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Sub-inhibitory concentrations of different pharmaceutical products affect the meta-transcriptome of river biofilm communities cultivated in rotating annular reactors

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Running head: Pharmaceutical products effects on river biofilms

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Summary

Surface waters worldwide are contaminated by pharmaceutical products that are released into the environment from wastewater treatment plants. Here, we hypothesize that pharmaceutical products have effects on organisms as well as genes related to nutrient cycling in complex microbial communities. To test this hypothesis, biofilms were grown in reactors and subjected low concentrations of three antibiotics (erythromycin, ER, sulfamethoxazole, SL and sulfamethazine, SN) and a lipid regulator (gemfibrozil, GM). Total community RNA was extracted and sequenced together with PCR amplicons of the 16S rRNA gene using 454 pyrosequencing. Exposure to pharmaceutical products resulted in very little change in bacterial community composition at the phylum level based on 16S rRNA gene amplicons, even though some genera were significantly affected. In contrast, large shifts were observed in the active community composition based on taxonomic affiliations of mRNA sequences. Consequently, expression of gene categories related to N, P and C cycling were strongly affected by the presence of pharmaceutical products, with each treatment having specific effects. These results indicate that low pharmaceutical product concentrations rapidly provoke a variety of functional shifts in river bacterial communities. In the longer term these shifts in gene expression and microbial activity could lead to a disruption of important ecosystem processes like nutrient cycling.

Introduction

Surface waters worldwide are contaminated by pharmaceutical and personal care products (PPCP) at very low concentrations (Daughton and Ternes, 1999; Kolpin *et al.*, 2002; Metcalfe *et al.*, 2003). These products typically contaminate surface waters through effluent water release from wastewater treatment plants (Jones *et al.*, 2004). Since many PPCP's are often specifically designed to resist degradation, it is not surprising that they are relatively unaffected by the wastewater treatment process (Kolpin *et al.*, 2002; Metcalfe *et al.*, 2003). Furthermore, the typically low concentrations in wastewater make PPCP's difficult to remove by any means (Daughton and Ternes, 1999). Although present at low concentrations, PPCP's are considered pseudo-persistent in that they are constantly being added to receiving waters (Daughton and Ternes, 1999). Of great concern is their role, not only in endocrine disruption (Kidd *et al.*, 2007), but in the potential development of antibiotic-resistant bacteria (Costanzo *et al.*, 2005). One of the more subtle but equally important effects, however, is the likelihood of PPCP's having an effect on bacterial processes that are crucial for the health and integrity of aquatic ecosystems. Several pharmaceutical products, like antibiotics, may act as signaling molecules in addition to their role as inhibitors of microbial processes (Fajardo and Martínez, 2008). Lending support to this hypothesis is the fact that the same antibiotic can trigger different responses in different bacteria (Goh *et al.*, 2002). Different antibiotics are also known to elicit different responses in the same organism (Lin *et al.*, 2005; Ng *et al.*, 2003). Because pharmaceutical products have the ability to act as bacterial community functional regulators, chronic bacterial exposure may disrupt the functioning of complex microbial assemblages, and thereby alter ecosystem dynamics (Lawrence *et al.*, 2005; Lawrence *et al.*, 2009; Lawrence *et al.*, 2011).

Low pharmaceutical product concentrations have been shown to affect transcription in isolated bacterial strains (reviewed in Davies *et al.*, 2006). While useful, these studies did not establish if low concentrations of pharmaceutical products in aquatic environments might lead to changes in ecosystem level relevant bacterial processes (such as nutrient (N, P, C) cycling). We previously assessed the meta-transcriptomic responses of reactor-grown biofilms to various pharmaceutical products using a novel anonymous microarray approach (Yergeau *et al.*, 2010). Although this approach highlighted several dominant genes, whose expression was significantly affected by pharmaceutical products, it could not yield information about the changes in abundance of the less numerous transcripts and in the active community composition. This information is crucial in view of the potential impact on ecosystem processes or what are referred to as ecosystem services in terms of maintenance of water quality. We therefore decided to take a complementary ecological approach and sequenced the meta-transcriptome and 16S rRNA gene amplicons from nutrient-rich river biofilms to search for indications of shifts in ecosystem-related processes (nutrient cycles, photosynthesis and carbon utilization), at the level of both community composition and gene expression.

In this study, microbial biofilms grown in water from Wascana Creek, Saskatchewan, Canada, were subjected to low concentrations of erythromycin, sulfamethoxazole and sulfamethazine (three antibiotics) as well as gemfibrozil (a lipid regulator). Sequencing of 16S rRNA gene amplicons was used to determine if these pharmaceutical products caused any shifts in bacterial community composition. In addition, mRNA sequencing was used to determine the potential of these pharmaceutical products to change active bacterial community composition and gene expression. Our results suggested that in the short term, pharmaceutical products cause relatively minor changes in bacterial community composition, but large shifts in gene expression in the active community. Furthermore, several gene categories (photosynthesis, carbon utilization and N- and P-metabolism), crucial for ecosystem processes, showed shifts in their relative expression following exposure to pharmaceutical products. Overall, the results suggested that chronic exposure of aquatic ecosystems to pharmaceutical products could seriously alter ecosystem processes and lead to shifts in microbial community composition.

Results and discussion

In this study, a metagenomic and metatranscriptomic approach (Table 1) was used to test the hypothesis that exposing complex microbial biofilm communities to pharmaceutical products causes changes in the community composition and in the expression of genes related to important ecosystem processes. For biofilm development, we used rotating annular reactors (Lawrence *et al.*, 2000; Lawrence *et al.*, 2004) inoculated with water from Wascana Creek (WC), upstream from the city of Regina, SK, Canada, sewage treatment plant (50°24’587.42” N, 104°32’56.95”W). Treatments included: 1 µg L^{-1} erythromycin (ER), 1 µg L^{-1} gemfibrozil (GM), 0.5 µg L^{-1} sulfamethazine (SN), and 0.5 µg L^{-1} sulfamethoxazole (SL). Nothing was added to the control reactors (CO). All treatments were replicated independently three times and the experiment was run for 8 weeks. The rotating annular reactor approach was used to mimic the environmental conditions under which river biofilms grow, but without fluctuating water levels, temperature and nutrient inputs that are normally observed in the field. In view of the already high variability observed between replicated reactors, this approach had the major advantage of enabling us to identify significant trends in gene expression. Most of the previous literature related to the effects of pharmaceutical products on microbial communities used a similar experimental design.

Shifts in community composition

These treatments did not result in large changes to the biofilm microbial community composition at the DNA level (based on 16S rRNA gene amplicon sequencing) (Fig. 1a). The large variability between replicated reactors, as previously reported (Yergeau *et al.*, 2010), probably prevented the detection of significant trends in this dataset. This lack of large shifts at the phylum/class level (Fig. 1a) could also be related to the fact that pharmaceutical products were added at low, environmentally-relevant concentrations and the incubation time was relatively short. Results presented here contrast with other studies that used the same rotating annular reactor approach and demonstrated that biofilm architecture (thickness) and community composition at the major functional group level are highly sensitive to environmental stress (Lawrence *et al.*, 2004; Lawrence *et al.*, 2005). The antiseptic chlorhexidine and antimicrobial triclosan, for instance, were shown to significantly alter the microbial community composition of biofilms grown in rotating annular reactors at concentrations of 10-100µg/L (Lawrence *et al.*, 2008; Lawrence *et al.*, 2009). In another study, exposure of rotating annular biofilms to four different PPCPs resulted in a significant increase in *Betaproteobacteria* (nutrient effect), and a concomitant decrease in *Gammaproteobacteria* (toxic effect) (Lawrence *et al.*, 2005). Such shifts, which have also been observed in response to the addition of carbon, nitrogen and phosphorus (CNP), are thought to be indicative of nutrient enrichment or pollution (Brümmer *et al.*, 2000; Neu *et al.*, 2005). One reason for the lack of nutrient response of the bacterial community in our study may have been the low pharmaceutical product concentration used (0.5 to 1 µg/L). Such concentrations were probably too low to significantly increase Wascana Creek nutrients, which are already significantly elevated (Waiser *et al.*, 2011a) with dissolved organic carbon levels of 15 mg/L and total dissolved N of 3 mg/L versus an addition of < 1 µg/L C and < 0.1 µg/L N by the antibiotic treatments. Another reason for the differing results obtained is that two different molecular methods were used. In the Lawrence and colleagues (2005) study *in* *situ* hybridization or PCR-DGGE was utilized, while in the present study, pyrosequencing of the 16S rRNA gene was used. That being said, there were some genera in the Wascana study, which were particularly sensitive to low exposure levels of pharmaceutical products (Table 2). Several genera were affected either positively or negatively by the treatments, and these almost exclusively belonged to the *Cyanobacteria*, *Planctomycetes*, and *Proteobacteria* phyla. The impact at the genus level, however, was not enough to significantly change the bacterial community composition at higher taxonomic levels.

In contrast to the small differences observed at the DNA level (16S rRNA gene amplicon sequencing), the active community composition at the RNA level (taxonomic affiliation of the mRNA sequences) was strongly affected by exposure to low concentrations of pharmaceutical products, even at the phylum level (Fig. 1b). At the phylum level, the largest changes occurred in the *Cyanobacteria* and the *Proteobacteria* for ER and SL treatments. This result suggests that some phyla members modify their general activity when exposed to pharmaceutical products. *Cyanobacteria*, for instance, exhibited a strong decrease in activity in response to both ER and SL (Fig. 1b). Interestingly, even though the general activity of *Cyanobacteria* decreased, significant increases in the relative abundance of some genera (based on 16S rRNA gene amplicon sequencing) were also noted (Table 2). This observation is in line with previous work showing differential sensitivity of isolated *Cyanobacteria* to antibiotics (Lawrence *et al.*, 2009). Similarly direct biofilm imaging in another study demonstrated that exposure to four different pharmaceutical products reduced *Cyanobacteria* biomass (Lawrence *et al.*, 2005). Results presented here suggest that *Cyanobacteria* could be used as a bioindicator phylum for ecosystem pollution by pharmaceutical products. Of concern is that this phylum is one of the most important ones in aquatic ecosystems, being involved in both carbon and nitrogen cycling. Any decrease in the activity of this group, therefore, has the potential to disrupt aquatic nutrient cycling.

Treatments also significantly influenced the activity of the biofilm community at the organism level (Table 3). Most of the significant changes were found in the ER and the SL treatments, and organisms most significantly affected belonged to the *Proteobacteria*, the *Actinobacteria* or the *Firmicutes* (Table 3). ER caused a significant increase in the relative activity for most organisms, with the exception of two *Cyanobacteria* species that exhibited decreased activity (Table 3). Similarly, the only organism showing a significant decrease in activity following the SL treatment was the *Bacteroidetes*, *Croicebacter atlanticus* (Table 3). In contrast, the two organisms that were significantly affected by the GM treatments showed significant decreases in their activity. No significant effect of SN on any organism was observed at $P<0.05$. Even though each treatment affected specific organisms, most of the active microorganisms were shared between the treatments (Fig. 2a). Some organisms were more or less active in the different treatments, but the majority of the organisms detected in the mRNA dataset showed some activity in all treatments. This indicates that the pharmaceutical products used elicited some common microbial responses.

Shifts in function

Large shifts in the relative abundance of different transcript categories were observed based on the functional classification of the mRNA reads (Fig. 3). These changes were highly variable and pharmaceutical product-specific with the ER and SL treatments having the strongest effect (Fig. 3). However, as for the active microorganisms, most of the actively expressed functions were common to all treatments (Fig. 2b), suggesting that most of the differences observed between treatments were related to shifts in the relative expression of different gene categories and not to shifts in the gene categories being expressed. However, when compared to the control, several genes were uniquely expressed under specific treatments, especially the SL and ER treatments (Table 4), which led to a large difference in metabolic networks (Fig. 4). The most striking feature of this metabolic network analysis is the large number of genes uniquely expressed in the ER and SL treatments as compared to the controls, which lends support to the idea that at low concentrations, antibiotics might act as signaling molecules triggering the expression of specific genes (Fajardo and Martínez, 2008).

Because CO_2 and N_2 fixation are major ecophysiological processes that allow biofilms to be self-sufficient (Van Gemerden, 1993), our analyses also focused on C- and N-cycle related gene categories. In control biofilms, photosynthesis-related transcripts were the most abundant category (Fig. 3). In sulfamethoxazole (SL) exposed biofilms, however, this category decreased dramatically, to the point where it was no longer the most dominant ecosystem process (Fig. 3). Photosynthesis inhibition could have major consequences on ecosystem processes, as photosynthesis is the major source of fixed carbon in aquatic ecosystems. A recent laboratory study reported that the antibiotics triclosan and triclocarban, at concentrations of 10 µg/L, shifted river biofilms from an autotrophic dominated community to one controlled by heterotrophs (Lawrence *et al.*, 2009). A similar observation was recently made in a field-based study on Wascana

Creek (Waiser *et al.*, 2011a). Here the planktonic microbial community shifted from net autotrophy at a site above the Regina sewage treatment plant to net heterotrophy 0.4 km below it, based on primary production to bacterial production ratios (Waiser *et al.*, 2011a). A suite of pharmaceutical products, including the ones in this study, are regularly found at this particular creek site (Waiser *et al.*, 2011b).

We also observed shifts in transcripts related to carbohydrate metabolism (Fig. 3 and Table 4). Using BIOLOG plates, shifts in carbon utilization patterns were previously reported as a typical effect of pharmaceutical products on river biofilm communities growing in rotating annular reactors (Lawrence *et al.*, 2005; Lawrence *et al.*, 2008; Lawrence *et al.*, 2009). In our dataset, carbohydrate-related genes were mostly positively affected by exposure to pharmaceutical products (Fig. 3 and Table 4). Four different pharmaceutical products were previously observed to have significant positive effects on the utilization of carbohydrates, while most of these pharmaceutical products had negative effects on the utilization of carboxylic acids and phosphorylated compounds and no effects were observed on the utilization of polymers, esters and amino acids (Lawrence *et al.*, 2005). In contrast, general negative effects of exposure to pharmaceutical product on carbon utilization have been reported in other studies (Lawrence *et al.*, 2008; Lawrence *et al.*, 2009).

In addition to the shifts observed in carbohydrate and photosynthesis related genes, we also observed changes in genes related to N and P metabolism (Fig. 3 and Table 4). Based on previous reports (Dokianakis *et al.*, 2004; Lawrence *et al.*, 2004), Lawrence and colleagues (2009) proposed that the antibiotics triclosan and triclocarban might act on microbial communities by disrupting critical biogeochemical processes such as the nitrogen cycle. Accordingly, most of the pharmaceutical products tested in the present study reduced the relative abundance of transcripts related to nitrite reductase and ammonia assimilation (Fig .3). In other studies, sulfamethoxazole (SL) significantly inhibited nitrite oxidation in isolated strains (Dokianakis *et al.*, 2004). Some effects on gene categories related to this process were also observed in our dataset. The observed shifts in the expression of N-cycle related genes could influence the ability of aquatic ecosystems to deal with excess nitrate and nitrate originating from sewage treatment plants. In Wascana Creek, for example, although some nitrification is occurring, the persistence of high concentrations of nitrate and nitrite for many kilometers downstream of the STP would suggest some inhibition of denitrification (Waiser *et al.*, 2011a). Whether or not this inhibition is occurring in response to chronic pharmaceutical product exposure remains to be determined.

We previously assessed the metatranscriptomic response of the current samples to pharmaceutical products using an anonymous microarray approach (Yergeau *et al.*, 2010). Although the two methods (pyrosequencing and microarrays) are highly complementary, each gave a different view of the shifts occurring following exposure of river biofilms to pharmaceutical products. Anonymous microarrays were highly effective in detecting shifts in dominant genes, but could not give a complete overview of the community. Shifts in ecosystem-related processes reported here, for instance, were missed by the anonymous microarray approach because these genes comprise only a small part of the total expressed gene pool (less than 2% for N and P metabolism and less than 5% for carbohydrates). Furthermore, classification of mRNA in the subsystem hierarchy of the MG-RAST server allowed us to sum several individual genes and carry out tests on these sums, something not possible using anonymous microarrays. In contrast, the large amount of data involved in metatranscriptomic sequencing makes it difficult to identify particular genes that are strongly affected by pharmaceutical products as was possible with the anonymous microarray approach. Using the two approaches, we were able to highlight both shifts in ecosystem processes and large changes in the expression of individual genes. We believe that using the two approaches on a common set of samples resulted in very useful information that would not have been revealed by using either method alone.

Conclusions

In contrast to previous reports, we did not observe short-term effects of pharmaceutical products on bacterial community composition, probably because of the lower concentrations of pharmaceutical products used. Based on RNA analysis, however, a range of significant shifts in the active community composition and in the relative abundance of a range of transcript categories were observed. The data presented here demonstrates the usefulness of RNA-based studies. They appear to be especially useful, as demonstrated in this study, in detecting subtle changes in microbial communities after short-term exposure to low pharmaceutical product concentrations. The shifts observed were in line with previous reports, and suggest that low concentrations of pharmaceutical products may potentially affect critical biofilm functions in river ecosystems. One of the most significant changes observed was a decrease in *Cyanobacteria* activity and in the expression of photosynthesis-related genes after exposure to erythromycin and sulfamethoxazole. Longer-term studies are needed to understand how the pharmaceutical product-induced shifts at the RNA-level observed in this study translate into effects on important aquatic ecosystem process rates.

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Table 1: Sequencing statistics (average per sample). Total DNA and RNA were simultaneously extracted from 500 mg biofilm subsamples (Yergeau *et al.*, 2007; Yergeau and Kowalchuk, 2008). Pyrosequencing of 16S rRNA gene amplicons was performed as previously described (Bell *et al.*, 2011). mRNA was enriched using the MicrobExpress kit (Ambion, Austin, TX). mRNA was then sent for cDNA generation, library construction and Roche 454 GS FLX Titanium sequencing at The Centre for Applied Genomics, The Hospital for Sick Children, Toronto, ON, Canada. Sequence data produced in the current study were deposited in the GenBank database under accession numbers XX000000 to XX000000 (16S rRNA gene amplicons) and XX000000 to XX000000 (RNA).

	Raw		After *in silico* rRNA removal	
	nb reads	bp	nb reads	bp
16S rRNA sequencing				
CO	37,979	7,675,660		
ER	19,789	4,051,123		
GM	21,959	4,527,673		
SL	26,723	5,466,712		
SN	33,300	7,088,289		
RNA sequencing				
CO	73,762	13,846,719	16,718	1,543,302
ER	76,223	18,191,920	20,619	3,080,393
GM	58,574	12,205,107	12,499	1,197,220
SL	91,372	18,655,602	34,077	4,149,027
SN	63,410	15,806,579	12,183	1,431,968

Table 2: Bacterial genera that showed significant differences between treatments and controls for their relative abundance based on 16S rRNA gene amplicons. Significance was measured using a t-test carried out with the R package. Fold change was calculated as the average for the treatment divided by the average for the control. If the fold change was lower than 1, it was reversed (1/x) and made negative. If one of the two averages used for fold change calculation was equal to zero, it was replaced by the minimal value (1 sequence detected among all replicates) and values are given as “greater than” or “lower than” the value obtained. See legend to Figure 1 for more details about 16S rRNA gene amplicon analysis.

	avg. CO	avg. treat.	Fold change	P-value	Phylum/Class	Genus/Group
ER	0.00774	0.01248	1.61	0.023	*Cyanobacteria*	GpIV
	0.00003	0.00000	<-4.76	0.036	*Bacteroidetes*	*Alistipes*
	0.00004	0.00000	<-6.97	0.048	*Gammaproteobacteria*	*Cellvibrio*
	0.00002	0.00008	4.60	0.049	*Deltaproteobacteria*	*Bacteriovorax*
GM	0.00774	0.01281	1.65	0.035	*Cyanobacteria*	GpIV
	0.00002	0.00008	3.55	0.044	*Alphaproteobacteria*	*Beijerinckia*
SL	0.00007	0.00000	<-15.11	0.013	*Alphaproteobacteria*	*Seohaeicola*
	0.00066	0.00034	-1.97	0.032	*Alphaproteobacteria*	*Pedomicrobium*
	0.00022	0.00040	1.87	0.038	*Planctomycetes*	*Planctomyces*
	0.00006	0.00000	<-13.60	0.040	*Planctomycetes*	*Rhodopirellula*
	0.00008	0.00003	-3.30	0.040	*Alphaproteobacteria*	*Oceanibaculum*
	0.00004	0.00000	<-9.91	0.048	*Gammaproteobacteria*	*Cellvibrio*
SN	0.00022	0.00051	2.36	0.013	*Planctomycetes*	*Planctomyces*
	0.00001	0.00018	13.21	0.019	*Gammaproteobacteria*	*Nevskia*
	0.00093	0.00194	2.08	0.022	*OD1*	OD1_genera_incertae_sedis
	0.00007	0.00003	-2.11	0.043	*Alphaproteobacteria*	*Seohaeicola*
	0.00032	0.00081	2.51	0.044	*Betaproteobacteria*	*Inhella*

Table 3: Bacterial species that showed significant differences between treatments and controls for their relative abundance based on classified mRNA sequences in MG-RAST v. 2.0. Significance was measured using a t-test carried out with the R package. See legend to Table 2 for details about fold change calculation. See legend to Figure 3 for more details about mRNA sequence analysis.

	avg. CO	avg. treat.	Fold change	P-value	Phylum/Class	Species
ER	0.00	0.14	>8.05	0.001	*Actinobacteria*	*Mycobacterium bovis*
	0.00	0.14	>8.05	0.001	*Firmicutes*	*Bacillus subtilis*
	0.00	0.14	>8.05	0.001	*Firmicutes*	*Staphylococcus aureus*
	0.32	0.03	-10.62	0.023	*Cyanobacteria*	*Synechococcus sp.*
	0.04	0.22	5.95	0.027	*Bacteroidetes*	*Flavobacteriales* bacterium
	0.00	0.15	>8.63	0.043	*Gammaproteobacteria*	*Colwellia psychrerythraea*
	0.00	0.07	>4.31	0.043	*Gammaproteobacteria*	*Alteromonas macleodii*
	0.00	0.07	>4.31	0.043	*Gammaproteobacteria*	*Pseudomonas resinovorans*
	0.00	0.06	>3.74	0.048	*Chloroflexi*	*Dehalococcoides sp.*
	0.00	0.06	>3.74	0.048	*Gammaproteobacteria*	*Shewanella putrefaciens*
	5.23	2.35	-2.23	0.049	*Cyanobacteria*	*Prochlorococcus marinus*
GM	0.43	0.06	-6.66	0.022	*Bacteroidetes*	*Croceibacter atlanticus*
	0.32	0.04	-8.19	0.019	*Gammaproteobacteria*	*Xanthomonas campestris*
SL	0.05	0.51	11.06	0.004	*Gammaproteobacteria*	*Actinobacillus actinomycetemcomitans*
	0.09	0.98	10.55	0.004	*Deltaproteobacteria*	*Desulfococcus oleovorans*
	0.00	0.04	>2.44	0.004	*Firmicutes*	*Bacillus clausii*
	0.00	0.04	>2.44	0.004	*Firmicutes*	*Bacillus thuringiensis*
	0.00	0.04	>2.44	0.004	*Alphaproteobacteria*	*Wolbachia sp.*
	0.00	0.04	>2.44	0.004	*Gammaproteobacteria*	*Yersinia enterocolitica*
	0.00	0.04	>2.44	0.004	*Gammaproteobacteria*	*Acinetobacter sp.*
	0.00	0.04	>2.44	0.004	*Gammaproteobacteria*	*Vibrio vulnificus*
	0.00	0.13	>7.32	0.004	*Thermotogae*	*Petrotoga mobilis*
	0.00	0.08	>4.88	0.004	*Acidobacteria*	*Acidobacteria* bacterium
	0.00	0.08	>4.88	0.004	*Gammaproteobacteria*	*Yersinia intermedia*
	0.00	0.08	>4.88	0.004	*Deltaproteobacteria*	*Sorangium cellulosum*
	1.01	4.16	4.11	0.009	*Epsilonproteobacteria*	*Campylobacter coli*
	0.41	1.11	2.73	0.010	*Deltaproteobacteria*	*Bdellovibrio bacteriovorus*
	0.00	0.16	>9.45	0.016	*Actinobacteria*	*Mycobacterium tuberculosis*
	0.04	0.26	7.01	0.019	*Alphaproteobacteria*	*Oceanicola batsensis*
	0.00	0.43	>25.01	0.020	*Alphaproteobacteria*	*Mesorhizobium sp.*
	0.04	0.42	11.36	0.022	*Betaproteobacteria*	*Dechloromonas aromatica*
	0.08	0.32	3.81	0.023	*Actinobacteria*	marine actinobacterium
	0.00	0.12	>7.01	0.023	*Firmicutes*	*Listeria innocua*
	0.00	0.12	>7.01	0.023	*Firmicutes*	*Thermoanaerobacter pseudethanolicus*
	0.00	0.24	>14.03	0.023	*Gammaproteobacteria*	*Xylella fastidiosa*
	0.05	0.30	6.55	0.025	*Alphaproteobacteria*	*Oceanicaulis alexandrii*
	0.00	0.13	>7.63	0.030	*Gammaproteobacteria*	*Pseudomonas aeruginosa*
	0.35	0.53	1.50	0.032	*Chloroflexi*	*Roseiflexus sp.*

0.04	0.29	7.86	0.034	*Actinobacteria*	*Streptomyces coelicolor*
0.04	0.39	10.38	0.037	*Epsilonproteobacteria*	*Campylobacter hominis*
0.00	0.08	>4.57	0.038	*Alphaproteobacteria*	*Sphingomonas wittichii*
0.08	0.29	3.50	0.039	*Bacteroidetes*	*Gramella forsetii*
0.05	0.29	6.20	0.040	*Spirochaetes*	*Borrelia garinii*
0.00	0.09	>5.19	0.042	*Firmicutes*	*Candidatus Desulforudis audaxviator*
0.00	0.18	>10.37	0.042	*Gammaproteobacteria*	*Xanthomonas campestris*
0.43	0.10	-4.08	0.042	*Bacteroidetes*	*Croceibacter atlanticus*
0.07	0.40	5.32	0.043	*Alphaproteobacteria*	*Gluconobacter oxydans*
0.04	0.21	5.61	0.044	*Actinobacteria*	*Propionibacterium acnes*
0.04	0.18	4.91	0.045	*Alphaproteobacteria*	*Roseobacter sp.*
0.00	0.19	>11.28	0.047	*Alphaproteobacteria*	*Sinorhizobium meliloti*
0.00	0.23	>13.12	0.049	*Betaproteobacteria*	*Polaromonas sp.*

Table 4: Subsystems that showed significant differences between treatments and controls for their relative abundance based on classified mRNA sequences in MG-RAST v. 2.0. Significance was measured using a t-test carried out with the R package. Subsystems related to carbohydrate metabolism are in boldface. Details about the individual reads classified in each subsystem are available in supplementary Table S1. See legend to Table 2 for details about fold change calculation. See legend to Figure 3 for more details about mRNA sequence analysis.

	avg CO	avg treat	Fold change	P	Subsystem Name
ER	0.00	0.32	>11.42	0.0195	Bacterial Cell Division
	0.07	0.36	5.46	0.0323	**Maltose and Maltodextrin Utilization**
	0.00	0.12	>4.18	0.0385	Lipid A modifications
	0.00	0.12	>4.18	0.0385	Pyrimidine utilization
	0.13	0.42	3.19	0.0409	**Sucrose Metabolism**
GM	0.44	0.00	<-13.32	0.0128	Beta-lactamase
SL	0.00	0.37	>13.47	0.0045	Bacterial Cell Division
	0.06	0.65	10.09	0.0047	**Acetyl-CoA fermentation to Butyrate**
	0.00	0.06	>2.29	0.0090	Glutamine synthetases
	0.00	0.06	>2.29	0.0090	**D-galactarate, D-glucarate and D-glycerate catabolism**
	0.00	0.06	>2.29	0.0090	**Di-Inositol-Phosphate biosynthesis**
	0.00	0.06	>2.29	0.0090	Lipid A modifications
	0.00	0.06	>2.29	0.0090	Major Outer Membrane Proteins
	0.00	0.06	>2.29	0.0090	Transport of Molybdenum
	0.00	0.06	>2.29	0.0090	Two-component sensor regulator linked to Carbon Starvation Protein A
	0.00	0.13	>4.59	0.0090	Arginine and Ornithine Degradation
	0.00	0.13	>4.59	0.0090	Choline Transport
	0.00	0.19	>6.88	0.0090	Pterin metabolism 3
	0.00	0.25	>8.88	0.0115	Branched chain amino acid degradation regulons
	0.06	0.46	7.14	0.0143	Glycerolipid and Glycerophospholipid Metabolism in Bacteria
	0.07	0.48	7.17	0.0166	**Maltose and Maltodextrin Utilization**
	0.00	0.18	>6.59	0.0187	Benzoate transport and degradation cluster
	0.00	0.18	>6.59	0.0187	Resistance to fluoroquinolones
	0.00	0.30	>10.88	0.0245	Pyoverdine biosynthesis
	0.00	0.26	>9.46	0.0283	Synthesis of osmoregulated periplasmic glucans
	0.00	0.20	>7.17	0.0344	**Glycerol and Glycerol-3-phosphate Uptake and Utilization**
	0.07	0.36	5.39	0.0358	Type IV pilus
	0.00	0.29	>10.59	0.0426	Serine Biosynthesis
	0.58	0.14	-4.03	0.0444	Transcription factors cyanobacterial RpoD-like sigma factors
	0.84	0.27	-3.08	0.0460	Terminal cytochrome C oxidases
	0.25	0.88	3.53	0.0465	Cobalt-zinc-cadmium resistance
	0.00	0.18	>6.30	0.0488	Phenylacetate pathway of aromatic compound degradation
SN	0.64	0.10	-6.46	0.0472	Copper homeostasis

Figure legends

Figure 1: Bacterial community composition for the controls (CO) and the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. Community composition was calculated based on the relative abundance of phylum-classified 16S rRNA genes sequences (a) or the relative abundance of the phylum-classified mRNA sequences (b). Analysis of the 16S rRNA gene amplicons was carried out essentially as previously described (Bell *et al.*, 2011; Yergeau *et al.*, 2012). Sequence data were analyzed mainly by using the RDP pyrosequencing pipeline (http://pyro.cme.msu.edu/). The sequences were then deconvoluted and binned according to their multiplex tags, and the tag was trimmed by using the Pipeline Initial Process tool. Datasets were individually classified using the RDP Classifier tool with a 50% bootstrap cutoff.

Figure 2: Venn diagram showing the overlap in the detection of organisms (a) and subsystems (b) in the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. Diagrams were drawn using VENNY (http://bioinfogp.cnb.csic.es/tools/venny/index.html) based on presence-absence of the subsystems or the organisms in the datasets pooled for each treatment following analysis in MG-RAST v. 2.0. See legend of Figure 3 for more details about mRNA sequences analysis.

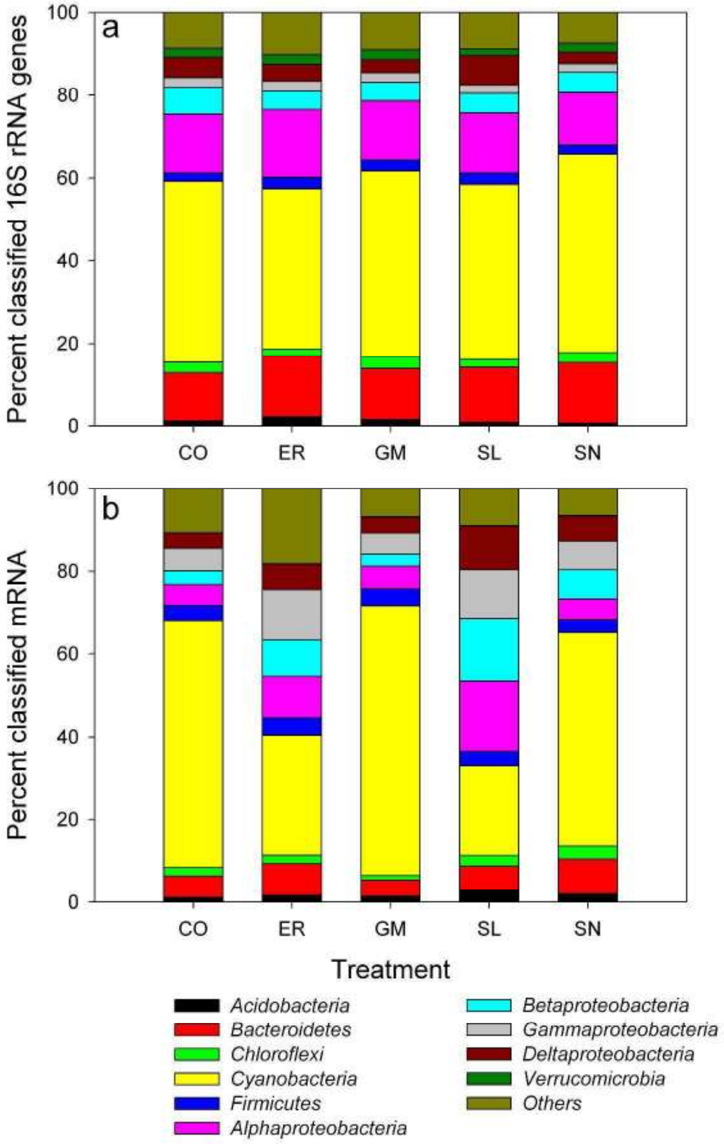
Figure 3: Functional microbial community composition for the controls (CO) and the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. The sequences were deconvoluted and binned according to their MID tags, and the MID was trimmed using custom made Perl scripts. Sequences from each sample

were then compared against a database containing representative bacterial and archaeal 16S and 23S and fungal and algal 18S and 28S sequences using the local NCBI blastall program (blastn option). All sequences having significant hits to the database (e-value of 10^{-5} or less) were removed from the dataset, leaving mostly mRNA sequences. The sequences were then annotated using the MG-RAST server version 2.0 (Meyer *et al.*, 2008). The maximum e-value for a significant match was set to 10^{-5} and the minimum alignment length was set to 50 bp.

Figure 4: Metabolic network analysis for (a) controls, (b) erythromycin and (c) sulfamethoxazole. The pathways detected are highlighted in blue. The metabolic network analyses were carried out in MG-RAST v 3.0 using the KEGG mapper tool. The maximum e-value for a significant match was set to 10^{-5} and the minimum alignment length was set to 50 bp. See legend to Figure 3 for more details about mRNA sequence analysis.

Supplementary material legend

Supplementary Table S1: Subsystems that showed significant differences between treatments and controls for their relative abundance based on classified mRNA sequences in MG-RAST v. 2.0. Significance was measured using a t-test carried out with the R package. Details about the individual reads classified in each subsystem are given.



Bacterial community composition for the controls (CO) and the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. Community composition was calculated based on the relative abundance of phylum-classified 16S rRNA genes sequences (a) or the relative abundance of the phylum-classified mRNA sequences (b). Analysis of the 16S rRNA gene amplicons was carried out essentially as previously described (Bell et al., 2011; Yergeau et al., 2012). Sequence data were analyzed mainly by using the RDP pyrosequencing pipeline (http://pyro.cme.msu.edu/). The sequences were then deconvoluted and binned according to their multiplex tags, and the tag was trimmed by using the Pipeline Initial Process tool. Datasets were individually classified using the RDP Classifier tool with a 50% bootstrap cutoff.

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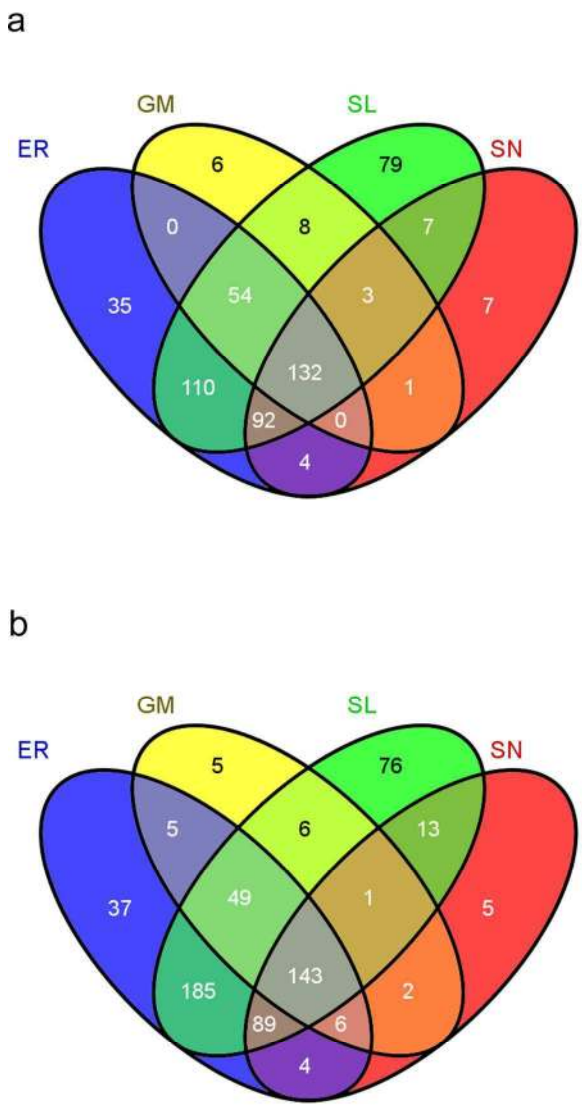
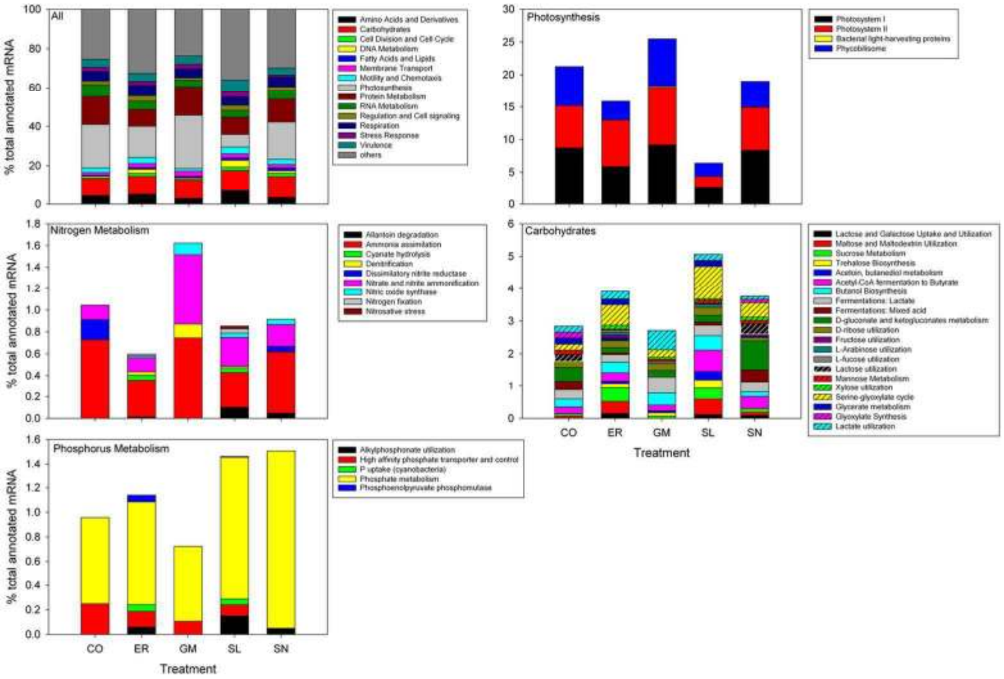
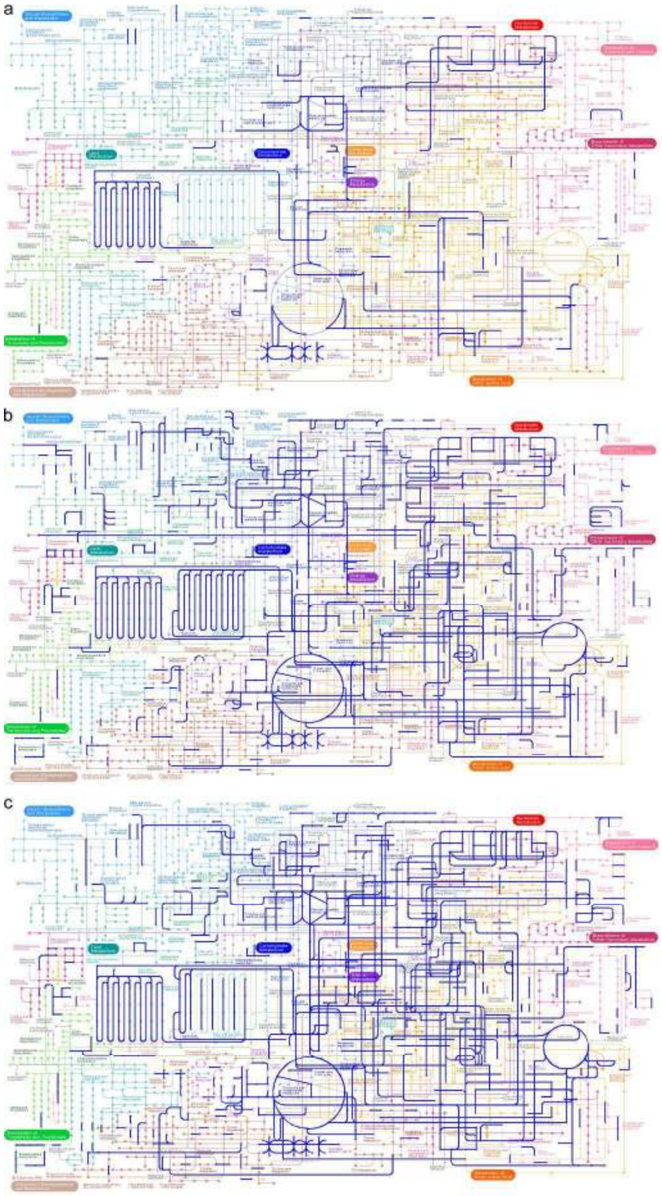


Venn diagram showing the overlap in the detection of organisms (a) and subsystems (b) in the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. Diagrams were drawn using VENNY (http://bioinfogp.cnb.csic.es/tools/venny/index.html) based on presence-absence of the subsystems or the organisms in the datasets pooled for each treatment following analysis in MG-RAST v. 2.0. See legend of Figure 3 for more details about mRNA sequences analysis.
86x171mm (300 x 300 DPI)



Functional microbial community composition for the controls (CO) and the erythromycin (ER), gemfibrozil (GM), sulfamethoxazole (SL) and sulfamethazine (SN) treatments. The sequences were deconvoluted and binned according to their MID tags, and the MID was trimmed using custom made Perl scripts. Sequences from each sample were then compared against a database containing representative bacterial and archaeal 16S and 23S and fungal and algal 18S and 28S sequences using the local NCBI blastall program (blastn option). All sequences having significant hits to the database (e-value of 10-5 or less) were removed from the dataset, leaving mostly mRNA sequences. The sequences were then annotated using the MG-RAST server version 2.0 (Meyer et al., 2008). The maximum e-value for a significant match was set to 10-5 and the minimum alignment length was set to 50 bp.
121x83mm (300 x 300 DPI)



Metabolic network analysis for (a) controls, (b) erythromycin and (c) sulfamethoxazole. The pathways detected are highlighted in blue. The metabolic network analyses were carried out in MG-RAST v 3.0 using the KEGG mapper tool. The maximum e-value for a significant match was set to 10-5 and the minimum alignment length was set to 50 bp. See legend to Figure 3 for more details about mRNA sequence analysis.
180x330mm (300 x 300 DPI)

Treatment	P-value	Subsystem Hierarchy 1
ER	0.0195	Cell Division and Cell Cycle
ER	0.0323	Carbohydrates
ER	0.0385	Cell Wall and Capsule
ER	0.0385	Nucleosides and Nucleotides

ER	0.0409	Carbohydrates
GM	0.0128	Virulence
SL	0.0045	Cell Division and Cell Cycle

SL	0.0047	Carbohydrates

SL	0.0048	Clustering-based subsystems
SL	0.0090	Amino Acids and Derivatives
SL	0.0090	Carbohydrates
SL	0.0090	Carbohydrates
SL	0.0090	Cell Wall and Capsule
SL	0.0090	Cell Wall and Capsule
SL	0.0090	Clustering-based subsystems
SL	0.0090	Membrane Transport
SL	0.0090	Unclassified
SL	0.0090	Amino Acids and Derivatives

SL	0.0090	Membrane Transport
SL	0.0090	Cofactors, Vitamins, Prosthetic Groups, Pigments
SL	0.0115	Unclassified

SL	0.0143	Fatty Acids and Lipids

SL	0.0166	Carbohydrates
SL	0.0187	Metabolism of Aromatic Compounds
SL	0.0187	Virulence

SL	0.0231	Clustering-based subsystems
SL	0.0245	Virulence
SL	0.0283	Stress Response
SL	0.0296	Clustering-based subsystems
SL	0.0309	Clustering-based subsystems

SL	0.0344	Carbohydrates
SL	0.0358	Virulence

SL	0.0426	Amino Acids and Derivatives

SL	0.0444	RNA Metabolism

SL	0.0460	Respiration
SL	0.0465	Virulence

SL	0.0465	Protein Metabolism

SL	0.0488	Metabolism of Aromatic Compounds
SN	0.0472	Stress Response

Subsystem Hierarchy 2
Cell cycle in Prokaryota
Di- and oligosaccharides
Capsular and extracellular polysacchrides
Pyrimidines

Di- and oligosaccharides
Resistance to antibiotics and toxic compounds
Cell cycle in Prokaryota

Fermentation

Fatty acid metabolic cluster
Glutamine, glutamate, aspartate, asparagine; ammonia assimilation
Monosaccharides
Sugar alcohols
Capsular and extracellular polysacchrides
Gram-Negative cell wall components
Sarcosine oxidase
Unclassified
Unclassified
Arginine; urea cycle, polyamines

Unclassified

Folate and pterines

Unclassified

Phospholipids

Di- and oligosaccharides

Unclassified

Resistance to antibiotics and toxic compounds

Cytochrome biogenesis
Iron Scavenging Mechanisms
Osmotic stress
Putative asociate of RNA polymerase sigma-54 factor rpoN
Tricarboxylate transporter

Sugar alcohols

Type III, Type IV, ESAT secretion systems

Alanine, serine, and glycine

Transcription

Electron accepting reactions

Resistance to antibiotics and toxic compounds

Protein biosynthesis
Metabolism of central aromatic intermediates
Unclassified

Subsystem Name	CONTROL Relative abundance
Bacterial Cell Division	0.00
Maltose and Maltodextrin Utilization	0.07
Lipid A modifications	0.00
Pyrimidine utilization	0.00

Sucrose Metabolism	0.13
Beta-lactamase	0.44
Bacterial Cell Division	0.00

Acetyl-CoA fermentation to Butyrate	0.06

CBSS-218491.3.peg.427	0.06
Glutamine synthetases	0.00

D-galactarate, D-glucarate and D-glycerate catabolism	0.00

Di-Inositol-Phosphate biosynthesis	0.00
Lipid A modifications	0.00
Major Outer Membrane Proteins	0.00

CBSS-188.1.peg.6170	0.00
Transport of Molybdenum	0.00

Two-component sensor regulator linked to Carbon Starvation Protein A	0.00
Arginine and Ornithine Degradation	0.00

Choline Transport	0.00
Pterin metabolism 3	0.00
Branched chain amino acid degradation regulons	0.00

Glycerolipid and Glycerophospholipid Metabolism in Bacteria	0.06

Maltose and Maltodextrin Utilization	0.07
Benzoate transport and degradation cluster	0.00
Resistance to fluoroquinolones	0.00

CBSS-196164.1.peg.1690	0.13
Pyoverdine biosynthesis new	0.00
Synthesis of osmoregulated periplasmic glucans	0.00
CBSS-316057.3.peg.1308	0.13
CBSS-49338.1.peg.459	0.00

Glycerol and Glycerol-3-phosphate Uptake and Utilization	0.00
Type IV pilus	0.07

Serine Biosynthesis	0.00
Transcription factors cyanobacterial RpoD-like sigma factors	0.58

Terminal cytochrome C oxidases	0.84
Cobalt-zinc-cadmium resistance	0.25

Ribosome SSU bacterial	2.06
Phenylacetate pathway of aromatic compound degradation	0.00
Copper homeostasis	0.64

fragment	organism
None	
NA	
None	
None	

NA
NA
None

NA

NA
None
None
None
None
None
None
None
None
None

None

None

None

4451548.3	GLP7T0L01AO7AP	Clostridium botulinum (strain Alaska E43 / Type E3)

NA

None

None

NA

None

None

None

None

None

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4451547.3 GLP7T0L01BC61H	Trichodesmium erythraeum IMS101
4451547.3 GLP7T0L01CW8DA	Cyanothece sp. PCC 8801
4451547.3 GLP7T0L01CW8DA	Cyanothece sp. PCC 8801
4451547.3 GLP7T0L01BI96X	Thermosynechococcus elongatus BP-1
4451548.3 GLP7T0L01C7MDW	Nostoc punctiforme PCC 73102
4451548.3 GLP7T0L01C4CO9	Anabaena variabilis ATCC 29413
4451548.3 GLP7T0L01DO9Z9	Trichodesmium erythraeum IMS101
4451547.3 GLP7T0L01BEHPR	Anabaena variabilis ATCC 29413

None

4451546.3 GLP7T0L01DGH06	Crocosphaera watsonii WH 8501
4451547.3 GLP7T0L01A1CAI	Thermosynechococcus elongatus BP-1
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4451547.3 GLP7T0L01D4G1B	Maribacter sp. HTCC2170
4451548.3 GLP7T0L01DE2TI	Synechococcus elongatus PCC 7942

4451548.3 GLP7T0L01AL1I2	Synechococcus elongatus PCC 7942
4451548.3 GLP7T0L01D1I7N	Cyanothece sp. PCC 7424
4451547.3 GLP7T0L01A1CAI	Cyanothece sp. PCC 7424
4451547.3 GLP7T0L01C3Q0E	Microcystis aeruginosa NIES-843
4451547.3 GLP7T0L01EQFSU	Chitinophaga pinensis DSM 2588
4451548.3 GLP7T0L01DPFP4	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)
NA	

4451547.3 GLP7T0L01C0P3T	Thermosynechococcus elongatus BP-1
4451547.3 GLP7T0L01CM0UL	Mycoplasma bovis PG45
4451547.3 GLP7T0L01BLIF5	Syntrophobacter fumaroxidans MPOB
4451547.3 GLP7T0L01B162W	Polaromonas sp. JS666
4451547.3 GLP7T0L01AWTD0	Anabaena variabilis ATCC 29413
4451547.3 GLP7T0L01BQXAI	Anabaena variabilis ATCC 29413
4451547.3 GLP7T0L01BQXAI	Anabaena variabilis ATCC 29413
4451547.3 GLP7T0L01CQS56	Flavobacterium psychrophilum JIP02/86
4451548.3 GLP7T0L01D58NM	Bacteroides thetaiotaomicron VPI-5482
4451548.3 GLP7T0L01D7IDN	Odontella sinensis (Marine centric diatom) (Biddulphia sinensis)
4451548.3 GLP7T0L01CLEFI	Moorella thermoacetica ATCC 39073
4451548.3 GLP7T0L01A4P52	Idiomarina loihiensis L2TR
4451548.3 GLP7T0L01DKEK6	Cyanothece sp. PCC 7425
4451548.3 GLP7T0L01EOQB4	Synechocystis sp. PCC 6803
4451548.3 GLP7T0L01E4M7U	Cyanothece sp. PCC 8801
4451546.3 GLP7T0L01DXVN9	Anabaena variabilis ATCC 29413
4451546.3 GLP7T0L01CNFZ2	Streptococcus pyogenes MGAS9429 (serotype M12)

None	
4451547.3 GLP7T0L01BB1GN	Methylobacillus flagellatus KT
4451547.3 GLP7T0L01BNN00	Lactobacillus gasseri ATCC 33323

SEED ID

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fig|240292.3.peg.883
fig|203124.1.peg.4675
fig|240292.3.peg.883

fig|165597.1.peg.4227
fig|197221.1.peg.264
fig|203124.1.peg.5211
fig|313603.3.peg.757
fig|1140.3.peg.881

fig|269084.3.peg.123
fig|65393.5.peg.2897
fig|65393.5.peg.2897
fig|449447.3.peg.2110
fig|485918.5.peg.3066
fig|269799.3.peg.279

fig|197221.1.peg.94
fig|347257.4.peg.550
fig|335543.6.peg.2185
fig|296591.1.peg.2817
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fig|240292.3.peg.2134
fig|240292.3.peg.2134
fig|402612.4.peg.449
fig|226186.1.peg.2785
fig|2839.1.peg.138
fig|264732.9.peg.2496
fig|283942.3.peg.432
fig|395961.4.peg.1270
fig|1148.1.peg.747
fig|41431.3.peg.1896
fig|240292.3.peg.1205
fig|370553.3.peg.46

fig|265072.7.peg.638
fig|324831.10.peg.1704

function

Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)

Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Type IV fimbrial assembly, ATPase PilB
Type IV pilin PilA
Type IV pilus biogenesis protein PilE
Type IV pilin PilA
Type IV pilus biogenesis protein PilE

Cyanobacteria-specific RpoD-like sigma factor, type-7
Cyanobacteria-specific RpoD-like sigma factor, type-2 @ Group 2 RNA polymerase sigma factor
Cyanobacteria-specific RpoD-like sigma factor, type-2 @ Group 2 RNA polymerase sigma factor
RNA polymerase sigma factor RpoD
Cyanobacteria-specific RpoD-like sigma factor, type-2 @ Group 2 RNA polymerase sigma factor

Group 2 RNA polymerase sigma factor @ Cyanobacteria-specific RpoD-like sigma factor, type-7
Cyanobacteria-specific RpoD-like sigma factor, type-3 @ Group 2 RNA polymerase sigma factor
Cyanobacteria-specific RpoD-like sigma factor, type-3 @ Group 2 RNA polymerase sigma factor

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Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
Alternative cytochrome c oxidase polypeptide CoxP (EC 1.9.3.1)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1)

SSU ribosomal protein S8p (S15Ae)
SSU ribosomal protein S13p (S18e)
SSU ribosomal protein S1p
SSU ribosomal protein S1p
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S2p (SAe)
SSU ribosomal protein S15p (S13e)
SSU ribosomal protein S2p (SAe), chloroplast
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S3p (S3e)
SSU ribosomal protein S11p (S14e)
SSU ribosomal protein S20p
SSU ribosomal protein S11p (S14e)
SSU ribosomal protein S10p (S20e)

Type cbb3 cytochrome oxidase biogenesis protein CcoI; Copper-translocating P-type ATPase (EC 3.6.3.4)
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPas

			TREATMENT	
e-value	score	identity	Relative abundance	fragment
			0.32	4451573.3 GLP7T0L02F99RW
				4451573.3 GLP7T0L02GKWRV
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				4451573.3 GLP7T0L02JPP6J
				4451573.3 GLP7T0L02GR7FO
				4451573.3 GLP7T0L02G8E5S
				4451573.3 GLP7T0L02JOWOB
				4451573.3 GLP7T0L02IWQIW
				4451573.3 GLP7T0L02JF07F
				4451573.3 GLP7T0L02JNJH9
				4451573.3 GLP7T0L02FQ6NK
				4451573.3 GLP7T0L02FUJQG
				4451573.3 GLP7T0L02GOE23
				4451573.3 GLP7T0L02FM077
				4451573.3 GLP7T0L02HSUAM
				4451573.3 GLP7T0L02GV9NK
				4451573.3 GLP7T0L02FIG8Q
				4451573.3 GLP7T0L02IIUQ3
				4451573.3 GLP7T0L02HFJIV
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			0.36	4451573.3 GLP7T0L02FV9YC
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				4451573.3 GLP7T0L02GF03U
				4451573.3 GLP7T0L02HIPEX
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				4451574.3 GLP7T0L02FHUU9
			0.12	4451573.3 GLP7T0L02HTXK5
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				4451573.3 GLP7T0L02JS4ZN
				4451573.3 GLP7T0L02I5870
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				4451579.3 GLP7T0L02HGNQA
				4451579.3 GLP7T0L02HZVFO
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	4451579.3	GLP7T0L02GKUTA
	4451579.3	GLP7T0L02IH8X7
	4451579.3	GLP7T0L02GAL2H
	4451578.3	GLP7T0L02GTLQD
	4451578.3	GLP7T0L02I4FQV
0.30	NA	
0.26	4451579.3	GLP7T0L02FW0R5
	4451579.3	GLP7T0L02INOHF
	4451579.3	GLP7T0L02F0KE8
	4451579.3	GLP7T0L02FM0TR
	4451579.3	GLP7T0L02FMEOG
	4451579.3	GLP7T0L02I5BU0
	4451579.3	GLP7T0L02H0TTS
	4451579.3	GLP7T0L02JVWQM
	4451579.3	GLP7T0L02FGFNO
	4451579.3	GLP7T0L02IIH8Y
	4451578.3	GLP7T0L02IVK4Y
	4451578.3	GLP7T0L02JK69I
0.76	4451579.3	GLP7T0L02F9LXF
	4451579.3	GLP7T0L02IZE19
	4451579.3	GLP7T0L02GOBSJ
	4451579.3	GLP7T0L02HCUF6
	4451579.3	GLP7T0L02HXP04
	4451579.3	GLP7T0L02ISKBC
	4451579.3	GLP7T0L02JATHH
	4451579.3	GLP7T0L02ISI9S
	4451579.3	GLP7T0L02I3K3Z
	4451579.3	GLP7T0L02GZKBQ
	4451579.3	GLP7T0L02F1NTL
	4451578.3	GLP7T0L02FWMOC
	4451578.3	GLP7T0L02JA2X9
0.46	4451579.3	GLP7T0L02IYXG5
	4451579.3	GLP7T0L02I86QL
	4451579.3	GLP7T0L02JLFN5

				4451579.3	GLP7T0L02JP44K
				4451579.3	GLP7T0L02ITIXI
				4451579.3	GLP7T0L02ITF4W
				4451579.3	GLP7T0L02HA4L1
				4451579.3	GLP7T0L02FZERU
				4451578.3	GLP7T0L02IYXLU
				4451578.3	GLP7T0L02H6VJE
				4451578.3	GLP7T0L02I60XF
				4451578.3	GLP7T0L02IJQXO
			0.20	4451578.3	GLP7T0L02HRTSQ
				4451578.3	GLP7T0L02HZJ5C
				4451578.3	GLP7T0L02GPEL0
				4451578.3	GLP7T0L02IOFF2
				4451579.3	GLP7T0L02H0ESE
				4451579.3	GLP7T0L02J4P3T
				4451579.3	GLP7T0L02JH08A
				4451579.3	GLP7T0L02HZVFO
				4451579.3	GLP7T0L02HK339
				4451579.3	GLP7T0L02IB1YB
				4451579.3	GLP7T0L02JRIR3
				4451579.3	GLP7T0L02I6SK4
				4451579.3	GLP7T0L02JFTUV
				4451579.3	GLP7T0L02G65DX
				4451579.3	GLP7T0L02GQFNY
				4451579.3	GLP7T0L02II2LI
				4451579.3	GLP7T0L02II2LI
				4451579.3	GLP7T0L02G7920
				4451579.3	GLP7T0L02G3JSK
				4451579.3	GLP7T0L02JL9K5
				4451579.3	GLP7T0L02HBEBR
				4451579.3	GLP7T0L02JAX5I
				4451579.3	GLP7T0L02JGDZQ
				4451579.3	GLP7T0L02IMO1B
				4451579.3	GLP7T0L02H4QKU
				4451579.3	GLP7T0L02J17P3
				4451579.3	GLP7T0L02IRT25
				4451579.3	GLP7T0L02HX15R
3.00E-03	40 bits (103)	19/21 (90%)	0.36	4451579.3	GLP7T0L02JS3VO
1.00E-38	158 bits (407)	74/104 (71%)		4451579.3	GLP7T0L02JPYD3
6.00E-05	46 bits (118)	21/27 (78%)		4451579.3	GLP7T0L02FK7LK
6.00E-05	46 bits (118)	21/27 (78%)		4451579.3	GLP7T0L02JTQDL
2.00E-47	187 bits (481)	93/104 (89%)		4451579.3	GLP7T0L02H1ALW
4.00E-13	73 bits (188)	36/51 (71%)		4451579.3	GLP7T0L02F75RC
5.00E-09	59 bits (153)	33/36 (92%)		4451579.3	GLP7T0L02G23UY
4.00E-05	46 bits (119)	22/29 (76%)		4451579.3	GLP7T0L02H4K36
3.00E-07	53 bits (138)	27/39 (69%)		4451579.3	GLP7T0L02FHLCE
				4451579.3	GLP7T0L02GRDMG

				4451579.3 GLP7T0L02FZJT9
				4451579.3 GLP7T0L02H42E4
				4451579.3 GLP7T0L02IIOUI
				4451579.3 GLP7T0L02JJHCS
				4451579.3 GLP7T0L02H0M52
				4451579.3 GLP7T0L02IENTM
				4451579.3 GLP7T0L02FTCTG
				4451579.3 GLP7T0L02IZ81I
				4451579.3 GLP7T0L02HL2KS
				4451579.3 GLP7T0L02IJFVC
				4451579.3 GLP7T0L02I4DMS
				4451579.3 GLP7T0L02IDKJJ
				4451579.3 GLP7T0L02HG1BI
				4451579.3 GLP7T0L02FRBDZ
				4451579.3 GLP7T0L02G37I6
				4451578.3 GLP7T0L02FTB1C
				4451578.3 GLP7T0L02JHX3M
			0.29	4451579.3 GLP7T0L02HIHNM
				4451579.3 GLP7T0L02JP54Z
				4451579.3 GLP7T0L02H3C2K
				4451579.3 GLP7T0L02GHTRS
				4451579.3 GLP7T0L02I5R57
				4451579.3 GLP7T0L02I1MIX
				4451579.3 GLP7T0L02G6UCP
				4451579.3 GLP7T0L02H5ABV
				4451579.3 GLP7T0L02FUG54
				4451579.3 GLP7T0L02H932O
				4451579.3 GLP7T0L02GUDOS
				4451579.3 GLP7T0L02IUY86
				4451579.3 GLP7T0L02GXALY
				4451579.3 GLP7T0L02IVV1X
				4451579.3 GLP7T0L02HOUMA
				4451579.3 GLP7T0L02F4CLU
				4451579.3 GLP7T0L02GF9P7
				4451579.3 GLP7T0L02IQO56
				4451579.3 GLP7T0L02H3C2K
				4451579.3 GLP7T0L02IPY5K
				4451579.3 GLP7T0L02IIGKL
				4451579.3 GLP7T0L02G1N2L
				4451579.3 GLP7T0L02H4Z4Z
				4451578.3 GLP7T0L02HWQKK
				4451578.3 GLP7T0L02G6IQ1
6.00E-03	39 bits (101)	21/28 (75%)	0.14	4451579.3 GLP7T0L02JJAZ0
3.00E-17	86 bits (223)	44/70 (63%)		4451579.3 GLP7T0L02IZGBD
5.00E-10	62 bits (161)	32/38 (84%)		4451579.3 GLP7T0L02GI3O5
2.00E-40	163 bits (421)	85/97 (88%)		4451579.3 GLP7T0L02GOOLU
6.00E-09	59 bits (152)	30/47 (64%)		4451579.3 GLP7T0L02JZDBE

7.00E-06	49 bits (126)	25/31 (81%)		4451579.3 GLP7T0L02HCFLA
2.00E-30	130 bits (336)	61/80 (76%)		4451579.3 GLP7T0L02HJ3FG
4.00E-14	76 bits (196)	38/57 (67%)		4451579.3 GLP7T0L02GMO2P
				4451579.3 GLP7T0L02FPYRC
				4451579.3 GLP7T0L02H68QS
				4451578.3 GLP7T0L02GUMTK
				4451578.3 GLP7T0L02G6T20
3.00E-17	86 bits (223)	37/52 (71%)	0.27	4451578.3 GLP7T0L02HIFL4
8.00E-07	52 bits (134)	23/30 (77%)		4451578.3 GLP7T0L02HRZ8B
3.00E-04	43 bits (112)	18/26 (69%)		4451578.3 GLP7T0L02FGWW3
				4451579.3 GLP7T0L02GQPO6
				4451579.3 GLP7T0L02G9QJR
				4451579.3 GLP7T0L02JMS0F
				4451579.3 GLP7T0L02F93YH
				4451579.3 GLP7T0L02JTC8T
				4451579.3 GLP7T0L02IIE5I
				4451579.3 GLP7T0L02JQ080
				4451579.3 GLP7T0L02GTXGW
				4451579.3 GLP7T0L02ICNVI
				4451579.3 GLP7T0L02H4TC1
				4451579.3 GLP7T0L02GROTZ
				4451579.3 GLP7T0L02FQPID
				4451579.3 GLP7T0L02IV9AT
			0.88	4451578.3 GLP7T0L02GH7VJ
				4451578.3 GLP7T0L02JRQ6Q
				4451578.3 GLP7T0L02JNN9H
				4451578.3 GLP7T0L02JM5NE
				4451578.3 GLP7T0L02G6XSP
				4451579.3 GLP7T0L02JVYSA
				4451579.3 GLP7T0L02FEYUP
				4451579.3 GLP7T0L02G9ADP
				4451579.3 GLP7T0L02G2J36
				4451579.3 GLP7T0L02HNWQQ
				4451579.3 GLP7T0L02JL4M1
				4451579.3 GLP7T0L02I8NIP
				4451579.3 GLP7T0L02JBL7R
				4451579.3 GLP7T0L02I3UNU
				4451579.3 GLP7T0L02FM3R7
				4451579.3 GLP7T0L02I5FK3
				4451579.3 GLP7T0L02HXNFJ
				4451579.3 GLP7T0L02FHBXG
				4451579.3 GLP7T0L02IW9CR
				4451579.3 GLP7T0L02GZ26A
				4451579.3 GLP7T0L02JH87N
				4451579.3 GLP7T0L02FR3PN
				4451579.3 GLP7T0L02G25RI
				4451579.3 GLP7T0L02ITCX3

				4451579.3 GLP7T0L02IDYFM
				4451579.3 GLP7T0L02JZLAO
				4451579.3 GLP7T0L02H5IYL
				4451579.3 GLP7T0L02GOVA8
				4451579.3 GLP7T0L02GP1R1
3.00E-29	126 bits (326)	60/82 (73%)	0.75	4451578.3 GLP7T0L02IOOYZ
7.00E-16	82 bits (211)	38/48 (79%)		4451578.3 GLP7T0L02H401Y
4.00E-10	63 bits (162)	29/49 (59%)		4451578.3 GLP7T0L02HT8ZC
1.00E-04	44 bits (115)	23/23 (100%)		4451578.3 GLP7T0L02FG8V5
2.00E-23	107 bits (276)	50/78 (64%)		4451578.3 GLP7T0L02HMJED
2.00E-06	51 bits (131)	23/38 (61%)		4451578.3 GLP7T0L02FQUUP
2.00E-06	51 bits (131)	23/38 (61%)		4451578.3 GLP7T0L02I67KW
6.00E-22	102 bits (263)	53/93 (57%)		4451578.3 GLP7T0L02JU3K8
3.00E-13	73 bits (189)	36/62 (58%)		4451578.3 GLP7T0L02GW0DG
7.00E-22	102 bits (262)	49/65 (75%)		4451578.3 GLP7T0L02JSFOF
2.00E-11	67 bits (173)	35/50 (70%)		4451578.3 GLP7T0L02IUJRY
9.00E-04	42 bits (108)	21/27 (78%)		4451579.3 GLP7T0L02HL6EZ
6.00E-26	115 bits (298)	54/57 (95%)		4451579.3 GLP7T0L02I3I40
3.00E-15	80 bits (206)	42/44 (95%)		4451579.3 GLP7T0L02FZ5UR
3.00E-03	40 bits (103)	21/29 (72%)		4451579.3 GLP7T0L02I2EWO
6.00E-26	115 bits (298)	59/65 (91%)		4451579.3 GLP7T0L02GO8V0
9.00E-23	105 bits (270)	52/56 (93%)		4451579.3 GLP7T0L02GYU2W
				4451579.3 GLP7T0L02GS36Z
				4451579.3 GLP7T0L02IX6BF
				4451579.3 GLP7T0L02JKYP5
				4451579.3 GLP7T0L02GEPN2
				4451579.3 GLP7T0L02JCYXX
				4451579.3 GLP7T0L02IRVTF
				4451579.3 GLP7T0L02IJP7R
				4451579.3 GLP7T0L02G13MH
				4451579.3 GLP7T0L02FG4UM
				4451579.3 GLP7T0L02HJDVY
				4451579.3 GLP7T0L02G81KI
				4451579.3 GLP7T0L02H2XZ3
				4451579.3 GLP7T0L02I1XW4
				4451579.3 GLP7T0L02JKD3M
				4451579.3 GLP7T0L02FVOCZ
				4451579.3 GLP7T0L02I8V0V
				4451579.3 GLP7T0L02IFJCU
				4451579.3 GLP7T0L02F3CHD
				4451579.3 GLP7T0L02H9KSP
				4451579.3 GLP7T0L02I8GY7
				4451579.3 GLP7T0L02G4V7O
			0.18	NA
2.00E-04	44 bits (114)	23/36 (64%)	0.10	NA
1.00E-07	55 bits (141)	28/53 (53%)		

organism
Geobacter uraniumreducens Rf4
Trichodesmium erythraeum IMS101
Anabaena variabilis ATCC 29413
Dinoroseobacter shibae DFL 12
Cyanothece sp. PCC 8801
Cyanothece sp. CCY0110
Trichodesmium erythraeum IMS101
Shewanella woodyi ATCC 51908
Nostoc punctiforme PCC 73102
Rubrobacter xylanophilus DSM 9941
Nostoc punctiforme PCC 73102
Xanthomonas campestris pv. campestris 8004 (Beijing)
Treponema pallidum subsp. pallidum SS14
Mesorhizobium loti MAFF303099
Trichodesmium erythraeum IMS101
Cytophaga hutchinsonii ATCC 33406
Hahella chejuensis KCTC 2396
Cyanothece sp. CCY0110
Methylacidiphilum infernorum V4
Sinorhizobium meliloti 1021
Thermoanaerobacter tengcongensis MB4(T)
Gluconobacter oxydans 621H
Xanthomonas campestris pv. campestris B100
Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)
Sphingopyxis alaskensis RB2256
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Solibacter usitatus Ellin6076
Bacteroides thetaiotaomicron VPI-5482
Moorella thermoacetica ATCC 39073
marine actinobacterium PHSC20C1
Sphingopyxis alaskensis RB2256
Acidovorax sp. JS42
Thermosynechococcus elongatus BP-1
Methylococcus capsulatus Bath
Sulfitobacter sp. EE-36
Brucella suis 1330
Anabaena variabilis ATCC 29413
Brucella suis
Brucella suis
Aurantimonas sp. SI85-9A1
Methylobacterium sp. 4-46
Pseudomonas fluorescens SBW25
Rhodobacter sphaeroides ATCC 17025
Methylobacterium extorquens PA1

Cyanothece sp. PCC 8802
Xanthomonas oryzae pv. oryzae KACC10331
Rhodospirillum centenum SW
Sulfitobacter sp. EE-36
Microcystis aeruginosa NIES-843
Maricaulis maris MCS10
Microcystis aeruginosa NIES-843
Porphyromonas gingivalis ATCC 33277
Parabacteroides distasonis ATCC 8503
Bordetella parapertussis 12822
Synechococcus sp. (strain WH7805)
Bacillus cereus ATCC 14579
Caulobacter crescentus NA1000
Brucella melitensis bv. 1 16M
Xanthomonas campestris pv. campestris B100
Ralstonia solanacearum GMI1000
Salmonella enterica subsp. enterica serovar Typhi Ty2
Xylella fastidiosa M23
Xylella fastidiosa M23
Jonesia denitrificans DSM 20603
Parvibaculum lavamentivorans DS-1
Leptothrix cholodni SP-6
Alkalilimnicola ehrlichei MLHE-1
Rhodobacter sphaeroides ATCC 17029
Cyanobacteria bacterium Yellowstone B-Prime (Synechococcus sp. JA- 2-3B'a(2-13))
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Trichodesmium erythraeum IMS101
Methylobacterium sp. 4-46
Polaromonas sp. JS666
Bacteriovorax marinus (strain ATCC BAA-682 / DSM 15412 / SJ)
Methylobacterium sp. 4-46
Pseudomonas entomophila L48
Bordetella parapertussis 12822
Thermoanaerobacter tengcongensis MB4(T)
Xanthomonas oryzae pv. oryzae MAFF 311018
Opitutus terrae PB90-1
Ralstonia solanacearum GMI1000
Anaeromyxobacter dehalogenans 2CP-C
Prochlorococcus marinus NATL2A
Rhodopirellula baltica SH 1 (Pirellula sp. strain 1)
Xylella fastidiosa subsp. sandyi Ann-1
Saccharopolyspora erythraea NRRL 2338
Rhodobacter sphaeroides ATCC 17029
Stenotrophomonas maltophilia K279a
Opitutus terrae PB90-1

Nostoc punctiforme PCC 73102
Nostoc punctiforme PCC 73102
Pseudomonas putida F1

Photorhabdus luminescens subsp. laumondii TTO1
Deinococcus radiodurans R1
Burkholderia pseudomallei 668
Leptothrix cholodnii SP-6
Magnetospirillum magnetotacticum
Hyphomonas neptunium ATCC 15444
Sphaerobacter thermophilus DSM 20745
Bradyrhizobium sp. ORS278
Mycobacterium avium subsp. paratuberculosis k10
Cupriavidus metallidurans CH34
Desulfitobacterium hafniense DCB-2
Rhodoferax ferrireducens T118 (DSM 15236)
Herpetosiphon aurantiacus ATCC 23779
Methylibium petroleiphilum PM1
Burkholderia sp. 383
Syntrophus aciditrophicus SB
Sorangium cellulosum So ce 56
Sphaerobacter thermophilus DSM 20745
Rhodoferax ferrireducens T118 (DSM 15236)
Haliangium ochraceum DSM 14365
Brucella abortus 9-941 (biovar 1)
marine actinobacterium PHSC20C1
Nocardia farcinica IFM 10152
Rhodospirillum rubrum ATCC 11170
Parvularcula bermudensis HTCC2503
Solibacter usitatus Ellin6076
Silicibacter pomeroyi DSS-3
Caulobacter sp. K31
Methylobacterium sp. 4-46
Chloroherpeton thalassium ATCC 35110
Bacillus halodurans C-125
Sorangium cellulosum So ce 56
Rhodoferax ferrireducens T118 (DSM 15236)
Acinetobacter baumannii AB307-0294
Azoarcus sp. BH72
Janibacter sp. HTCC2649
Acinetobacter baumannii AB307-0294
Marinobacter aquaeolei VT8
Roseovarius sp. 217
Xanthomonas campestris pv. campestris ATCC 33913
Burkholderia pseudomallei K96243
Geobacillus thermodenitrificans NG80-2
Xanthomonas oryzae pv. oryzae KACC10331
Actinobacillus actinomycetemcomitans HK1651

Burkholderia xenovorans LB400
Mycobacterium sp. JLS
Mycobacterium leprae Br4923
Pseudoalteromonas atlantica T6c
Methylobacterium sp. 4-46
Rhizobium leguminosarum bv. viciae 3841

Herpetosiphon aurantiacus ATCC 23779
Prochlorococcus marinus MIT 9515
Xanthomonas campestris pv. campestris ATCC 33913
Photobacterium profundum SS9
Thiomicrospira crunogena XCL-2
Myxococcus xanthus DK 1622
Synechococcus elongatus PCC6301

Acidovorax sp. JS42
Burkholderia cenocepacia AU 1054
Polaromonas sp. JS666
Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))

Delftia acidovorans SPH-1
Pectobacterium wasabiae WPP163
Delftia acidovorans SPH-1
Shewanella amazonensis SB2B
Delftia acidovorans (strain DSM 14801 / SPH-1)
Delftia acidovorans (strain DSM 14801 / SPH-1)

Brucella suis ATCC 23445
Rhodospirillum centenum SW
Rhodothermus marinus DSM 4252
Ralstonia eutropha JMP134
Bordetella bronchiseptica (Alcaligenes bronchisepticus)

Chitinophaga pinensis DSM 2588
Anaeromyxobacter dehalogenans 2CP-C
Burkholderia dolosa AUO158
Rhodobacter sphaeroides 2.4.1
Rhodospirillum rubrum ATCC 11170
Photorhabdus luminescens subsp. laumondii TTO1
Pseudomonas syringae pv. phaseolicola 1448A
Sphingopyxis alaskensis RB2256
Cytophaga hutchinsonii ATCC 33406
Hyphomonas neptunium ATCC 15444
Thermus thermophilus HB8
Chloroflexus aggregans DSM 9485
Chloroflexus aggregans DSM 9485
Mesorhizobium loti MAFF303099

Cyanothece sp. PCC 7425
Novosphingobium aromaticivorans DSM 12444
Leptothrix cholodni SP-6
Cyanothece sp. PCC 7425
Blastopirellula marina DSM 3645
Photorhabdus luminescens subsp. laumondii TTO1
Acidovorax avenae subsp. citrulli AAC00-1
Bacteroides fragilis YCH46
Brucella suis 1330
Vibrio vulnificus CMCP6
Nitrococcus mobilis Nb-231

Rhodobacter sphaeroides 2.4.1
Ralstonia eutropha JMP134
Roseobacter sp. GAI101

Xylella fastidiosa M23
Methylibium petroleiphilum PM1
Oceanicola batsensis HTCC2597
Solibacter usitatus Ellin6076
Ralstonia solanacearum GMI1000
Polaromonas sp. JS666
Delftia acidovorans SPH-1
Delftia acidovorans SPH-1
Neisseria meningitidis MC58 (serogroup B)
Rhodospirillum centenum SW
Pseudomonas syringae pv. tomato DC3000
Delftia acidovorans SPH-1
Burkholderia cenocepacia HI2424
Verminephrobacter eiseniae EF01-2
Rhodospirillum centenum SW
Methylocella silvestris BL2
Azoarcus sp. BH72
Leptothrix cholodnii SP-6
Azoarcus sp. BH72
Pseudomonas syringae pv. syringae B728a
Methylibium petroleiphilum PM1
Aromatoleum aromaticum EbN1
Cupriavidus metallidurans CH34
Flavobacterium psychrophilum JIP02/86
Rhodothermus marinus DSM 4252
Flavobacterium johnsoniae UW101
Roseobacter sp. MED193
Parvibaculum lavamentivorans DS-1
Synechocystis sp. PCC 6803
Synechococcus elongatus PCC 7942

Mycobacterium smegmatis MC2 155
Burkholderia ambifaria MC40-6
Aeropyrum pernix K1

Pseudoalteromonas atlantica T6c
Anaeromyxobacter sp. K
Roseiflexus castenholzii DSM 13941
Alkalilimnicola ehrlichii MLHE-1
Burkholderia pseudomallei 1710b
Mycobacterium vanbaalenii PYR-1
Burkholderia pseudomallei 668
Leptothrix cholodnii SP-6
Oceanicola batsensis HTCC2597
Rhodoferax ferrireducens T118 (DSM 15236)
Polaromonas sp. JS666
Dechloromonas aromatica RCB
Sphaerobacter thermophilus DSM 20745
Leptothrix cholodni SP-6
Burkholderia vietnamiensis G4
Cupriavidus metallidurans CH34
Oceanicaulis alexandrii HTCC2633
Sorangium cellulosum So ce 56
Methylibium petroleiphilum PM1
Burkholderia cenocepacia HI2424
Bordetella parapertussis 12822
Rhodoferax ferrireducens T118 (DSM 15236)
Psychrobacter sp. PRwf-1
Haliangium ochraceum DSM 14365
Mycobacterium smegmatis MC2 155
Verminephrobacter eiseniae EF01-2
Maricaulis maris MCS10
Parvularcula bermudensis HTCC2503
Sphingomonas wittichii RW1
Ruegeria sp. TM1040
Verminephrobacter eiseniae EF01-2
Chloroherpeton thalassium ATCC 35110
Pseudoalteromonas haloplanktis TAC125
Pseudomonas mendocina ymp
Sorangium cellulosum So ce 56
Acidovorax sp. JS42
Azoarcus sp. BH72
Acidovorax sp. JS42
Marinobacter aquaeolei VT8
Myxococcus xanthus DK 1622
Mycobacterium smegmatis MC2 155
Rhodospirillum rubrum ATCC 11170
Haliangium ochraceum DSM 14365
Bacillus halodurans C-125
Dechloromonas aromatica RCB
Leptothrix cholodni SP-6
Chloroflexus sp. Y-400-fl

Congregibacter litoralis KT71
Ruegeria sp. TM1040
Polaromonas sp. JS666
Leeuwenhoekiella blandensis (strain CECT 7118 / CCUG 51940 / MED217) (Flavobacterium sp. (strain MED217))

Polaromonas sp. JS666
Polaromonas sp. JS666
Xanthomonas campestris pv. vesicatoria 85-10
Clostridium difficile 630 (PCR-ribotype 012)
Deinococcus radiodurans R1
Rhodoferax ferrireducens T118 (DSM 15236)
Methylibium petroleiphilum PM1
Nocardioides sp. JS614
Rubrobacter xylanophilus DSM 9941
Ralstonia solanacearum GMI1000
Ralstonia eutropha JMP134
Ralstonia eutropha JMP134
Acidovorax sp. JS42
Flavobacteria bacterium (strain BBFL7)
Pseudomonas fluorescens Pf-5
Microcystis aeruginosa NIES-843
Rhodobacter sphaeroides ATCC 17029
Sphaerobacter thermophilus DSM 20745
Verminephrobacter eiseniae EF01-2
Aurantimonas sp. SI85-9A1
Bacillus licheniformis ATCC 14580
Novosphingobium aromaticivorans DSM 12444
Sorangium cellulosum So ce 56
Rhodospirillum centenum SW
Mycobacterium sp. MCS
Methylibium petroleiphilum PM1
Caulobacter crescentus NA1000
Sphingopyxis alaskensis RB2256
Burkholderia xenovorans LB400
Cyanothece sp. ATCC 51142
Rhodoferax ferrireducens T118 (DSM 15236)
Methylibium petroleiphilum PM1
Microcystis aeruginosa NIES-843
Leptothrix cholodnii SP-6
Citrobacter koseri ATCC BAA-895
Sphaerobacter thermophilus DSM 20745
Sorangium cellulosum So ce 56
Serratia proteamaculans 568
Halorhodospira halophila SL1
Myxococcus xanthus DK 1622
Symbiobacterium thermophilum IAM14863
Solibacter usitatus Ellin6076
Verminephrobacter eiseniae EF01-2

Hyphomonas neptunium ATCC 15444
Azorhizobium caulinodans ORS 571
Myxococcus xanthus DK 1622
Rhizobium leguminosarum bv. viciae 3841
Mannheimia haemolytica
Xanthomonas axonopodis pv. citri 306
Rhodococcus jostii RHA1
Shewanella sp. MR-4
Clavibacter michiganensis subsp. michiganensis NCPPB 382
Dinoroseobacter shibae DFL 12
Opitutus terrae PB90-1
Burkholderia cepacia AMMD
Herpetosiphon aurantiacus ATCC 23779
Burkholderia xenovorans LB400
Anabaena variabilis ATCC 29413
Clavibacter michiganensis subsp. michiganensis NCPPB 382
Syntrophus aciditrophicus SB
Sulfolobus tokodaii strain7
Rhodopseudomonas palustris CGA009
Leptothrix cholodni SP-6
Bradyrhizobium sp. BTAi1
Nostoc punctiforme PCC 73102
Leptothrix cholodni SP-6
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Verminephrobacter eiseniae EF01-2
Rhodopseudomonas palustris CGA009
Burkholderia xenovorans LB400
Myxococcus xanthus DK 1622
Leptothrix cholodnii SP-6
Bradyrhizobium japonicum USDA110
Leeuwenhoekiella blandensis (strain CECT 7118 / CCUG 51940 / MED217) (Flavobacterium sp. (strain MED217))
Catenulispora acidiphila DSM 44928
Haliangium ochraceum DSM 14365
Burkholderia xenovorans LB400
Oceanicaulis alexandrii HTCC2633
Xanthomonas campestris pv. campestris B100
Synechococcus sp. CC9605
Methylibium petroleiphilum PM1
Chlamydia trachomatis D/UW-3/CX (serovar D)
Methylibium petroleiphilum PM1
Rickettsia typhi Wilmington (ATCC VR-144)
Cyanothece sp. PCC 8801
Polaromonas sp. JS666
Gloeobacter violaceus PCC7421
Shewanella piezotolerans WP3
Thioalkalivibrio sp. HL-EbGR7
Yersinia pestis Z176003

Polaromonas sp. JS666
Thermotoga petrophila RKU-1
Bordetella pertussis Tohama I
Anabaena variabilis ATCC 29413
Alteromonas macleodii Deep ecotype
Trichodesmium erythraeum IMS101
Actinobacillus actinomycetemcomitans HK1651
Sorangium cellulosum So ce 56

Colwellia psychrerythraea 34H
Burkholderia cepacia AMMD
Novosphingobium aromaticivorans
Anabaena variabilis ATCC 29413
Anabaena variabilis ATCC 29413
Sphingomonas wittichii RW1
Methylibium petroleiphilum PM1
Bacteroides fragilis YCH46
Methylobacillus flagellatus KT
Chromohalobacter salexigens DSM 3043

Minibacterium massiliensis (Janthinobacterium sp. Marseille)
Magnetospirillum gryphiswaldense MSR-1
Nitrosospira multiformis ATCC 25196
Nitrosospira multiformis ATCC 25196
Pseudomonas putida W619
Anaeromyxobacter dehalogenans 2CP-C
Minibacterium massiliensis (Janthinobacterium sp. Marseille)
Aeromonas salmonicida subsp. salmonicida A449
Nitrosomonas eutropha C91
Aeromonas salmonicida subsp. salmonicida A449
Anaeromyxobacter sp. K
Candidatus Methanosphaerula palustris E1-9c

Minibacterium massiliensis (Janthinobacterium sp. Marseille)
Brucella suis ATCC 23445
Pseudomonas fluorescens Pf0-1
Rhizobium leguminosarum bv. viciae 3841
Ralstonia solanacearum GMI1000
Burkholderia pseudomallei 1710b
Caulobacter crescentus NA1000
Candidatus Desulfococcus oleovorans Hxd3
Solibacter usitatus Ellin6076
Xanthomonas axonopodis pv. citri 306
Caulobacter crescentus NA1000
Burkholderia pseudomallei 1106a
Shewanella frigidimarina NCIMB 400

Rhodospirillum rubrum ATCC 11170
Polaromonas sp. JS666
Dinoroseobacter shibae DFL 12

Brucella suis ATCC 23445
Bordetella pertussis Tohama I
Rhodothermus marinus DSM 4252
Polaromonas sp. JS666
Leptothrix cholodni SP-6
Dinoroseobacter shibae DFL 12
Leptothrix cholodni SP-6
Maritimibacter alkaliphilus HTCC2654
Cupriavidus metallidurans CH34

Cytophaga hutchinsonii ATCC 33406
Delftia acidovorans SPH-1
Myxococcus xanthus DK 1622
Symbiobacterium thermophilum IAM14863
Deinococcus radiodurans R1
Rhodoferax ferrireducens T118 (DSM 15236)
Deinococcus radiodurans R1
Rubrobacter xylanophilus DSM 9941
Erythrobacter sp. NAP1
Flavobacteria bacterium (strain BBFL7)
Polaromonas sp. JS666
Oceanicola batsensis HTCC2597
Staphylococcus aureus subsp. aureus MRSA252, methicillin-resistant
Sphaerobacter thermophilus DSM 20745
Ralstonia eutropha JMP134
Ralstonia eutropha JMP134
Ralstonia eutropha JMP134
Rhodobacter sphaeroides ATCC 17029
Novosphingobium aromaticivorans DSM 12444
Rhodospirillum centenum SW
Mycobacterium sp. MCS
Pseudomonas syringae pv. syringae B728a
Leptothrix cholodnii SP-6
Sphaerobacter thermophilus DSM 20745
Hyphomonas neptunium ATCC 15444
Bordetella avium 197N
Rhodopseudomonas palustris CGA009
Leptothrix cholodnii SP-6

Dichelobacter nodosus VCS1703A
Desulfitobacterium hafniense Y51
Pelobacter carbinolicus DSM 2380
Burkholderia pseudomallei MSHR346
Geobacter uraniumreducens Rf4
Aromatoleum aromaticum EbN1
Geobacter metallireducens GS-15
Geobacter bemidjiensis Bem
Blastopirellula marina DSM 3645
Acidothermus cellulolyticus 11B

Geobacter bemidjiensis Bem
Burkholderia pseudomallei 1710b
Acidovorax sp. JS42
Xylella fastidiosa M23
Geobacter metallireducens GS-15
Sorangium cellulosum So ce 56
Stenotrophomonas maltophilia K279a
Rhodospirillum rubrum
Pelobacter carbinolicus DSM 2380
Methylibium petroleiphilum PM1
Verminephrobacter eiseniae EF01-2
Cytophaga hutchinsonii ATCC 33406
Leptothrix cholodni SP-6
Desulfitobacterium hafniense Y51
Erythrobacter litoralis HTCC2594
Haliangium ochraceum DSM 14365
Thermosynechococcus elongatus BP-1

Veillonella parvula DSM 2008
Colwellia psychrerythraea 34H
Polaromonas sp. JS666
Sphingomonas wittichii RW1
Pseudomonas putida GB-1
Coxiella burnetii CbuK_Q154
Synechococcus elongatus PCC 7942
Crocosphaera watsonii WH 8501
Rhizobium leguminosarum bv. viciae 3841
Cyanothece sp. PCC 8801
Sorangium cellulosum So ce 56
Mesoplasma florum L1
Burkholderia xenovorans LB400
Roseiflexus castenholzii DSM 13941
Roseovarius nubinhibens ISM
Parvibaculum lavamentivorans DS-1
Acidiphilium cryptum JF-5
Anaeromyxobacter dehalogenans 2CP-C
Polaromonas sp. JS666
Polaromonas sp. JS666
Rhodospirillum rubrum ATCC 11170
Bradyrhizobium japonicum USDA110
Delftia acidovorans SPH-1
Candidatus Desulfococcus oleovorans Hxd3
Flavobacterium psychrophilum JIP02/86

Porphyromonas gingivalis W83
Brucella abortus 9-941 (biovar 1)
Blastopirellula marina DSM 3645
Rickettsia prowazekii Madrid E
Rhodoferax ferrireducens T118 (DSM 15236)

Cyanothece sp. PCC 7424
Cyanobacteria bacterium Yellowstone A-Prime (Synechococcus sp. JA- 3-3Ab)
Hyphomonas neptunium ATCC 15444
Rhodoferax ferrireducens T118 (DSM 15236)
Cyanobacteria bacterium Yellowstone A-Prime (Synechococcus sp. JA- 3-3Ab)
Cyanothece sp. PCC 7425
Haliangium ochraceum DSM 14365

Cafeteria roenbergensis
Planctomyces limnophilus DSM 3776
Cyanobacteria bacterium Yellowstone B-Prime (Synechococcus sp. JA- 2-3B'a(2-13))
Shewanella sp. MR-7
Bradyrhizobium sp. BTAi1
Rickettsia conorii Malish 7
Cyanothece sp PCC 7425
Blastopirellula marina DSM 3645
Ralstonia solanacearum GMI1000
Polaribacter sp. MED152
Erythrobacter litoralis HTCC2594
Polaromonas sp. JS666
Acidovorax ebreus TPSY
Acidovorax ebreus TPSY
Acidovorax ebreus TPSY
Mesorhizobium sp. BNC1

Syntrophobacter fumaroxidans MPOB
Bacteroides vulgatus ATCC 8482
Burkholderia xenovorans LB400
Rhodopseudomonas palustris CGA009
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Legionella pneumophila Paris
Acidovorax sp. JS42
Geobacter metallireducens GS-15
Symbiobacterium thermophilum IAM14863
Methylibium petroleiphilum PM1
Delftia acidovorans SPH-1
Azotobacter vinelandii DJ
Gramella forsetii KT0803
Acidithiobacillus ferrooxidans ATCC 53993
Anaeromyxobacter sp. Fw109-5
Anaeromyxobacter sp. Fw109-5
Rhodoferax ferrireducens T118 (DSM 15236)
Parvibaculum lavamentivorans DS-1
Idiomarina loihiensis L2TR
Methylococcus capsulatus Bath
Campylobacter curvus 525.92
Dyadobacter fermentans DSM 18053
Magnetospirillum magneticum AMB-1
Solibacter usitatus Ellin6076

Anaeromyxobacter sp. Fw109-5
Myxococcus xanthus DK 1622
Methylibium petroleiphilum PM1
Blastopirellula marina DSM 3645
Dyadobacter fermentans DSM 18053
Trichodesmium erythraeum IMS101
Syntrophus aciditrophicus SB
Paracoccus denitrificans PD1222
Chitinophaga pinensis DSM 2588
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Desulfitobacterium hafniense Y51
Bacteroides thetaiotaomicron VPI-5482
Bacillus amyloliquefaciens FZB42
Staphylococcus aureus subsp. aureus USA300_TCH1516, community- acquired meticillin-susceptible
Shewanella sp. W3-18-1
Crocosphaera watsonii WH 8501
Delftia acidovorans SPH-1
Haliangium ochraceum DSM 14365
Geobacter sulfurreducens PCA
Gramella forsetii KT0803
Methylocella silvestris BL2
Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293
Novosphingobium aromaticivorans DSM 12444
Burkholderia dolosa AUO158
Denitrovibrio acetiphilus DSM 12809
Zymomonas mobilis subsp. mobilis ZM4
Xylella fastidiosa M23
Chloroflexus aggregans DSM 9485
Thermosynechococcus elongatus BP-1
Candidatus Amoebophilus asiaticus 5a2
Anabaena sp. PCC 7120 (Nostoc sp. PCC 7120)
Meiothermus silvanus DSM 9946
Cyanothece sp. PCC 8801
Nocardia farcinica IFM 10152
Leptospira interrogans serovar Copenhageni Fiocruz L1-130
Magnetospirillum magneticum AMB-1
Anaeromyxobacter sp. K
Kytococcus sedentarius DSM 20547
Anaeromyxobacter sp. K
Idiomarina loihiensis L2TR
Opitutus terrae PB90-1
Aliivibrio salmonicida LFI1238
Verminephrobacter eiseniae EF01-2

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fig|232721.5.peg.3159
fig|62928.7.peg.2536
fig|232721.5.peg.3759
fig|351348.5.peg.1780
fig|246197.19.peg.3334
fig|246196.1.peg.6912
fig|1085.1.peg.2827
fig|502025.5.peg.367
fig|272558.1.peg.214
fig|159087.4.peg.190
fig|395495.3.peg.4002
fig|324602.4.peg.1988

fig|314285.3.peg.173
fig|292414.1.peg.702
fig|296591.1.peg.827
fig|313593.3.peg.1860

fig|296591.1.peg.5195
fig|296591.1.peg.5195
fig|316273.3.peg.375
fig|1496.1.peg.2655
fig|243230.1.peg.2110
fig|338969.3.peg.3722
fig|420662.8.peg.1857
fig|196162.6.peg.3653
fig|266117.6.peg.981
fig|267608.1.peg.1049
fig|264198.3.peg.2205
fig|264198.3.peg.2205
fig|232721.5.peg.2671
fig|156586.3.peg.2547
fig|220664.3.peg.128
fig|449447.3.peg.4506
fig|349101.4.peg.1329
fig|479434.4.peg.869
fig|391735.5.peg.2530
fig|314269.3.peg.614
fig|279010.5.peg.2795
fig|48935.1.peg.1026
fig|448385.11.peg.3650
fig|414684.4.peg.247
fig|164756.6.peg.3355
fig|420662.8.peg.462
fig|190650.1.peg.3554
fig|317655.9.peg.1739
fig|36873.1.peg.2881
fig|43989.3.peg.2665
fig|338969.3.peg.2720
fig|420662.8.peg.1243
fig|449447.3.peg.4506
fig|395495.3.peg.3637
fig|290338.6.peg.3661
fig|479434.4.peg.1733
fig|448385.11.peg.3650
fig|399741.3.peg.3081
fig|349124.5.peg.959
fig|246197.19.peg.6030
fig|292459.1.peg.1148
fig|234267.9.peg.361
fig|391735.5.peg.756

fig|228405.5.peg.3338
fig|438753.3.peg.4391
fig|246197.19.peg.4804
fig|216596.5.peg.183
fig|75985.2.peg.663
fig|190486.1.peg.2552
fig|101510.15.peg.1465
fig|60480.16.peg.1683
fig|443906.9.peg.1432
fig|398580.3.peg.1408
fig|452637.4.peg.903
fig|339670.3.peg.3988
fig|316274.3.peg.1163
fig|36873.1.peg.3186
fig|240292.3.peg.294
fig|443906.9.peg.1432
fig|56780.10.peg.1004
fig|273063.1.peg.2175
fig|258594.1.peg.658
fig|395495.3.peg.3484
fig|288000.5.peg.6460
fig|63737.4.peg.5221
fig|395495.3.peg.3489
fig|103690.1.peg.5110
fig|391735.5.peg.707
fig|258594.1.peg.658
fig|36873.1.peg.5722
fig|246197.19.peg.3334
fig|395495.3.peg.3491
fig|224911.1.peg.1076
fig|313593.3.peg.1860
fig|479433.4.peg.6294
fig|502025.5.peg.2959
fig|36873.1.peg.830
fig|314254.3.peg.1723
fig|509169.3.peg.4
fig|110662.3.peg.2534
fig|420662.8.peg.2108
fig|272561.1.peg.191
fig|420662.8.peg.2108
fig|257363.1.peg.211
fig|41431.3.peg.1422
fig|296591.1.peg.4800
fig|251221.1.peg.3082
fig|225849.3.peg.19
fig|396588.3.peg.4
fig|386656.4.peg.2484

fig|296591.1.peg.4975
fig|390874.10.peg.95
fig|257313.1.peg.824
fig|240292.3.peg.1414
fig|314275.6.peg.7
fig|203124.1.peg.5093
fig|714.2.peg.469
fig|448385.11.peg.4114
fig|167879.3.peg.972
fig|339670.3.peg.2959
fig|48935.1.peg.3669
fig|240292.3.peg.1307
fig|240292.3.peg.1307
fig|392499.4.peg.3074
fig|420662.8.peg.2971
fig|295405.3.peg.729
fig|265072.7.peg.245
fig|290398.4.peg.1225

fig|375286.6.peg.1976
fig|431944.4.peg.3233
fig|323848.3.peg.1293
fig|323848.3.peg.1293
fig|390235.3.peg.2127
fig|290397.13.peg.3174
fig|375286.6.peg.1976
fig|382245.6.peg.3006
fig|335283.5.peg.1967
fig|382245.6.peg.3006
fig|447217.4.peg.3339
fig|521011.3.peg.651
fig|375286.6.peg.1938
fig|470137.3.peg.1513
fig|205922.3.peg.2809
fig|216596.1.peg.4152
fig|267608.1.peg.2544
fig|320372.3.peg.4016
fig|190650.1.peg.3573
fig|96561.3.peg.506
fig|234267.9.peg.3280
fig|190486.1.peg.2925
fig|190650.1.peg.388
fig|243160.4.peg.1461
fig|318167.10.peg.805
fig|1085.1.peg.3714
fig|296591.1.peg.4113
fig|398580.3.peg.1034

fig|470137.3.peg.2576
fig|257313.1.peg.3615
fig|518766.5.peg.1711
fig|296591.1.peg.591
fig|395495.3.peg.3074
fig|398580.8.peg.51
fig|395495.3.peg.310
fig|314271.3.peg.4038
fig|266264.4.peg.4599

fig|269798.12.peg.961
fig|398578.3.peg.5450
fig|246197.19.peg.6030
fig|292459.1.peg.1148
fig|243230.1.peg.2110
fig|338969.3.peg.3722
fig|243230.1.peg.113
fig|266117.6.peg.981
fig|237727.3.peg.1783
fig|156586.3.peg.2547
fig|296591.1.peg.2881
fig|252305.3.peg.1531
fig|282458.1.peg.1204
fig|479434.4.peg.869
fig|264198.3.peg.2738
fig|264198.3.peg.2738
fig|264198.3.peg.2738
fig|349101.4.peg.3948
fig|48935.1.peg.1026
fig|414684.4.peg.247
fig|164756.6.peg.3355
fig|205918.4.peg.4941
fig|395495.3.peg.3215
fig|479434.4.peg.866
fig|228405.5.peg.882
fig|360910.3.peg.1919
fig|258594.1.peg.123
fig|395495.3.peg.3637

fig|246195.3.peg.430
fig|272564.4.peg.883
fig|338963.3.peg.157
fig|334803.3.peg.663
fig|351605.4.peg.2632
fig|76114.4.peg.1047
fig|269799.3.peg.230
fig|404380.3.peg.80
fig|314230.3.peg.5266
fig|351607.5.peg.1317

fig|404380.3.peg.187
fig|320372.3.peg.5227
fig|232721.5.peg.866
fig|405440.3.peg.1913
fig|269799.3.peg.1235
fig|448385.11.peg.5772
fig|40324.1.peg.1076
fig|1085.1.peg.1173
fig|338963.3.peg.157
fig|420662.8.peg.1698
fig|391735.5.peg.2644
fig|269798.12.peg.1803
fig|395495.3.peg.4188
fig|272564.4.peg.883
fig|314225.3.peg.753
fig|502025.5.peg.842
fig|197221.1.peg.122

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fig|479436.4.peg.359
fig|167879.3.peg.2411
fig|296591.1.peg.1616
fig|392499.4.peg.4694
fig|76869.3.peg.342
fig|434924.4.peg.306
fig|1140.3.peg.266
fig|165597.1.peg.2131
fig|216596.1.peg.4090
fig|41431.3.peg.2525
fig|448385.11.peg.5073
fig|265311.3.peg.93
fig|36873.1.peg.7068
fig|383372.4.peg.597
fig|89187.3.peg.1833
fig|402881.6.peg.2432
fig|349163.4.peg.3109
fig|290397.13.peg.2736
fig|296591.1.peg.1616
fig|296591.1.peg.1616
fig|1085.1.peg.3267
fig|224911.1.peg.6687
fig|398578.3.peg.5950
fig|96561.3.peg.2806
fig|402612.4.peg.65

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fig|242619.1.peg.522
fig|262698.3.peg.1380
fig|314230.3.peg.4419
fig|272947.1.peg.810
fig|338969.3.peg.3304

fig|65393.5.peg.2897
fig|321327.20.peg.2010
fig|228405.5.peg.2767
fig|338969.3.peg.3304
fig|321327.20.peg.2010
fig|395961.4.peg.1491
fig|502025.5.peg.2204

fig|33653.1.peg.4
fig|521674.4.peg.4050
fig|321332.10.peg.2698
fig|94122.5.peg.2172
fig|288000.5.peg.2848
fig|272944.1.peg.553
fig|395961.4.peg.1183
fig|314230.3.peg.718
fig|267608.1.peg.1280
fig|313598.3.peg.635
fig|314225.3.peg.2538
fig|296591.1.peg.2014
fig|232721.5.peg.1211
fig|232721.5.peg.1211
fig|232721.5.peg.1212
fig|266779.1.peg.1323

fig|335543.6.peg.2511
fig|435590.6.peg.1912
fig|36873.1.peg.8399
fig|258594.1.peg.217
fig|103690.3.peg.126
fig|297246.3.peg.2858
fig|232721.5.peg.4018
fig|269799.3.peg.1388
fig|292459.1.peg.3144
fig|420662.8.peg.2011
fig|398578.3.peg.18
fig|354.1.peg.3946
fig|411154.5.peg.1222
fig|380394.3.peg.1157
fig|404589.4.peg.3503
fig|404589.4.peg.3503
fig|338969.3.peg.4288
fig|402881.6.peg.2440
fig|283942.3.peg.1357
fig|243233.4.peg.1447
fig|360105.6.peg.1558
fig|471854.4.peg.3873
fig|342108.5.peg.2245
fig|234267.9.peg.16

fig|404589.4.peg.3503
fig|246197.19.peg.455
fig|420662.8.peg.1533
fig|314230.3.peg.3185
fig|471854.4.peg.5298
fig|203124.1.peg.2488
fig|56780.10.peg.1574
fig|318586.4.peg.705
fig|485918.5.peg.1970
fig|103690.1.peg.4509
fig|272564.4.peg.3014
fig|226186.1.peg.2709
fig|326423.3.peg.140
fig|93062.4.peg.1045
fig|351745.7.peg.161
fig|165597.1.peg.209
fig|398578.3.peg.4930
fig|502025.5.peg.3163
fig|243231.1.peg.898
fig|411154.5.peg.2659
fig|395965.4.peg.117
fig|203120.4.peg.217
fig|48935.1.peg.1944
fig|350701.3.peg.3044
fig|522772.4.peg.1185
fig|264203.3.peg.1878
fig|405440.3.peg.1452
fig|326427.3.peg.3118
fig|197221.1.peg.1746
fig|452471.3.peg.675
fig|103690.1.peg.3044
fig|526227.4.peg.2251
fig|395962.3.peg.1579
fig|247156.1.peg.4784
fig|267671.1.peg.2775
fig|431944.4.peg.3772
fig|455488.3.peg.2472
fig|478801.4.peg.2308
fig|455488.3.peg.2472
fig|283942.3.peg.1850
fig|452637.4.peg.242
fig|316275.9.peg.599
fig|391735.5.peg.2893

function
Cell division protein FtsX
Cell division protein FtsQ
Septum site-determining protein MinD
rRNA small subunit methyltransferase H # 16S rRNA m(4) C1402 methyltransferase
Cell division topological specificity factor MinE
Cell division trigger factor (EC 5.2.1.8)
Septum site-determining protein MinC
Cell division protein FtsH (EC 3.4.24.-)
Cell division protein FtsW
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsW
Rod shape-determining protein MreB
Cell division protein FtsK
Cell division protein MraZ
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)
Rod shape-determining protein MreB
Cell division trigger factor (EC 5.2.1.8)
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Cell division protein FtsK
Cell division protein FtsZ (EC 3.4.24.-)
Cell division protein FtsH (EC 3.4.24.-)
Cell division protein FtsZ (EC 3.4.24.-)
Rod shape-determining protein MreB
Maltodextrin glucosidase (EC 3.2.1.20)
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)
Alpha-glucosidase (EC 3.2.1.20)
Cytoplasmic alpha-amylase (EC 3.2.1.1)
Neopullulanase (EC 3.2.1.135)
Alpha-glucosidase (EC 3.2.1.20)
Transcriptional regulator of maltose utilization, LacI family
Glucoamylase (EC 3.2.1.3)
Glycogen phosphorylase (EC 2.4.1.1)
Glycogen phosphorylase (EC 2.4.1.1)
Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)
Lipid A export ATP-binding/permease protein MsbA
Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)
Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)
allantoate amidohydrolase
phenylhydantoinase
dihydropyrimidine dehydrogenase
luciferase family protein

Fructokinase (EC 2.7.1.4)

Cell division protein FtsZ (EC 3.4.24.-)
Cell division protein FtsW
Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)
Cell division protein FtsZ (EC 3.4.24.-)
Chromosome partitioning protein ParA
Cell division protein FtsZ (EC 3.4.24.-)
Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Cell division protein FtsH (EC 3.4.24.-)
Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1)
Cell division protein FtsH (EC 3.4.24.-)
GTP-binding protein Era
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Cell division protein FtsQ
Rod shape-determining protein MreB
Cell division protein FtsA
Cell division protein FtsA
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsA
Septum site-determining protein MinD
Cell division protein FtsX
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsK
Rod shape-determining protein MreC
Rod shape-determining protein MreB
GTP-binding protein Era
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-)
Rod shape-determining protein MreB
Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.-)
Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
Cell division protein FtsK
Rod shape-determining protein MreB
Cell division topological specificity factor MinE
Cell division protein FtsK
Cell division protein FtsQ
Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1)
rRNA small subunit methyltransferase H # 16S rRNA m(4) C1402 methyltransferase
Cell division protein BolA
Cell division protein FtsZ (EC 3.4.24.-)

Cell division protein FtsH (EC 3.4.24.-)
Cell division protein FtsH (EC 3.4.24.-)
rRNA small subunit methyltransferase H # 16S rRNA m(4) C1402 methyltransferase

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Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Electron transfer flavoprotein, alpha subunit
Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Isovaleryl-CoA dehydrogenase (EC 1.3.99.10); Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Electron transfer flavoprotein, alpha subunit
3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-C
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Enoyl-CoA hydratase (EC 4.2.1.17) / 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogena
Electron transfer flavoprotein, beta subunit
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Enoyl-CoA hydratase (EC 4.2.1.17)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Acetoacetyl-CoA reductase (EC 1.1.1.36)
Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-
3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)
3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)
Enoyl-CoA hydratase (EC 4.2.1.17)
3-ketoacyl-CoA thiolase (EC 2.3.1.16); Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Electron transfer flavoprotein, alpha subunit
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Electron transfer flavoprotein, alpha subunit
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Electron transfer flavoprotein, alpha subunit
Butyryl-CoA dehydrogenase (EC 1.3.99.2)
Enoyl-CoA hydratase (EC 4.2.1.17)
Enoyl-CoA hydratase (EC 4.2.1.17)
3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)
Enoyl-CoA hydratase (EC 4.2.1.17) / 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogena
Acetyl-CoA acetyltransferase (EC 2.3.1.9)

Enoyl-CoA hydratase (EC 4.2.1.17)
Acetyl-CoA acetyltransferase (EC 2.3.1.9) @ Beta-ketoadipyl CoA thiolase (EC 2.3.1.-)
Enoyl-CoA hydratase (EC 4.2.1.17)
Electron transfer flavoprotein, alpha subunit
Enoyl-CoA hydratase (EC 4.2.1.17)
Acetyl-CoA C-acyltransferase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
Glutamine synthetase type I (EC 6.3.1.2)
D-galactarate dehydratase (EC 4.2.1.42)
D-galactarate dehydratase (EC 4.2.1.42)
D-galactarate dehydratase (EC 4.2.1.42)
Glucarate dehydratase (EC 4.2.1.40)
Osmolarity sensory histidine kinase EnvZ
Two-component system response regulator OmpR
Osmolarity sensory histidine kinase EnvZ
Two-component system response regulator OmpR
Osmolarity sensory histidine kinase EnvZ
Osmolarity sensory histidine kinase EnvZ
Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)
Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)
Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)
Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)
Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)
Agmatine deiminase (EC 3.5.3.12)
Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)
Histidine ABC transporter, ATP-binding protein HisP (TC 3.A.1.3.1)
Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) / Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.1
Ornithine cyclodeaminase (EC 4.3.1.12)
Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71)
Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)
Ornithine decarboxylase (EC 4.1.1.17)
Ornithine aminotransferase (EC 2.6.1.13)
Ornithine carbamoyltransferase (EC 2.1.3.3)
Ornithine carbamoyltransferase (EC 2.1.3.3)
Ornithine carbamoyltransferase (EC 2.1.3.3)
Ornithine carbamoyltransferase (EC 2.1.3.3)
Agmatinase (EC 3.5.3.11)

Biosynthetic arginine decarboxylase (EC 4.1.1.19)
N-carbamoylputrescine amidase (3.5.1.53)
Arginase (EC 3.5.3.1)
Biosynthetic arginine decarboxylase (EC 4.1.1.19)
NADP-specific glutamate dehydrogenase (EC 1.4.1.4)
Succinylarginine dihydrolase (EC 3.5.3.23)
Transcriptional repressor of PutA and PutP / Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) / Delta-1-pyrro
Biosynthetic arginine decarboxylase (EC 4.1.1.19)
Agmatinase (EC 3.5.3.11)
Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) / Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.1
NAD-specific glutamate dehydrogenase (EC 1.4.1.2); NADP-specific glutamate dehydrogenase (EC 1.4.1.4)

Choline-sulfatase (EC 3.1.6.6)
Choline-sulfatase (EC 3.1.6.6)
Choline-sulfatase (EC 3.1.6.6)

COGs COG3146
GTP cyclohydrolase I (EC 3.5.4.16) type 2
Acetoacetyl-CoA synthetase (EC 6.2.1.16)
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)
FolM Alternative dihydrofolate reductase 1
COGs COG3146
Aromatic-amino-acid aminotransferase (EC 2.6.1.57)
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)
Dihydropteroate synthase (EC 2.5.1.15)
Phenylalanine-4-hydroxylase (EC 1.14.16.1)
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)
Homogentisate 1,2-dioxygenase (EC 1.13.11.5)
Acetoacetyl-CoA synthetase (EC 6.2.1.16)
Fumarylacetoacetase (EC 3.7.1.2)
Fumarylacetoacetate hydrolase family protein
Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)
Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)
Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)
Fumarylacetoacetase (EC 3.7.1.2)
Maleylacetoacetate isomerase (EC 5.2.1.2) / Glutathione S-transferase
COGs COG3146
Fumarylacetoacetate hydrolase family protein
Homogentisate 1,2-dioxygenase (EC 1.13.11.5)
Fumarylacetoacetate hydrolase family protein
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)
FolM Alternative dihydrofolate reductase 1
Fumarylacetoacetate hydrolase family protein
GTP cyclohydrolase I (EC 3.5.4.16) type 1
COGs COG3146

Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)

Electron transfer flavoprotein, alpha subunit
Branched-chain amino acid aminotransferase (EC 2.6.1.42)
Branched-chain amino acid aminotransferase (EC 2.6.1.42)
Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Electron transfer flavoprotein, alpha subunit
Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
Acetoacetyl-CoA synthetase (EC 6.2.1.16)
Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)
Isovaleryl-CoA dehydrogenase (EC 1.3.99.10); Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)
Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)
Electron transfer flavoprotein, alpha subunit
Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.
Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
Electron transfer flavoprotein, beta subunit
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)
Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)
Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Acetoacetyl-CoA synthetase (EC 6.2.1.16)
Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Electron transfer flavoprotein, alpha subunit
Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)
Electron transfer flavoprotein, alpha subunit
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Electron transfer flavoprotein, alpha subunit
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)
Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)
Isovaleryl-CoA dehydrogenase (EC 1.3.99.10); Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)
Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)

Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)
Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)

Aldehyde dehydrogenase (EC 1.2.1.3)
Aldehyde dehydrogenase (EC 1.2.1.3)
Cardiolipin synthetase (EC 2.7.8.-)
Aldehyde dehydrogenase (EC 1.2.1.3)
Glycerol kinase (EC 2.7.1.30)
Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
Phosphatidate cytidylyltransferase (EC 2.7.7.41)
Aldehyde dehydrogenase (EC 1.2.1.3)
Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
Phosphate:acyl-ACP acyltransferase PlsX
Cardiolipin synthetase (EC 2.7.8.-)
Cardiolipin synthetase (EC 2.7.8.-)
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
Phosphatidate cytidylyltransferase (EC 2.7.7.41)
Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)
Phosphate:acyl-ACP acyltransferase PlsX
Glycerol kinase (EC 2.7.1.30)
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
Aldehyde dehydrogenase (EC 1.2.1.3)
Alcohol dehydrogenase (EC 1.1.1.1)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
Alcohol dehydrogenase (EC 1.1.1.1)
Glycerol kinase (EC 2.7.1.30)
Possible Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
Aldehyde dehydrogenase B (EC 1.2.1.22)
Aldehyde dehydrogenase B (EC 1.2.1.22)
Phosphate:acyl-ACP acyltransferase PlsX
Diacylglycerol kinase (EC 2.7.1.107)
Alcohol dehydrogenase (EC 1.1.1.1)
Acyl carrier protein (ACP1)
Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
Alcohol dehydrogenase (EC 1.1.1.1)
Phosphate:acyl-ACP acyltransferase PlsX
Alcohol dehydrogenase (EC 1.1.1.1)
Aldehyde dehydrogenase (EC 1.2.1.3), PaaZ
Cardiolipin synthetase (EC 2.7.8.-)
Glycerol kinase (EC 2.7.1.30)
Glycerol kinase (EC 2.7.1.30)
Cardiolipin synthetase (EC 2.7.8.-)
Aldehyde dehydrogenase B (EC 1.2.1.22)

Alcohol dehydrogenase (EC 1.1.1.1)
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)
Maltose/maltodextrin ABC transporter, permease protein MalF
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)
Glycogen phosphorylase (EC 2.4.1.1)
Transcriptional regulator of maltose utilization, LacI family
Glycogen phosphorylase (EC 2.4.1.1)
Transcriptional regulator of maltose utilization, LacI family
Glycogen phosphorylase (EC 2.4.1.1)
Maltose/maltodextrin ABC transporter, permease protein MalG
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)
Glycogen phosphorylase (EC 2.4.1.1)
Glycogen phosphorylase (EC 2.4.1.1)
Glycogen phosphorylase (EC 2.4.1.1)
Glycogen phosphorylase (EC 2.4.1.1)
Glycogen phosphorylase (EC 2.4.1.1)
Glucoamylase (EC 3.2.1.3)
Benzoate-CoA ligase (EC 6.2.1.25)
Benzoate transport, inner-membrane translocator precursor # FIG predicted
Benzoate-CoA ligase (EC 6.2.1.25)
Periplasmic aromatic aldehyde oxidoreductase, FAD binding subunit YagS @ 4-hydroxybenzoyl-CoA reductase, bet
P-hydroxylaminobenzoate lyase
Predicted 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase
Benzoyl-CoA oxygenase component A
Benzoate-CoA ligase (EC 6.2.1.25)
Benzoyl-CoA oxygenase component B
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)
benzoyl-CoA-dihydrodiol lyase (BoxC)
Regulatory protein of benzoate catabolism # HTH-XRE-family like protein/AroE I homolog
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)
Benzoyl-CoA oxygenase component B
Benzoyl-CoA oxygenase component B
benzoyl-CoA-dihydrodiol lyase (BoxC)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
Topoisomerase IV subunit B (EC 5.99.1.-)
DNA gyrase subunit B (EC 5.99.1.3)
Topoisomerase IV subunit A (EC 5.99.1.-)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)

DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit A (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3)
DNA gyrase subunit B (EC 5.99.1.3) @ intein-containing
DNA gyrase subunit B (EC 5.99.1.3)
Topoisomerase IV subunit B (EC 5.99.1.-)

ABC-type multidrug transport system, permease component
ABC-type multidrug transport system, permease component
Iron-sulfur cluster assembly protein SufB
Iron-sulfur cluster assembly protein SufB
Iron-sulfur cluster assembly protein SufB
Iron-sulfur cluster assembly ATPase protein SufC
Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB
Iron-sulfur cluster assembly ATPase protein SufC
ABC-type multidrug transport system, permease component
Iron-sulfur cluster assembly protein SufB

Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)

RNA polymerase sigma-70 factor, ECF subfamily
macromolecule metabolism; macromolecule synthesis, modification; dna - replication, repair, restr./modif.
RNA polymerase sigma-54 factor RpoN
RNA polymerase sigma-70 factor, ECF subfamily
macromolecule metabolism; macromolecule synthesis, modification; dna - replication, repair, restr./modif.
DNA-directed RNA polymerase specialized sigma subunit, sigma24-like
RNA polymerase sigma-54 factor RpoN
RNA polymerase sigma-54 factor RpoN
RNA polymerase sigma-54 factor RpoN
RNA polymerase sigma-54 factor RpoN
RNA polymerase sigma-70 factor, ECF subfamily
RNA polymerase sigma-70 factor, ECF family
RNA polymerase sigma-70 factor, ECF subfamily

TRAP-type C4-dicarboxylate transport system, large permease component
TRAP-type C4-dicarboxylate transport system, periplasmic component
TRAP-type C4-dicarboxylate transport system, large permease component

TRAP-type uncharacterized transport system, fused permease component
TRAP-type C4-dicarboxylate transport system, large permease component
TRAP-type C4-dicarboxylate transport system, periplasmic component
TRAP-type C4-dicarboxylate transport system, large permease component
TRAP-type C4-dicarboxylate transport system, periplasmic component
TRAP-type C4-dicarboxylate transport system, periplasmic component
TRAP-type C4-dicarboxylate transport system, periplasmic component
TRAP-type C4-dicarboxylate transport system, large permease component
Putative tricarboxylic transport TctC

Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)
Glycerol kinase (EC 2.7.1.30)
Glycerol kinase (EC 2.7.1.30)
Glycerol kinase (EC 2.7.1.30)
Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)
Glycerol uptake facilitator protein
Glycerol kinase (EC 2.7.1.30)
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)
Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
Glycerol kinase (EC 2.7.1.30)
Possible Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerol uptake facilitator protein
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)

Type IV fimbriae expression regulatory protein PilR
Twitching motility protein PilT
Type IV fimbriae expression regulatory protein PilR
3-dehydroquinate synthase (EC 4.2.3.4) # AroB
Type IV fimbrial assembly protein PilC
Type IV pilin PilA
Twitching motility protein PilT
Twitching motility protein PilT
3-dehydroquinate synthase (EC 4.2.3.4) # AroB
Twitching motility protein PilT

Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Type IV pilus biogenesis protein PilM
Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)
Twitching motility protein PilT
Type IV fimbrial assembly protein PilC
Type IV pilus biogenesis protein PilQ
3-dehydroquinate synthase (EC 4.2.3.4) # AroB
Type IV fimbriae expression regulatory protein PilR
Twitching motility protein PilT
Type IV fimbrial biogenesis protein PilY1
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Type IV pilus biogenesis protein PilO
Twitching motility protein PilT
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
Type IV fimbrial assembly, ATPase PilB
Serine hydroxymethyltransferase (EC 2.1.2.1)
Serine hydroxymethyltransferase (EC 2.1.2.1)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
Serine hydroxymethyltransferase (EC 2.1.2.1)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
Serine hydroxymethyltransferase (EC 2.1.2.1)
Serine hydroxymethyltransferase (EC 2.1.2.1)
Phosphoserine aminotransferase (EC 2.6.1.52)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
Serine hydroxymethyltransferase (EC 2.1.2.1)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
Serine hydroxymethyltransferase (EC 2.1.2.1)
Phosphoserine phosphatase (EC 3.1.3.3)
Phosphoserine aminotransferase (EC 2.6.1.52)
Serine hydroxymethyltransferase (EC 2.1.2.1)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
Phosphoserine aminotransferase (EC 2.6.1.52)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD

Cyanobacteria-specific RpoD-like sigma factor, type-3 @ Group 2 RNA polymerase sigma factor
Group 2 RNA polymerase sigma factor @ Cyanobacteria-specific RpoD-like sigma factor, type-7
RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD
Group 2 RNA polymerase sigma factor @ Cyanobacteria-specific RpoD-like sigma factor, type-7
Group 2 RNA polymerase sigma factor @ RNA polymerase sigma factor RpoD
RNA polymerase sigma factor RpoD

Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
probable cytochrome oxidase (cbb3-type)
Cytochrome c oxidase polypeptide III (EC 1.9.3.1)
Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)
Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
probable cytochrome oxidase (cbb3-type)
Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation
Cytochrome c oxidase subunit CcoN (EC 1.9.3.1) / Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)
Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)
Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)
Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1) / Cytochrome c oxidase polypeptide III (EC 1.9.3.1) ## putative

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Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcD
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcD
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcD
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Zn(II) and Co(II) transmembrane diffusion facilitator
Probable Co/Zn/Cd efflux system membrane fusion protein
Probable Co/Zn/Cd efflux system membrane fusion protein
Transcriptional regulator, MerR family

Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Heavy metal RND efflux outer membrane protein, CzcC family
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
SSU ribosomal protein S4p (S9e)
SSU ribosomal protein S2p (SAe)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S8p (S15Ae)
SSU ribosomal protein S8p (S15Ae)
SSU ribosomal protein S5p (S2e)
SSU ribosomal protein S5p (S2e)
SSU ribosomal protein S7p (S5e)
SSU ribosomal protein S3p (S3e)
SSU ribosomal protein S2p (SAe)
SSU ribosomal protein S2p (SAe)
SSU ribosomal protein S2p (SAe)
SSU ribosomal protein S21p
SSU ribosomal protein S4p (S9e)
SSU ribosomal protein S4p (S9e)
SSU ribosomal protein S5p (S2e)
SSU ribosomal protein S15p (S13e)
SSU ribosomal protein S5p (S2e)
SSU ribosomal protein S18p
SSU ribosomal protein S1p
SSU ribosomal protein S1p
SSU ribosomal protein S14p (S29e)
SSU ribosomal protein S12p (S23e)
SSU ribosomal protein S1p
SSU ribosomal protein S4p (S9e)
SSU ribosomal protein S3p (S3e)
SSU ribosomal protein S19p (S15e)
SSU ribosomal protein S14p (S29e) ## Zinc-independent
SSU ribosomal protein S8p (S15Ae)
SSU ribosomal protein S10p (S20e)
SSU ribosomal protein S1p
SSU ribosomal protein S9p (S16e)
SSU ribosomal protein S1p
SSU ribosomal protein S5p (S2e)
SSU ribosomal protein S12p (S23e)
SSU ribosomal protein S20p
SSU ribosomal protein S1p

e-value	score	identity
4.00E-04	43 bits (111)	22/35 (63%)
4.00E-17	86 bits (222)	42/85 (49%)
3.00E+02	23 bits (60)	12/14 (86%)
9.00E-48	188 bits (484)	100/138 (72%)
4.00E-10	63 bits (162)	32/46 (70%)
8.00E-02	35 bits (90)	17/20 (85%)
3.00E-17	86 bits (223)	40/56 (71%)
7.00E-03	39 bits (100)	21/29 (72%)
3.00E-05	47 bits (121)	21/29 (72%)
3.00E-04	43 bits (112)	21/29 (72%)
3.00E-03	40 bits (103)	19/27 (70%)
3.00E-56	216 bits (557)	107/142 (75%)
1.00E+02	25 bits (63)	13/14 (93%)
3.00E-03	40 bits (103)	19/23 (83%)
7.00E-14	75 bits (194)	33/47 (70%)
6.00E-13	72 bits (186)	35/40 (88%)
5.00E-16	82 bits (212)	42/74 (57%)
1.00E-25	115 bits (295)	56/92 (61%)
2.00E-08	57 bits (148)	28/37 (76%)
7.00E-03	39 bits (100)	21/27 (78%)
2.00E-16	84 bits (216)	43/69 (62%)
2.00E-78	289 bits (747)	142/164 (87%)
9.00E-25	111 bits (287)	56/80 (70%)
1.00E-23	108 bits (277)	56/73 (77%)
7.00E-10	62 bits (160)	27/36 (75%)
1.00E-02	38 bits (98)	18/22 (82%)
3.00E-05	47 bits (121)	22/34 (65%)
4.00E-15	79 bits (205)	40/68 (59%)
3.00E-04	43 bits (112)	21/32 (66%)
3.00E-04	43 bits (112)	22/33 (67%)
9.00E-06	48 bits (125)	24/34 (71%)
5.00E-06	49 bits (127)	26/41 (63%)
2.00E-08	57 bits (147)	28/48 (58%)
2.00E-06	50 bits (130)	24/33 (73%)
2.00E-21	100 bits (258)	52/87 (60%)
2.00E-11	67 bits (173)	35/61 (57%)
1.00E-08	58 bits (150)	27/40 (68%)
2.00E-11	67 bits (173)	35/61 (57%)
2.00E-11	67 bits (173)	35/61 (57%)
7.00E-22	102 bits (262)	46/69 (67%)
8.00E-26	115 bits (297)	57/89 (64%)
1.00E-68	257 bits (663)	118/156 (76%)
1.00E-33	141 bits (363)	67/85 (79%)
4.00E-02	36 bits (93)	18/24 (75%)

3.00E-04	43 bits (112)	22/33 (67%)

8.00E-05	45 bits (117)	24/30 (80%)
6.00E-03	39 bits (101)	17/22 (77%)
7.00E-18	88 bits (228)	46/60 (77%)
2.00E-07	54 bits (139)	29/49 (59%)
4.00E-18	89 bits (230)	41/55 (75%)
2.00E-26	117 bits (303)	62/69 (90%)
2.00E-15	81 bits (208)	39/54 (72%)
6.00E-09	59 bits (152)	25/40 (63%)
7.00E-14	75 bits (194)	35/47 (74%)
2.00E-09	61 bits (157)	32/44 (73%)
1.00E-05	48 bits (124)	24/42 (57%)
1.00E-23	108 bits (278)	53/62 (85%)
2.00E-20	97 bits (250)	50/66 (76%)
5.00E-09	59 bits (153)	28/49 (57%)
4.00E-07	53 bits (136)	23/36 (64%)
5.00E-14	76 bits (195)	39/61 (64%)
9.00E-25	111 bits (287)	55/66 (83%)
2.00E-40	163 bits (421)	80/93 (86%)
2.00E-03	41 bits (105)	20/23 (87%)
2.00E-08	57 bits (148)	28/47 (60%)
4.00E-10	63 bits (162)	31/45 (69%)
4.00E-10	63 bits (162)	29/37 (78%)
2.00E-14	77 bits (198)	38/43 (88%)
2.00E-26	117 bits (303)	58/76 (76%)
3.00E-15	80 bits (206)	37/46 (80%)
7.00E-06	49 bits (126)	25/40 (63%)
4.00E-06	49 bits (128)	24/36 (67%)
1.00E-02	38 bits (98)	18/27 (67%)
9.00E-06	48 bits (125)	23/31 (74%)
9.00E-10	62 bits (159)	30/44 (68%)
1.00E-12	71 bits (184)	35/57 (61%)
6.00E-20	95 bits (246)	46/59 (78%)
1.00E-04	45 bits (116)	22/33 (67%)
7.00E-06	49 bits (126)	24/28 (86%)
4.00E-21	99 bits (256)	49/74 (66%)
1.00E-05	48 bits (123)	26/39 (67%)
6.00E-15	79 bits (203)	38/47 (81%)
1.00E-03	41 bits (106)	22/38 (58%)
3.00E-09	60 bits (154)	30/45 (67%)
1.00E+03	21 bits (54)	10/10 (100%)
1.00E-06	51 bits (132)	25/33 (76%)
4.00E-10	63 bits (162)	34/48 (71%)
7.00E-06	49 bits (126)	22/29 (76%)
9.00E-08	55 bits (142)	26/31 (84%)

2.00E-23	107 bits (275)	54/59 (92%)
1.00E-19	95 bits (244)	48/59 (81%)
4.00E-12	69 bits (179)	35/64 (55%)
3.00E-03	40 bits (103)	18/23 (78%)
5.00E-06	49 bits (127)	24/44 (55%)
2.00E-09	60 bits (156)	30/39 (77%)
8.00E-26	115 bits (297)	50/62 (81%)
9.00E-08	55 bits (142)	25/43 (58%)
2.00E-06	50 bits (130)	26/43 (60%)
1.00E-20	98 bits (252)	46/85 (54%)
3.00E-03	40 bits (104)	22/34 (65%)
2.00E-04	44 bits (113)	20/30 (67%)
3.00E-11	67 bits (172)	34/60 (57%)
7.00E-12	69 bits (177)	31/46 (67%)
5.00E-16	82 bits (212)	39/43 (91%)
4.00E-02	36 bits (93)	15/23 (65%)
2.00E-27	120 bits (311)	62/77 (81%)
5.00E-09	59 bits (153)	31/53 (58%)
7.00E-03	39 bits (100)	20/30 (67%)
7.00E-06	49 bits (126)	24/37 (65%)
3.00E-03	40 bits (104)	22/35 (63%)
3.00E-02	37 bits (94)	18/28 (64%)
2.00E-04	44 bits (113)	22/34 (65%)
4.00E-18	89 bits (230)	44/72 (61%)
5.00E-04	42 bits (110)	23/38 (61%)
2.00E-18	90 bits (233)	46/74 (62%)
1.00E-13	74 bits (192)	35/57 (61%)
2.00E-06	51 bits (131)	25/37 (68%)
1.00E-06	51 bits (132)	26/30 (87%)
8.00E-07	52 bits (134)	26/43 (60%)
1.00E-17	88 bits (227)	43/76 (57%)
1.00E-01	34 bits (88)	19/26 (73%)
7.00E-06	49 bits (126)	23/40 (58%)
3.00E-04	43 bits (112)	22/28 (79%)
3.00E-03	40 bits (103)	22/31 (71%)
6.00E-02	35 bits (91)	18/22 (82%)
5.00E+01	26 bits (66)	13/13 (100%)
7.00E-06	49 bits (126)	31/54 (57%)
2.00E-03	41 bits (105)	21/33 (64%)
1.00E-02	38 bits (97)	19/22 (86%)
1.00E-04	45 bits (116)	22/28 (79%)
7.00E-08	55 bits (143)	29/49 (59%)
1.00E-04	45 bits (116)	23/27 (85%)
4.00E-05	46 bits (119)	22/34 (65%)
5.00E-09	59 bits (153)	30/41 (73%)
4.00E-01	33 bits (84)	17/26 (65%)
9.00E-04	42 bits (108)	23/36 (64%)

3.00E-17	86 bits (223)	41/57 (72%)
7.00E-03	39 bits (100)	21/34 (62%)
9.00E-08	55 bits (142)	26/34 (76%)
7.00E-16	82 bits (211)	44/58 (76%)
4.00E-03	39 bits (102)	20/27 (74%)
4.00E-04	43 bits (111)	21/28 (75%)
2.00E-11	67 bits (173)	31/46 (67%)
2.00E-08	57 bits (147)	27/43 (63%)
6.00E-21	99 bits (254)	44/61 (72%)
1.00E+01	28 bits (71)	13/19 (68%)
7.00E-04	42 bits (109)	24/43 (56%)
9.00E-04	42 bits (108)	21/29 (72%)
7.00E-37	152 bits (391)	76/83 (92%)
7.00E-08	55 bits (143)	27/29 (93%)
2.00E-06	50 bits (130)	25/28 (89%)
3.00E-09	60 bits (154)	28/31 (90%)
7.00E-12	69 bits (177)	35/45 (78%)
6.00E-26	115 bits (298)	58/81 (72%)
1.00E-06	51 bits (133)	25/32 (78%)
6.00E-26	115 bits (298)	61/80 (76%)
7.00E-22	102 bits (262)	49/80 (61%)
6.00E-26	115 bits (298)	58/81 (72%)
6.00E-26	115 bits (298)	61/80 (76%)
3.00E-11	67 bits (172)	33/40 (83%)
2.00E-06	51 bits (131)	27/38 (71%)
3.00E-03	40 bits (104)	19/24 (79%)
2.00E-11	67 bits (173)	37/57 (65%)
4.00E-22	102 bits (264)	49/72 (68%)
2.00E-11	67 bits (173)	32/41 (78%)
8.00E-26	115 bits (297)	54/72 (75%)
1.00E-19	94 bits (243)	48/59 (81%)
5.00E-17	86 bits (221)	45/74 (61%)
1.00E-25	115 bits (295)	57/85 (67%)
5.00E+03	19 bits (49)	10/11 (91%)
1.00E-06	51 bits (133)	27/45 (60%)
3.00E-03	40 bits (103)	20/29 (69%)
4.00E-03	39 bits (102)	19/22 (86%)
8.00E-24	108 bits (279)	54/76 (71%)
3.00E-06	50 bits (129)	24/39 (62%)
1.00E-15	81 bits (209)	39/60 (65%)
7.00E-06	49 bits (126)	22/36 (61%)
1.00E-02	38 bits (98)	19/23 (83%)

6.00E-22	102 bits (263)	49/63 (78%)
1.00E-03	41 bits (106)	21/31 (68%)
5.00E-25	112 bits (289)	52/69 (75%)
8.00E-26	115 bits (297)	54/82 (66%)
2.00E-10	63 bits (164)	30/37 (81%)
5.00E-15	79 bits (204)	41/64 (64%)
6.00E-01	32 bits (83)	15/18 (83%)
2.00E-10	63 bits (164)	30/40 (75%)
7.00E-12	69 bits (177)	30/42 (71%)
6.00E-03	39 bits (101)	21/24 (88%)
2.00E-07	54 bits (140)	24/28 (86%)
4.00E-03	39 bits (102)	22/35 (63%)
3.00E-05	46 bits (120)	21/32 (66%)
2.00E-11	67 bits (173)	31/48 (65%)
2.00E-08	57 bits (148)	26/46 (57%)
2.00E-06	51 bits (131)	24/26 (92%)
2.00E-08	57 bits (147)	25/34 (74%)
5.00E-27	119 bits (307)	55/82 (67%)
3.00E-04	43 bits (112)	23/37 (62%)
3.00E-13	73 bits (189)	35/48 (73%)
2.00E-10	63 bits (164)	33/50 (66%)
2.00E-23	107 bits (275)	54/68 (79%)
9.00E-06	48 bits (125)	26/42 (62%)
5.00E-09	59 bits (153)	30/40 (75%)
2.00E-11	67 bits (174)	36/44 (82%)
3.00E-13	73 bits (189)	36/47 (77%)
3.00E-04	43 bits (112)	19/22 (86%)
1.00E-06	51 bits (132)	25/34 (74%)
1.00E-14	78 bits (201)	37/54 (69%)
3.00E-10	63 bits (163)	32/53 (60%)
2.00E-02	37 bits (96)	17/22 (77%)
3.00E-18	90 bits (231)	42/55 (76%)
2.00E-02	37 bits (96)	17/22 (77%)
1.00E-06	51 bits (132)	23/26 (88%)
2.00E-07	54 bits (140)	25/33 (76%)
3.00E-02	37 bits (94)	19/26 (73%)
2.00E-14	77 bits (199)	35/47 (74%)
3.00E-03	40 bits (103)	18/27 (67%)
6.00E-03	39 bits (101)	20/34 (59%)
4.00E-03	39 bits (102)	20/24 (83%)
4.00E-23	106 bits (273)	52/88 (59%)
1.00E-25	115 bits (295)	53/79 (67%)
1.00E-02	38 bits (97)	20/25 (80%)
2.00E-06	51 bits (131)	21/32 (66%)
2.00E-16	84 bits (216)	40/65 (62%)
5.00E-19	92 bits (238)	43/54 (80%)
7.00E-03	39 bits (100)	18/30 (60%)

7.00E-16	82 bits (211)	44/58 (76%)
6.00E-03	39 bits (101)	20/34 (59%)
1.00E-02	38 bits (98)	21/32 (66%)
1.00E-18	91 bits (234)	45/71 (63%)
2.00E-08	57 bits (148)	28/38 (74%)
2.00E-04	44 bits (113)	21/27 (78%)
2.00E-09	60 bits (156)	30/39 (77%)
8.00E-26	115 bits (297)	50/62 (81%)
2.00E-08	57 bits (147)	25/34 (74%)
2.00E-04	44 bits (113)	23/23 (100%)
2.00E-08	57 bits (148)	28/34 (82%)
1.00E-12	71 bits (184)	35/46 (76%)
1.00E-20	98 bits (252)	46/85 (54%)
6.00E-45	178 bits (460)	90/105 (86%)
3.00E-01	33 bits (85)	17/28 (61%)
4.00E-03	39 bits (102)	20/28 (71%)
1.00E-18	91 bits (234)	42/65 (65%)
5.00E-17	86 bits (221)	42/69 (61%)
2.00E-27	120 bits (311)	62/77 (81%)
7.00E-12	69 bits (177)	33/44 (75%)
6.00E-20	95 bits (246)	47/72 (65%)
2.00E-08	57 bits (147)	29/49 (59%)
7.00E-12	69 bits (177)	35/61 (57%)
2.00E-04	44 bits (113)	22/34 (65%)
9.00E-14	75 bits (193)	39/52 (75%)
2.00E-06	51 bits (131)	28/37 (76%)
8.00E-05	45 bits (117)	21/26 (81%)
2.00E-06	51 bits (131)	25/37 (68%)
6.00E-02	35 bits (91)	18/23 (78%)
6.00E-07	52 bits (135)	24/40 (60%)
1.00E-06	51 bits (132)	25/34 (74%)
7.00E-06	49 bits (126)	23/40 (58%)
3.00E-04	43 bits (112)	19/25 (76%)
2.00E-08	57 bits (147)	30/36 (83%)
3.00E-03	40 bits (103)	22/31 (71%)
3.00E-03	40 bits (104)	21/23 (91%)
7.00E-06	49 bits (126)	31/54 (57%)
8.00E-05	45 bits (117)	23/32 (72%)
1.00E-04	45 bits (116)	22/28 (79%)
2.00E-18	90 bits (233)	51/82 (62%)
4.00E-22	102 bits (264)	54/84 (64%)
5.00E-14	76 bits (195)	38/53 (72%)
1.00E-04	45 bits (116)	23/38 (61%)
4.00E-03	39 bits (102)	18/28 (64%)
6.00E-18	89 bits (229)	41/51 (80%)
1.00E-37	154 bits (398)	75/90 (83%)
5.00E-14	76 bits (195)	35/55 (64%)

1.00E-12	71 bits (183)	35/48 (73%)
2.00E-25	114 bits (293)	56/75 (75%)
7.00E+01	25 bits (65)	15/17 (88%)
7.00E-16	82 bits (211)	41/71 (58%)
2.00E-04	44 bits (114)	21/27 (78%)
8.00E+00	28 bits (73)	15/17 (88%)
1.00E+02	25 bits (63)	13/15 (87%)
2.00E-10	63 bits (164)	28/42 (67%)
3.00E+00	30 bits (77)	15/20 (75%)
5.00E-04	42 bits (110)	22/34 (65%)
2.00E-06	51 bits (131)	24/35 (69%)
7.00E-06	49 bits (126)	24/36 (67%)
4.00E-04	43 bits (111)	23/29 (79%)
8.00E-02	35 bits (90)	22/33 (67%)
2.00E-05	47 bits (122)	22/27 (81%)
6.00E-05	46 bits (118)	21/26 (81%)
2.00E-22	104 bits (267)	52/64 (81%)
7.00E-08	55 bits (143)	28/37 (76%)
1.00E-06	51 bits (133)	26/42 (62%)
9.00E-25	111 bits (287)	49/67 (73%)
2.00E+00	30 bits (78)	16/21 (76%)
4.00E+01	26 bits (67)	14/15 (93%)
1.00E-05	48 bits (124)	23/30 (77%)
7.00E-03	39 bits (100)	22/32 (69%)
2.00E-08	57 bits (147)	26/37 (70%)
2.00E-06	50 bits (130)	28/41 (68%)
1.00E-06	51 bits (133)	24/36 (67%)
2.00E+02	24 bits (61)	12/12 (100%)
8.00E-05	45 bits (117)	22/34 (65%)
5.00E-30	129 bits (333)	58/69 (84%)
1.00E-19	95 bits (244)	41/47 (87%)
6.00E-22	102 bits (263)	48/57 (84%)
4.00E-05	46 bits (119)	24/27 (89%)
1.00E-06	51 bits (132)	30/37 (81%)
3.00E-07	53 bits (137)	26/39 (67%)
1.00E-05	48 bits (124)	24/35 (69%)
9.00E-25	111 bits (287)	54/84 (64%)
1.00E-16	84 bits (217)	45/60 (75%)
1.00E-01	34 bits (88)	14/20 (70%)
1.00E-06	51 bits (133)	27/39 (69%)
7.00E-01	32 bits (82)	15/23 (65%)
2.00E-06	51 bits (131)	27/45 (60%)
2.00E-04	44 bits (113)	26/39 (67%)
1.00E-01	35 bits (89)	18/19 (95%)
2.00E-15	81 bits (208)	37/52 (71%)
1.00E-02	38 bits (98)	21/32 (66%)
1.00E-03	41 bits (106)	20/30 (67%)

7.00E-08	55 bits (143)	25/36 (69%)
1.00E-06	51 bits (132)	22/32 (69%)
1.00E-03	41 bits (106)	18/22 (82%)
4.00E-15	79 bits (205)	41/46 (89%)
1.00E+00	31 bits (80)	15/18 (83%)
2.00E-14	77 bits (199)	43/64 (67%)
1.00E-06	51 bits (132)	27/39 (69%)
2.00E-11	67 bits (174)	31/57 (54%)
1.00E-09	61 bits (158)	27/36 (75%)
5.00E-09	59 bits (153)	28/36 (78%)
2.00E-06	51 bits (131)	27/33 (82%)
4.00E-05	46 bits (119)	19/26 (73%)
2.00E-06	51 bits (131)	28/47 (60%)
1.00E-18	91 bits (234)	40/58 (69%)
4.00E-18	89 bits (230)	38/58 (66%)
1.00E-05	48 bits (124)	21/31 (68%)
3.00E-04	43 bits (112)	21/24 (88%)
7.00E-03	39 bits (100)	19/23 (83%)
1.00E-14	78 bits (201)	41/49 (84%)
1.00E-23	108 bits (278)	59/73 (81%)
6.00E-09	59 bits (152)	29/32 (91%)
5.00E-04	42 bits (110)	21/33 (64%)
8.00E-26	115 bits (297)	53/65 (82%)
4.00E-13	73 bits (188)	36/47 (77%)
1.00E-40	164 bits (423)	76/88 (86%)
2.00E-13	74 bits (191)	40/47 (85%)
1.00E-16	84 bits (217)	40/53 (75%)
2.00E-18	90 bits (233)	51/82 (62%)
1.00E-18	91 bits (235)	45/56 (80%)
4.00E-03	39 bits (102)	20/32 (63%)
7.00E-16	82 bits (211)	41/71 (58%)
5.00E-16	82 bits (212)	42/56 (75%)
8.00E-07	52 bits (134)	23/32 (72%)
1.00E-23	108 bits (277)	51/66 (77%)
6.00E-02	35 bits (91)	17/21 (81%)
6.00E-03	39 bits (101)	19/21 (90%)
2.00E-19	94 bits (242)	48/63 (76%)
4.00E-19	93 bits (239)	47/57 (82%)
4.00E-04	43 bits (111)	22/29 (76%)
1.00E-03	41 bits (106)	20/25 (80%)
3.00E-04	43 bits (112)	19/22 (86%)
1.00E-03	41 bits (107)	18/22 (82%)
7.00E-06	49 bits (126)	23/27 (85%)
7.00E-03	39 bits (100)	20/29 (69%)
5.00E-08	56 bits (144)	27/35 (77%)
1.00E-03	41 bits (107)	21/28 (75%)
3.00E-05	47 bits (121)	23/30 (77%)

2.00E+00	30 bits (78)	16/28 (57%)
3.00E-07	53 bits (137)	24/33 (73%)
1.00E-16	84 bits (217)	43/70 (61%)
2.00E-07	54 bits (139)	27/37 (73%)
3.00E-09	60 bits (155)	26/33 (79%)
6.00E-13	72 bits (186)	36/43 (84%)
2.00E-01	34 bits (87)	16/23 (70%)
1.00E-10	65 bits (167)	30/48 (63%)
2.00E-08	57 bits (147)	28/40 (70%)
2.00E-07	54 bits (139)	24/33 (73%)
6.00E-36	148 bits (383)	77/84 (92%)
3.00E-29	126 bits (326)	60/72 (83%)
5.00E-04	42 bits (110)	20/21 (95%)
1.00E-10	64 bits (166)	33/42 (79%)
4.00E-22	102 bits (264)	48/66 (73%)
1.00E-08	58 bits (149)	31/40 (78%)
5.00E-06	49 bits (127)	22/31 (71%)
5.00E-04	42 bits (110)	22/40 (55%)
4.00E+02	23 bits (59)	12/16 (75%)
3.00E-08	56 bits (146)	26/34 (76%)
2.00E-04	44 bits (113)	19/34 (56%)
4.00E-03	39 bits (102)	21/29 (72%)
4.00E-07	53 bits (136)	25/38 (66%)
1.00E-06	51 bits (132)	23/37 (62%)
2.00E-07	54 bits (140)	26/40 (65%)
1.00E-03	41 bits (106)	19/27 (70%)
7.00E-03	39 bits (100)	17/24 (71%)
4.00E+02	23 bits (59)	11/12 (92%)
1.00E-06	51 bits (133)	25/35 (71%)
1.00E-07	55 bits (141)	31/52 (60%)
2.00E-06	51 bits (131)	24/37 (65%)
5.00E-08	56 bits (144)	31/42 (74%)
4.00E-10	63 bits (162)	33/50 (66%)
6.00E-11	65 bits (169)	33/49 (67%)
1.00E-16	85 bits (218)	46/70 (66%)
5.00E-08	56 bits (144)	28/31 (90%)
1.00E-01	35 bits (89)	19/23 (83%)
2.00E-04	44 bits (114)	22/35 (63%)
4.00E-17	86 bits (222)	40/63 (63%)
3.00E-03	40 bits (103)	20/25 (80%)
1.00E-14	78 bits (201)	41/50 (82%)
4.00E-10	63 bits (162)	32/52 (62%)
9.00E-04	42 bits (108)	22/33 (67%)
3.00E-03	40 bits (103)	19/23 (83%)
1.00E-02	38 bits (98)	17/21 (81%)
4.00E-10	63 bits (162)	30/44 (68%)

2.00E-10	63 bits (164)	31/42 (74%)
2.00E-09	60 bits (156)	32/58 (55%)
5.00E-10	62 bits (161)	32/50 (64%)
4.00E-17	86 bits (222)	40/50 (80%)
2.00E+00	31 bits (79)	13/15 (87%)
9.00E-16	81 bits (210)	37/51 (73%)
3.00E-07	53 bits (137)	28/39 (72%)
2.00E-21	100 bits (258)	50/71 (70%)
1.00E-09	61 bits (158)	27/40 (68%)
6.00E-03	39 bits (101)	18/23 (78%)
4.00E-27	119 bits (308)	62/70 (89%)
1.00E-01	35 bits (89)	18/19 (95%)
2.00E-15	81 bits (208)	37/52 (71%)
3.00E+00	30 bits (77)	15/20 (75%)
5.00E-04	42 bits (110)	22/34 (65%)
1.00E-06	51 bits (133)	26/39 (67%)
4.00E-04	43 bits (111)	23/29 (79%)
4.00E-03	39 bits (102)	20/35 (57%)
7.00E-08	55 bits (143)	28/37 (76%)
3.00E-03	40 bits (103)	19/26 (73%)
1.00E+01	28 bits (71)	14/17 (82%)
4.00E-10	63 bits (162)	30/41 (73%)
4.00E+01	26 bits (67)	14/15 (93%)
2.00E-11	67 bits (173)	34/52 (65%)
2.00E-11	67 bits (174)	34/52 (65%)
2.00E-11	67 bits (174)	34/52 (65%)
1.00E-10	65 bits (167)	30/39 (77%)
2.00E-06	50 bits (130)	28/41 (68%)
2.00E+02	24 bits (61)	12/12 (100%)
8.00E-05	45 bits (117)	22/34 (65%)
1.00E-06	51 bits (133)	27/39 (69%)
2.00E+01	27 bits (70)	14/19 (74%)
3.00E-09	60 bits (154)	31/53 (58%)
6.00E-20	95 bits (246)	43/62 (69%)
2.00E-18	90 bits (233)	45/50 (90%)
5.00E-08	56 bits (144)	26/40 (65%)
1.00E-16	84 bits (217)	45/60 (75%)
3.00E-01	33 bits (85)	18/28 (64%)
1.00E-03	41 bits (107)	20/26 (77%)
2.00E-04	44 bits (114)	23/37 (62%)
1.00E-23	108 bits (277)	52/58 (90%)
4.00E-25	113 bits (290)	55/84 (65%)
2.00E-06	51 bits (131)	28/30 (93%)
1.00E-06	51 bits (132)	26/37 (70%)
8.00E-09	58 bits (151)	29/53 (55%)
2.00E-06	51 bits (131)	23/35 (66%)
4.00E-04	43 bits (111)	25/37 (68%)

2.00E-09	60 bits (156)	29/44 (66%)
1.00E-14	78 bits (201)	39/46 (85%)
9.00E+01	25 bits (64)	13/14 (93%)
5.00E-09	59 bits (153)	28/46 (61%)
1.00E-01	34 bits (88)	18/21 (86%)
4.00E-05	46 bits (119)	24/40 (60%)
9.00E-21	98 bits (253)	47/66 (71%)
1.00E-06	51 bits (132)	30/52 (58%)
3.00E-05	46 bits (120)	26/39 (67%)
4.00E-15	79 bits (205)	44/64 (69%)
9.00E-14	75 bits (193)	36/47 (77%)
2.00E-08	57 bits (147)	27/36 (75%)
1.00E-02	38 bits (98)	20/29 (69%)
2.00E-01	33 bits (86)	17/22 (77%)
9.00E-08	55 bits (142)	25/41 (61%)
2.00E-08	57 bits (147)	28/43 (65%)
6.00E-18	89 bits (229)	47/59 (80%)
3.00E-18	90 bits (231)	44/61 (72%)
5.00E-17	86 bits (221)	42/66 (64%)
3.00E-04	43 bits (112)	18/28 (64%)
4.00E-10	63 bits (162)	30/51 (59%)
1.00E-02	38 bits (98)	18/26 (69%)
1.00E-24	111 bits (286)	56/81 (69%)
1.00E-01	35 bits (89)	16/17 (94%)
2.00E-04	44 bits (114)	23/38 (61%)
2.00E-14	77 bits (199)	38/58 (66%)
5.00E-16	82 bits (212)	40/48 (83%)
2.00E-08	57 bits (147)	29/52 (56%)
9.00E-04	42 bits (108)	21/27 (78%)
7.00E-16	82 bits (211)	44/61 (72%)
5.00E-04	42 bits (110)	22/35 (63%)
1.00E-29	128 bits (330)	64/84 (76%)
2.00E-06	51 bits (131)	27/42 (64%)
5.00E-06	49 bits (127)	24/35 (69%)
2.00E+00	31 bits (79)	16/19 (84%)
3.00E-04	43 bits (112)	18/28 (64%)
1.00E-35	148 bits (381)	71/105 (68%)
3.00E-03	40 bits (104)	22/29 (76%)
1.00E-16	85 bits (218)	42/68 (62%)
4.00E-29	126 bits (325)	64/87 (74%)
3.00E-03	40 bits (103)	20/30 (67%)
3.00E-03	40 bits (103)	20/21 (95%)
2.00E-05	47 bits (122)	23/24 (96%)
3.00E+00	30 bits (77)	18/29 (62%)
1.00E-07	55 bits (141)	26/35 (74%)
1.00E-04	44 bits (115)	21/27 (78%)
3.00E-06	50 bits (129)	22/30 (73%)

4.00E-12	69 bits (179)	35/62 (56%)
2.00E+02	24 bits (61)	12/15 (80%)
6.00E-02	35 bits (91)	17/28 (61%)
9.00E-08	55 bits (142)	28/29 (97%)
6.00E-05	46 bits (118)	24/27 (89%)
4.00E-04	43 bits (111)	24/25 (96%)
7.00E-14	75 bits (194)	33/53 (62%)
3.00E-09	60 bits (154)	28/30 (93%)
2.00E-06	51 bits (131)	25/30 (83%)
2.00E-10	63 bits (164)	28/34 (82%)
2.00E-12	70 bits (181)	30/37 (81%)
3.00E-03	40 bits (103)	18/21 (86%)
1.00E-05	48 bits (123)	21/27 (78%)
3.00E-07	53 bits (138)	24/30 (80%)
7.00E-14	75 bits (194)	35/53 (66%)
8.00E-05	45 bits (117)	23/38 (61%)
2.00E-11	67 bits (174)	30/39 (77%)
3.00E-04	43 bits (112)	21/31 (68%)
4.00E-22	102 bits (264)	49/67 (73%)
7.00E-16	82 bits (211)	38/45 (84%)
2.00E-06	50 bits (130)	22/30 (73%)
4.00E-06	49 bits (128)	25/31 (81%)
4.00E+00	30 bits (76)	14/22 (64%)
2.00E-19	94 bits (242)	43/80 (54%)
7.00E-16	82 bits (211)	42/65 (65%)
9.00E-04	42 bits (108)	22/33 (67%)
1.00E-06	51 bits (133)	24/34 (71%)
3.00E-17	86 bits (223)	42/46 (91%)
2.00E-08	57 bits (147)	30/40 (75%)
2.00E-14	77 bits (198)	36/53 (68%)
1.00E-12	71 bits (183)	36/49 (73%)
6.00E-09	59 bits (152)	28/49 (57%)
7.00E-06	49 bits (126)	23/28 (82%)
3.00E-16	83 bits (214)	41/55 (75%)
4.00E-06	49 bits (128)	26/32 (81%)
4.00E-03	39 bits (102)	23/28 (82%)
2.00E-08	57 bits (147)	27/38 (71%)
7.00E-06	49 bits (126)	25/39 (64%)
5.00E-04	42 bits (110)	20/31 (65%)
5.00E-14	76 bits (195)	38/61 (62%)
3.00E-03	40 bits (104)	21/29 (72%)
2.00E+03	20 bits (52)	11/13 (85%)
1.00E-03	41 bits (107)	21/32 (66%)
6.00E-09	59 bits (152)	28/42 (67%)
3.00E-10	63 bits (163)	30/37 (81%)
2.00E+04	17 bits (44)	9/10 (90%)
3.00E-04	43 bits (112)	20/26 (77%)

5.00E-06	49 bits (127)	25/31 (81%)
4.00E-17	86 bits (222)	45/59 (76%)
5.00E-04	42 bits (110)	22/30 (73%)
8.00E-02	35 bits (90)	18/23 (78%)
1.00E-03	41 bits (107)	19/27 (70%)
3.00E-04	43 bits (112)	20/24 (83%)
3.00E-09	60 bits (154)	30/43 (70%)
3.00E-07	53 bits (137)	25/35 (71%)
9.00E-10	62 bits (159)	29/48 (60%)
7.00E-16	82 bits (211)	34/52 (65%)
7.00E-14	75 bits (194)	40/68 (59%)
8.00E-05	45 bits (117)	23/33 (70%)
1.00E-06	51 bits (132)	26/43 (60%)
4.00E-06	49 bits (128)	25/35 (71%)
3.00E-04	43 bits (112)	19/20 (95%)
1.00E-06	51 bits (132)	24/27 (89%)
1.00E-14	78 bits (201)	40/67 (60%)
1.00E-08	58 bits (149)	28/38 (74%)
3.00E-07	53 bits (137)	26/42 (62%)
4.00E-04	43 bits (111)	21/31 (68%)
7.00E-10	62 bits (160)	33/58 (57%)
4.00E-03	39 bits (102)	21/30 (70%)
1.00E-19	94 bits (243)	47/53 (89%)
5.00E-02	36 bits (92)	20/23 (87%)
3.00E-09	60 bits (154)	29/41 (71%)
2.00E-21	100 bits (258)	49/60 (82%)
1.00E-05	48 bits (123)	24/34 (71%)
1.00E-04	45 bits (116)	21/33 (64%)
3.00E-10	63 bits (163)	30/31 (97%)
2.00E-18	90 bits (232)	42/62 (68%)
2.00E-18	90 bits (233)	42/53 (79%)
5.00E-06	49 bits (127)	20/26 (77%)
4.00E-27	119 bits (308)	57/62 (92%)
7.00E-22	102 bits (262)	53/81 (65%)
2.00E-06	51 bits (131)	24/42 (57%)
6.00E-09	59 bits (152)	31/32 (97%)
6.00E-01	32 bits (83)	15/18 (83%)
7.00E-06	49 bits (126)	26/42 (62%)
8.00E-07	52 bits (134)	24/31 (77%)
2.00E+05	14 bits (35)	7/7 (100%)
8.00E-13	72 bits (185)	36/39 (92%)
4.00E-10	63 bits (162)	34/51 (67%)
4.00E-06	49 bits (128)	27/29 (93%)