



Table S1. Whole genome annotation of bacteria strain C33 with features of interest.

c	Subcategory	Subsystem	Role	
Cofactors, Vitamins, Prosthetic Groups, Pigments	Biotin	Biotin biosynthesis	Dethiobiotin synthetase (EC 6.3.3.3)	
			Biotin synthase (EC 2.8.1.6)	
			Biotin operon repressor	
			Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62)	
			8-amino-7-oxononanoate synthase (EC 2.3.1.47)	
		Biotin biosynthesis Experimental	Dethiobiotin synthetase (EC 6.3.3.3)	
			Biotin synthase (EC 2.8.1.6)	
			Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62)	
			8-amino-7-oxononanoate synthase (EC 2.3.1.47)	
			Hydroxymethylpyrimidine ABC transporter, substrate-binding component	
	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	Thiamin biosynthesis	Thiamin pyrophosphokinase (EC 2.7.6.2)	
			Thiamine-monophosphate kinase (EC 2.7.4.16)	
			1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	
			Thiamin ABC transporter, substrate-binding component	
			Hydroxymethylpyrimidine ABC transporter, transmembrane component	
			Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	
		Tetrapyrroles	Cobalamin synthesis	Hydroxyethylthiazole kinase (EC 2.7.1.50)
				L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)
				Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)
				Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130)
	Cobyric acid synthase (EC 6.3.5.10)			
	Cobalamin biosynthesis protein CbiG			
	Sirohydrochlorin cobaltochelataase CbiK (EC 4.99.1.3)			
	Adenosylcobinamide kinase (EC 2.7.1.156)			
	Cobalt-precorrin-6x reductase (EC 1.3.1.54)			
	Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)			
	Cobalt-precorrin-3b C17-methyltransferase			
	Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)			
	Adenosylcobinamide-phosphate synthase (EC 6.3.1.10)			
	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyl-transferase (EC 2.4.2.21)			
	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)			
	Heme and Siroheme Biosynthesis		Cobalt-precorrin-6 synthase, anaerobic	
			Cobalamin synthase (EC 2.7.8.26)	
			Cobyric acid A,C-diamide synthase	
			Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III oxidase, oxygen-independent	
			Hypothetical radical SAM family enzyme in heat shock gene cluster, similarity with CPO of BS HemN-type	
Glutamyl-tRNA synthetase (EC 6.1.1.17)				
Riboflavin, FMN, FAD		Uroporphyrinogen-III synthase (EC 4.2.1.75)		
		Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)		
		Precorrin-2 oxidase (EC 1.3.1.76)		
		Porphobilinogen synthase (EC 4.2.1.24)		
		Glutamyl-tRNA reductase (EC 1.2.1.70)		
		Porphobilinogen deaminase (EC 2.5.1.61)		
		Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)		
		Sirohydrochlorin ferrochelataase (EC 4.99.1.4)		
		FMN adenylyltransferase (EC 2.7.7.2)		
		FIG000859: hypothetical protein YebC		

Riboflavin, FMN and FAD metabolism in plants		Molybdopterin binding motif, CinA N-terminal domain
		Multi antimicrobial extrusion protein (Na ⁺)/drug antiporter), MATE family of MDR efflux pumps
		C-terminal domain of CinA type S
		6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)
		Adenosine deaminase (EC 3.5.4.4), alternative form
		5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
		tRNA pseudouridine synthase B (EC 4.2.1.70)
		Riboflavin kinase (EC 2.7.1.26)
		GTP cyclohydrolase II (EC 3.5.4.25)
		tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)
		Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)
		Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26)
		3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)
		FMN adenylyltransferase (EC 2.7.7.2)
riboflavin to FAD		Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)
		Riboflavin kinase (EC 2.7.1.26)
		3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)
		Flavodoxin
Flavodoxin		NAD(P)H oxidoreductase YRKL (EC 1.6.99.-)
		Flavodoxin 1
		Flavodoxin 2
Riboflavin, FMN and FAD metabolism		FMN adenylyltransferase (EC 2.7.7.2)
		6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)
		Adenosine deaminase (EC 3.5.4.4), alternative form
		5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
		Riboflavin kinase (EC 2.7.1.26)
		GTP cyclohydrolase II (EC 3.5.4.25)
		Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)
		Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26)
		3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)
		Nicotinate phosphoribosyltransferase (EC 2.4.2.11)
NAD and NADP	NAD and NADP cofactor biosynthesis global	NAD kinase (EC 2.7.1.23)
		Glutamine amidotransferase chain of NAD synthetase
		C-terminal domain of CinA type S
		Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)
		Nicotinamidase (EC 3.5.1.19)
Folate and pterines	Folate biosynthesis cluster	NAD synthetase (EC 6.3.1.5)
		GTP cyclohydrolase I (EC 3.5.4.16) type 1
		Cell division protein FtsH (EC 3.4.24.-)
		Dihydropteroate synthase (EC 2.5.1.15)
		Dihydropteridine aldolase (EC 4.1.2.25)
		2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3)
		tRNA(Ile)-lysine synthetase (EC 6.3.4.19)
		Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)
Coenzyme A	Coenzyme A Biosynthesis	Pantothenate:Na ⁺ symporter (TC 2.A.21.1.1)
		Phosphopantetheine adenylyltransferase (EC 2.7.7.3)
		Ketol-acid reductoisomerase (EC 1.1.1.86)
		Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)
		Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)
		Dephospho-CoA kinase (EC 2.7.1.24)
		Pantothenate kinase type III, CoaX-like (EC 2.7.1.33)

Cell Wall and Capsule	Capsular and extra-cellular polysaccharides	dTDP-rhamnose synthesis	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)
			Glucose-1-phosphate cytidyltransferase (EC 2.7.7.33)
			dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
			dTDP-rhamnosyl transferase RfbF (EC 2.-.-.-)
			dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)
		Capsular heptose biosynthesis	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
			Phosphoheptose isomerase (EC 5.3.1.-)
			GDP-mannose 4,6-dehydratase (EC 4.2.1.47)
			GDP-L-fucose synthetase (EC 1.1.1.271)
			dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)
		Polysaccharide deacetylases	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.-)
			Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.-)
		Rhamnose containing glycans	Polysaccharide deacetylase
			UDP-glucose 4-epimerase (EC 5.1.3.2)
			dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)
			capsular polysaccharide biosynthesis protein
			dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
	Sialic Acid Metabolism		dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)
			Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
			N-acetylneuraminate lyase (EC 4.1.3.3)
			Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)
			Predicted sialic acid transporter
			TRAP-type transport system, large permease component, predicted N-acetylneuraminate transporter
			TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter
			N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)
			Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)
			Glucosamine-6-phosphate deaminase (EC 3.5.99.6)
			Sialic acid-induced transmembrane protein YjhT(NanM), possible mutarotase
			PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.69)
			PTS system, N-acetylmuramic acid-specific IIB component (EC 2.7.1.69)
			N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)
			N-acetylmannosamine kinase (EC 2.7.1.60)
			Phosphoglucosamine mutase (EC 5.4.2.10)
			N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)
			TRAP-type transport system, periplasmic component, predicted N-acetylneuraminate-binding protein
Gram-Negative cell wall components	LOS core oligosaccharide biosynthesis		Sialic acid utilization regulator, RpiR family
			Putative two-domain glycosyltransferase
			Phosphoheptose isomerase (EC 5.3.1.-)
			Beta-1,3-glucosyltransferase
			ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20)
			D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.-)
			Lipopolysaccharide core biosynthesis protein RfaY
			ADP-heptose synthase (EC 2.7.-.-)
			ADP-heptose--lipooligosaccharide heptosyltransferase II (EC 2.4.1.-)
			D-glycero-beta-D-manno-heptose 7-phosphate kinase
		Lipoprotein sorting system	Lipoprotein releasing system transmembrane protein LolC
			Lipoprotein releasing system ATP-binding protein LolD
		Murein Hydrolases	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)

Cell Wall and Capsule - no subcategory	Peptidoglycan Biosynthesis	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
		Soluble lytic murein transglycosylase precursor (EC 3.2.1.-)
		Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)
		Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)
		UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)
		D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
		Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
		UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)
		Glutamine synthetase type III, GlnN (EC 6.3.1.2)
		UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
		UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)
		UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)
		Rod shape-determining protein RodA
		UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)
		Glutamate racemase (EC 5.1.1.3)
		UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
		D-alanine--D-alanine ligase (EC 6.3.2.4)
		Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)
		N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)
		Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
	UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)
	UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis	Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)
		Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)
		UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
	YjeE	Phosphoglucosamine mutase (EC 5.4.2.10)
		N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23)
		TsaB protein, required for threonylcarbamoyladenosine t(6)A formation in tRNA
	Recycling of Peptidoglycan Amino Acids	NAD(P)HX epimerase
		TsaE protein, required for threonylcarbamoyladenosine t(6)A37 formation in tRNA
		NAD(P)HX dehydratase
	Peptidoglycan biosynthesis--gjo	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
		Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)
		UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
		UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)
		UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)
	Virulence, Disease and Defense	D-alanine--D-alanine ligase (EC 6.3.2.4)
		UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)
Virulence, Disease and Defense	Adhesion	Streptococcus pyogenes recombinatorial zone
	Resistance to antibiotics and toxic compounds	Chaperonin (heat shock protein 33)
		Copper homeostasis
		Copper-translocating P-type ATPase (EC 3.6.3.4)
		Cobalt-zinc-cadmium resistance protein
		Probable Co/Zn/Cd efflux system membrane fusion protein
		Transcriptional regulator, MerR family
Virulence, Disease and Defense	Resistance to fluoroquinolones	DNA gyrase subunit B (EC 5.99.1.3)
		DNA gyrase subunit A (EC 5.99.1.3)

			Arsenic resistance	Arsenical-resistance protein ACR3
				Arsenate reductase (EC 1.20.4.1)
			Beta-lactamase	Beta-lactamase (EC 3.5.2.6)
			Zinc resistance	Response regulator of zinc sigma-54-dependent two-component system
			Multidrug Resistance Efflux Pumps	Multi antimicrobial extrusion protein (Na ⁽⁺⁾ /drug antiporter), MATE family of MDR efflux pumps
				Acridine resistance protein
			Invasion and intracellular resistance	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)
				SSU ribosomal protein S7p (S5e)
				Translation elongation factor G
				Translation elongation factor Tu
				SSU ribosomal protein S12p (S23e)
				Mycobacterium virulence operon involved in an unknown function with a Jag Protein and YidC and YidD
				RNA-binding protein Jag
				Protein YidD
				Inner membrane protein translocase component YidC, short form OxaI-like
				Mycobacterium virulence operon involved in DNA transcription
				DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)
				DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)
				Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)
				LSU ribosomal protein L35p
				Translation initiation factor 3
				LSU ribosomal protein L20p
Potassium metabolism	Potassium metabolism - no subcategory	Potassium homeostasis		FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)
				Trk system potassium uptake protein TrkA
				Large-conductance mechanosensitive channel
				Kup system potassium uptake protein
Miscellaneous	Plant-Prokaryote DOE project	Conserved gene cluster possibly involved in RNA metabolism		CysteinyI-tRNA synthetase (EC 6.1.1.16)
				RNA polymerase sporulation specific sigma factor SigH
				Serine acetyltransferase (EC 2.3.1.30)
				COG1939: Ribonuclease III family protein
	Phosphoglycerate mutase protein family			Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)
				Carboxyl-terminal protease (EC 3.4.21.102)
				2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)
	Miscellaneous - no subcategory	Muconate lactonizing enzyme family		L(+)-tartrate dehydratase beta subunit (EC 4.2.1.32)
				L(+)-tartrate dehydratase alpha subunit (EC 4.2.1.32)
		Broadly distributed proteins not in subsystems		YbbM seven transmembrane helix protein
				UPF0225 protein YchJ
				UPF0265 protein YeeX
Phages, Prophages, Transposable elements, Plasmids	Phages, Prophages	Phage DNA synthesis		Glutaredoxin
	Plasmid related functions	Rolling-circle replication		Replication initiation protein, topoisomerase
Membrane Transport	ABC transporters	ABC transporter alkylphosphonate (TC 3.A.1.9.1)		Phosphonate ABC transporter ATP-binding protein (TC 3.A.1.9.1)
				Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)
		ABC transporter oligopeptide (TC 3.A.1.5.1)		Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1)
				Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1)
				Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1)
				Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
		ABC transporter dipeptide (TC 3.A.1.5.2)		Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)
				Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)

			Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)	
			Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)	
			Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	
Protein translocation across cytoplasmic membrane	Bacterial signal recognition particle (SRP)		Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	
			Signal recognition particle associated protein	
			Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	
Cation transporters	Magnesium transport		Magnesium and cobalt transport protein CorA	
			Magnesium and cobalt efflux protein CorC	
	Copper Transport System		Mg/Co/Ni transporter MgtE	
			Mg(2+) transport ATPase, P-type (EC 3.6.3.2)	
Uni- Sym- and Antiporters	NhaA, NhaD and Sodium-dependent phosphate transporters		Copper-translocating P-type ATPase (EC 3.6.3.4)	
			Repressor CsoR of the copZA operon	
			Na+/H+ antiporter NhaD type	
	Choline Transport		Sodium-Choline Symporter	
Membrane Transport - no subcategory	ECF class transporters		Duplicated ATPase component MtsB of energizing module of methionine-regulated ECF transporter	
			Transmembrane component MtsC of energizing module of methionine-regulated ECF transporter	
			Substrate-specific component STY3230 of queuosine-regulated ECF transporter	
			Substrate-specific component MtsA of methionine-regulated ECF transporter	
	Ton and Tol transport systems		Ferric siderophore transport system, periplasmic binding protein TonB	
			Outer membrane lipoprotein omp16 precursor	
			MotA/TolQ/ExbB proton channel family protein	
			TPR repeat containing exported protein	
			Haemin uptake system outer membrane receptor	
			Biopolymer transport protein ExbD/TolR	
TRAP transporters	TRAP Transporter collection		TRAP-type C4-dicarboxylate transport system, large permease component	
			TRAP-type C4-dicarboxylate transport system, periplasmic component	
Iron acquisition and metabolism	Iron acquisition and metabolism - no subcategory	Hemin transport system	Haemin uptake system permease protein	
			Ferric siderophore transport system, periplasmic binding protein TonB	
			Haemin uptake system outer membrane receptor	
RNA Metabolism	RNA processing and modification	RNA pseudouridine syntheses	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	
			Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	
			Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	
			Ribosomal large subunit pseudouridine synthase B (EC 4.2.1.70)	
			RNA pseudouridylylase BT0642	
			tRNA pseudouridine synthase B (EC 4.2.1.70)	
			tRNA pseudouridine synthase A (EC 4.2.1.70)	
		tRNA nucleotidyltransferase	tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)	
		Methylthiotransferases		tRNA-t(6)A37 methylthiotransferase
				tRNA-i(6)A37 methylthiotransferase
				Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase
				Ribonucleases in Bacillus
				Ribonuclease HII (EC 3.1.26.4)
			Ribonuclease J2 (endoribonuclease in RNA processing)	

RNA processing and degradation, bacterial	Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
	3'-to-5' exoribonuclease RNase R
	FIG146085: 3'-to-5' oligoribonuclease A, Bacillus type
RNA methylation	Ribonuclease III (EC 3.1.26.3)
	tRNA (guanosine(18)-2'-O)-methyltransferase (EC 2.1.1.34)
	tRNA (adenine37-N(6))-methyltransferase TrmN6 (EC 2.1.1.223)
	Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)
	Ribosomal RNA large subunit methyltransferase F (EC 2.1.1.51)
	LSU m5C1962 methyltransferase RlmI
	SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)
	23S rRNA (guanosine-2'-O-) -methyltransferase rlmB (EC 2.1.1.-)
	tRNA (guanine46-N7)-methyltransferase (EC 2.1.1.33)
	Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-)
	tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)
	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)
	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)
	LSU m3Psi1915 methyltransferase RlmH
ATP-dependent RNA helicases, bacterial	rRNA small subunit 7-methylguanosine (m7G) methyltransferase GidB
	tRNA-specific 2-thiouridylase MnmA
16S rRNA modification within P site of ribosome	ATP-dependent RNA helicase RhlE
	ATP-dependent RNA helicase BA2475
	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
mm5U34 biosynthesis bacteria	rRNA small subunit methyltransferase H
	rRNA small subunit methyltransferase I
	GTPase and tRNA-U34 5-formylation enzyme TrmE
	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA
	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)
	Cysteine desulfurase (EC 2.8.1.7)
Queuosine-Archaeosine Biosynthesis	preQ1-regulated inosine-uridine nucleoside hydrolase (EC 3.2.2.1)
	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
	Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
	Putative preQ0 transporter
	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-)
	Permease of the drug/metabolite transporter (DMT) superfamily
	GTP cyclohydrolase I (EC 3.5.4.16) type 1
	tRNA-guanine transglycosylase (EC 2.4.2.29)
Ribonuclease H	Substrate-specific component STY3230 of queuosine-regulated ECF transporter
	Ribonuclease HII (EC 3.1.26.4)
	Ribonuclease P protein component (EC 3.1.26.5)
tRNA processing	tRNA-i(6)A37 methylthiotransferase
	tRNA dimethylallyltransferase (EC 2.5.1.75)
	tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)
	Ribonuclease PH (EC 2.7.7.56)
	tRNA pseudouridine synthase B (EC 4.2.1.70)
Transcription	tRNA pseudouridine synthase A (EC 4.2.1.70)
	RNA polymerase sigma-54 factor RpoN
	RNA polymerase sigma factor RpoD
	RNA polymerase sporulation specific sigma factor SigH
	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)

Nucleosides and Nucleotides	RNA polymerase bacterial	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)
		DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)
	Transcription factors bacterial	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)
		Transcription termination protein NusB
		Transcription accessory protein (S1 RNA-binding domain)
		Transcription termination factor Rho
		Transcription antitermination protein NusG
		Transcription-repair coupling factor
		ribosomal protein L7Ae family protein
		COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination
		FIG000325: clustered with transcription termination protein NusA
		Transcription termination protein NusA
	Rrf2 family transcriptional regulators	Rrf2 family transcriptional regulator
	RNA Metabolism - no subcategory	Group II intron-associated genes
	pyrimidine conversions	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)
		Nucleoside diphosphate kinase (EC 2.7.4.6)
		Uridine kinase (EC 2.7.1.48) [C1]
		Thymidylate kinase (EC 2.7.4.9)
		Cytosine deaminase (EC 3.5.4.1)
		Thioredoxin reductase (EC 1.8.1.9)
		Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)
		Cytidylate kinase (EC 2.7.4.25)
		Thymidine kinase (EC 2.7.1.21)
		Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)
Nucleosides and Nucleotides	Pyrimidines	Purine nucleoside phosphorylase (EC 2.4.2.1)
		5'-nucleotidase (EC 3.1.3.5)
		Cytidine deaminase (EC 3.5.4.5)
		Uridine kinase (EC 2.7.1.48)
		Uracil phosphoribosyltransferase (EC 2.4.2.9)
		2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)
		CTP synthase (EC 6.3.4.2)
		Uracil permease
		Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
		Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1)
Nucleosides and Nucleotides	De Novo Pyrimidine Synthesis	Aspartate carbamoyltransferase (EC 2.1.3.2)
		Dihydroorotate dehydrogenase, catalytic subunit (EC 1.3.3.1)
		Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)
		Orotate phosphoribosyltransferase (EC 2.4.2.10)
		Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
		Uracil phosphoribosyltransferase (EC 2.4.2.9)
		Dihydroorotase (EC 3.5.2.3)
		Phosphoribosylamine--glycine ligase (EC 6.3.4.13)
		IMP cyclohydrolase (EC 3.5.4.10)
		Amidophosphoribosyltransferase (EC 2.4.2.14)
Nucleosides and Nucleotides	Purines	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
		Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)
		Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)
		Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
		Adenylosuccinate lyase (EC 4.3.2.2)
		Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)

		Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
		Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3)
		Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)
		Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit (EC 6.3.5.3)
Xanthine Metabolism in Bacteria		Xanthine phosphoribosyltransferase (EC 2.4.2.22)
Purine Utilization		Xanthine/uracil/thiamine/ascorbate permease family protein
		Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family
		Uracil-xanthine permease
		preQ1-regulated inosine-uridine nucleoside hydrolase (EC 3.2.2.1)
		GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)
		Adenylosuccinate synthetase (EC 6.3.4.4)
		Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
		Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)
		Possible hypoxanthine oxidase XdhD (EC 1.-.-.-)
		Adenylosuccinate lyase (EC 4.3.2.2)
		Polyphosphate kinase (EC 2.7.4.1)
		Deoxyadenosine kinase (EC 2.7.1.76)
		Adenine phosphoribosyltransferase (EC 2.4.2.7)
Purine conversions		2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)
		Adenylate kinase (EC 2.7.4.3)
		Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
		Nucleoside diphosphate kinase (EC 2.7.4.6)
		Deoxyguanosine kinase (EC 2.7.1.113)
		Adenine deaminase (EC 3.5.4.2)
		Purine nucleoside phosphorylase (EC 2.4.2.1)
		5'-nucleotidase (EC 3.1.3.5)
		Xanthine phosphoribosyltransferase (EC 2.4.2.22)
		Adenosine deaminase (EC 3.5.4.4)
		Guanylate kinase (EC 2.7.4.8)
		Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)
		Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)
Ribonucleotide reduction		Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)
		Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)
		Ribonucleotide reductase transcriptional regulator NrdR
Pseudouridine catabolism		Pseudouridine 5'-phosphate glycosidase
		Pseudouridine kinase (EC 2.7.1.83)
		S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)
Adenosyl nucleosidases		Purine nucleoside phosphorylase (EC 2.4.2.1)
		5'-methylthioadenosine nucleosidase (EC 3.2.2.16)
	Nucleoside triphosphate pyrophosphohydrolase MazG	Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)
Detoxification	Nudix proteins (nucleoside triphosphate hydrolases)	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
		Hypothetical nudix hydrolase YeaB
		Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)

		Housecleaning nucleoside triphosphate pyrophosphatases	Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.15)
			5'-nucleotidase YjjG (EC 3.1.3.5)
Protein folding	GroEL GroES		Heat shock protein GrpE
			Heat-inducible transcription repressor HrcA
			Chaperone protein DnaK
			Chaperone protein DnaJ
			Heat shock protein 60 family chaperone GroEL
	Protein chaperones		Heat shock protein GrpE
			Chaperone protein DnaK
			Chaperone protein DnaJ
			Chaperone protein HtpG
			ClpB protein
Protein Metabolism	Periplasmic disulfide interchange		Cytochrome c-type biogenesis protein CcdA (DsbD analog)
	Peptidyl-prolyl cis-trans isomerase		Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8)
			FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)
	Selenoproteins	Selenocysteine metabolism	selenocysteine-containing
			L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)
			Selenophosphate-dependent tRNA 2-selenouridine synthase
			Selenocysteine-specific translation elongation factor
			Selenide, water dikinase (EC 2.7.9.3)
Protein biosynthesis	tRNA aminoacylation, Val		Valyl-tRNA synthetase (EC 6.1.1.9)
	tRNA aminoacylation, Met		Methionyl-tRNA synthetase (EC 6.1.1.10)
	tRNA aminoacylation, Ile		Isoleucyl-tRNA synthetase (EC 6.1.1.5)
	tRNA aminoacylation, Arg		Arginyl-tRNA synthetase (EC 6.1.1.19)
	Translation initiation factors bacterial		Translation initiation factor 1
			Methionyl-tRNA formyltransferase (EC 2.1.2.9)
			Translation initiation factor 3
			Translation initiation factor 2
	tRNA aminoacylation, Gly		Ribosome-binding factor A
	tRNA aminoacylation, Ala		Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)
			Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)
			Alanyl-tRNA synthetase family protein
			Alanyl-tRNA synthetase (EC 6.1.1.7)
	tRNA aminoacylation, Trp		
Protein biosynthesis	Ribosome biogenesis bacterial		Tryptophanyl-tRNA synthetase (EC 6.1.1.2)
			16S rRNA processing protein RimM
			TsaB protein, required for threonylcarbamoyladenosine (t(6)A) formation in tRNA
			Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
			Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)
			LSU m5C1962 methyltransferase RlmI
			SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)
			tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)
			Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)
Protein biosynthesis			Ribonuclease M5 (EC 3.1.26.8)
			LSU m3Psi1915 methyltransferase RlmH
Protein biosynthesis			Ribosomal protein L11 methyltransferase (EC 2.1.1.-)
			programmed frameshift-containing

	Peptide chain release factor 2
tRNA aminoacylation, Cys	Cysteinyl-tRNA synthetase (EC 6.1.1.16)
Translation termination factors bacterial	Protein-N(5)-glutamine methyltransferase PrmC, methylates poly-peptide chain release factors RF1 and RF2
	Ribosome recycling factor
	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
	Peptide deformylase (EC 3.5.1.88)
	tmRNA-binding protein SmpB
	Peptide chain release factor 1
Universal GTPases	Methionine aminopeptidase (EC 3.4.11.18)
	Peptide chain release factor 2
	Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)
	GTP-binding protein EngA
	GTP-binding protein YqeH, required for biogenesis of 30S ribosome subunit
	GTP-binding protein HflX
	Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)
	50S ribosomal subunit maturation GTPase RbgA (B. subtilis YlqF)
	GTP-binding protein TypA/BipA
	Translation elongation factor LepA
	Translation initiation factor 2
	Ribosome small subunit-stimulated GTPase EngC
	Probable GTPase related to EngC
	Translation elongation factor G
	GTP-binding protein Era
	GTPase and tRNA-U34 5-formylation enzyme TrmE
	GTP-binding and nucleic acid-binding protein YchF
	Translation elongation factor Tu
	GTP-binding protein Obg
	GTP-binding protein EngB
tRNA aminoacylation, His	Histidyl-tRNA synthetase (EC 6.1.1.21)
tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6)
	Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6)
tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA synthetase (EC 6.1.1.12)
	Asparaginyl-tRNA synthetase (EC 6.1.1.22)
	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6)
Translation elongation factors bacterial	Translation elongation factor G
	Translation elongation factor LepA
	Translation elongation factor Tu
	Translation elongation factor Ts
	Translation elongation factor P
	Translation elongation factor G-related protein
tRNA aminoacylation, Lys	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)
tRNA aminoacylation, Thr	Threonyl-tRNA synthetase (EC 6.1.1.3)
tRNA aminoacylation, Pro	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type
Translation elongation factor G family	Translation elongation factor G
	Tetracycline resistance protein TetP
	Translation elongation factor G-related protein
	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)

		Glutamyl-tRNA synthetase (EC 6.1.1.17)
		Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7)
	tRNA aminoacylation, Glu and Gln	Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)
		Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7)
	tRNA aminoacylation, Ser	Seryl-tRNA synthetase (EC 6.1.1.11)
	tRNA aminoacylation, Tyr	Tyrosyl-tRNA synthetase (EC 6.1.1.1)
	tRNA aminoacylation, Leu	Leucyl-tRNA synthetase (EC 6.1.1.4)
	Glycyl-tRNA synthetase	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)
		Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)
	tRNA aminoacylation, Phe	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
		Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)
Protein processing and modification	Lipoprotein Biosynthesis	Lipoprotein signal peptidase (EC 3.4.23.36)
		Prolipoprotein diacylglycerol transferase (EC 2.4.99.-)
	Signal peptidase	Signal peptidase I (EC 3.4.21.89)
		Lipoprotein signal peptidase (EC 3.4.23.36)
	Ribosomal protein S12p Asp methylthiotransferase	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase
		SSU ribosomal protein S12p (S23e)
	G3E family of P-loop GTPases (metallocenter biosynthesis)	Urease accessory protein UreD
		FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)
		Urease accessory protein UreF
		Urease beta subunit (EC 3.5.1.5)
		Urease accessory protein UreG
		Urease gamma subunit (EC 3.5.1.5)
		Urease alpha subunit (EC 3.5.1.5)
	Peptide methionine sulfoxide reductase	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)
		Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)
	Putative TldE-TldD proteolytic complex	TldE protein, part of TldE/TldD proteolytic complex
		TldD protein, part of TldE/TldD proteolytic complex
	Aminopeptidases (EC 3.4.11.-)	Xaa-Pro aminopeptidase (EC 3.4.11.9)
		Cytosol aminopeptidase PepA (EC 3.4.11.1)
Protein degradation	Protein degradation	Deblocking aminopeptidase (EC 3.4.11.-)
		Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)
	Metalloprotease (EC 3.4.17.-)	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
		Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)
		Thermostable carboxypeptidase 1 (EC 3.4.17.19)
	Proteolysis in bacteria, ATP-dependent	DNA repair protein RadA
		ATP-dependent Clp protease ATP-binding subunit ClpX
		ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)
		ClpB protein
	Omega peptidases (EC 3.4.19.-)	ATP-dependent protease La (EC 3.4.21.53) Type I
		Pyrrolidone-carboxylate peptidase (EC 3.4.19.3)
Cell Division and Cell Cycle	YgjD and YeaZ	TsaD/Kae1/Qri7 protein, required for threonylcarbamoyladenine t(6)A37 formation in tRNA
		TsaB protein, required for threonylcarbamoyladenine t(6)A formation in tRNA
	Macromolecular synthesis operon	TsaD/Kae1/Qri7 protein, required for threonylcarbamoyladenine t(6)A37 formation in tRNA
		RNA polymerase sigma factor RpoD
		DNA primase (EC 2.7.7.-)
		Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)
		Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)

Regulation and Cell signaling	Regulation and Cell signaling - no sub-category	Bacterial Cytoskeleton	Septum site-determining protein MinC
			Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
			Rod shape-determining protein RodA
			Cell division protein FtsW
			Cell division protein FtsZ (EC 3.4.24.-)
			Cell division protein FtsA
			Rod shape-determining protein MreB
			Rod shape-determining protein MreC
			Septum formation protein Maf
			Septum site-determining protein MinD
			Cell division topological specificity factor MinE
			Chromosome (plasmid) partitioning protein ParA
			ElaA protein
			ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)
			Adenylate cyclase (EC 4.6.1.1)
			Adenine phosphoribosyltransferase (EC 2.4.2.7)
			3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)
			Catabolite control protein A
			HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)
Regulation and Cell signaling	Regulation and Cell signaling - no sub-category	cAMP signaling in bacteria	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I
		HPr catabolite repression system	
		Stringent Response, (p)ppGpp metabolism	
		Programmed Cell Death and Toxin-antitoxin Systems	
		Toxin-antitoxin replicon stabilization systems	DNA-damage-inducible protein J
Secondary Metabolism	Plant Alkaloids	Alkaloid biosynthesis from L-lysine	Oxalyl-CoA decarboxylase (EC 4.1.1.8)
		Uracil-DNA glycosylase	Uracil-DNA glycosylase, family 1
		DNA repair, bacterial MutL-MutS system	Recombination inhibitory protein MutS2
			DNA mismatch repair protein MutS
			DNA mismatch repair protein MutL
		DNA repair, UvrABC system	Excinuclease ABC subunit C
			Excinuclease ABC subunit A
			Excinuclease ABC subunit B
		DNA repair, bacterial photolyase	Deoxyribodipyrimidine photolyase, type II (EC 4.1.99.3)
		DNA repair, bacterial DinG and relatives	DinG family ATP-dependent helicase YoaA
DNA Metabolism	DNA repair	DNA repair system including RecA, MutS and a hypothetical protein	DNA mismatch repair protein MutS
			RecA protein
			Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
			DNA repair protein RadaA
			Exonuclease SbcD
			DNA repair protein RecN
			DNA repair protein RadC
			DNA polymerase IV (EC 2.7.7.7)
			Exonuclease SbcC
		DNA repair, bacterial	DNA-damage-inducible protein J
			Single-stranded DNA-binding protein
			Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)
			Endonuclease IV (EC 3.1.21.2)
			RecA protein
			Exodeoxyribonuclease III (EC 3.1.11.2)
			Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
			ATP-dependent DNA helicase RecQ

		DNA repair, bacterial RecFOR pathway	Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)
			Single-stranded DNA-binding protein
			Recombination protein RecR
			RecA protein
			DNA recombination and repair protein RecO
			DNA recombination and repair protein RecF
		DNA Repair Base Excision	Endonuclease III (EC 4.2.99.18)
			Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)
			Uracil-DNA glycosylase, family 1
			DNA-3-methyladenine glycosylase (EC 3.2.2.20)
			DNA polymerase I (EC 2.7.7.7)
			DNA ligase (EC 6.5.1.2)
		DNA repair, bacterial UvrD and related helicases	ATP-dependent DNA helicase UvrD/PcrA
	CRISPs	CRISPRs	CRISPR-associated protein, Csn1 family
			CRISPR-associated protein Cas1
			CRISPR-associated protein, Csm1 family
	DNA Metabolism - no subcategory	Type I Restriction-Modification	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)
			Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)
			Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)
		Restriction-Modification System	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)
			Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)
			Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)
		YcfH	Putative predicted metal-dependent hydrolase
			Putative deoxyribonuclease YcfH
		DNA structural proteins, bacterial	Chromosome partition protein smc
			DNA-binding protein HU
	DNA replication	DNA topoisomerases, Type I, ATP-independent	DNA topoisomerase III (EC 5.99.1.2)
			DNA topoisomerase I (EC 5.99.1.2)
		DNA topoisomerases, Type II, ATP-dependent	DNA gyrase subunit B (EC 5.99.1.3)
			DNA gyrase subunit A (EC 5.99.1.3)
	DNA recombination	RuvABC plus a hypothetical	FIG000859: hypothetical protein YebC
			Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4)
			Holliday junction DNA helicase RuvA
	DNA uptake, competence	DNA processing cluster	Holliday junction DNA helicase RuvB
			FIG000557: hypothetical protein co-occurring with RecR
			Recombination protein RecR
			DNA topoisomerase III (EC 5.99.1.2)
			DNA polymerase III subunits gamma and tau (EC 2.7.7.7)
Fatty Acids, Lipids, and Isoprenoids	Phospholipids	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Cardiolipin synthesis
			Cardiolipin synthetase (EC 2.7.8.-)
			Alcohol dehydrogenase (EC 1.1.1.1)
			Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY
			Phosphatidylglycerophosphatase A (EC 3.1.3.27)
			CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)
			Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
			Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
			Glycerol kinase (EC 2.7.1.30)

			Phosphatidylserine decarboxylase (EC 4.1.1.65)
			Aldehyde dehydrogenase (EC 1.2.1.3)
			1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
			Diacylglycerol kinase (EC 2.7.1.107)
			CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
			Cardiolipin synthetase (EC 2.7.8.-)
			Dihydroxyacetone kinase family protein
			Acyl carrier protein
			Phosphatidate cytidyltransferase (EC 2.7.7.41)
			Phosphate:acyl-ACP acyltransferase PlsX
			Glycerate kinase (EC 2.7.1.31)
Triacylglycerols	Triacylglycerol metabolism		Monoglyceride lipase (EC 3.1.1.23)
			Lysophospholipase (EC 3.1.1.5)
Fatty acids	Fatty Acid Biosynthesis FASII		3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
			Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)
			Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)
			Biotin carboxyl carrier protein of acetyl-CoA carboxylase
			Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)
			Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)
			Acyl carrier protein
			Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)
			3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)
			Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9)
Isoprenoids	Isoprenoinds for Quinones		Undecaprenyl diphosphate synthase (EC 2.5.1.31)
			Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)
			1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)
	Isoprenoid Biosynthesis		Undecaprenyl diphosphate synthase (EC 2.5.1.31)
			4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)
			1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)
			4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
			2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
			2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)
			1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
			1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)
			4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)
			1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)
			4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
			2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
			2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)
			1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
Nitrogen Metabolism	Nitrogen Metabolism - no subcategory	Nitrosative stress	Hydroxylamine reductase (EC 1.7.-.-)
		Nitrate and nitrite ammonification	Nitrite reductase probable electron transfer 4Fe-S subunit (EC 1.7.1.4)
			Assimilatory nitrate reductase large subunit (EC:1.7.99.4)
			Nitrite reductase probable [NAD(P)H] subunit (EC 1.7.1.4)
Dormancy and Sporulation	Spore Core Dehydration		Spore maturation protein B
			Spore maturation protein A

	Dormancy and Sporulation - no subcategory	Sporulation-associated proteins with broader functions	Protein of unknown function identified by role in sporulation (SpoVG)	
			Peptidyl-tRNA hydrolase (EC 3.1.1.29)	
Respiration	Electron accepting reactions	Anaerobic respiratory reductases	RNA polymerase sporulation specific sigma factor SigH	
			Anaerobic sulfite reductase subunit C (EC 1.8.1.-)	
			Anaerobic sulfite reductase subunit A	
			Arsenate reductase (EC 1.20.4.1)	
			Anaerobic sulfite reductase subunit B	
		Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Anaerobic dehydrogenases, typically selenocysteine-containing	
			Electron transport complex protein RnfE	
			Electron transport complex protein RnfA	
			Electron transport complex protein RnfG	
			Electron transport complex protein RnfD	
	Respiration - no subcategory	Respiratory dehydrogenases 1	Electron transport complex protein RnfB	
			Electron transport complex protein RnfC	
			Glycerol dehydrogenase (EC 1.1.1.6)	
			NADH dehydrogenase (EC 1.6.99.3)	
			Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	
		Succinate dehydrogenase	L-lactate dehydrogenase (EC 1.1.2.3)	
			Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	
			Biogenesis of c-type cytochromes	
			Cytochrome c-type biogenesis protein ResA	
			Cytochrome c-type biogenesis protein CcdA (DsbD analog)	
Stress Response	Osmotic stress	Soluble cytochromes and functionally related electron carriers	Ferredoxin	
			Aquaporin Z	
		Osmoregulation	Glycerol uptake facilitator protein	
			L-proline glycine betaine ABC transport system permease protein ProV (TC 3.A.1.12.1)	
		Choline and Betaine Uptake and Betaine Biosynthesis	Glycine betaine transporter OpuD	
			Sarcosine oxidase alpha subunit (EC 1.5.3.1)	
			L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)	
			Rubrerythrin	
	Oxidative stress	Oxidative stress	Ferric uptake regulation protein	
			transcriptional regulator, Crp/Fnr family	
			Superoxide reductase (EC 1.15.1.2)	
			Fe2+/Zn2+ uptake regulation proteins	
			Peroxide stress regulator	
			Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	
		Glutathione: Biosynthesis and gamma-glutamyl cycle	Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3)	
			Lactoylglutathione lyase (EC 4.4.1.5)	
	Oxidative stress	Glutathione: Non-redox reactions	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	
			Rubrerythrin	
		Rubrerythrin	Rubredoxin	
			Superoxide reductase (EC 1.15.1.2)	
		Redox-dependent regulation of nucleus processes	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	
			Nicotinamidase (EC 3.5.1.19)	
			NAD-dependent protein deacetylase of SIR2 family	
			NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	
		Glutathione: Redox cycle	Glutaredoxin	

Glutaredoxins		Glutaredoxin
Cold shock	Cold shock, CspA family of proteins	Cold shock protein CspA
Heat shock	Heat shock dnaK gene cluster extended	Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III oxidase, oxygen-independent
		Hypothetical radical SAM family enzyme in heat shock gene cluster, similarity with CPO of BS HemN-type
		Heat-inducible transcription repressor HrcA
		Chaperone protein DnaK
		tRNA-t(6)A37 methylthiotransferase
		Chaperone protein DnaJ
		Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)
		tmRNA-binding protein SmpB
		Heat shock protein GrpE
		Translation elongation factor LepA
		Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.15)
		Ribosomal protein L11 methyltransferase (EC 2.1.1.-)
		Signal peptidase-like protein
		FIG009886: phosphoesterase
Stress Response - no subcategory	SigmaB stress response regulation	Ribonuclease PH (EC 2.7.7.56)
		rRNA small subunit methyltransferase I
		Serine phosphatase RsbU, regulator of sigma subunit
Periplasmic Stress	Periplasmic Stress Response	GTP-binding protein HflX
		Carbon starvation protein A
		Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8)
Metabolism of Aromatic Compounds	Peripheral pathways for catabolism of aromatic compounds	Outer membrane protein H precursor
		3-dehydroquinate dehydratase II (EC 4.2.1.10)
Amino Acids and Derivatives	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	L-asparaginase I, cytoplasmic (EC 3.5.1.1)
		L-asparaginase (EC 3.5.1.1)
		Aspartate--ammonia ligase (EC 6.3.1.1)
		Aspartate aminotransferase (EC 2.6.1.1)
		Glutamate racemase (EC 5.1.1.3)
		Glutaminase (EC 3.5.1.2)
		Glutamate synthase [NADPH] small chain (EC 1.4.1.13)
		Glutamine synthetase type III, GlnN (EC 6.3.1.2)
		Aspartate ammonia-lyase (EC 4.3.1.1)
		Glutamine synthetases
	Histidine Metabolism	Glutamine synthetase type III, GlnN (EC 6.3.1.2)
		N-formylglutamate deformylase (EC 3.5.1.68)
		Formiminoglutamase (EC 3.5.3.8)
		Imidazolonepropionase (EC 3.5.2.7)
		Urocanate hydratase (EC 4.2.1.49)
	Histidine Degradation	Histidine ammonia-lyase (EC 4.3.1.3)
		Glutamate formiminotransferase (EC 2.1.2.5)
		Urease accessory protein UreD
		Urease accessory protein UreF
	Arginine; urea cycle, polyamines	Urease beta subunit (EC 3.5.1.5)
		Urease accessory protein UreG
		Urea channel UreI
		Urease gamma subunit (EC 3.5.1.5)
		Urease alpha subunit (EC 3.5.1.5)

Polyamine Metabolism	Arginine/ornithine antiporter ArcD
	Spermidine Putrescine ABC transporter permease component potC (TC 3.A.1.11.1)
	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)
	Arginine decarboxylase, catabolic (EC 4.1.1.19)
	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)
	Agmatine deiminase (EC 3.5.3.12)
	Arginine decarboxylase (EC 4.1.1.19)
	Ornithine decarboxylase (EC 4.1.1.17)
	N-carbamoylputrescine amidase (3.5.1.53)
	5'-methylthioadenosine nucleosidase (EC 3.2.2.16)
Arginine and Ornithine Degradation	ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)
	Arginine/ornithine antiporter ArcD
	Arginine decarboxylase, catabolic (EC 4.1.1.19)
	Arginine decarboxylase (EC 4.1.1.19)
	Agmatine deiminase (EC 3.5.3.12)
	Ornithine decarboxylase (EC 4.1.1.17)
	Lysine-arginine-ornithine-binding periplasmic protein precursor (TC 3.A.1.3.1)
Urea decomposition	N-carbamoylputrescine amidase (3.5.1.53)
	Urease accessory protein UreD
	Urease accessory protein UreF
	Urease beta subunit (EC 3.5.1.5)
	Urease accessory protein UreG
	Urea channel UreI
	Urease gamma subunit (EC 3.5.1.5)
Methionine Degradation	Urease alpha subunit (EC 3.5.1.5)
	S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)
	Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)
	Methionine ABC transporter substrate-binding protein
	Methionine ABC transporter ATP-binding protein
	Methionine ABC transporter permease protein
	S-adenosylmethionine synthetase (EC 2.5.1.6)
	Methionine transporter MetT
	Adenosylhomocysteinase (EC 3.3.1.1)
	Methionine ABC transporter ATP-binding protein
Lysine, threonine, methionine, and cysteine	Duplicated ATPase component MtsB of energizing module of methionine-regulated ECF transporter
	S-adenosylmethionine synthetase (EC 2.5.1.6)
	O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)
	Serine acetyltransferase (EC 2.3.1.30)
	Homoserine O-succinyltransferase (EC 2.3.1.46)
	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)
	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49)
	Transmembrane component MtsC of energizing module of methionine-regulated ECF transporter
	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)
	Homoserine dehydrogenase (EC 1.1.1.3)
	Methionine ABC transporter substrate-binding protein
	S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)
	Methionine ABC transporter permease protein
	Methionine transporter MetT
	Adenosylhomocysteinase (EC 3.3.1.1)

		Substrate-specific component MtsA of methionine-regulated ECF transporter
Threonine and Homoserine Biosynthesis		Homoserine dehydrogenase (EC 1.1.1.3)
		Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
		Aspartate aminotransferase (EC 2.6.1.1)
		Aspartokinase (EC 2.7.2.4)
Threonine degradation		Threonine dehydratase (EC 4.3.1.19)
Lysine Biosynthesis DAP Pathway, GJO scratch		Diaminopimelate decarboxylase (EC 4.1.1.20)
		N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)
		Diaminopimelate epimerase (EC 5.1.1.7)
		Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
		2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89)
		4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)
		Aspartokinase (EC 2.7.2.4)
Lysine degradation		4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)
		Lysine decarboxylase (EC 4.1.1.18)
Lysine Biosynthesis DAP Pathway		Diaminopimelate decarboxylase (EC 4.1.1.20)
		N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)
		Diaminopimelate epimerase (EC 5.1.1.7)
		Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
		2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89)
		4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)
		Aspartokinase (EC 2.7.2.4)
Amino Acids and Derivatives - no subcategory	Creatine and Creatinine Degradation	4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)
		Cytosine permease
Branched-chain amino acids	Branched-Chain Amino Acid Biosynthesis	Cytosine deaminase (EC 3.5.4.1)
		Branched-chain amino acid aminotransferase (EC 2.6.1.42)
		Threonine dehydratase (EC 4.3.1.19)
		Ketol-acid reductoisomerase (EC 1.1.1.86)
		Dihydroxy-acid dehydratase (EC 4.2.1.9)
		Acetolactate synthase large subunit (EC 2.2.1.6)
Aromatic amino acids and derivatives	Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate)	Acetolactate synthase small subunit (EC 2.2.1.6)
		Shikimate kinase I (EC 2.7.1.71)
		5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)
		Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
		3-dehydroquinate dehydratase II (EC 4.2.1.10)
		2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)
		3-dehydroquinate synthase (EC 4.2.3.4)
	Chorismate Synthesis	Chorismate synthase (EC 4.2.3.5)
		Shikimate kinase I (EC 2.7.1.71)
		5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)
		Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
		3-dehydroquinate dehydratase II (EC 4.2.1.10)
		2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)
		3-dehydroquinate synthase (EC 4.2.3.4)
		Chorismate synthase (EC 4.2.3.5)
	Chorismate: Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxy-anthranilate and more.	Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)
		Isochorismatase (EC 3.3.2.1)

Sulfur Metabolism	Sulfur Metabolism - no subcategory	Phenylalanine and Tyrosine Branches from Chorismate	Cyclohexadienyl dehydratase (EC 4.2.1.51)(EC 4.2.1.91) Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57)
		Proline Synthesis	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
		A Hypothetical Protein Related to Proline Metabolism	Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC
		Glycine Biosynthesis	Pyrroline-5-carboxylate reductase (EC 1.5.1.2) Serine hydroxymethyltransferase (EC 2.1.2.1)
		Alanine, serine, and glycine	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
			Cysteine desulfurase (EC 2.8.1.7)
			Alanine racemase (EC 5.1.1.1)
			Phosphoserine phosphatase (EC 3.1.3.3)
			Serine hydroxymethyltransferase (EC 2.1.2.1)
		Thioredoxin-disulfide reductase	Thiol peroxidase, Tpx-type (EC 1.11.1.15)
			Alkyl hydroperoxide reductase protein F (EC 1.6.4.-)
			Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)
			Thioredoxin reductase (EC 1.8.1.9)
			Alpha-galactosidase (EC 3.2.1.22)
			Beta-galactosidase (EC 3.2.1.23)
		Galactosylceramide and Sulfatide metabolism	probable beta-D-galactosidase
Phosphorus Metabolism	Phosphorus Metabolism - no subcategory	High affinity phosphate transporter and control of PHO regulon	Phosphate regulon transcriptional regulatory protein PhoB (SphR)
			Phosphate transport system permease protein PstC (TC 3.A.1.7.1)
			Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)
			Phosphate transport system permease protein PstA (TC 3.A.1.7.1)
			Phosphate transport system regulatory protein PhoU
			Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)
			Polyphosphate kinase (EC 2.7.4.1)
			Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
			Phosphate regulon transcriptional regulatory protein PhoB (SphR)
			Phosphate transport system permease protein PstC (TC 3.A.1.7.1)
		Phosphate metabolism	Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)
			Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)
			Phosphate transport system permease protein PstA (TC 3.A.1.7.1)
			Exopolyphosphatase (EC 3.6.1.11)
			Phosphate transport system regulatory protein PhoU
			Predicted ATPase related to phosphate starvation-inducible protein PhoH
			Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)
			Alkaline phosphatase (EC 3.1.3.1)
			Alkaline phosphatase like protein
			Polyphosphate kinase (EC 2.7.4.1)
			Sodium-dependent phosphate transporter
			Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
		Polyphosphate	Polyphosphate kinase (EC 2.7.4.1)
			Exopolyphosphatase (EC 3.6.1.11)
Carbohydrates	Central carbohydrate metabolism	Methylglyoxal Metabolism	Methylglyoxal synthase (EC 4.2.3.3)
			Lactoylglutathione lyase (EC 4.4.1.5)
			Aldehyde dehydrogenase (EC 1.2.1.3)
		Pyruvate:ferredoxin oxidoreductase	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)
			Pyruvate:ferredoxin oxidoreductase, delta subunit (EC 1.2.7.1)
			Pyruvate:ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.1)
			Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)
			Pyruvate:ferredoxin oxidoreductase, beta subunit (EC 1.2.7.1)
			Pyruvate:ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.1)

Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Aldehyde dehydrogenase (EC 1.2.1.3)
	Acetaldehyde dehydrogenase (EC 1.2.1.10)
	Phosphate acetyltransferase (EC 2.3.1.8)
	Acetate kinase (EC 2.7.2.1)
	NAD-dependent protein deacetylase of SIR2 family
Pyruvate Alanine Serine Interconversions	Acylphosphate phosphohydrolase (EC 3.6.1.7), putative
	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
	L-serine dehydratase (EC 4.3.1.17)
Dihydroxyacetone kinases	Alanine racemase (EC 5.1.1.1)
	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), subunit DhaM
	DHA-specific IIA component
	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), ADP-binding subunit DhaL
	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), dihydroxyacetone binding subunit DhaK
Glycolysis and Gluconeogenesis	6-phosphofructokinase (EC 2.7.1.11)
	Triosephosphate isomerase (EC 5.3.1.1)
	Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11)
	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)
	Glucose-6-phosphate isomerase (EC 5.3.1.9)
	Pyruvate kinase (EC 2.7.1.40)
	Enolase (EC 4.2.1.11)
Pentose phosphate pathway	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
	Phosphoglycerate kinase (EC 2.7.2.3)
	Transketolase, N-terminal section (EC 2.2.1.1)
	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
	6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type
	Transaldolase (EC 2.2.1.2)
	Ribose 5-phosphate isomerase B (EC 5.3.1.6)
	Transketolase, C-terminal section (EC 2.2.1.1)
Pyruvate metabolism I: anaplerotic reactions, PEP	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)
	Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)
	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)
	NADP-dependent malic enzyme (EC 1.1.1.40)
Aminosugars	Pyruvate kinase (EC 2.7.1.40)
	Malate permease
	PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.69)
	Glucosamine-6-phosphate deaminase (EC 3.5.99.6)
	N-Acetyl-D-glucosamine ABC transport system, permease protein 2
Chitin and N-acetylglucosamine utilization	Chitinase (EC 3.2.1.14)
	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)
	Sucrose operon repressor ScrR, LacI family
	PTS system, sucrose-specific IIC component (EC 2.7.1.69)
	PTS system, sucrose-specific IIB component (EC 2.7.1.69)
Sucrose utilization	Fructokinase (EC 2.7.1.4)
	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)
	Maltose/maltodextrin ABC transporter, permease protein MalF
	Maltose-6'-phosphate glucosidase (EC 3.2.1.122)
	Neopullulanase (EC 3.2.1.135)
Di- and oligosaccharides	Glycogen phosphorylase (EC 2.4.1.1)
	Alpha-glucosidase (EC 3.2.1.20)
	Aldose 1-epimerase (EC 5.1.3.3)
	Maltose and Maltodextrin Utilization

		PTS system, maltose and glucose-specific IIC component (EC 2.7.1.69)
		Multiple sugar ABC transporter, ATP-binding protein
		Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)
		PTS system, maltose and glucose-specific IIB component (EC 2.7.1.69)
		Maltoporin (maltose/maltodextrin high-affinity receptor, phage lambda receptor protein)
		Maltose/maltodextrin ABC transporter, permease protein MalG
		PTS system, cellobiose-specific IIB component (EC 2.7.1.69)
		Outer surface protein of unknown function, cellobiose operon
		6-phospho-beta-glucosidase (EC 3.2.1.86)
		PTS system, cellobiose-specific IIC component (EC 2.7.1.69)
Beta-Glucoside Metabolism		PTS system, cellobiose-specific IIA component (EC 2.7.1.69)
		Beta-glucosidase (EC 3.2.1.21)
		UDP-glucose 4-epimerase (EC 5.1.3.2)
		Galactose/methyl galactoside ABC transport system, permease protein MglC (TC 3.A.1.2.3)
		Alpha-galactosidase (EC 3.2.1.22)
		Galactokinase (EC 2.7.1.6)
		Aldose 1-epimerase (EC 5.1.3.3)
		Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3)
		Beta-galactosidase (EC 3.2.1.23)
		Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17)
Lactose and Galactose Uptake and Utilization		Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)
		Beta-galactosidase (EC 3.2.1.23)
		Evolved beta-D-galactosidase, alpha subunit
		Evolved beta-D-galactosidase transcriptional repressor
		Galactoside O-acetyltransferase (EC 2.3.1.18)
		Formate--tetrahydrofolate ligase (EC 6.3.4.3)
		Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)
		Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)
		5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)
		Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)
One-carbon Metabolism	One-carbon metabolism by tetrahydropterines	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
		D-glycerate transporter (predicted)
		Pyruvate kinase (EC 2.7.1.40)
		Glycerate kinase (EC 2.7.1.31)
		L-lactate dehydrogenase (EC 1.1.2.3)
		Na(+)/Citrate OH(-) antiporter
		Citrate lyase gamma chain, acyl carrier protein (EC 4.1.3.6)
		[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)
		Citrate lyase beta chain (EC 4.1.3.6)
		Citrate lyase alpha chain (EC 4.1.3.6)
Organic acids	Citrate Metabolism, Transport, and Regulation	D-lactate dehydrogenase (EC 1.1.1.28)
		Alcohol dehydrogenase (EC 1.1.1.1)
		Acetaldehyde dehydrogenase (EC 1.2.1.10)
		Formate efflux transporter (TC 2.A.44 family)
		Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)
		L-lactate dehydrogenase (EC 1.1.1.27)
		Sugar/maltose fermentation stimulation protein homolog
		Pyruvate formate-lyase (EC 2.3.1.54)
		Acetate kinase (EC 2.7.2.1)
		Phosphate acetyltransferase (EC 2.3.1.8)
Fermentation	Fermentations: Mixed acid	Acetolactate synthase large subunit (EC 2.2.1.6)

Acetolactate synthase subunits		Acetolactate synthase small subunit (EC 2.2.1.6)	
Fermentations: Lactate		D-lactate dehydrogenase (EC 1.1.1.28)	
		L-lactate dehydrogenase (EC 1.1.1.27)	
		Acetaldehyde dehydrogenase (EC 1.2.1.10)	
		Phosphate acetyltransferase (EC 2.3.1.8)	
		Acetate kinase (EC 2.7.2.1)	
Sugar alcohols	Glycerol and Glycerol-3-phosphate Uptake and Utilization	NADH peroxidase (EC 1.11.1.1)	
		Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)	
		Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	
		Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	
		Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)	
		Glycerol kinase (EC 2.7.1.30)	
		Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	
		Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	
		Glycerol uptake facilitator protein	
Polysaccharides	Glycogen metabolism	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	
		1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)	
		Glycogen biosynthesis protein GlgD, glucose-1-phosphate adenylyltransferase family	
		Glycogen phosphorylase (EC 2.4.1.1)	
		Glycogen debranching enzyme (EC 3.2.1.-)	
		Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)	
Mannose Metabolism		Mannose-6-phosphate isomerase (EC 5.3.1.8)	
		Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	
D-ribose utilization		Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	
		Ribokinase (EC 2.7.1.15)	
Monosaccharides	Deoxyribose and Deoxynucleoside Catabolism	Ribose 5-phosphate isomerase B (EC 5.3.1.6)	
		Purine nucleoside phosphorylase (EC 2.4.2.1)	
		Ribokinase (EC 2.7.1.15)	
		Phosphopentomutase (EC 5.4.2.7)	
	L-ascorbate utilization (and related gene clusters)	Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	
		Deoxyribose-phosphate aldolase (EC 4.1.2.4)	
		L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	
		3-keto-L-gulonate 6-phosphate decarboxylase	
	D-galactarate, D-glucarate and D-glycerate catabolism		L-xylulose 5-phosphate 3-epimerase (EC 5.1.3.-)
			Probable L-ascorbate-6-phosphate lactonase UlaG (EC 3.1.1.-) (L-ascorbate utilization protein G)
		Ascorbate-specific PTS system, EIIC component	
		2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	
		D-glycerate transporter (predicted)	
		Glycerate kinase (EC 2.7.1.31)	
Fructose utilization			Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)
			PTS system, fructose-specific IIC component (EC 2.7.1.69)
			Transcriptional repressor of the fructose operon, DeoR family
			PTS system, fructose-specific IIB component (EC 2.7.1.69)
			Transaldolase (EC 2.2.1.2)
			PTS system, fructose-specific IIA component (EC 2.7.1.69)
	Fructokinase (EC 2.7.1.4)		
		2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	

D-galactarate, D-glucose and D-glycerate catabolism - gjo

D-glycerate transporter (predicted)
Glycerate kinase (EC 2.7.1.31)
