COG2084 COG3485 COG3206 COG2223 COG0664 COG2180 COG0247 COG5615	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UPP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components	R M T G K F I Q M P T C C S E	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG0402 COG0402 COG2084 COG3280 COG2223 COG0664 COG2180 COG02559 COG0683	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - Catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component	R M S M T G K F I Q M P T C C S E E	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism Amino acid transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG3448 COG3280 COG1802 COG0402 COG2084 COG3286 COG2223 COG0664 COG2180 COG2180 COG2180 COG256 COG256 COG256 COG256 COG556 COG0559 COG0683 COG0583	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component Transcriptional regulator	R M T G K F I Q M P T C C S E	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Transcription
COG1846 COG0596 COG0451 COG0397 COG3448 COG3280 COG1802 COG2084 COG3285 COG3206 COG2223 COG0664 COG2180 COG0247 COG5615 COG0559 COG0683 COG0583 COG0227	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component Transcriptional regulator AraC-type DNA-binding domain-containing proteins	R M S M T G K F I Q M P T C C S E E K	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Transcription Transcription
COG1846 COG0596 COG0451 COG0397 COG3448 COG3280 COG1802 COG2084 COG3285 COG3206 COG2223 COG0664 COG2180 COG2559 COG0683 COG0583 COG0583 COG0583 COG0583 COG0587 COG3185	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component Transcriptional regulator AraC-type DNA-binding domain-containing proteins 4-hydroxyphenylpyruvate dioxygenase and related hemolysins	R M S M T G K F I Q M P T C S E E K K	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism Transcription Transcription Amino acid transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG0677 COG3448 COG3280 COG0402 COG0402 COG02223 COG0664 COG2223 COG0664 COG225 COG06683 COG0559 COG0583 COG0583 COG0583 COG0597	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component Transcriptional regulator AraC-type DNA-binding domain-containing proteins 4-hydroxyphenylpyruvate dioxygenase and related hemolysins Permeases of the drug/metabolite transporter (DMT) superfamily	R M T G K F I Q M P T C C S E E K K E	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism Amino acid transport and metabolism Transcription Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism
COG1846 COG0596 COG0451 COG0397 COG3448 COG3280 COG1802 COG0402 COG2084 COG2223 COG0664 COG2180 COG2283 COG06651 COG0559 COG0583 COG2207 COG3185 COG2207 COG3185 COG0697 COG2388	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) Nucleoside-diphosphate-sugar epimerases Uncharacterized conserved protein UDP-N-acetyl-D-mannosaminuronate dehydrogenase CBS-domain-containing membrane protein Maltooligosyl trehalose synthase Transcriptional regulators Cytosine deaminase and related metal-dependent hydrolases 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Protocatechuate 3,4-dioxygenase beta subunit Uncharacterized protein involved in exopolysaccharide biosynthesis Nitrate/nitrite transporter cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases Nitrate reductase delta subunit Fe-S oxidoreductase Predicted integral membrane protein Branched-chain amino acid ABC-type transport system, permease components ABC-type branched-chain amino acid transport systems, periplasmic component Transcriptional regulator AraC-type DNA-binding domain-containing proteins 4-hydroxyphenylpyruvate dioxygenase and related hemolysins	R M S M T G K F I Q M P T C C S E E K K E	Cell wall/membrane/envelope biogenesis Function unknown Cell wall/membrane/envelope biogenesis Signal transduction mechanisms Carbohydrate transport and metabolism Transcription Nucleotide transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Inorganic ion transport and metabolism Signal transduction mechanisms Energy production and conversion Energy production and conversion Function unknown Amino acid transport and metabolism Transcription Transcription Amino acid transport and metabolism

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
	ABC-type multidrug transport system, ATPase component	V	Defense mechanisms
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
COG0069	Glutamate synthase domain 2	E	Amino acid transport and metabolism
	Glutamate synthase domain 3	E	Amino acid transport and metabolism
	Glutamate synthase domain 1	E	Amino acid transport and metabolism
	Predicted membrane protein	S	Function unknown
	Asp-tRNAAsn/Glu-tRNAGIn amidotransferase A subunit and related amidases	J	Translation, ribosomal structure and biogenesis
	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	M	Cell wall/membrane/envelope biogenesis
	Nucleoside-diphosphate-sugar epimerases	M	Cell wall/membrane/envelope biogenesis
	Site-specific recombinase XerD	L	Replication, recombination and repair
	Site-specific recombinases, DNA invertase Pin homologs	L	Replication, recombination and repair
	Methyl-accepting chemotaxis protein	N	Cell motility
	Predicted outer membrane protein	S P	Function unknown
	NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain Lactoy/glutathione lyase and related lyases	E	Inorganic ion transport and metabolism Amino acid transport and metabolism
	DnaJ-class molecular chaperone with C-terminal Zn finger domain	0	Posttranslational modification, protein turnover, chaperones
	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport and metabolism
	Predicted branched-chain amino acid permease (azaleucine resistance)	E	Amino acid transport and metabolism
	Tetrahydrodipicolinate N-succinyltransferase	E	Amino acid transport and metabolism
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Predicted hydrolase (HAD superfamily)	R	General function prediction only
	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	c	Energy production and conversion
	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	P	Inorganic ion transport and metabolism
	Predicted permeases	R	General function prediction only
	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q	Secondary metabolites biosynthesis, transport and catabolism
	tRNA-dihydrouridine synthase	j	Translation, ribosomal structure and biogenesis
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Predicted enzyme of the cupin superfamily	R	General function prediction only
	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
COG3713	Outer membrane protein V	М	Cell wall/membrane/envelope biogenesis
	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	С	Energy production and conversion
	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
	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	0	Posttranslational modification, protein turnover, chaperones
COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	1	Linid transport and protoholism
0000510	1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	'	Lipid transport and metabolism
	Acetyl-CoA acetyltransferase	i	Lipid transport and metabolism
COG0183		l S	
COG0183 COG5454	Acetyl-CoA acetyltransferase	S	Lipid transport and metabolism
COG0183 COG5454 COG2510 COG2370	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein	s O	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones
COG0183 COG5454 COG2510 COG2370 COG0583	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator	S O K	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulators	S O K K	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulators Methyl-accepting chemotaxis protein	S O K K	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulators Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria	S O K K N S	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	S O K K N S	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulators Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily	S O K K N S P	Lipid transport and metabolism Function unknown Fustranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulators Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria	S O K K N S P G	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG2841 COG0065	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit	S O K K N S P G S	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG4773 COG0697 COG2841 COG0065 COG0697	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily	S O K K N S P G S E	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG4773 COG0697 COG2841 COG0065 COG0697 COG3791	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein	S O K K N S P G S E G S	Lipid transport and metabolism Function unknown Fustranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Function unknown
COG0183 COG5454 COG2510 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG2841 COG0665 COG0697 COG3791 COG4663	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component	S O K N S P G S E G G Q	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG2841 COG065 COG0697 COG3791 COG4663 COG1247	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases	S O K N S P G S E G M	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG04773 COG0697 COG267 COG0655 COG0697 COG3791 COG065 COG0657 COG0657 COG067 C	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases	S O K K N S P G S E G S Q M C	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Secondary metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG046773 COG0697 COG2841 COG0697 COG3791 COG4663 COG1247 COG1247	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein	S O K N S P G S E G M	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only
COG0183 COG5454 COG5510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG2841 COG0697 COG697 COG3791 COG4663 COG1247 COG1012 COG2005 COG050	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit	SOKKNSPGSEGSQMCR	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism General function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism
COG0183 COG5454 COG5101 COG2370 COG0583 COG1522 COG0807 COG697 COG2841 COG0697 COG3697	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase	S O K K N S P G S E G G M C R E	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG4773 COG0697 COG2065 COG0697 COG3791 COG4065 COG1247 COG1012 COG2005 COG1012 COG2005 COG146 COG0684 COG0146	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylhmenaquinone methyltransferase Transcriptional regulator	SOKKNSPGSEGSQMCREHK	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG040 COG1376 COG697 COG0697 COG0697 COG1247 COG1024	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation	SOKKNSPGSSEGMCREH	Lipid transport and metabolism Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones
COG0183 COG5454 COG5510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG2841 COG0697 COG26663 COG1012 COG0690 COG01012 COG06065 COG01012 COG06065 COG0146 COG0684 COG0684 COG0684 COG0715	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylhmenaquinone methyltransferase Transcriptional regulator	SOKKNSPGSEGSQMCREHKO	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription
COG0183 COG2454 COG2510 COG2370 COG0583 COG1522 COG0697 COG2841 COG0697 COG2841 COG0697 COG3761 COG0697 COG3761 COG0697 COG3761 COG0697 COG0761 COG0697	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-t-erminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulators	SOKKNSPGSEGSQMCREHKOP	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG04773 COG0697 COG267 COG267 COG267 COG267 COG205 COG0697 COG3791 COG4065 COG0697 COG3791 COG4065 COG0124 COG1012 COG2005 COG0146 COG0684 COG0583 COG1764 COG0715 COG1396 COG0765	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	SOKKNSPGSEGSQMCREHKOPK	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG2841 COG0657 COG2841 COG0657 COG2841 COG0657 COG697 COG697 COG697 COG697 COG7067 COG7065 COG7065 COG7065	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulators ABC-type amino acid transport system, permease component	SOKKNSPGSEGSQMCREHKOPKE	Lipid transport and metabolism Function unknown Function unknown Fosttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Amino acid transport and metabolism
COG0183 COG5454 COG5210 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG2841 COG0697 COG26663 COG102 COG06664 COG06664 COG06664 COG06664 COG066667 COG0715 COG1366 COG0765 COG0765 COG0765 COG0765	Acetyl-CoA acetyltransferase Predicted gecreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulators ABC-type amino acid transport system, permease component	SOKKNSPGSEGSQMCREHKOPKEE	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG0183 COG5454 COG5210 COG2370 COG0583 COG1522 COG0804 COG1376 COG697 COG2841 COG0657 COG2841 COG0657 COG0697 COG1012 COG0654	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases NAD-dependent aldehyde dehydrogenases NAD-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulators ABC-type amino acid transport system, permease component ABC-type amino acid transport system, permease component ABC-type polar amino acid transport system, ATPase component	SOKKNSPGSEGSQMCREHKOPKEEEE	Lipid transport and metabolism Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG0183 COG5454 COG2510 COG2370 COG0583 COG1522 COG0840 COG1376 COG4773 COG0697 COG3791 COG4065 COG0065 COG0065 COG0065 COG0065 COG0124 COG1012 COG2005 COG0146 COG00684 COG0684 COG0765 COG0765 COG0765 COG0765 COG0765 COG0765	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-t-erminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type amino acid transport system, permease component ABC-type amino acid transport system, permease component ABC-type amino acid transport system, ATPase component 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	SOKKNSPGSEGSQMCREHKOPKEEEH	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Amino acid transport and metabolism Coenzyme transport and metabolism
COG0183 COG5454 COG5216 COG62370 COG62370 COG6937 COG62841 COG6065 COG60697 COG62841 COG60697 COG62841 COG60697	Acetyl-CoA acetyltransferase Predicted gereted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases NAD-dependent aldehyde dehydrogenases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulators ABC-type amino acid transport system, permease component ABC-type amino acid transport system, ATPase component 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases Arabinose efflux permease Transcriptional regulator ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	SOKKNSPGSEGSQMCREHKOPKEEEHGKE	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Coenzyme transport and metabolism Transcription Amino acid transport and metabolism Transcription Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Coenzyme transport and metabolism Carbohydrate transport and metabolism Transcription Amino acid transport and metabolism
COG0183 COG5454 COG5454 COG5450 COG62370 COG0583 COG1522 COG0697 COG0765 COG0654 COG06	Acetyl-CoA acetyltransferase Predicted secreted protein Predicted membrane protein Hydrogenase/urease accessory protein Transcriptional regulator Methyl-accepting chemotaxis protein Uncharacterized protein conserved in bacteria Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized protein conserved in bacteria 3-isopropylmalate dehydratase large subunit Permeases of the drug/metabolite transporter (DMT) superfamily Uncharacterized conserved protein TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component Sortase and related acyltransferases N-terminal domain of molybdenum-binding protein N-methylhydantoinase B/acetone carboxylase, alpha subunit Demethylmenaquinone methyltransferase Transcriptional regulator Predicted redox protein, regulator of disulfide bond formation ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components Predicted transcriptional regulator ABC-type amino acid transport system, permease component ABC-type amino acid transport system, permease component ABC-type polar amino acid transport system, permease component 2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases Arabinose efflux permease Transcriptional regulator ABC-type polar amino acid transport system, permease component ABC-type polar permease Transcriptional regulator ABC-type polar permease Transcriptional regulator system, permease component	SOKKNSPGSEGSQMCREHKOPKEEEHGKEE	Lipid transport and metabolism Function unknown Function unknown Posttranslational modification, protein turnover, chaperones Transcription Transcription Cell motility Function unknown Inorganic ion transport and metabolism Carbohydrate transport and metabolism Function unknown Amino acid transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Function unknown Secondary metabolites biosynthesis, transport and catabolism Cell wall/membrane/envelope biogenesis Energy production and conversion General function prediction only Amino acid transport and metabolism Conzyme transport and metabolism Transcription Posttranslational modification, protein turnover, chaperones Inorganic ion transport and metabolism Transcription Amino acid transport and metabolism Amino acid transport and metabolism Coenzyme transport and metabolism Coenzyme transport and metabolism Coenzyme transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Transcription Amino acid transport and metabolism Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism
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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	Т	Signal transduction mechanisms
	Transcriptional regulator	К	Transcription
	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
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Dihydroorotase and related cyclic amidohydrolases	F	Nucleotide transport and metabolism
	Coenzyme F420-reducing hydrogenase, beta subunit	С	Energy production and conversion
	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain	Т	Signal transduction mechanisms
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	M	Cell wall/membrane/envelope biogenesis
	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	Gamma-aminobutyrate permease and related permeases	E	Amino acid transport and metabolism
	Universal stress protein UspA and related nucleotide-binding proteins	T	Signal transduction mechanisms
	Predicted transcriptional regulators	K	Transcription
	Putative translation initiation inhibitor, yigF family	J E	Translation, ribosomal structure and biogenesis
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Glycine/D-amino acid oxidases (deaminating) Transcriptional regulators	K	Amino acid transport and metabolism Transcription
	Transcriptional regulators ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	P	·
	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Inorganic ion transport and metabolism Coenzyme transport and metabolism
	Predicted acyltransferase	R	General function prediction only
	Predicted hydrolase (HAD superfamily)	R	General function prediction only
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	Deacetylases, including yeast histone deacetylase and acetoin utilization protein	В	Chromatin structure and dynamics
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport and metabolism
	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components ABC-type nitrate/sulfonate/bicarbonate transport systems, ATPase component	P	Inorganic ion transport and metabolism
	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)		Lipid transport and metabolism
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	Enoyl-CoA hydratase/carnithine racemase	I I	Lipid transport and metabolism
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	Heme/copper-type cytochrome/quinol oxidase, subunit 4	C	Energy production and conversion
	Transcriptional regulators	K	Transcription
	ABC-type branched-chain amino acid transport systems, ATPase component	E E	Amino acid transport and metabolism
	Amidases related to nicotinamidase	Q	Secondary metabolites biosynthesis, transport and catabolism
	Amidases related to nicotinamidase	Q.	Secondary metabolites biosynthesis, transport and catabolism
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Transposase and inactivated derivatives	 L	Replication, recombination and repair
	Glutathione S-transferase	0	Posttranslational modification, protein turnover, chaperones
	Mu-like prophage I protein	R	General function prediction only
	Mu-like prophage major head subunit gpT	R	General function prediction only
	Phage-related baseplate assembly protein	R	General function prediction only
	Phage tail sheath protein FI	R	General function prediction only
	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
	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	1	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	0	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
	Glycerophosphoryl diester phosphodiesterase	С	Energy production and conversion
	D-alanyl-D-alanine carboxypeptidase	M	Cell wall/membrane/envelope biogenesis
COG0563	Adenylate kinase and related kinases	F	Nucleotide transport and metabolism
	Predicted membrane protein	S	Function unknown
COG0260	Leucyl aminopeptidase	E	Amino acid transport and metabolism
	N-methylhydantoinase A/acetone carboxylase, beta subunit	E	Amino acid transport and metabolism
	Phosphoglycerate dehydrogenase and related dehydrogenases	Н	Coenzyme transport and metabolism
		S	Function unknown
	Uncharacterized membrane-associated protein		
	Uncharacterized protein conserved in bacteria	S	Function unknown
COG2148	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis	M	Cell wall/membrane/envelope biogenesis
COG2148 COG1123	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase	M R	Cell wall/membrane/envelope biogenesis General function prediction only
COG2148 COG1123 COG1522	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators	M R K	Cell wall/membrane/envelope biogenesis General function prediction only Transcription
COG2148 COG1123 COG1522 COG5573	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain	M R K R	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only
COG2148 COG1123 COG1522 COG5573 COG5345	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria	M R K R	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase	M R K R S R	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria	M R K R S R	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain	M R K R S R S K	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II	M R K R S R S K	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177 COG0580	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	M R K S R S K E G	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3795 COG4941 COG1177 COG0580 COG1176	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I	M R K S R S K E G	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177 COG0580 COG1176 COG2355	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I Zn-dependent dipeptidase, microsomal dipeptidase homolog	M R R S R S K E G E	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177 COG0580 COG1176 COG2355 COG1335	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I Zn-dependent dipeptidase, microsomal dipeptidase homolog Amidases related to nicotinamidase	M R K S R S K E G E Q	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3395 COG4941 COG1177 COG0580 COG4176 COG2355 COG1335 COG0600	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I Zn-dependent dipeptidase, microsomal dipeptidase homolog Amidases related to nicotinamidase ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	M R K S R S K E G E Q P	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Inorganic ion transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177 COG0580 COG1176 COG2355 COG1335 COG0600 COG0687	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I Zn-dependent dipeptidase, microsomal dipeptidase homolog Amidases related to nicotinamidase ABC-type nitrate/sulfonate/bicarbonate transport system, permease component Spermidine/putrescine-binding periplasmic protein	M R K S R S K E G E Q P E	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Inorganic ion transport and metabolism Amino acid transport and metabolism
COG2148 COG1123 COG1522 COG5573 COG5345 COG3324 COG3795 COG4941 COG1177 COG0580 COG1176 COG2355 COG0600 COG0687	Uncharacterized protein conserved in bacteria Sugar transferases involved in lipopolysaccharide synthesis ATPase components of various ABC-type transport systems, contain duplicated ATPase Transcriptional regulators Predicted nucleic-acid-binding protein, contains PIN domain Uncharacterized protein conserved in bacteria Predicted enzyme related to lactoylglutathione lyase Uncharacterized protein conserved in bacteria Predicted RNA polymerase sigma factor containing a TPR repeat domain ABC-type spermidine/putrescine transport system, permease component II Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family) ABC-type spermidine/putrescine transport system, permease component I Zn-dependent dipeptidase, microsomal dipeptidase homolog Amidases related to nicotinamidase ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	M R K S R S K E G E Q P	Cell wall/membrane/envelope biogenesis General function prediction only Transcription General function prediction only Function unknown General function prediction only Function unknown Transcription Amino acid transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Inorganic ion transport and metabolism

	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	L E	Replication, recombination and repair
	Spermidine synthase Transcriptional regulators	K	Amino acid transport and metabolism Transcription
	Transcriptional regulator	K	Transcription
COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	G	Carbohydrate transport and metabolism
	Prephenate dehydratase	E	Amino acid transport and metabolism
	TRAP-type C4-dicarboxylate transport system, large permease component TRAP-type mannitol/chloroaromatic compound transport system, small permease component	G Q	Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
	CMP-2-keto-3-deoxyoctulosonic acid synthetase	M	Cell wall/membrane/envelope biogenesis
	Methylase involved in ubiquinone/menaquinone biosynthesis	н	Coenzyme transport and metabolism
COG0262	Dihydrofolate reductase	Н	Coenzyme transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	Transcriptional regulators	K -	Transcription
	Signal transduction histidine kinase Uncharacterized protein affecting Mg2+/Co2+ transport	T P	Signal transduction mechanisms Inorganic ion transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
COG1012	NAD-dependent aldehyde dehydrogenases	С	Energy production and conversion
	Trans-aconitate methyltransferase	R	General function prediction only
	ABC-type dipeptide transport system, periplasmic component Transcriptional regulator.	E K	Amino acid transport and metabolism
	Transcriptional regulator Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreducta	C	Transcription Energy production and conversion
	Na+/H+-dicarboxylate symporters	c	Energy production and conversion
	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport and metabolism
	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	E	Amino acid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
	Amidases related to nicotinamidase Predicted hydrolase (HAD superfamily)	Q R	General function prediction only
	Putative homoserine kinase type II (protein kinase fold)	R	General function prediction only
	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R	General function prediction only
	Choline dehydrogenase and related flavoproteins	E	Amino acid transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
	N-methylhydantoinase A/acetone carboxylase, beta subunit High-affinity Fe2+/Pb2+ permease	E P	Amino acid transport and metabolism Inorganic ion transport and metabolism
	Sugar phosphate permease	G	Carbohydrate transport and metabolism
	Uncharacterized conserved protein	S	Function unknown
COG3408	Glycogen debranching enzyme	G	Carbohydrate transport and metabolism
COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	С	Energy production and conversion
	Uncharacterized conserved protein	S	Function unknown
	Putative intracellular protease/amidase Uncharacterized conserved protein	R S	General function prediction only Function unknown
	Uncharacterized protein conserved in bacteria	S	Function unknown
	Uncharacterized conserved protein	S	Function unknown
COG1228	Imidazolonepropionase and related amidohydrolases	Q	Secondary metabolites biosynthesis, transport and catabolism
	Uncharacterized conserved protein	S	Function unknown
	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport and metabolism
	Predicted permeases Uncharacterized conserved protein	R S	General function prediction only Function unknown
	Enoyl-CoA hydratase/carnithine racemase	ı	Lipid transport and metabolism
	Predicted ring-cleavage extradiol dioxygenase	R	General function prediction only
COG3246	Uncharacterized conserved protein	S	Function unknown
	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	Н	Coenzyme transport and metabolism
	Transcriptional regulator	K	Transcription
	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit) Uncharacterized conserved protein	C S	Energy production and conversion Function unknown
	NAD-dependent aldehyde dehydrogenases	c	Energy production and conversion
	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
	Periplasmic protease	М	Cell wall/membrane/envelope biogenesis
	Limonene-1,2-epoxide hydrolase Predicted integral membrane protein	Q S	Secondary metabolites biosynthesis, transport and catabolism Function unknown
	Cytochrome c biogenesis protein	0	Posttranslational modification, protein turnover, chaperones
	Na+-driven multidrug efflux pump	V	Defense mechanisms
COG1576	Uncharacterized conserved protein	S	Function unknown
	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	H	Coenzyme transport and metabolism
	Alkaline phosphatase Uncharacterized homolog of plant lojap protein	P S	Inorganic ion transport and metabolism
	ABC-type antimicrobial peptide transport system, ATPase component	. V	Function unknown Defense mechanisms
	ABC-type transport system, involved in lipoprotein release, permease component	M	Cell wall/membrane/envelope biogenesis
	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	E	Amino acid transport and metabolism
	Nicotinic acid mononucleotide adenylyltransferase	Н	Coenzyme transport and metabolism
	Transcriptional regulator	K	Transcription
	Imidazolonepropionase and related amidohydrolases	Q	Secondary metabolites biosynthesis, transport and catabolism
	ABC-type branched-chain amino acid transport systems, periplasmic component ABC-type branched-chain amino acid transport system, permease component	E E	Amino acid transport and metabolism Amino acid transport and metabolism
	Gamma-glutamyl phosphate reductase	E	Amino acid transport and metabolism
COG1573	Uracil-DNA glycosylase	L	Replication, recombination and repair
	Leucyl aminopeptidase	E	Amino acid transport and metabolism
	Predicted DNA-binding protein with the Helix-hairpin-helix motif	R	General function prediction only
	Nucleoside-diphosphate-sugar epimerases Cytochrome c, mono- and diheme variants	M C	Cell wall/membrane/envelope biogenesis Energy production and conversion
	Transcriptional regulator	К	Transcription
	Arginine/lysine/ornithine decarboxylases	E	Amino acid transport and metabolism
COG0524	Sugar kinases, ribokinase family	G	Carbohydrate transport and metabolism
	Predicted permeases	R	General function prediction only
	Homoserine acetyltransferase Predicted phosphatase/phosphohayamutase	E R	Amino acid transport and metabolism
	Predicted phosphatase/phosphohexomutase Transcriptional regulator	K K	General function prediction only Transcription
	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	Н	Coenzyme transport and metabolism
			

COG0747	ABC-type dipeptide transport system, periplasmic component	E	Amino acid transport and metabolism
	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	E	Amino acid transport and metabolism
	Glutamate 5-kinase	E	Amino acid transport and metabolism
	Uncharacterized anaerobic dehydrogenase	R	General function prediction only
	Mg2+ and Co2+ transporters	P	Inorganic ion transport and metabolism
	Uncharacterized protein conserved in bacteria	S	Function unknown
	·	D D	
	K+ transport systems, NAD-binding component	P	Inorganic ion transport and metabolism
	Esterase/lipase	I	Lipid transport and metabolism
	4-diphosphocytidyl-2-methyl-D-erithritol synthase	1	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	С	Energy production and conversion
	Predicted PP-loop superfamily ATPase	R	General function prediction only
	Organic radical activating enzymes	0	Posttranslational modification, protein turnover, chaperones
	Nitroreductase	c	Energy production and conversion
	Fe-S oxidoreductase	c	Energy production and conversion
	Transcriptional regulators	ĸ	Transcription
		K.	•
	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		Lipid transport and metabolism
	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure and biogenesis
	6-pyruvoyl-tetrahydropterin synthase	H	Coenzyme transport and metabolism
	Predicted thioesterase	R	General function prediction only
	Acyl-CoA dehydrogenases	1	Lipid transport and metabolism
	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	С	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	1	Lipid transport and metabolism
	UDP-N-acetylglucosamine 2-epimerase	M	Cell wall/membrane/envelope biogenesis
	Flagellar basal body-associated protein	N	Cell motility
	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	T	Signal transduction mechanisms
	Flagellin-specific chaperone FliS	N N	Cell motility
			· · · · · · · · · · · · · · · · · · ·
	Flagellar basal body protein	N	Cell motility
	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	н	Coenzyme transport and metabolism
	Uncharacterized protein involved in cation transport	P	Inorganic ion transport and metabolism
	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	M	Cell wall/membrane/envelope biogenesis
	Plasmid maintenance system antidote protein	R	General function prediction only
	Guanosine polyphosphate pyrophosphohydrolases/synthetases	T.	Signal transduction mechanisms
	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms
	Transcriptional regulator	K	Transcription
	Threonine dehydrogenase and related Zn-dependent dehydrogenases	E	Amino acid transport and metabolism
	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	E	Amino acid transport and metabolism
	Transcriptional regulator	K	Transcription
COG2197	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Т	Signal transduction mechanisms
COG3193	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	R	General function prediction only
COCOCCE	Glycine/D-amino acid oxidases (deaminating)		Amino acid transport and metabolism
COG0665		E	
	TRAP-type C4-dicarboxylate transport system, periplasmic component	E G	Carbohydrate transport and metabolism
COG1638			Carbohydrate transport and metabolism
COG1638 COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G G	Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1638 COG3090 COG1593	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component	G G G	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1638 COG3090 COG1593 COG1305	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases	G G G E	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein	G G E S	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components	G G E S V	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain	G G E S V S	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase	G G E S V S G	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis	G G E S V S G Q	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	G G G E S V S G Q I	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3715 COG1028 COG3618	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold	G G E S V S G Q I R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG3961	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes	G G G E S V S G Q I	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG37155 COG1028 COG3618 COG3961 COG2084	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	G G E S V S G Q I R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG1305 COG1917 COG3717 COG3155 COG1028 COG3618 COG36618 COG2084 COG0625	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase	G G E S V S G Q I R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Secondary metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG1305 COG1917 COG3717 COG3155 COG1028 COG3618 COG36618 COG2084 COG0625	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	G G E S V S G Q I R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG1305 COG1917 COG3117 COG3155 COG1028 COG3618 COG36616 COG2084 COG0625 COG0008	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase	G G E S V S G Q I R G I O	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Secondary metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG3961 COG2084 COG0625 COG0008	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases	G G E S V S G Q I R G G J	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Sepondary and metabolism Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Translation, ribosomal structure and biogenesis
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG3961 COG2084 COG0625 COG0008	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain S-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	G G G E S V S G Q I R G I O R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Upid transport and metabolism Control or prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only
COG1638 COG3090 COG1593 COG1305 COG1305 COG1917 COG3717 COG3155 COG1028 COG3618 COG3618 COG2084 COG0625 COG0008 COG1721 COG0662 COG0662	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases	G G E S V S G Q I R G I O J R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG11302 COG1917 COG3155 COG1028 COG3618 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG16835 COG2146	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione 5-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Feredicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases	G G G E S V S G Q I R G I P	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG3084 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG1835 COG2146 COG5554	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-decovyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pryruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione 5-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein	G G S V S G Q I R G I O J R G I	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG1835 COG2146 COG5554 COG1143	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	G G G E S V S G Q I R G I O J R G I O J R G Q I O D R G O D R G O D R G O D R D R D D R D D D D D D D D D D D D	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG2084 COG0625 COG0008 COG1721 COG662 COG1835 COG2146 COG25554 COG2144 COG65554	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Truncated hemoglobins	G G E S V S G Q I R G I P Q C R	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Posttranslation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Secondary metabolism Lipid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG11305 COG3717 COG3155 COG30618 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG1835 COG2146 COG5554 COG1143 COG2346 COG0119	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Truncated hemoglobins Isopropylmalate/homocitrate/citramalate synthases	G G E S V S G Q I R G I O J R G C R E	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion General function prediction only Amino acid transport and metabolism
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3061 COG2084 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG1835 COG2146 COG5554 COG1143 COG2346 COG2346 COG2346 COG05554 COG1149 COG0565	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Predicted acyltransferases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Truncated hemoglobins Isopropylmalate/homocitrate/citramalate synthases RNA methylase	G G E S V S G Q I R G I O J R G C R E J	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Secondary metabolism and metabolism Lipid transport and metabolism Lipid transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion General function prediction only Amino acid transport and metabolism Translation, ribosomal structure and biogenesis
COG1638 COG3090 COG1593 COG1305 COG2308 COG1132 COG1917 COG3717 COG3155 COG1028 COG3618 COG3961 COG2084 COG0625 COG0008 COG1721 COG0662 COG1835 COG1143 COG2346 COG2346 COG0119 COG0565 COG3279	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Truncated hemoglobins Isopropylmalate/homocitrate/citramalate synthases RRNA methylase Response regulator of the LytR/AlgR family	G G E S V S G Q I R G I O J R G C R E I V S I V S I V S I V S I V S I V S I V S I V S I V S I V S I V S I V S I S I	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Inorganic ion transport and metabolism Inorganic ion transport and metabolism Energy production and conversion General function prediction only Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Transcription
COG1638 COG3090 COG1593 COG1305 COG2308 COG11302 COG1917 COG3155 COG31618 COG3961 COG2084 COG0625 COG0008 COG1721 COG6625 COG10835 COG2146 COG5554 COG1143 COG2346 COG0119 COG05657 COG05572	TRAP-type C4-dicarboxylate transport system, small permease component TRAP-type C4-dicarboxylate transport system, large permease component Transglutaminase-like enzymes, putative cysteine proteases Uncharacterized conserved protein ABC-type multidrug transport system, ATPase and permease components Uncharacterized conserved protein, contains double-stranded beta-helix domain 5-keto 4-deoxyuronate isomerase Uncharacterized protein involved in an early stage of isoprenoid biosynthesis Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) Predicted metal-dependent hydrolase of the TIM-barrel fold Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes 3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases Glutathione S-transferase Glutamyl- and glutaminyl-tRNA synthetases Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) Mannose-6-phosphate isomerase Predicted acyltransferases Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases Nitrogen fixation protein Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) Truncated hemoglobins Isopropylmalate/homocitrate/citramalate synthases RRNA methylase Response regulator of the LytR/AlgR family Predicted integral membrane protein	G G E S V S G Q I R G I P Q C R E J K S S S S S S S S S S S S S S S S S S	Carbohydrate transport and metabolism Carbohydrate transport and metabolism Carbohydrate transport and metabolism Amino acid transport and metabolism Function unknown Defense mechanisms Function unknown Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Lipid transport and metabolism General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Posttranslational modification, protein turnover, chaperones Translation, ribosomal structure and biogenesis General function prediction only Carbohydrate transport and metabolism Lipid transport and metabolism Lipid transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Energy production and conversion General function prediction only Amino acid transport and metabolism Translation, ribosomal structure and biogenesis Transcription Function unknown
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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	Н	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