Title

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Metagenomic and metatranscriptomic analyses reveal structure and dynamics of a dechlorinating community containing *Dehalococcoides mccartyi* and corrinoid-providing microorganisms under cobalamin-limited condition

Running title: Meta-omic sequencing of dechlorinating communities

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Abstract

The aim of this study is to obtain a systems level understanding of the interactions between *Dehalococcoides* and corrinoid-supplying microorganisms by analyzing community structures and functional compositions, activities and dynamics in trichloroethene (TCE) - dechlorinating enrichments. Metagenomes and metatranscriptomes of the dechlorinating enrichments with and without exogenous cobalamin were compared. Seven putative draft genomes were binned from the metagenomes. At an early stage (2 d), more transcripts of genes in the *Veillonellaceae* bin-genome were detected in the metatranscriptome of the enrichment with exogenous cobalamin compared to the one without cobalamin addition. Among these genes, sporulation-related genes exhibited the highest differential expression when cobalamin was not added, suggesting a possible release route of corrinoids from corrinoid-producers. Other differentially expressed genes include those involved in energy conservation and nutrient transport (including cobalt transport). The most highly expressed corrinoid *de novo* biosynthesis pathway was also assigned to the *Veillonellaceae* bin-genome. Targeted qPCR analyses confirmed higher transcript abundances of those corrinoid biosynthesis genes in the enrichment without exogenous cobalamin. Furthermore, *Dehalococcoides*' corrinoid salvaging and modification pathway was upregulated in response to the cobalamin stress. This study provides important insights into the microbial interactions and roles of members of dechlorinating communities under cobalamin-limited conditions.

Importance

The key chloroethene-dechlorinating bacterium *Dehalococcoides mccartyi* is cobalamin auxotroph, thus acquires corrinoids from other community members. Therefore, it is important to investigate the microbe-microbe interactions between *Dehalococcoides* and the corrinoid-providing microorganisms in a community. This study provides systems level information, i.e.,

taxonomic and functional compositions and dynamics of the supportive microorganisms in dechlorinating communities under different cobalamin conditions. The findings shed light on the important roles of *Veillonellaceae* species in the communities compared to other co-existing community members in producing and providing corrinoids for *Dehalococcoides* species under cobalamin-limited condition.

Keywords: *Dehalococcoides*, reductive dechlorination, corrinoid, *Veillonellaceae*, metagenome, metatranscriptome

Introduction

Chlorinated solvents such as tetra- and tri-chloroethene (PCE and TCE) are common groundwater contaminants in the United States (1, 2). Bioremediation is a cost-effective and environmentally friendly approach to clean up solvent-contaminated field sites (3, 4). *Dehalococcoides mccartyi* is the only known bacterium capable of carrying out complete reductive dechlorination of chloroethenes to ethene (5, 6). Numerous studies have been performed on the physiology (7-10), genomics (11-15) and metabolic pathways (16-19) of this bacterium to optimize bioremediation processes. Corrinoids are a group of cyclic compounds containing four pyrrole rings, many of which are vitamins and/or enzyme cofactors. *D. mccartyi* requires hydrogen, acetate and corrinoid cofactors (e.g., cobalamin, a.k.a. vitamin B_{12}) during reductive dechlorination (5). However, all sequenced strains lack the genetic potential for forming hydrogen or acetate via fermentation as well as the capabilities of *de novo* synthesis of corrinoid cofactors (6, 11, 20). Consequently, *D. mccartyi* must acquire each of these essential substrates and nutrients from the environment or through interactions with other co-existing organisms. In a typical groundwater bioremediation site amended with low-cost organic substrates like whey and molasses, hydrogen and acetate can readily be provided by fermenters (21-23). Since a number of environmental microorganisms are capable of *de novo* corrinoid biosynthesis (24), corrinoid cofactors may also be available for *Dehalococcoides* in an environmental microbial community. *D. mccartyi* strains are able to utilize corrinoid forms other than cobalamin, and modify them into cobalamin in the presence of the favorable lower ligand dimethylbenzimidazole (DMB) (9, 25, 26). Therefore, understanding the capabilities of microorganisms supportive of *D. mccartyi* and how they interact will provide important guidance for manipulations of site conditions towards better bioremediation strategies.

Previous community studies focused primarily on the physiological and transcriptional responses of *D. mccartyi* to different growth conditions (27-31), with limited knowledge of the corresponding responses of the co-existing supportive microorganisms, particularly at the transcriptional level. Total RNA sequencing (metatranscriptomics) can complement total DNA sequencing (metagenomics) by providing information about active community members and the taxonomic or functional dynamics over a time course or across different environmental conditions (32). Metagenomics or 16S rRNA gene amplicon sequencing, sometimes followed by metatranscriptomics have been successfully applied to a wide range of environmental microbiomes, including ocean surface waters (33, 34), acid mine drainage (35), permafrost (32) and microbial fuel cells (36). Microbial compositions and functional genes of *Dehalococcoides*-containing dechlorinating communities have been reported in several metagenomic studies (19, 36, 37), and the active community members and the genes involved in carbon metabolism in the community have been investigated by BrdU-incorporated DNA sequencing (38). Metatranscriptomics sequencing can further provide insights into a comprehensive profile of functional activity and dynamics, which is important for identifying the roles played by the supportive microorganisms in dechlorinating communities under various environmental conditions.

The goal of this study is to get a systems level understanding of taxonomic and functional compositions in dechlorinating communities without exogenous cobalamin, and the roles of supportive microorganisms in corrinoid supplying for *D. mccartyi*. We constructed enrichment cultures from contaminated groundwater that were able to reductively dechlorinate TCE using lactate as the primary electron donor, with and without exogenous cobalamin cofactor. The microbial compositions and functional potentials were first analyzed by metagenomic sequencing. Draft genomes were binned from the metagenomes representing dominant community members of the enrichment community. Subsequently, the active members and their functional roles in the community were revealed by metatranscriptomics, reverse transcription quantitative PCR (RT-qPCR) and microarrays.

Results

Metagenomic analysis

A total of 101,964,968 reads from both HiTCEB12 and HiTCE metagenomes were filtered out after quality control and dynamic trimming with an average length of 100 bp. Using *de novo* assembly, 16,404 contigs with an average length of 2,463 bp were obtained. The coverages of the assembled contigs for HiTCEB12 and HiTCE metagenomes were 89.7% and 83.0%, respectively, which indicates a reliable accuracy of the *de novo* assembly. The assembled contigs consist of 49,488 predicted open reading frames (ORFs). Nine clusters of metagenome bins were retrieved using a modified differential coverage method (39) (Fig. 1). Seven metagenome bins (bins1-6, and bin9) with relatively high coverage and long contig length were subjected to further analysis, including those related to *Dehalococcoides*, *Veillonellaceae*, *Desulfovibrio*, *Sedimentibacter*, *Spirochaetaceae*, *Bacteroides*, and *Clostridium* (Fig. 1 & Table 1), which are referred to as bin-genomes hereafter. The bin-genome sizes, in terms of the number of predicted ORFs, were comparable with fully-sequenced genomes of related taxa (Table 1) (http://www.ncbi.nlm.nih.gov/). *Dehalococcoides*, *Desulfovibrio*, and *Sedimentibacter* bin-genomes exhibited an average of more than 90% amino acid sequence identity with the corresponding sequenced genomes, whereas the other bin-genomes exhibited less than 70% amino acid sequence identity, indicating that they represent novel species (Table 1). Detailed gene annotations of each bin-genome are listed in Table S2 of supplementary information.

Differential gene expression from metatranscriptomic sequencing

In addition to the metagenomes, which represent the taxonomic composition and metabolic potentials of each taxonomic group (i.e., bin-genome), the metatranscriptomes provide additional information on the dynamics of these taxonomic groups and their functional activities. Over 70% of the detected gene transcripts from the metatranscriptomes were assigned to the seven analyzed bin-genomes (Table 1), indicating that they represent the most active community members. In order to investigate the structural and functional activity dynamics in the community when no exogenous cobalamin was available, we first compared the metatranscriptomes of HiTCE (without B_{12}) and HiTCEB12 (with B_{12}) on day 2. Although similar numbers of transcripts were detected in the two metatranscriptomes (Table 1), approximately 550 functional genes exhibited more than 5-fold greater transcript abundances in HiTCE than in HiTCEB12 (Fig. 2A). Moreover, about 75% of those up-regulated genes were assigned to the *Veillonellaceae* bin-genome (Fig. 2A). Similar taxonomic distribution was obtained using BLASTx to annotate the up-regulated gene sequences (Fig. 2B).

Community dynamics were also analyzed by metatranscriptomic sequencing over a time series in the HiTCE enrichment. Transcript abundances of most annotated genes between the two replicates at T3 were at similar levels, so as for the remaining 16S rRNA if assuming the removal of structural RNA was the same among samples (Fig. S3). Therefore, the averaged transcript abundance at T3 was used for analysis. *Veillonellaceae* cells were most active on day 2 (T1), while *Desulfovibrio* dominated on day 9 (T2). On day 13 (T3), activities of all the other community members decreased substantially, resulting in a relatively higher activity of *Dehalococcoides* (Fig. 3). This suggests that the *Veillonellaceae* taxon likely plays a key role in corrinoid exchange during the first two days in the culture without exogenous cobalamin.

Corrinoid biosynthesis

The corrinoid biosynthesis pathway is one of the most complex pathways in nature, containing more than 30 enzymatic steps (24). In the *Dehalococcoides* bin-genome, only three up-stream corrinoid biosynthesis genes were detected (Fig. 4 & Table S3), consistent with its reported inability for *de novo* corrinoid synthesis (40, 41). Nevertheless, a full set of genes involved in the downstream corrinoid salvaging and remodeling pathway is present in the *Dehalococcoides* bin genome (Fig. 4), suggesting its potential for corrinoid remodeling when corrinoids are made available by others (9). Three of the non-*Dehalococcoides* bin-genomes, *Veillonellaceae*, *Desulfovibrio* and *Sedimentibacter* possess near-complete *de novo* corrinoid biosynthesis pathways (Fig. 4 & Table S3), indicating their potential for providing corrinoids to *Dehalococcoides*. However, transcripts of those corrinoid biosynthesis genes were not positively detected in the metatranscriptomes. Only *cysG* (gene_id_944) and *cobS*_2 (gene_id_5485) transcripts in the *Veillonellaceae* bin-genome were detected in both enrichments at T1, and higher transcript abundances (> 5-fold) were observed in HiTCE than HiTCEB12 (Fig. 4 & Table S4).

Corrinoid-dependent metabolic pathways

Considering the complexity and energy cost of *de novo* corrinoid biosynthesis, presumably corrinoids would only be synthesized if they were required as co-factors for enzymes in essential metabolic pathways. Therefore, we analyzed the presence of known corrinoid-dependent metabolic pathways in the bin-genomes, as well as their transcriptional activities, in order to further identify the active corrinoid producers.

One known corrinoid-dependent metabolic pathway is the methylmalonyl-CoA pathway used for propionate formation during lactate fermentation. The methylmalonyl-CoA mutase in this pathway is a corrinoid-dependent isomerase. This pathway was annotated in the *Veillonellaceae*, *Sedimentibacter*, *Spirochaetaceae*, and *Bacteroides* bin-genomes. Those in the

Veillonellaceae and *Spirochaetaceae* bin-genomes were actively transcribed (Fig. 5 & Table S5). In the *Veillonellaceae* bin-genome, the transcripts of the two genes encoding the corrinoid-dependent methylmalonyl-CoA mutase and methylmalonyl-CoA carboxyltransferase were less abundant in HiTCE than in HiTCEB12, whereas the other genes in this pathway exhibited higher expression in HiTCE, especially for lactate permease. In contrast, in the *Spirochaetaceae* bin-genome, similar transcript abundances were observed for HiTCE and HiTCEB12. In addition, transcriptional dynamics of the methylmalonyl-CoA pathway over a time course were observed. The activity in *Veillonellaceae* was relatively higher at T2, while that in *Spirochaetaceae* was higher at T1 (Fig. 5 & Table S5).

Another corrinoid-dependent metabolic pathway that might activate corrinoid *de novo* synthesis in corrinoid producers is methionine synthesis. The corrinoid-dependent methionine synthase (MetH) is a methyltransferase. It was detected in all of the non-*Dehalococcoides* bin-genomes, except for the *Clostridium* bin-genome (Table S2). However, only the one in *Veillonellaceae* was actively transcribed, and exhibited higher abundances in HiTCE (RPKM: 12) than in HiTCEB12 (RPKM: 6) (Fig. 5). One gene encoding the alternative corrinoid-independent methionine synthase (MetE) was also detected in the *Desulfovibrio* bin-genome, suggesting the ability to synthesize methionine when corrinoids are limited. However, the corresponding gene transcript was not detected in the culture, suggesting that corrinoids were available to the community in some form. Other corrinoid-dependent methyltransferases important for energy metabolism and carbon cycle in anaerobic acetogenic bacteria include vanillate O-demethylase, a corrinoid iron-sulfur protein and its corresponding methyltransferase (AcsE) involved in the Wood-Ljungdahl pathway for CO_2/CO fixation (42). However, we were not able to detect genes encoding those methyltransferases in any of the non-*Dehalococcoides* bin-genomes (data not shown).

Cobalt and corrinoid transport

Cobalt is the key metal element in a corrinoid molecule, which is transported into cells via ATP-binding cassette (ABC) transporters for *de novo* corrinoid synthesis. The uptake of cobalt may also indicate corrinoid biosynthesis activities, and help to identify active corrinoid producers. We discovered four operons annotated as cobalt ABC-transporters (*cbiMQO*) in the *Veillonellaceae* bin-genome, and one in the *Desulfovibrio*, but not in the other non-*Dehalococcoides* bin-genomes. Three of the four cobalt transporters in *Veillonellaceae* were transcribed with higher abundance in HiTCE than HiTCEB12, while the *cbiQ* transcript in *Desulfovibrio* was less abundant in HiTCE (Fig. 5 & Table S4). In addition, the transcripts of cobalt ABC transporters were only detected at T1, indicating that corrinoid biosynthesis occurred at an early phase, and its activity decreased afterwards when corrinoids reached an adequate level.

We also analyzed the presence and transcriptional activities of the corrinoid ABC transporter operon (*btuFCD*) in all bin-genomes. As the *btuFCD* operon exhibits similarity with other ABC transporters leading to potential mis-annotations, we manually annotated the *btuFCD* homologous genes in each bin-genome by blasting against a customized protein database containing the known amino acid sequences of the BtuFCD operon from all bacterial species extracted from the NCBI non-redundant database. A 30% amino acid sequence identity was set as the cutoff value. Genes homologous to *btuFCD* were detected in the *Veillonellaceae*, *Desulfovibrio*, *Sedimentibactor*, and *Dehalococcoides* bin-genomes. However, only the *Dehalococcoides btuD* gene (gene_id_5163) transcript was detected in the metatranscriptomes, with about 2 times more abundance in the enrichment without exogenous cobalamin than that with exogenous cobalamin (Table S4).

Sporulation-related genes in the Veillonellaceae bin-genome

Interestingly, a distinctive difference between the metatranscriptomes of HiTCE and HiTCEB12 was related to sporulation (Fig. 5). For all of the detected *Veillonellaceae* transcripts, abundances were substantially higher (up to 28-fold) in HiTCE than HiTCEB12 at T1, but were dramatically lower at T2 and T3 (Fig. 5, Table S4 & S5). Although the other two *Firmicutes* bin-genomes, *Sedimentibacter* and *Clostridium*, also possess a suite of sporulation related genes, the sporulation activities were insignificant with only 2-4 genes actively transcribed (Table S4 & S5).

Complementary molecular approaches for differential gene expression analyses

Although the detected activities of corrinoid-dependent metabolic pathways and cobalt transport strongly suggests the need for *de novo* corrinoid synthesis within the HiTCE community, transcripts of genes involved in the corrinoid biosynthesis pathway in the *Veillonellaceae* bin-genome were not detected in the metatranscriptome. In order to query the expression of low abundant mRNAs of the corrinoid biosynthesis pathway in *Veillonellaceae*, specific qPCR primers were designed and applied to the same RNA samples used for sequencing. With this complementary approach, we were able to detect and quantify the relative expression of the corrinoid biosynthesis genes in the *Veillonellaceae* bin-genome. Since the transcript abundances of the *tceA* gene among all samples were at similar levels, we used *tceA* as the reference gene for the relative RT-qPCR analysis. Corrinoid biosynthesis activities of *Veillonellaceae* in HiTCE at T1 were higher than HiTCEB12 under the same dechlorination activity (Fig. 6). Interestingly, consistent with the metatranscriptomic data (Fig. 4 & Table S4), one gene annotated as *cobS_1* (gene_id_5485) exhibited higher relative expression in HiTCE, while another annotated *cobS_2* (gene_id_6498) had higher transcript abundance in HiTCEB12 (Fig. 6) in this analysis.

Microarrays are another complementary approach to analyze differential gene expression. To further validate the metatranscriptomic sequencing results related to *Dehalococcoides* bin-genome, we compared differential gene expression obtained from a *Dehalococcoides* genus-wide microarray to those obtained from the metatranscriptomic sequencing. The targeted *D. mccartyi* genomes of the microarray include strain 195, which is the closest genome to the identified *Dehalococcoides* bin-genome. According to microarray results, 96 genes were up-regulated and 2 genes were down-regulated in HiTCE comparing to HiTCEB12. Eighty-six out of the 96 up-regulated genes and one of the two down-regulated genes were detected in the metatranscriptomes (Table S6), although the transcript abundance ratios of HiTCE to HiTCEB12 according to RNA sequencing were less significant than the signal intensity ratios by RNA microarray. The results of microarray and RNA sequencing were more consistent when there was a more than 4-fold difference (Table S6). We further examined the *Dehalococcoides* genes involved in corrinoid salvaging and remodeling pathways. In general, metatranscriptomes and microarrays give similar gene regulation trends. Consistently up-regulated genes include *cbiZ* (DET0653), *cobD* (DET0655), *cobT* (DET0657), and *btuCD* (DET0651, 0652), although several genes (i.e., *cbiP*, *butF*, DET1175, and DET1176) did not show differential expression based on metatranscriptome, but were significantly upregulated according to microarray analysis (Fig. S4). Since we only included technical replicates for the RNA samples of HiTCE at T3 (due to relatively high cost of sequencing at the time of this study and the budget limitation), it is unavailable to get the statistical significance of the comparison between metatranscriptomic and microarray results.

Discussion

Metagenomic and metatranscriptomic analyses provide powerful cultivation independent tools to disentangle microbial interactions, given that most environmental microorganisms are excluded from lab cultivation and many grow in important syntrophy. This study is the first combined application of both metagenomic and metatranscriptomic sequencing to dechlorinating communities. Here we compared enrichments with and without exogenous cobalamin to uncover the phylogenetic composition, functional potentials, activities, and dynamics of the communities, with a focus on the function of materials exchanges, including corrinoids. We acknowledge that the lack of biological replicates for metatranscriptomic sequencing makes the comparative analyses without statistical significance. Nevertheless, we still carried out some qualitative and semi-quantitative comparison of gene expression using the RNA sequencing data. We then conducted qPCR and microarray analyses with three biological replicates as a validation.

Among the bin-genomes with *de novo* corrinoid biosynthesis pathways, we observed the most differential gene expression of *Veillonellaceae* bin-genome at an early stage in the enrichment without exogenous cobalamin compared to that with cobalamin, including genes related to cobalt transport and *de novo* corrinoid biosynthesis. *Veillonellaceae* is one of the three bin-genomes capable of *de novo* corrinoid synthesis that also exhibited activities of corrinoid-dependent metabolic pathways, such as propionate-formation methylmalonyl CoA and MetH-mediated methionine synthesis (42). Moreover, the *Veillonellaceae* bin-genome in HiTCE exhibited the highest activity on day 2 (T1), when the corrinoid production reached a maximum production (41). In addition, *p*-cresolyl cobamide was the dominant corrinoid form produced endogenously by supportive microorganisms in this enrichment (41), and the phenolic corrinoids are known to be produced by *Veillonellaceae* species (i.e., *Pelosinus* and *Sporomusa*) similar to the *Veillonellaceae* bin-genome detected in this study (43, 44). Collectively, the above evidence suggests that the cells associated with the *Veillonellaceae* bin-genome are the corrinoid cofactor (i.e., *p*-cresolyl cobamide) suppliers for *Dehalococcoides* in this community. *Pelosinus* and *Sporomusa* species are among the commonly detected species in dechlorinating communities (22, 40, 45, 46).

In the *p*-cresolylcobamide molecule, the lower ligand cannot form the coordination to the cobalt ion (base-off conformation) (43). Only several corrinoid-dependent enzymes can use corrinoids with base-off conformation as cofactors, and the corrinoid-dependent methylmalonyl CoA mutase in the propionate-producing methylmalonyl CoA pathway is one such enzyme (42). Therefore, *p*-cresolyl cobamide is most likely produced and utilized by the *Veillonellaceae* bin-genome as the corrinoid cofactor for the methylmalonyl CoA pathway to generate propionate from lactate fermentation.

The *de novo* synthesis and utilization of corrinoid cofactors generally occur intracellularly. Therefore, it is still an enigma how corrinoids are made available extracellularly to other community members such as *Dehalococcoides*. Possibilities include positive secretion and passive release via lysis. So far, no active mechanisms of corrinoid export has been identified (47). The transcript abundances of corrinoid ABC transporter genes (*btuFCD*) in the *Veillonellaceae* bin-genome were rather low, and no difference was observed between the enrichments with and without B_{12} addition, suggesting little positive corrinoid exchange via corrinoid ABC transporters. Nevertheless, the sporulation activity of *Veillonellaceae* was substantially induced in the enrichment without exogenous cobalamin on day 2. This suggests that the cell lysis during sporulation likely served as a possible mechanism of the corrinoid release. Similarly, some nutrients may also be released during the nocturnal sporulation of *Epulopiscium* spp. symbiont, which is beneficial for its host surgeonfish (48). Once released into the environment, corrinoids could be salvaged by *D. mccartyi* for remodeling to the preferred cobalamin form with the corresponding lower ligand dimethylbenzimidazole (DMB), as shown previously (9, 41, 44). Sporulation is an important strategy for spore-forming species within the phylum *Firmicutes* to survive in adverse conditions, presumably triggered by nutrient depletion or the presence of toxic compounds (49, 50). As both enrichments with and without exogenous cobalamin encountered the same level of TCE toxicity and the same lactate depletion after the first two days, it seems to be other conditions, possibly the limited cobalamin that stimulated the sporulation of the *Veillonellaceae* cells in the enrichment without cobalamin. Therefore, regarding the interactions between the corrinoid suppliers and the dechlorinators in the investigated community without exogenous cobalamin, it is not unreasonable to speculate that during the first two days, corrinoids were produced by *Veillonellaceae* cells via corrinoid-dependent fermentation pathways, then passively released to the culture suspension during the induced sporulation, which made them available for *Dehalococcoides* to utilize for dechlorination afterwards.

If *Dehalococcoides* was obtaining cobalamin by modifying other corrinoid forms using the lower ligand DMB when there was no exogenous cobalamin, the availability of DMB in the community would become essential. DMB was detected in the enrichment cultures (41), indicating that some community members were able to produce it anaerobically. An anaerobic DMB synthesis operon (*bzaABCDE*) has been identified very recently (51), but we were not able to detect homologous genes in our metagenomes (data not shown), so the DMB producers here remain unknown.

High-throughput DNA/RNA sequencing allows us to obtain the compositions, activities and dynamics of complex communities at systems levels. In this study we complemented metagenomic and metatranscriptomic sequencing with qPCR and microarray analyses to gain a comprehensive understanding of microbial communities involved in reductive dechlorination. The corrinoid biosynthesis genes are not highly expressed, probably because the pathway complexity makes it energy-demanding, and corrinoid cofactors are only needed in trace amounts to function (24). Here, RT-qPCR using specific primers targeting corrinoid synthesis genes identified from the *Veillonellaceae* bin-genome, as well as microarrays seemed to be more sensitive in detecting the differential gene expression than metatranscriptomic sequencing, by avoiding the interference of structural RNAs and house-keeping. All these complementary tools are important for the differential gene expression analyses, especially for the rare genes in complex communities. We also recognize the limitation of all RNA-based function and activity analyses, as mRNA abundance does not necessarily reflect the actual metabolic activity. Nevertheless, valuable hypotheses regarding the research questions can still be derived from the mRNA-level differential gene expression, and then be further tested by gene modification, as well as protein and metabolite level analyses.

In summary, metagenomic and metatranscriptomic sequencing together with downstream qPCR and microarray analyses gave a comprehensive view of the genomic information, phylogenetic and functional dynamics of supportive microorganisms in TCE-dechlorinating enrichments without exogenous cobalamin. *Veillonellaceae* with corrinoid biosynthesis pathways are important for corrinoid supply to *Dehalococcoides*. The induced sporulation activity of *Veillonellaceae* species is likely a response to exogenous corrinoid limitation, and might contribute to the release of *de novo* synthesized corrinoids. Our findings provide insights into the ecological interactions between *Dehalococcoides* and other community members, and lead to further hypothesis-driven validations for a better understanding of dechlorinating communities.

Materials and Methods

Enrichment cultures

Two TCE-dechlorinating enrichments with (HiTCEB12) and without (HiTCE) exogenous cobalamin were constructed using contaminated groundwater, and were stably maintained in 160 mL serum bottles (with 60 mL headspace of N_2/CO_2, v/v: 90/10) at 34 °C in the dark, and sub-cultured (5% v/v transfer to fresh defined medium) every two weeks for over 3 years prior to this study. Lactate was supplied as the primary electron donor (20 mM on day 0, 2.5 mM on day 6 and 8, 25 mM in total) (Fig. S1), along with high concentrations of TCE (~770 µM) as primary electron acceptor, which completely inhibited methanogens. The composition of the defined medium used and the details of growth conditions were described elsewhere (40). Both HiTCEB12 and HiTCE enrichments were performed in triplicates for TCE measurement and microarray analysis.

Cell harvest

For metagenomic sequencing, 40 mL cell samples from one bottle of HiTCEB12 or HiTCE culture were collected on the last day (day 13) of incubation. For metatranscriptomic sequencing, in order to compare the activities of specific microorganisms in the enrichments, particularly corrinoid-related activities between the enrichment with exogenous cobalamin and without, 40 mL sample from one bottle of both HiTCEB12 and HiTCE were sampled on day 2 (T1) (Fig. S1), when the corrinoids were observed to be actively produced (41). Moreover, 40 mL sample from the second bottle of HiTCE enrichment on day 9 (T2) and 2 × 40 mL sample from the third bottle of HiTCE on day 13 (T3) (Fig. S1) were also sampled, in order to obtain the temporal dynamics of gene expression. The two HiTCE samples taken on day 13 were sequenced as technical duplicates to test the reliability of the sequencing technique. All cell samples were collected by centrifugation at 15,000 × g, at 4 ºC for 10 min, and stored at -80 °C prior to use.

High molecular weight DNA isolation

High molecular weight (HMW) DNA samples were isolated following the steps described in the “Bacterial DNA Isolation CTAB Protocol” on the JGI website (www.jgi.doe.gov). The isolated HMW DNA was visualized using gel electrophoresis (0.7% agarose) for integrity check, and was then quantified by Nanophotometer P-300 (Implen, Inc., Westlake Village, CA). The DNA samples were adjusted to 1µg/10µL using nuclease-free water and stored at -20 °C till proceeded to metagenomic sequencing.

RNA isolation

Total RNA was isolated using the acid phenol-chloroform protocol described previously (44). Briefly, cell pellets were resuspended in 250 µL of lysis buffer (50 mM sodium acetate, 10 mM EDTA, pH 5.1), 100 µL of 10% sodium dodecylsulfate, and 1.0 mL of buffer-equilibrated phenol (pH 4.3) (Sigma-Aldrich, St. Louis, MO). After bead beating, the aqueous lysate was extracted twice with one volume of acid (pH 4.3) phenol-chloroform-isoamyl alcohol (25:24:1) and once with one volume of chloroform-isoamyl alcohol (24:1) (Sigma-Aldrich). RNA was then precipitated, collected, washed, vacuum dried, and resuspended in 100 µL of nuclease-free water. DNA contamination was removed by DNase I treatment using a Turbo DNAfree kit (Ambion, Life Technologies, Grand Island, NY) according to the manufacturer’s instructions. Purified RNA was stored at -80°C until library construction.

Library preparation for metatranscriptomic sequencing

First, mRNA in the total RNA samples was enriched by removing the biotinylated structural RNA using streptavidin-coated magnetic beads. Second, first-strand cDNA was synthesized by using Super Script II reverse transcriptase, and the second strand of cDNA was then synthesized by NEB Next mRNA Second Strand Synthesis Module (New England Biolabs, Inc., Ipswich, WA) according to the manufacturer’s instructions. Third, the double stranded cDNA was then subjected to T7 Linear Amplification for Deep Sequencing (LADS) procedure developed by Hoeijmakers *et al* (52). Detailed procedure is provided in the Supplemental Material.

High-throughput sequencing

The overall workflow of the high-throughput DNA and RNA sequencing is outlined in Fig. S2. The genomic DNA and double stranded cDNA (~ 100 ng per sample) were submitted to QB3 sequencing facility of University of California, Berkeley, for Illumina HiSeq2000 sequencing (paired-end, 150 bp) (http://qb3.berkeley.edu/qb3/gsl/index.cfm).

Metagenomic and metatranscriptomic analyses

Raw sequencing reads were trimmed and screened according to sequencing quality (Supplemental methods). The DNA reads after quality control were subjected to *de novo* assembly using CLC genomics workbench version 6 (CLC bio, Boston, MA), and genome reconstruction (i.e., metagnome binning) by a bi-dimension binning process as reported previously (39) (Supplemental methods). A genome evaluation software, checkM was used to evaluate the genome completeness using maker genes (53). The RNA reads were mapped against the assembled DNA sequences, and transcript abundances were determined as RPKM (the number of Reads Per Kilobase pair transcript per Million total reads mapped) values. Transcript abundances of HiTCE and HiTCEB12 2d-samples, as well as those of HiTCE time course samples were then compared (see details in Supplemental material).

RT-qPCR

For genes involved in corrinoid *de novo* biosynthesis that are usually present in low transcript abundance, specific qPCR primers were designed using primer-BLAST (Table S1). The relative gene expression ratios were determined using two-step RT-qPCR. The first strand cDNA was synthesized from the same RNA samples submitted for Illumina sequencing using Super Script III kit (Invitrogen) according to manufacturer's instructions. The cDNA was then relatively quantified by qPCR using Fast SYBR Green PCR reagent (Applied Biosystems, Life Technologies, Grand Island, NY) following the manufacturer's instructions.

The relative gene expression ratio was calculated using the following equation:

$$R = 2^{[\Delta Ct_{HiTCE}(ref-target)-\Delta Ct_{HiTCEB12}(ref-target)]} = 2^{\Delta\Delta Ct}$$

Where ΔCt_{HiTCE}(*ref-target*) and $\Delta Ct_{HiTCEB12}$(*ref-target*) are the difference in Ct values of a reference gene and the targeted corrinoid-related gene in the HiTCE and HiTCEB12 samples, respectively. As the transcript abundances of *tceA* gene in HiTCE and HiTCEB12 at T1 were at about the same level, it was used as the reference gene for the relative gene expression ratio calculation.

Microarray analysis

The custom designed microarray (Affymetrix, Santa Clara, CA, USA) targeting four sequenced *D. mccartyi* genomes: strain CBDB1, BAV1, 195, and VS, as well as 348 outside genes was described elsewhere (31). Biological triplicates were performed. The gDNA (40) and RNA microarrays were processed according to the instructions provided in section 3 of the Affymetrix GeneChip Expression Analysis technical manual (Affymetrix, Santa Clara, CA, USA) and data analysis is provided in the supplementary information.

Microarray (DNA and RNA) data were analyzed using Affymetrix GeneChip software and the MAS5 algorithm. Each microarray was normalized by scaling the signal intensities of the positive control spike-mix to a target signal intensity of 2,500 to allow comparison between microarrays. A gene (DNA microarray) or gene transcript (RNA microarray) was considered "present" in a culture if the probe set across all three replicated samples had signal intensities greater than 140 (DNA microarray) or 250 (RNA microarray) and p values less than 0.05.

Accession numbers

The assembled DNA sequences and predicted ORF sequences are deposited into the MG-RAST database under the project ID 7649. Raw reads of metagenomics and metatranscriptomic sequencing are deposited to SRA database under PRJNA344005 (SRP090641), and the accession numbers for each of the metagenomes/metatranscriptomes are: SAMN05817823 (HiTCEB12_DNA), SAMN05817824 (HiTCE_DNA), SAMN05817822 (HiTCEB12_2d_RNA), SAMN05817821 (HiTCE_2d_RNA), SAMN05817818 (HiTCE_9d_RNA), SAMN05817819 (HiTCE_13d_RNA_rep1), SAMN05817820 (HiTCE_13d_RNA_rep2). The microarray data are deposited into the NCBI Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE94143.

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The authors have no conflict of interest to declare.

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Table and Figure Legends

Table 1. Summary of bin-genome reconstruction from metagenomes and corresponding transcripts detected in metatranscriptomes

Figure 1. Metagenome binning using differential coverages of HiTCE and HiTCEB12 (Note: the taxonomic assignment of the bin-genomes was based on BLAST results of the unique 16S rRNA gene sequence included in each metagenome bin against SILVA structural RNA database, with the resolution at genus or family level.).

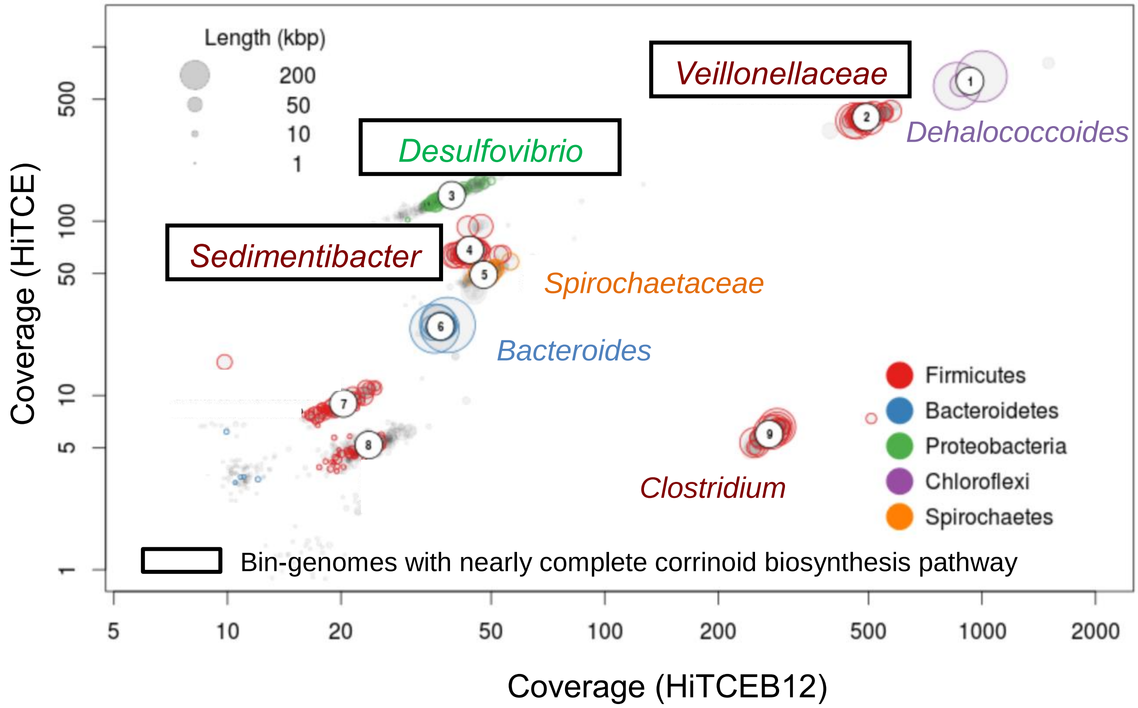
Figure 2. Taxonomic (A: by genomic reconstruction; B: by BLASTx and MEGAN5) distribution of genes up-regulated (> 5-fold) in HiTCE compared to HiTCEB12, numbers of up-regulated genes are indicated next to the names.

Figure 3. Taxonomic distribution of the up-regulated genes in HiTCE (> 5-fold difference) based on metatranscriptomic analysis over a time course.

Figure 4. Corrinoid biosynthesis pathways in 4 bin-genomes.

Figure 5. Heatmap of RPKM values of selected genes in the Veillonellaceae bin-genome.

Figure 6. Relative gene expression ratios (HiTCE/HiTCEB12 at T1) by RT-qPCR targeting corrinoid biosynthesis genes in the *Veillonellaceae* bin-genome (the lines indicate more than 2-fold difference; reference genes: tceA, representing dechlorination activity).



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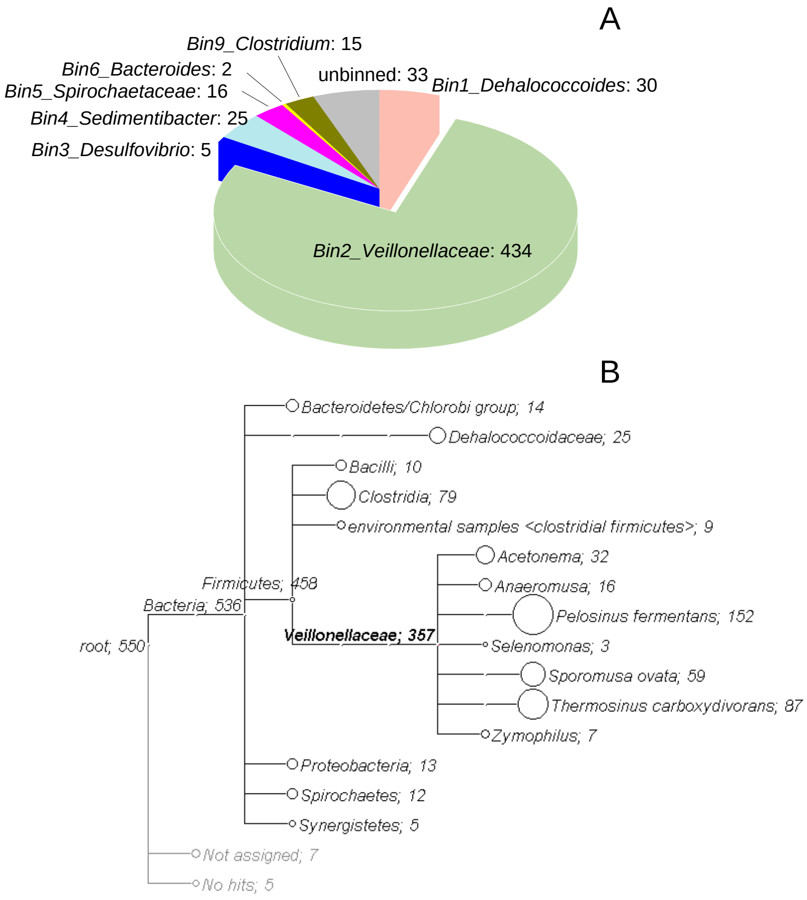

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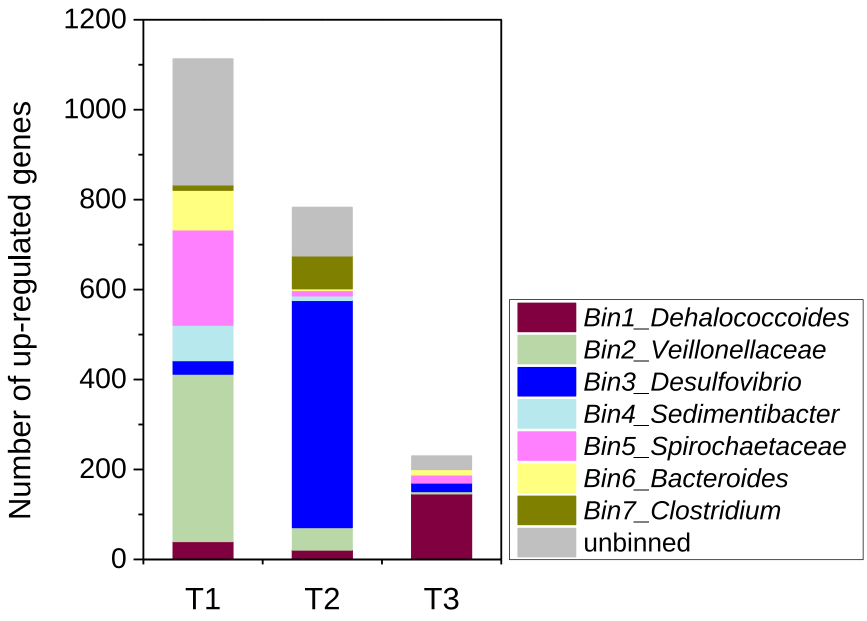

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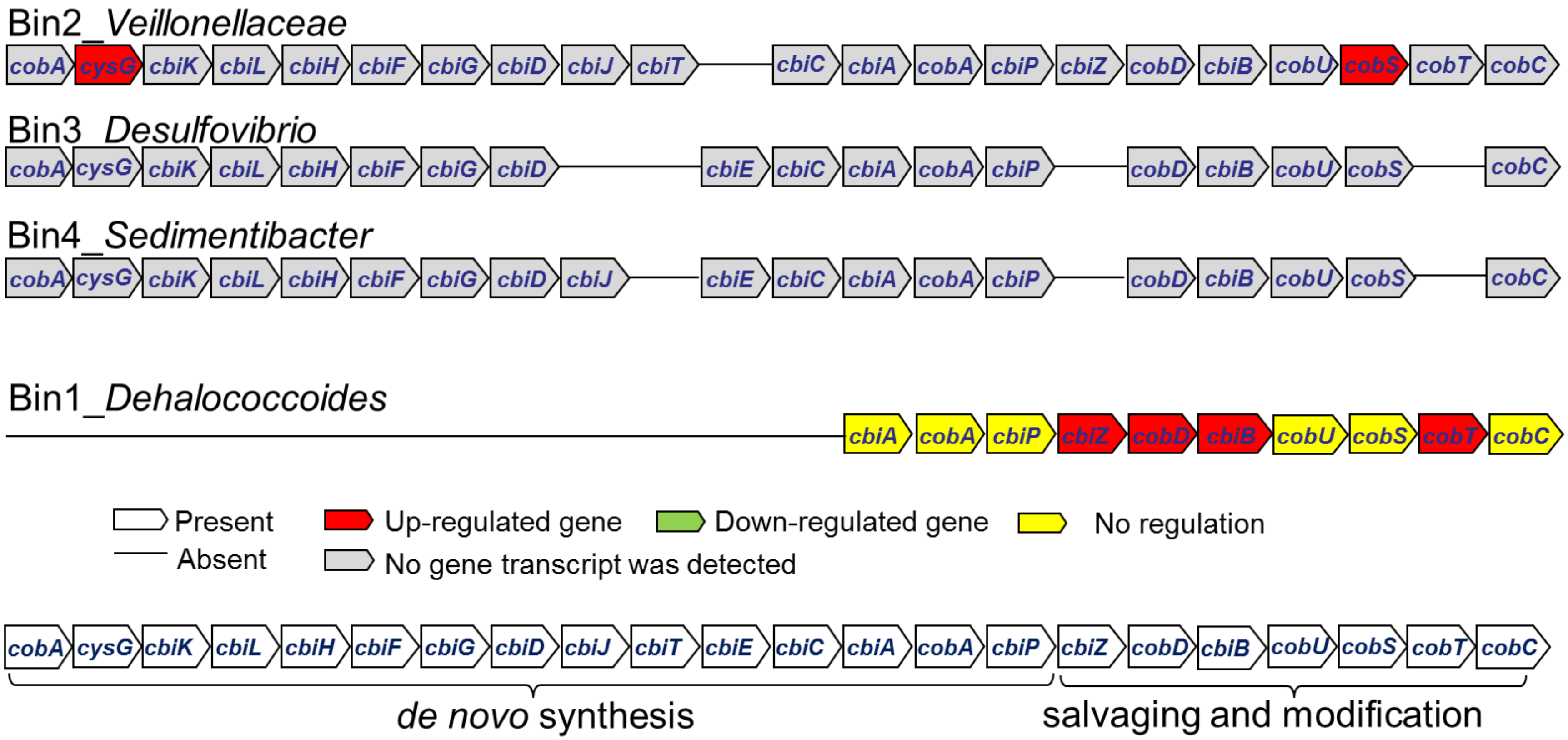

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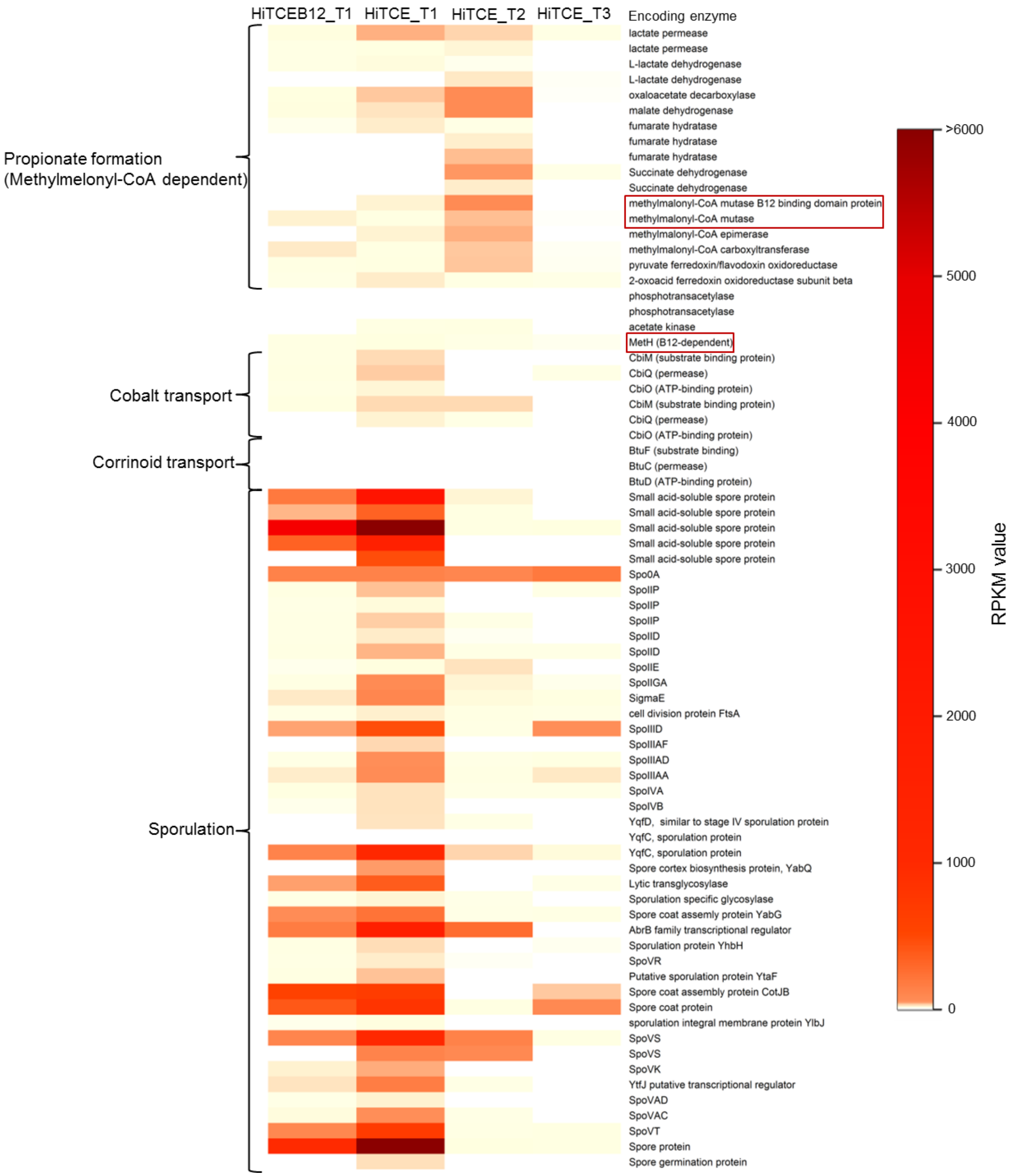

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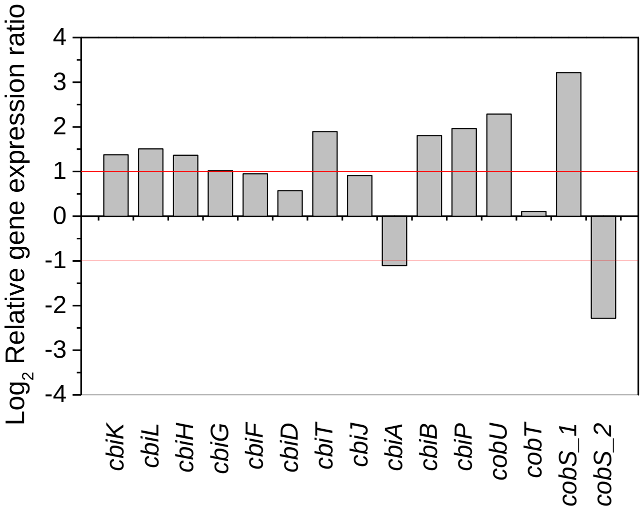

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Table 1. Summary of bin-genome reconstruction from metagenomes and corresponding transcripts detected in metatranscriptomes

Bin-genome	**Size (Mbp)**	**Number of predicted ORFs**	**Estimated genome completeness (%)**	**Average amino acid sequence identity (%)**	**Number of transcripts detected in metatranscriptomes**			
					HiTCEB12_T1	**HiTCE_T1**	**HiTCE_T2**	**HiTCE_T3**
Bin1_Dehalococcoides	1.3	1431	99.3	95	1300	1308	1333	1334
Bin2_Veillonellaceae	3.6	3856	99.9	66	808	910	99	466
Bin3_Desulfovibrio	3.4	3390	91.1	91	222	221	1483	641
Bin4_Sedimentibacter	3.5	3659	93.3	90	274	278	286	89
Bin5_Spirochaetaceae	2.7	2682	92.1	56	892	891	853	571
Bin6_Bacterioides	2.4	2203	96.4	68	728	724	494	449
Bin9_Clostridium	2.6	2871	99.0	67	57	60	216	63
unbinned		29396			1530	1551	196	239
Total		***49488***			***5811***	***5943***	***5852***	***3852***

Supplemental Information

Metagenomic and metatranscriptomic analyses reveal structure and dynamics of a dechlorinating community containing *Dehalococcoides mccartyi* and corrinoid-providing microorganisms under cobalamin-limited condition

Running title: High-throughput sequencing of dechlorinating communities

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Supplemental methods

1. Library preparation for RNA sequencing

Structural RNA removal and mRNA enrichment

The purified total RNA was subjected to first strand cDNA synthesis using biotinylated universal 16S and 23S rRNA probes (1) and SuperScript® II reverse transcription (RT) system (Invitrogen, Life Technologies, Grand Island, NY) according to the manufacturer's instructions. A mixture of 2 µL dNTP (10 mM each), 2 µL biotinylated universal 16S primer mix (2.5 mM each), 2 µL biotinylated universal 23S primer mix (2.5 mM each), 1 µL SUPERaseIn RNase inhibitor (20U/µL), together with 8 µL RNA sample (100 ng total) was denatured at 65 °C for 3 min and cooled on ice for 2 min. Then, the reaction mix was amended with 4 µL 5X First-Strand buffer and 1 µL (200 U) SuperScript II reverse transcriptase and incubated at 42 °C for 50 min.) Dynabeads® MyOne™ Streptavidin C1 magnetic beads (Invitrogen) were then used to capture the structural RNA from the above RT mix. (A 1.5-mL microcentrifuge tube containing 20 µL suspension of beads was put on a magnetic stand for 1 min, the supernatant was then discarded. The beads were washed by 20 µL of solution A (DEPC-treated 0.1 M NaOH and DEPC-treated 0.05 M NaCl, filter sterilized), B (DEPC-treated 0.1 M NaCl, filter sterilized) and 1X First-Strand buffer, respectively. The washed beads were resuspended into 10 µL 1X First-Strand buffer.) A mixture of 5 µL washed beads were added into the 20 µL RT mix, and incubated at room temperature for 15 min. The beads were captured on a magnetic stand and the supernatant was transfered into another tube, with another 5 µL of washed beads added for a 30 min-incubation at room temperature. The beads were captured and the supernatant was transferred into a new tube. The collected beads were resuspended in 10 µL 1X First-Strand buffer, and the supernatant was separated from the beads and combined with the previous ones, resulting in a total of 40 µL enriched mRNA solution.

Double stranded cDNA synthesis for linear amplification of mRNA

First stranded cDNA was first synthesized using random hexamer. 1µL primer (1µg/µL), 1µL dNTPs (10 mM each), and 1 µL (200 U) of SuperScript II reverse transcriptase were added into the 40 µL enriched mRNA solution and hybridized at 25 °C for 2 min, followed by incubation at 42 °C for 50 min. The reaction was then inactivated at 70 °C for 10 min.

The second strand was synthesized using NEBNext mRNA Second Strand Synthesis Module (New England Biolabs, Inc., Ipswich, WA) according to the manufacturer's instructions. The synthesized double stranded cDNA was purified and eluted into 10 µL nuclease-free water using MinElute PCR purification kit (Qiagen, Valencia, CA, USA) according to the manufacturer's instructions.

Linear amplification

T7 amplification requires addition of the T7 promoter to DNA fragments through the ligation of a T7-incorporated adapter. This enables T7 RNA polymerase-mediated transcription in an in vitro reaction, which amplifies the template in a linear rather than an exponential manner (2). The resulting RNA fragments are subsequently converted to cDNA, in which the representation of different DNA fragments is highly similar to that of the original samples (2). The entire procedure includes steps of end repair, "A" tailing, adapter ligation, size selection, linear amplification, and final double stranded cDNA synthesis. (The details of each step are described in supplementary information).

The purified and quantified ds cDNA was blunted and phosphorylated using End-It DNA End-repair Kit (Epicentre, Madison, WI) according to the manufacturer's instructions. An adenine was added to the 3'-end of DNA fragments using Klenow fragment (New England Biolabs) according to the manufacturer's instructions. The adapter A (containing P5 primer) and adapter B (containing T7 promoter and P7 primer) for Illumina sequencing were then ligated onto the DNA fragments using Ligalast rapid DNA ligation system (Promega, Madison, WI) according to the manufacturer's instructions). The 400-500 bp DNA fragments (including the adapters) shown on the E-gel system (Invitrogen) were excised and purified using QIAquick Gel Extraction Kit following the manufacturer's instructions. The adapter-ligated and size-selected DNA fragments were then linearly transcribed into RNA using MEGA short script T7 kit (Ambion, Life Technologies, Grand Island, NY) according to the manufacturer's instructions. The transcribed RNA was purified using RNeasy MinElute cleanup kit (Qiagen) following the manufacturer's instructions, and then reverse transcribed into double stranded cDNA using P5 primer (first strand cDNA synthesis) and P7 (second strand cDNA synthesis) primer according to the protocols described by others (2).

2. High throughput sequencing data analysis

The high throughput sequencing data were analyzed according to steps shown in Fig. S2. The following describes details of the major steps.

De novo assembly and ORF prediction

The raw DNA reads were first trimmed to 100 bp and filtered using criteria that all of the nucleotides in one read have a quality score equal or above 20. The trimmed and quality filtered reads from both HiTCEB12 and HiTCE samples were then submitted for de novo assembly by CLC genomics workbench version 6 (CLC bio, Boston, MA), using a kmer value of 63 and a minimum contig length of 1 kbp. The assembled contigs were submitted to Metagenmark server (3) for ORF/gene prediction.

Bin-genome construction and annotation

The difference in enrichment conditions of HiTCEB12 (with exogenous cobalamin) and HiTCE (without exogenous cobalamin) may result in shifts of microbial population abundances. A sequence-composition-independent, differential coverage binning method developed by others (4) was modified and applied to reconstruct the bin-genomes from the metagenomic datasets. Briefly, the coverage of each contig was calculated by mapping the reads after quality control against the contig sequence with a minimum similarity of 95% over 100% of the read length. Binning contigs into microbial population genomes were carried out by first plotting the coverage estimates of the two enrichments against each other for all contigs. The contigs clustered by differential coverage binning were further binned by tetranucleotide frequency and then extracted as bin-genomes.

The taxonomic assignment of the predicted ORFs was made by MEGAN5 (5) using the output file of BLASTx against the NCBI non-retardant protein sequence database (nr). The functional annotation of the predicted ORFs was assigned according to SEED subsystems database through MG-RAST, with a cut-off e-value of 10^{-5}.

Metatranscriptomic analysis

A rapid rRNA filter using DUK, an efficient kmer matching tool developed by JGI (https://sourceforge.net/projects/duk/) was applied to separate rRNA reads from the metatranscriptomic sequence pool. The non-rRNA reads were analyzed using modified Tophat and Cufflinks packages (6). In general, the RNA fragments were mapped against the predicted ORF/gene sequences. RPKM (Reads Per Kilobase pair transcript per Million total reads mapped) values were calculated using Cuffdiff, a part of Cufflinks package. Transcripts detected under both conditions with 5-fold difference in RPKM values were considered to be significantly differentially expressed, and were subjected to subsequent analyses. In order to investigate the gene regulation at a single-cell level, RPKM values normalized to one specific bin-genome (i.e.

reads per kilobase pair transcript per million reads mapped in one bin-genome) were also calculated using Bowtie2 alignment.

Supplemental Figures and Tables

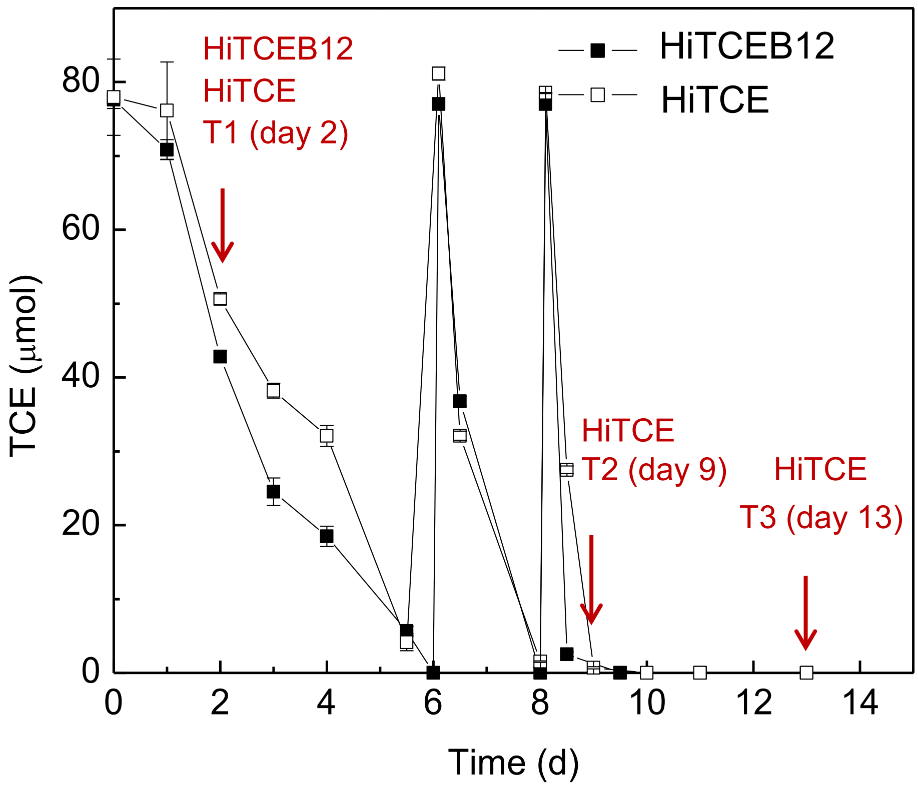

Figure S1. TCE degradation during a 13-day incubation (TCE was re-amended on day 6 and 8; red arrows indicate the time points at which samples were taken for metatranscriptomic sequencing)

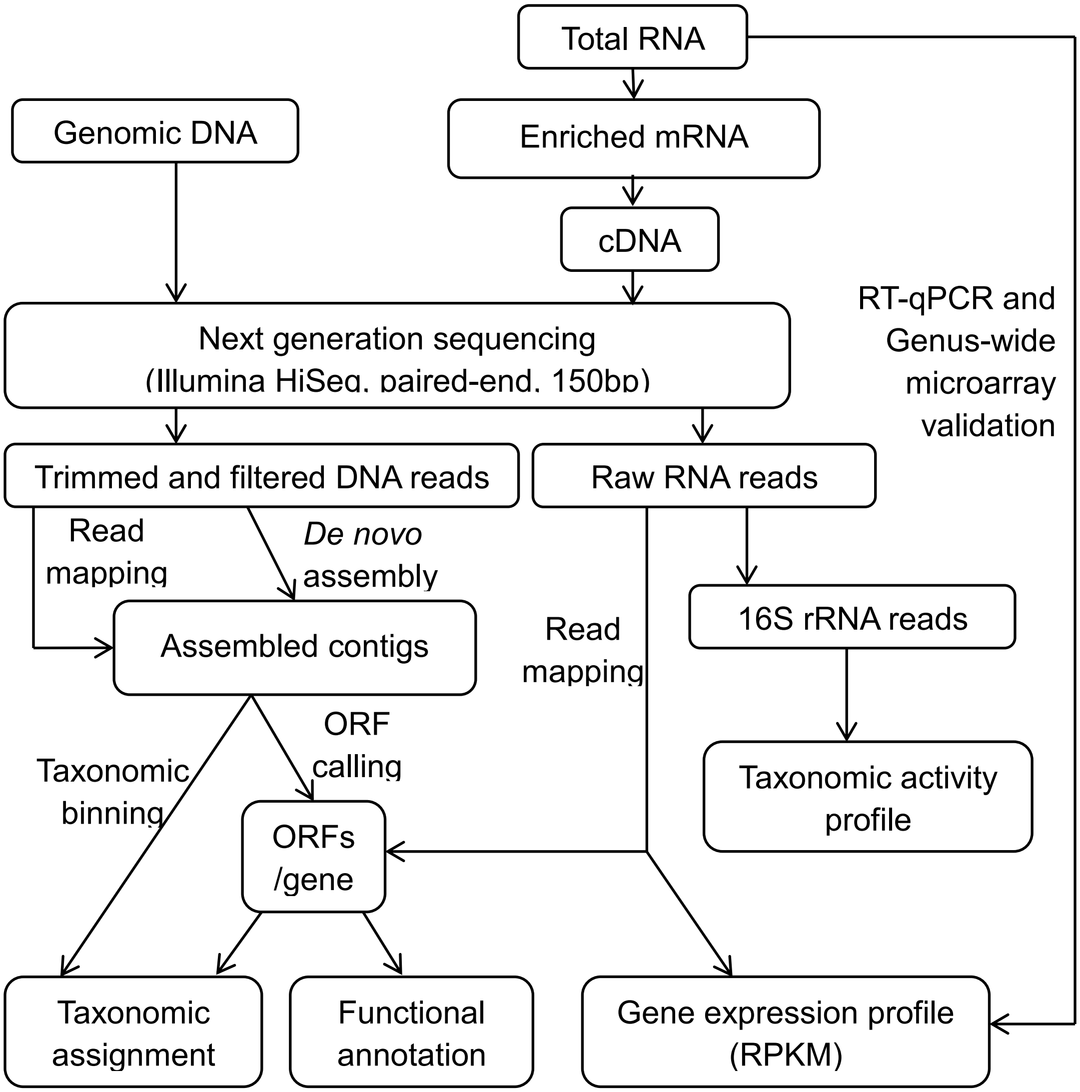

Figure S2. Schematic workflow of metagenomic and metatranscriptomic analysis. (ORF: open reading frame; RPKM: reads per kilobase pair of transcript per million reads mapped)

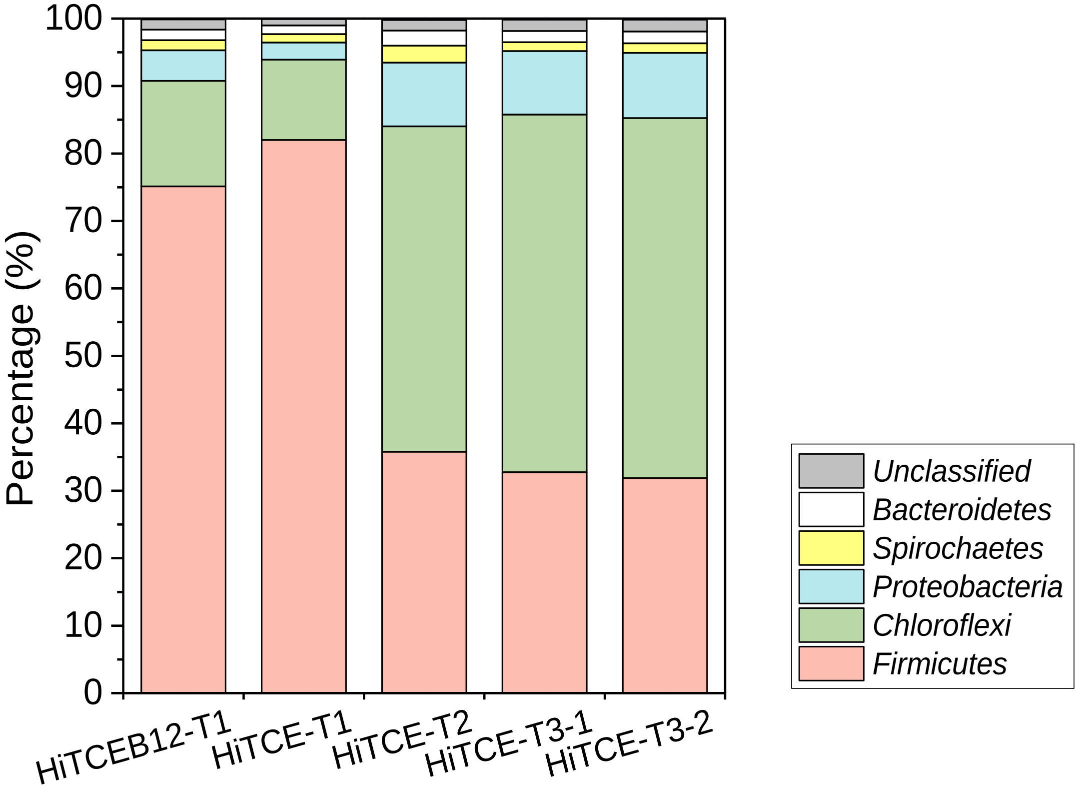

Figure S3. 16S rRNA distribution (at Phylum level) in metatranscriptomes (HiTCE-T3-1 and HiTCE-T3-2 are replicates).

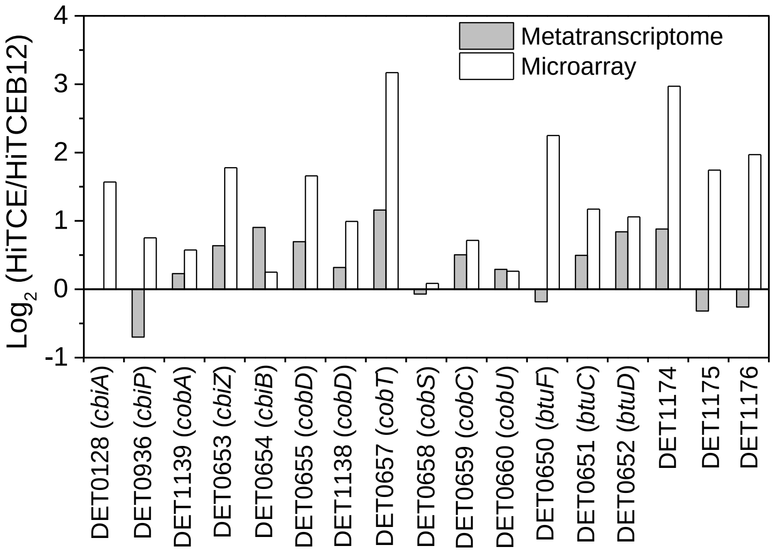

Figure S4. Differential expression of B_{12}-related genes in *Dehalococcoides* bin-genome at T1 by metatranscriptome and *Dehalococcoides* genus-wide microarray.

Table S1 Quantitative PCR primers targeting genes involved in cobalamin biosynthesis

Cobalamin biosynthesis enzymes		Gene ID	Primers (5’→ 3’)
CobA	uroporphyrin-III C-methyltransferase	947	F440: AAGATCCAACCAAGGGCGAG R571: CCGGACGGCCATTTTCAATC
CysG	precorrin-2 dehydrogenase/siroheme synthase	944	F282: TGGGCGGGGTTTGTTATTCA R392: TTGCCGGCTGTAGAAACAGT
CbiK	cobalt chelatase	1227	F376: ACGGGGCAAGAAAATCAACC R519: GAGTGCTGCATAGGCGGTAT
CbiL	precorrin-2 C20-methyltransferase	6488	F483: TCCAGAAGAGTTGCGTGTCA R667: CACCGCGGAGACTGTCTAAA
CbiH	precorrin-3B C17-methyltransferase	6491	F176: TTGCTGTGGTTTCAAGTGGC R308: GATGCTCCTACCGCACTGAT
CbiF	precorrin-4 C11-methyltransferase	6489	F129: ATTTGCCAAACAGGGTGCTG R254: CTCGGGTCTCCCGTATGAAC
CbiG	cobalamin biosynthesis protein	6490	F540: TGTTAGAACCGCGACTGAGC R654: CGAATCCACGGTCAGCTCTT
CbiD	cobalt-precorrin-6A synthase	6485	F735: ATACAACCTTCCCGCTGAGG R906: CCTGGCATCTGCCATACGAT
CbiJ	precorrin-6x reductase	6492	F531: CGCCATGCAAGGTCCATTTT R636: ATCACTACCGCCAAGGTTGC
CbiT	precorrin-6B (C15)-methyltransferase	6487	F207: AGAAGAAGGCGTTCGCTTGA R314: GCTTGCGGTAAATCGCTCAG
CbiE	precorrin-7 (C5)-methyltransferase	N.D.	N/A
CbiC	Precorrin-8x methylmutase	6493	F176: AGGCTGGATGCCAAGCTTTA R307: TGCCAGGGTCTGCGATTAAG
CbiA	cobyrinic acid a,c-diamide synthase	6494	F591: TACAGAGCATGTTGCCGAGG R697: ATAAAGGCGGGGCAGTTTGA
CobA	cob(I)alamin adenosyltransferase	5467	F306: ACGCATTCCCCAACGGTATT R423: GGTACGCTTGAGGGTGACAA
CbiP	cobyric acid synthase	6496	F1308: TGGCTTGGTAATGGGCACTT R1416: TGTGCCGAGTGGTGTTAGAC
CbiB/ CobD	cobalamin biosynthesis protein	6497	F244: ATCGCAGTATGGGTTGGTGG R370: CCTTATAGCGTGCCTGCTCA
CobU	adenosylcobinamide-phosphate guanylyltransferase	6495	F406: GGCATGAGCATCGTACCTGA R526: CTGGGATTCCGCTGACAACT
CobT	nicotinate-nucleotide dimethylbenzimidazole-P phophoribosyl transferase	5484	F659: GCTGTGTTGGCGGTTTTGAT R787: CATTGATCTTGGCCGCACAC
CobC	alpha-ribazole-5'-P phosphatase	6501	F171: TAGAGCCTACCATACGGCGG R269: CCTTCCCATTCCCCAAAGGA
CobS_1	cobalamin 5'-phosphate synthase	5485	F86: GTTGGTCACCGGAGTCCTTT R211: GGACGGGTACATCATTGCCA
CobS_2	cobalamin 5'-phosphate synthase	6498	F463: TTAGGCCGCTTTGCTATGGT R635: ACCGCAATACAAATGGCAGC
CbiZ	adenosylcobinamide amidohydrolase	1215	F710: ACGGCTTATCGCCCAATCAA R879: GGTCACTAAGGCAGGCAGTT
RpoB	RNA polymerase beta subunit	103	F1775: TCTCGCCTAAGCAGGTCGTA R1911: AACAATTGGAGCCTGCGTTC
TceA	Reductive dehalogenase	9272	F: ATCCAGATTATGACCCTGGTGAA R: GCGGCATATATTAGGGCATCTT

N.D.: not detected; N/A: not available

Table S3 Presence of anaerobic cobalamin biosynthesis genes in bingenomes and the corresponding transcripts in the metatranscriptomes

Gene	Corresponding enzymes	Bingenomes			
		Veillonellaceae	*Desulfovibrio*	*Sedimentibacter*	*Dehalococcoides*
		(presence of gene/transcript)			
cobA	uroporphyrin-III C-methyltransferase	+/-	+/-	+/-	-
cysG	precorrin-2 dehydrogenase/siroheme synthase	**+/+**	+/-	+/-	-
cbiK	cobalt chelatase	+/-	+/-	+/-	-
cbiL	precorrin-2 C20-methyltransferase	+/-	+/-	+/-	-
cbiH	precorrin-3B C17-methyltransferase	+/-	+/-	+/-	-
cbiF	precorrin-4 C11-methyltransferase	+/-	+/-	+/-	-
cbiG	cobalamin biosynthesis protein	+/-	+/-	+/-	-
cbiD	cobalt-precorrin-6A synthase	+/-	+/-	+/-	-
cbiJ	precorrin-6x reductase	+/-	-	+/-	-
cbiT	precorrin-6B (C15)-methyltransferase	+/-	-	-	-
cbiE	precorrin-7 (C5)-methyltransferase	-	+/-	+/-	-
cbiC	Precorrin-8x methylmutase	+/-	+/-	+/-	-
cbiA	cobyrinic acid a,c-diamide synthase	+/-	+/-	+/-	**+/+**
cobA	cob(I)alamin adenosyltransferase	+/-	+/-	+/-	**+/+**
cbiP	cobyric acid synthase	+/-	+/-	+/-	**+/+**
cbiB/ cobD	cobalamin biosynthesis protein	+/-	+/-	+/-	**+/+**
cobU	adenosylcobinamide-phosphate guanylyltransferase	+/-	+/-	+/-	**+/+**
cobT	nicotinate-nucleotide dimethylbenzimidazole-P phophoribosyl transferase	+/-	-	-	**+/+**
cobC	alpha-ribazole-5'-P phosphatase	+/-	+/-	+/-	**+/+**
cobS	cobalamin 5'-phosphate synthase	**+/+***	+/-	+/-	**+/+**
cbiZ	adenosylcobinamide amidohydrolase	+/-	-	-	**+/+**

*Transcripts of one out of two *cobS* genes were detected in the metatranscriptome.

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Gene ID	Length (aa)	Identity	e-value
gene_id_1	157	94.9	3.00E-67
gene_id_2	375	99.73	0
gene_id_3	189	89.42	9.00E-95
gene_id_4	151	99.34	3.00E-102
gene_id_5	401	100	0
gene_id_6	778	99.87	0
gene_id_7	93	97.85	3.00E-56
gene_id_8	104	100	1.00E-68
gene_id_9	72	100	5.00E-45
gene_id_10	179	99.44	1.00E-128
gene_id_11	286	99.65	0
gene_id_12	280	99.64	0
gene_id_13	336	98.51	0
gene_id_14	284	100	0
gene_id_15	323	100	0
gene_id_16	398	99.75	0
gene_id_17	160	100	3.00E-101
gene_id_18	231	99.57	1.00E-145
gene_id_19	306	98.69	0
gene_id_20	69	98.55	2.00E-40
gene_id_21	124	100	3.00E-69
gene_id_22	154	100	1.00E-98
gene_id_23	486	99.18	0
gene_id_24	95	100	2.00E-60
gene_id_25	126	100	2.00E-58
gene_id_26	269	96.65	0
gene_id_27	152	98.03	2.00E-107
gene_id_28	104	98.08	4.00E-70
gene_id_29	307	99.67	0
gene_id_30	68	100	7.00E-43
gene_id_31	84	100	3.00E-53
gene_id_32	134	97.76	2.00E-76
gene_id_33	302	99.67	0
gene_id_34	181	100	2.00E-127
gene_id_35	73	94.52	4.00E-40
gene_id_36	250	99.2	0
gene_id_37	237	98.73	2.00E-155
gene_id_38	64	98.44	3.00E-37
gene_id_39	152	100	9.00E-104
gene_id_40	74	98.65	2.00E-44
gene_id_41	302	99.01	4.00E-180
gene_id_42	345	100	0
gene_id_43	413	98.55	0
gene_id_44	72	98.61	2.00E-43
gene_id_45	182	100	2.00E-115
gene_id_46	452	99.78	0
gene_id_47	275	98.91	0
gene_id_48	62	100	9.00E-37
gene_id_49	115	100	7.00E-77

gene_id_50	187	98.93	5.00E-132
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gene_id_68	373	99.46	0
gene_id_69	289	97.92	0
gene_id_70	122	95.9	4.00E-63
gene_id_71	478	50.63	2.00E-149
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gene_id_75	234	62.39	4.00E-95
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gene_id_269	71	98.59	3.00E-44
gene_id_270	87	100	3.00E-59
gene_id_271	140	100	9.00E-96
gene_id_272	142	100	4.00E-100
gene_id_273	288	96.18	0
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gene_id_276	782	97.44	0
gene_id_277	166	98.19	2.00E-103
gene_id_278	221	99.1	7.00E-157
gene_id_279	134	100	2.00E-91
gene_id_280	142	100	2.00E-82
gene_id_281	481	100	0
gene_id_282	454	99.78	0
gene_id_283	316	100	0
gene_id_284	219	95.89	2.00E-152
gene_id_285	333	99.7	0
gene_id_286	205	99.51	1.00E-133
gene_id_287	96	100	1.00E-60
gene_id_288	282	100	0
gene_id_289	465	99.78	0
gene_id_290	70	100	3.00E-41
gene_id_291	177	99.44	6.00E-126
gene_id_292	200	98.5	5.00E-140
gene_id_293	46	100	2.00E-17
gene_id_294	123	99.19	1.00E-81
gene_id_295	148	97.97	2.00E-98
gene_id_296	367	99.73	0
gene_id_297	80	100	8.00E-51
gene_id_298	342	98.54	0
gene_id_299	203	99.51	6.00E-138
gene_id_300	321	99.07	0
gene_id_301	871	98.85	0

gene_id_302	133	99.25	4.00E-90
gene_id_303	392	98.98	0
gene_id_304	380	99.47	0
gene_id_305	824	100	0
gene_id_306	462	98.92	0
gene_id_307	227	100	1.00E-161
gene_id_308	157	100	3.00E-97
gene_id_309	458	98.91	0
gene_id_310	126	64.29	7.00E-47
gene_id_311	107	97.2	3.00E-70
gene_id_312	485	42.68	1.00E-111
gene_id_313	189	98.94	6.00E-138
gene_id_314	332	96.39	0
gene_id_315	159	94.97	4.00E-100
gene_id_316	181	90.61	4.00E-116
gene_id_317	76	94.74	7.00E-44
gene_id_318	803	91.16	0
gene_id_319	257	49.81	1.00E-71
gene_id_320	319	87.15	0
gene_id_321	268	69.78	2.00E-133
gene_id_322	1009	96.04	0
gene_id_323	237	95.78	3.00E-167
gene_id_324	154	90.26	6.00E-98
gene_id_325	105	93.33	7.00E-67
gene_id_326	160	93.75	6.00E-110
gene_id_327	111	96.4	3.00E-70
gene_id_328	62	98.39	9.00E-35
gene_id_329	365	98.08	0
gene_id_330	183	97.81	4.00E-130
gene_id_331	146	71.92	2.00E-68
gene_id_333	176	91.48	1.00E-105
gene_id_334	514	84.44	0
gene_id_335	101	91.09	5.00E-63
gene_id_336	231	91.77	4.00E-157
gene_id_337	126	88.1	8.00E-76
gene_id_338	201	85.57	2.00E-118
gene_id_339	128	75.78	6.00E-55
gene_id_340	237	94.94	4.00E-156
gene_id_341	283	86.22	1.00E-162
gene_id_342	65	84.62	1.00E-31
gene_id_343	108	87.04	2.00E-60
gene_id_344	417	93.76	0
gene_id_345	236	91.53	6.00E-147
gene_id_346	180	91.67	1.00E-117
gene_id_347	157	86.62	6.00E-99
gene_id_348	180	87.78	7.00E-78
gene_id_349	58	87.93	7.00E-27
gene_id_350	151	90.73	4.00E-77
gene_id_351	192	92.71	1.00E-113
gene_id_353	69	89.86	6.00E-17

gene_id_354	70	98.57	2.00E-42
gene_id_355	55	98.18	3.00E-29
gene_id_356	82	87.8	4.00E-43
gene_id_357	92	92.39	7.00E-57
gene_id_358	273	87.91	4.00E-116
gene_id_359	307	94.14	0
gene_id_360	104	81.73	5.00E-56
gene_id_361	73	90.41	3.00E-39
gene_id_362	730	96.71	0
gene_id_363	326	96.93	0
gene_id_364	75	96	4.00E-45
gene_id_365	131	100	7.00E-76
gene_id_366	309	86.08	0
gene_id_367	535	86.73	0
gene_id_368	268	35.82	3.00E-62
gene_id_369	428	43.22	5.00E-106
gene_id_370	138	55.8	3.00E-48
gene_id_371	536	31.34	1.00E-60
gene_id_372	720	59.86	0
gene_id_373	154	66.88	2.00E-71
gene_id_374	97	51.55	1.00E-23
gene_id_375	71	70.42	4.00E-29
gene_id_376	90	100	6.00E-45
gene_id_377	370	98.11	0
gene_id_378	479	100	0
gene_id_379	268	98.88	0
gene_id_380	270	99.26	0
gene_id_381	172	98.84	2.00E-107
gene_id_382	237	99.16	6.00E-169
gene_id_383	38	97.37	2.00E-16
gene_id_384	676	98.96	0
gene_id_385	102	95.1	2.00E-61
gene_id_386	238	98.32	8.00E-173
gene_id_387	89	100	1.00E-55
gene_id_388	384	97.92	0
gene_id_389	229	98.69	2.00E-156
gene_id_390	1070	99.16	0
gene_id_391	393	99.75	0
gene_id_392	312	99.04	0
gene_id_393	328	99.7	0
gene_id_394	121	100	2.00E-69
gene_id_395	279	100	0
gene_id_396	433	99.31	0
gene_id_397	639	98.75	0
gene_id_398	160	99.38	4.00E-110
gene_id_399	526	100	0
gene_id_400	326	99.08	0
gene_id_401	229	100	6.00E-170
gene_id_402	333	99.7	0
gene_id_403	352	98.86	0

gene_id_404	288	99.65	0
gene_id_405	182	98.35	1.00E-127
gene_id_406	180	99.44	7.00E-124
gene_id_407	566	99.47	0
gene_id_408	481	100	0
gene_id_409	95	100	6.00E-62
gene_id_410	31	93.55	7.00E-11
gene_id_411	599	100	0
gene_id_412	341	98.24	0
gene_id_413	374	99.2	0
gene_id_414	1061	99.81	0
gene_id_415	463	99.14	0
gene_id_416	138	97.1	5.00E-80
gene_id_417	123	100	2.00E-83
gene_id_418	130	99.23	4.00E-88
gene_id_419	190	91.05	1.00E-89
gene_id_420	70	100	4.00E-44
gene_id_421	139	97.84	3.00E-58
gene_id_422	230	99.57	1.00E-157
gene_id_423	581	99.66	0
gene_id_424	137	100	7.00E-93
gene_id_425	278	100	9.00E-174
gene_id_426	286	100	6.00E-163
gene_id_427	283	99.65	3.00E-146
gene_id_428	251	100	0
gene_id_429	218	99.54	7.00E-154
gene_id_430	139	99.28	6.00E-96
gene_id_431	184	97.28	8.00E-130
gene_id_432	155	100	2.00E-107
gene_id_433	417	100	0
gene_id_434	573	100	0
gene_id_435	167	100	2.00E-108
gene_id_436	277	99.64	0
gene_id_437	86	100	5.00E-55
gene_id_438	240	98.75	3.00E-175
gene_id_439	297	99.33	0
gene_id_440	183	98.36	8.00E-131
gene_id_441	232	100	9.00E-168
gene_id_442	503	98.21	0
gene_id_443	510	100	0
gene_id_444	72	87.5	9.00E-25
gene_id_445	226	100	4.00E-162
gene_id_446	596	99.83	0
gene_id_447	197	98.48	2.00E-139
gene_id_448	144	97.22	1.00E-92
gene_id_449	36	100	2.00E-18
gene_id_450	95	100	2.00E-47
gene_id_451	561	99.11	0
gene_id_452	309	100	0
gene_id_453	282	98.94	0

gene_id_454	403	99.75	0
gene_id_455	956	99.9	0
gene_id_456	35	97.14	3.00E-15
gene_id_457	192	99.48	5.00E-124
gene_id_458	53	100	4.00E-29
gene_id_459	88	100	5.00E-55
gene_id_460	162	100	9.00E-93
gene_id_461	267	98.5	0
gene_id_462	813	99.14	0
gene_id_463	435	99.31	0
gene_id_464	91	100	2.00E-57
gene_id_465	165	98.18	4.00E-102
gene_id_466	303	97.03	2.00E-149
gene_id_467	366	98.36	0
gene_id_468	410	99.51	0
gene_id_469	331	99.4	0
gene_id_470	312	99.68	0
gene_id_471	209	100	1.00E-153
gene_id_472	325	99.38	0
gene_id_473	216	99.54	3.00E-154
gene_id_474	280	98.93	0
gene_id_475	539	98.7	0
gene_id_476	256	99.61	7.00E-179
gene_id_477	404	99.26	0
gene_id_478	231	99.13	3.00E-166
gene_id_479	431	95.36	0
gene_id_480	131	97.71	5.00E-89
gene_id_481	440	98.86	0
gene_id_482	265	99.25	0
gene_id_483	324	98.46	0
gene_id_484	117	99.15	2.00E-77
gene_id_485	153	99.35	2.00E-100
gene_id_486	730	98.63	0
gene_id_487	408	99.26	0
gene_id_488	182	100	4.00E-125
gene_id_489	663	99.25	0
gene_id_490	225	98.67	5.00E-157
gene_id_491	374	95.99	0
gene_id_492	94	94.68	2.00E-43
gene_id_493	60	96.67	3.00E-35
gene_id_494	107	100	3.00E-69
gene_id_495	189	99.47	1.00E-121
gene_id_496	68	42.65	5.00E-09
gene_id_498	65	46.15	6.00E-07
gene_id_501	146	32.19	4.00E-09
gene_id_503	123	28.46	2.00E-08
gene_id_504	185	32.97	2.00E-18
gene_id_505	210	32.38	4.00E-12
gene_id_506	134	32.09	3.00E-08
gene_id_507	202	55.45	5.00E-66

gene_id_512	81	56.79	1.00E-18
gene_id_513	100	77	3.00E-38
gene_id_516	156	71.79	7.00E-71
gene_id_517	492	31.91	1.00E-59
gene_id_518	100	99	7.00E-63
gene_id_519	530	99.62	0
gene_id_520	199	98.99	2.00E-132
gene_id_521	401	97.51	0
gene_id_522	206	100	4.00E-122
gene_id_523	341	99.41	0
gene_id_524	311	99.68	0
gene_id_525	301	99.67	0
gene_id_526	449	99.78	0
gene_id_527	493	98.17	0
gene_id_528	133	100	2.00E-89
gene_id_529	815	98.65	0
gene_id_530	136	99.26	2.00E-70
gene_id_531	237	98.73	8.00E-159
gene_id_532	142	100	6.00E-99
gene_id_533	340	99.71	0
gene_id_534	408	100	0
gene_id_535	376	100	0
gene_id_536	175	99.43	2.00E-106
gene_id_537	845	95.98	0
gene_id_538	35	100	4.00E-13
gene_id_539	194	100	5.00E-143
gene_id_540	544	98.71	0
gene_id_541	138	100	2.00E-91
gene_id_542	32	100	2.00E-13
gene_id_543	587	91.99	0
gene_id_544	113	98.23	8.00E-75
gene_id_545	102	99.02	2.00E-65
gene_id_546	210	95.71	2.00E-140
gene_id_547	48	100	1.00E-25
gene_id_548	241	97.51	7.00E-152
gene_id_549	80	100	7.00E-52
gene_id_550	377	99.47	0
gene_id_551	346	99.13	0
gene_id_552	809	99.38	0
gene_id_553	211	100	1.00E-151
gene_id_554	569	98.59	0
gene_id_555	348	98.56	0
gene_id_556	327	99.39	0
gene_id_557	377	98.67	0
gene_id_558	267	99.63	6.00E-171
gene_id_559	218	99.08	5.00E-156
gene_id_560	185	100	3.00E-129
gene_id_561	241	100	5.00E-174
gene_id_562	167	99.4	9.00E-116
gene_id_563	245	99.59	0

gene_id_564	255	99.61	2.00E-176
gene_id_565	953	99.06	0
gene_id_566	293	100	0
gene_id_567	132	93.94	1.00E-86
gene_id_568	236	99.15	5.00E-150
gene_id_569	381	100	0
gene_id_570	274	98.91	0
gene_id_571	71	100	6.00E-44
gene_id_572	553	99.64	0
gene_id_573	289	98.96	0
gene_id_574	35	97.14	4.00E-14
gene_id_575	604	100	0
gene_id_576	276	99.64	0
gene_id_577	114	99.12	2.00E-76
gene_id_578	142	100	2.00E-98
gene_id_579	456	98.03	0
gene_id_580	163	100	9.00E-113
gene_id_581	336	97.92	0
gene_id_582	258	100	0
gene_id_583	255	100	0
gene_id_584	364	100	0
gene_id_585	279	99.64	0
gene_id_586	200	100	3.00E-135
gene_id_587	243	99.59	5.00E-180
gene_id_588	291	100	0
gene_id_589	284	100	0
gene_id_590	165	99.39	4.00E-114
gene_id_591	79	98.73	2.00E-48
gene_id_592	263	100	2.00E-156
gene_id_593	418	97.61	0
gene_id_594	305	98.69	0
gene_id_595	255	100	3.00E-168
gene_id_596	183	100	1.00E-127
gene_id_597	157	99.36	1.00E-111
gene_id_598	301	99.34	0
gene_id_599	170	100	3.00E-119
gene_id_600	95	98.95	4.00E-48
gene_id_601	253	100	0
gene_id_602	273	100	0
gene_id_603	252	99.6	1.00E-170
gene_id_604	279	99.64	0
gene_id_605	316	100	0
gene_id_606	219	98.17	7.00E-153
gene_id_607	258	97.29	6.00E-170
gene_id_608	504	97.02	0
gene_id_609	258	98.06	0
gene_id_610	393	98.98	0
gene_id_611	880	99.09	0
gene_id_612	357	100	0
gene_id_613	232	100	1.00E-164

gene_id_614	227	99.12	1.00E-161
gene_id_615	939	99.57	0
gene_id_616	324	99.69	0
gene_id_617	415	99.52	0
gene_id_618	206	100	1.00E-148
gene_id_619	551	100	0
gene_id_620	814	99.14	0
gene_id_621	49	100	4.00E-14
gene_id_622	668	99.7	0
gene_id_623	194	99.48	5.00E-133
gene_id_624	165	98.79	2.00E-100
gene_id_625	251	100	2.00E-166
gene_id_626	119	99.16	2.00E-80
gene_id_627	154	99.35	6.00E-109
gene_id_628	516	99.81	0
gene_id_629	417	99.76	0
gene_id_630	167	100	1.00E-115
gene_id_631	359	99.72	0
gene_id_632	307	98.37	0
gene_id_633	123	98.37	2.00E-67
gene_id_634	257	99.22	7.00E-163
gene_id_635	188	99.47	3.00E-129
gene_id_636	90	98.89	5.00E-57
gene_id_637	176	99.43	3.00E-112
gene_id_638	158	99.37	1.00E-113
gene_id_639	284	98.59	0
gene_id_640	107	84.11	2.00E-55
gene_id_641	287	97.56	0
gene_id_642	358	100	0
gene_id_643	364	100	0
gene_id_644	420	99.76	0
gene_id_645	176	98.86	2.00E-122
gene_id_646	286	99.65	0
gene_id_647	222	97.75	6.00E-142
gene_id_648	359	99.44	0
gene_id_649	256	100	0
gene_id_650	329	96.05	0
gene_id_651	80	77.5	1.00E-36
gene_id_652	110	79.09	2.00E-56
gene_id_653	547	31.44	6.00E-82
gene_id_654	64	100	6.00E-38
gene_id_655	75	98.67	7.00E-45
gene_id_656	551	97.64	0
gene_id_657	154	100	3.00E-107
gene_id_658	141	100	1.00E-99
gene_id_659	81	100	4.00E-49
gene_id_660	576	99.65	0
gene_id_661	465	99.57	0
gene_id_662	172	98.26	1.00E-119
gene_id_663	258	99.61	0

gene_id_664	116	100	4.00E-77
gene_id_665	128	98.44	5.00E-80
gene_id_666	148	100	2.00E-105
gene_id_667	272	98.53	0
gene_id_668	195	99.49	1.00E-141
gene_id_669	255	97.65	8.00E-168
gene_id_670	399	99.5	0
gene_id_671	336	98.81	0
gene_id_672	219	96.8	4.00E-153
gene_id_673	259	97.68	1.00E-177
gene_id_674	341	100	0
gene_id_675	200	99	3.00E-144
gene_id_676	485	98.76	0
gene_id_677	39	100	2.00E-15
gene_id_678	137	100	5.00E-94
gene_id_679	236	97.03	5.00E-137
gene_id_680	1170	99.66	0
gene_id_681	84	100	1.00E-51
gene_id_682	271	99.26	0
gene_id_683	127	98.43	2.00E-84
gene_id_684	186	98.39	9.00E-108
gene_id_685	179	99.44	6.00E-126
gene_id_686	233	97.42	6.00E-167
gene_id_687	47	100	2.00E-25
gene_id_688	193	91.71	1.00E-123
gene_id_689	282	99.29	0
gene_id_690	197	98.48	2.00E-135
gene_id_691	133	100	3.00E-93
gene_id_692	325	100	0
gene_id_693	148	97.97	5.00E-103
gene_id_694	203	100	4.00E-124
gene_id_695	41	100	1.00E-19
gene_id_696	137	98.54	3.00E-93
gene_id_697	185	99.46	5.00E-108
gene_id_698	143	98.6	2.00E-46
gene_id_699	107	98.13	1.00E-68
gene_id_700	206	98.06	6.00E-143
gene_id_701	335	98.81	0
gene_id_702	364	99.73	0
gene_id_703	71	100	1.00E-42
gene_id_704	763	98.43	0
gene_id_705	217	100	1.00E-153
gene_id_706	119	100	2.00E-81
gene_id_707	402	100	0
gene_id_708	537	99.81	0
gene_id_709	88	100	5.00E-52
gene_id_710	326	99.39	0
gene_id_711	424	99.76	0
gene_id_712	166	98.19	9.00E-113
gene_id_713	392	98.21	0

gene_id_714	207	99.03	3.00E-150
gene_id_715	470	98.09	0
gene_id_716	280	98.93	6.00E-160
gene_id_717	82	100	3.00E-51
gene_id_718	333	99.4	0
gene_id_719	513	99.22	0
gene_id_720	340	99.12	0
gene_id_721	472	99.79	0
gene_id_722	216	99.54	9.00E-115
gene_id_723	812	99.38	0
gene_id_724	88	100	1.00E-54
gene_id_725	330	100	0
gene_id_726	523	100	0
gene_id_727	216	99.54	4.00E-138
gene_id_728	424	99.76	0
gene_id_729	1007	85.3	0
gene_id_730	41	95.12	2.00E-09
gene_id_731	165	98.79	1.00E-116
gene_id_732	509	99.21	0
gene_id_733	210	99.52	2.00E-148
gene_id_734	345	99.71	0
gene_id_735	187	100	4.00E-134
gene_id_736	637	100	0
gene_id_737	356	98.88	0
gene_id_738	359	99.72	0
gene_id_739	216	99.54	1.00E-118
gene_id_740	441	100	0
gene_id_741	311	99.36	0
gene_id_742	192	100	2.00E-139
gene_id_743	144	97.92	7.00E-98
gene_id_744	903	98.89	0
gene_id_745	207	98.07	1.00E-128
gene_id_746	270	99.26	0
gene_id_747	186	97.85	2.00E-130
gene_id_748	343	98.25	0
gene_id_749	418	98.09	0
gene_id_750	92	100	2.00E-45
gene_id_751	515	99.81	0
gene_id_752	285	100	0
gene_id_753	792	99.62	0
gene_id_754	543	99.82	0
gene_id_755	196	98.98	2.00E-123
gene_id_756	136	100	3.00E-89
gene_id_757	78	100	8.00E-48
gene_id_758	302	99.34	0
gene_id_759	160	98.75	4.00E-108
gene_id_760	123	100	3.00E-71
gene_id_761	310	98.39	0
gene_id_762	190	99.47	4.00E-137
gene_id_763	160	98.75	1.00E-108

gene_id_764	61	100	8.00E-36
gene_id_765	334	98.8	0
gene_id_766	85	97.65	2.00E-52
gene_id_768	459	98.47	0
gene_id_769	166	100	1.00E-97
gene_id_770	694	100	0
gene_id_771	255	98.82	3.00E-137
gene_id_772	117	94.02	7.00E-55
gene_id_773	371	99.73	0
gene_id_774	485	99.18	0
gene_id_775	191	98.95	6.00E-116
gene_id_776	132	37.12	9.00E-18
gene_id_777	859	98.84	0
gene_id_778	503	99.4	0
gene_id_779	86	98.84	9.00E-51
gene_id_780	143	99.3	5.00E-97
gene_id_781	247	100	2.00E-176
gene_id_782	310	98.39	0
gene_id_783	72	100	3.00E-31
gene_id_784	147	99.32	4.00E-102
gene_id_785	67	98.51	3.00E-27
gene_id_786	279	99.64	0
gene_id_787	61	100	4.00E-34
gene_id_788	556	98.92	0
gene_id_789	232	99.57	2.00E-171
gene_id_790	818	98.78	0
gene_id_791	281	99.64	0
gene_id_792	265	99.25	0
gene_id_793	281	99.64	0
gene_id_794	279	99.64	0
gene_id_795	544	99.63	0
gene_id_796	461	99.13	0
gene_id_797	406	100	0
gene_id_798	296	98.99	2.00E-178
gene_id_799	398	98.99	0
gene_id_800	272	99.63	0
gene_id_801	405	99.75	0
gene_id_802	358	99.16	0
gene_id_803	65	98.46	1.00E-39
gene_id_804	75	100	6.00E-48
gene_id_805	186	100	1.00E-132
gene_id_806	64	98.44	6.00E-24
gene_id_807	221	99.1	3.00E-136
gene_id_808	98	98.98	7.00E-62
gene_id_809	155	100	9.00E-110
gene_id_810	90	98.89	2.00E-57
gene_id_811	190	99.47	6.00E-135
gene_id_812	123	100	7.00E-86
gene_id_813	176	97.73	9.00E-125
gene_id_814	209	98.56	5.00E-137

gene_id_815	34	94.12	5.00E-14
gene_id_816	272	99.63	4.00E-165
gene_id_817	284	98.94	0
gene_id_818	84	100	3.00E-52
gene_id_819	120	98.33	2.00E-79
gene_id_820	223	99.55	1.00E-162
gene_id_821	222	99.1	2.00E-157
gene_id_822	448	99.33	0
gene_id_823	225	98.22	3.00E-147
gene_id_824	133	91.73	7.00E-82
gene_id_825	378	99.74	0
gene_id_826	199	96.48	4.00E-123
gene_id_827	365	100	0
gene_id_828	199	91.96	4.00E-123
gene_id_829	253	99.21	0
gene_id_830	120	100	6.00E-76
gene_id_831	72	100	1.00E-43
gene_id_832	858	98.6	0
gene_id_833	271	98.89	0
gene_id_834	163	98.77	4.00E-86
gene_id_835	607	99.51	0
gene_id_836	302	99.67	0
gene_id_837	68	100	4.00E-39
gene_id_838	185	99.46	3.00E-122
gene_id_839	655	99.85	0
gene_id_840	277	99.28	0
gene_id_841	355	99.72	0
gene_id_842	652	99.85	0
gene_id_843	361	99.17	0
gene_id_844	421	99.52	0
gene_id_845	433	100	0
gene_id_846	348	99.71	0
gene_id_847	189	99.47	2.00E-134
gene_id_848	261	98.47	0
gene_id_849	1079	99.54	0
gene_id_850	364	99.18	0
gene_id_851	427	98.36	0
gene_id_852	331	98.19	0
gene_id_853	181	100	2.00E-124
gene_id_854	738	99.05	0
gene_id_855	566	98.59	0
gene_id_856	175	100	1.00E-111
gene_id_857	187	100	1.00E-119
gene_id_858	186	99.46	4.00E-129
gene_id_859	254	100	2.00E-139
gene_id_860	365	100	0
gene_id_861	205	98.54	4.00E-143
gene_id_862	403	100	0
gene_id_863	155	100	9.00E-107
gene_id_864	98	97.96	8.00E-64

gene_id_865	70	100	3.00E-42
gene_id_866	215	98.14	4.00E-119
gene_id_867	602	99.17	0
gene_id_868	741	99.73	0
gene_id_869	159	100	2.00E-102
gene_id_870	261	97.32	0
gene_id_871	272	100	0
gene_id_872	359	99.72	4.00E-177
gene_id_873	367	99.46	0
gene_id_874	175	100	3.00E-127
gene_id_875	62	100	2.00E-24
gene_id_876	102	94.12	4.00E-64
gene_id_877	159	98.74	9.00E-109
gene_id_878	239	100	8.00E-159
gene_id_879	264	99.24	2.00E-180
gene_id_880	222	99.1	4.00E-154
gene_id_881	368	99.46	0
gene_id_882	274	100	0
gene_id_883	109	100	3.00E-70
gene_id_884	130	100	4.00E-86
gene_id_885	539	99.63	0
gene_id_886	432	99.77	0
gene_id_887	454	99.56	0
gene_id_888	451	99.11	0
gene_id_889	134	100	4.00E-91
gene_id_890	100	99	2.00E-66
gene_id_891	164	100	7.00E-114
gene_id_892	276	100	0
gene_id_893	135	100	3.00E-94
gene_id_894	891	99.66	0
gene_id_895	247	99.19	8.00E-155
gene_id_896	273	99.27	2.00E-148
gene_id_897	172	99.42	2.00E-105
gene_id_898	109	100	3.00E-72
gene_id_899	135	100	6.00E-95
gene_id_900	105	99.05	1.00E-62
gene_id_901	120	100	9.00E-80
gene_id_902	371	99.19	0
gene_id_903	314	98.41	0
gene_id_904	186	100	9.00E-131
gene_id_905	1014	99.61	0
gene_id_906	356	99.72	0
gene_id_907	271	99.63	0
gene_id_908	454	100	0
gene_id_909	507	98.82	0
gene_id_910	284	99.3	0
gene_id_911	200	96	8.00E-128
gene_id_912	495	99.39	0
gene_id_913	244	99.59	5.00E-176
gene_id_914	91	97.8	2.00E-58

gene_id_915	46	100	2.00E-22
gene_id_916	237	99.58	9.00E-145
gene_id_917	120	42.5	2.00E-21
gene_id_918	417	49.4	2.00E-124
gene_id_919	162	87.65	3.00E-97
gene_id_920	366	90.16	0
gene_id_922	110	94.55	3.00E-69
gene_id_923	1041	52.74	0
gene_id_924	211	58.29	5.00E-82
gene_id_925	73	95.89	1.00E-39
gene_id_926	189	96.83	5.00E-133
gene_id_927	67	97.01	1.00E-31
gene_id_929	185	48.11	3.00E-48
gene_id_930	136	41.18	2.00E-33
gene_id_931	973	82.94	0
gene_id_932	103	31.07	6.00E-13
gene_id_934	868	68.43	0
gene_id_935	259	40.15	4.00E-52
gene_id_936	83	45.78	1.00E-13
gene_id_937	1191	99.16	0
gene_id_938	439	99.77	0
gene_id_939	129	100	2.00E-86
gene_id_940	83	98.8	4.00E-28
gene_id_941	78	100	6.00E-50
gene_id_942	169	99.41	2.00E-115
gene_id_943	270	96.3	1.00E-171
gene_id_944	80	98.75	4.00E-46
gene_id_945	343	99.13	5.00E-175
gene_id_946	112	99.11	9.00E-76
gene_id_947	325	98.46	0
gene_id_948	405	99.01	0
gene_id_949	237	100	9.00E-177
gene_id_950	400	100	0
gene_id_951	55	100	9.00E-31
gene_id_952	72	97.22	8.00E-32
gene_id_953	177	100	2.00E-122
gene_id_954	140	99.29	1.00E-93
gene_id_955	237	100	5.00E-142
gene_id_956	176	99.43	5.00E-120
gene_id_957	124	100	2.00E-42
gene_id_958	214	100	2.00E-135
gene_id_959	144	99.31	1.00E-99
gene_id_960	274	100	0
gene_id_961	507	99.41	0
gene_id_962	491	99.39	0
gene_id_963	92	100	1.00E-59
gene_id_964	593	99.66	0
gene_id_965	118	100	6.00E-80
gene_id_966	300	99	0
gene_id_967	57	100	2.00E-32

gene_id_968	353	99.43	0
gene_id_969	382	99.48	0
gene_id_970	193	100	8.00E-108
gene_id_971	423	100	0
gene_id_972	209	98.56	1.00E-148
gene_id_973	207	99.52	2.00E-152
gene_id_974	297	100	0
gene_id_975	326	99.69	0
gene_id_976	263	99.62	1.00E-179
gene_id_977	698	99.71	0
gene_id_978	87	100	5.00E-43
gene_id_979	98	97.96	6.00E-52
gene_id_980	764	98.95	0
gene_id_981	260	100	1.00E-157
gene_id_982	210	100	2.00E-134
gene_id_983	566	99.47	0
gene_id_984	422	99.76	0
gene_id_985	413	96.61	0
gene_id_986	350	100	0
gene_id_987	258	96.12	3.00E-180
gene_id_988	99	100	4.00E-65
gene_id_989	192	98.96	1.00E-137
gene_id_990	275	98.55	0
gene_id_991	134	100	2.00E-71
gene_id_992	828	99.15	0
gene_id_993	80	100	6.00E-35
gene_id_994	127	100	7.00E-89
gene_id_995	66	100	2.00E-40
gene_id_996	145	100	2.00E-98
gene_id_997	194	98.97	2.00E-121
gene_id_998	598	98.66	0
gene_id_999	630	100	0
gene_id_1000	294	99.32	0
gene_id_1001	350	100	0
gene_id_1002	430	99.77	0
gene_id_1003	428	100	0
gene_id_1004	263	100	0
gene_id_1005	429	99.3	0
gene_id_1006	88	100	2.00E-57
gene_id_1007	270	99.63	0
gene_id_1008	136	100	2.00E-91
gene_id_1009	506	99.8	0
gene_id_1010	218	99.54	9.00E-159
gene_id_1011	264	98.86	9.00E-176
gene_id_1012	481	100	0
gene_id_1013	478	99.79	0
gene_id_1014	645	99.69	0
gene_id_1015	101	100	2.00E-62
gene_id_1016	134	100	3.00E-74
gene_id_1017	169	100	2.00E-121

gene_id_1018	353	100	0
gene_id_1019	367	99.73	0
gene_id_1020	148	98.65	1.00E-104
gene_id_1021	200	100	9.00E-134
gene_id_1022	123	99.19	8.00E-80
gene_id_1023	363	100	0
gene_id_1024	408	99.75	0
gene_id_1025	136	99.26	3.00E-94
gene_id_1026	244	99.59	6.00E-128
gene_id_1027	86	100	3.00E-54
gene_id_1028	39	97.44	4.00E-19
gene_id_1029	302	99.34	0
gene_id_1030	266	97.74	5.00E-175
gene_id_1031	233	98.71	8.00E-167
gene_id_1032	151	99.34	1.00E-91
gene_id_1033	369	99.19	0
gene_id_1034	461	99.13	0
gene_id_1035	424	96.7	0
gene_id_1036	96	100	1.00E-61
gene_id_1037	214	98.6	6.00E-152
gene_id_1038	981	98.88	0
gene_id_1039	161	99.38	1.00E-112
gene_id_1040	188	100	7.00E-134
gene_id_1041	309	97.09	0
gene_id_1042	111	100	1.00E-76
gene_id_1043	359	100	0
gene_id_1044	461	97.61	0
gene_id_1045	197	99.49	1.00E-136
gene_id_1046	640	99.53	0
gene_id_1047	161	100	2.00E-113
gene_id_1048	155	99.35	1.00E-93
gene_id_1049	282	99.65	5.00E-146
gene_id_1050	635	98.11	0
gene_id_1051	605	99.67	0
gene_id_1052	378	96.56	0
gene_id_1053	236	98.31	3.00E-163
gene_id_1054	407	98.28	0
gene_id_1055	71	100	4.00E-30
gene_id_1056	71	98.59	2.00E-44
gene_id_1057	405	99.01	0
gene_id_1058	280	100	0
gene_id_1059	183	98.91	5.00E-130
gene_id_1060	266	99.25	0
gene_id_1061	245	100	8.00E-137
gene_id_1062	96	94.79	6.00E-43
gene_id_1063	412	99.27	0
gene_id_1064	468	99.57	0
gene_id_1065	435	96.78	0
gene_id_1066	358	98.6	0
gene_id_1067	196	100	8.00E-139

gene_id_1068	304	99.01	0
gene_id_1069	442	100	0
gene_id_1070	147	100	5.00E-80
gene_id_1071	382	99.74	0
gene_id_1072	103	100	1.00E-70
gene_id_1073	560	95.89	0
gene_id_1074	213	99.06	1.00E-147
gene_id_1075	555	99.46	0
gene_id_1076	569	100	0
gene_id_1077	157	100	2.00E-98
gene_id_1078	332	100	0
gene_id_1079	505	100	0
gene_id_1080	133	100	1.00E-78
gene_id_1081	416	99.28	0
gene_id_1082	166	100	7.00E-116
gene_id_1083	365	99.45	0
gene_id_1084	533	99.25	0
gene_id_1085	205	100	2.00E-148
gene_id_1086	486	100	0
gene_id_1087	138	100	8.00E-82
gene_id_1088	196	98.98	2.00E-125
gene_id_1089	234	98.72	3.00E-166
gene_id_1090	217	99.54	4.00E-160
gene_id_1091	263	99.24	0
gene_id_1092	411	99.76	0
gene_id_1093	251	100	8.00E-180
gene_id_1094	241	100	1.00E-132
gene_id_1095	248	99.19	2.00E-180
gene_id_1096	196	98.47	2.00E-132
gene_id_1097	514	98.25	0
gene_id_1098	421	99.05	0
gene_id_1099	268	95.15	0
gene_id_1100	282	100	0
gene_id_1101	124	100	2.00E-84
gene_id_1102	285	94.74	0
gene_id_1103	187	100	6.00E-131
gene_id_1104	265	97.74	0
gene_id_1105	343	97.38	0
gene_id_1106	360	98.89	0
gene_id_1107	305	100	0
gene_id_1108	267	98.13	2.00E-127
gene_id_1109	181	99.45	8.00E-126
gene_id_1110	571	96.85	0
gene_id_1111	245	99.59	6.00E-137
gene_id_1112	415	97.11	0
gene_id_1113	443	99.55	0
gene_id_1114	193	98.45	2.00E-95
gene_id_1115	217	94.93	3.00E-146
gene_id_1116	679	99.71	0
gene_id_1117	210	99.52	2.00E-148

gene_id_1118	352	98.01	0
gene_id_1119	121	95.87	1.00E-77
gene_id_1120	211	99.05	1.00E-151
gene_id_1121	349	98.85	0
gene_id_1122	207	99.03	6.00E-147
gene_id_1123	509	99.61	0
gene_id_1124	235	94.47	5.00E-146
gene_id_1125	431	98.38	0
gene_id_1126	370	98.92	0
gene_id_1127	246	99.59	6.00E-120
gene_id_1129	379	97.36	0
gene_id_1130	265	99.62	0
gene_id_1131	380	99.21	0
gene_id_1132	109	100	1.00E-69
gene_id_1133	76	100	5.00E-24
gene_id_1134	702	100	0
gene_id_1135	54	100	5.00E-30
gene_id_1136	219	99.54	3.00E-141
gene_id_1137	116	100	9.00E-64
gene_id_1138	267	100	2.00E-180
gene_id_1139	167	98.8	5.00E-114
gene_id_1140	219	99.54	2.00E-161
gene_id_1141	220	98.18	7.00E-154
gene_id_1142	122	99.18	2.00E-84
gene_id_1143	223	99.1	5.00E-63
gene_id_1143	60	100	5.00E-12
gene_id_1144	292	99.32	8.00E-98
gene_id_1144	77	100	2.00E-23
gene_id_1144	72	98.61	3.00E-16
gene_id_1145	582	99.83	0
gene_id_1146	154	100	1.00E-105
gene_id_1147	64	100	4.00E-37
gene_id_1148	95	98.95	7.00E-59
gene_id_1149	472	92.16	0
gene_id_1150	177	98.87	4.00E-93
gene_id_1151	633	99.37	0
gene_id_1152	397	100	0
gene_id_1153	401	98.75	0
gene_id_1154	251	97.21	7.00E-168
gene_id_1155	325	97.54	0
gene_id_1156	284	100	0
gene_id_1157	388	99.48	0
gene_id_1158	67	100	1.00E-38
gene_id_1159	380	99.21	0
gene_id_1160	264	100	3.00E-171
gene_id_1161	103	100	2.00E-56
gene_id_1162	489	99.39	0
gene_id_1163	240	99.58	1.00E-173
gene_id_1164	623	99.84	0
gene_id_1165	159	99.37	1.00E-111

gene_id_1166	313	100	0
gene_id_1167	390	100	0
gene_id_1168	83	98.8	3.00E-54
gene_id_1169	190	100	3.00E-121
gene_id_1170	424	100	0
gene_id_1171	390	97.69	0
gene_id_1172	703	99.43	0
gene_id_1173	307	100	0
gene_id_1174	348	97.7	0
gene_id_1175	186	100	2.00E-134
gene_id_1176	206	100	8.00E-148
gene_id_1177	273	98.9	0
gene_id_1178	328	99.39	0
gene_id_1179	191	100	7.00E-136
gene_id_1180	448	100	0
gene_id_1181	598	99.16	0
gene_id_1182	111	98.2	6.00E-60
gene_id_1183	193	98.96	5.00E-131
gene_id_1184	597	98.49	0
gene_id_1185	640	97.97	0
gene_id_1186	260	99.23	1.00E-176
gene_id_1187	296	100	0
gene_id_1188	313	97.76	0
gene_id_1189	733	99.18	0
gene_id_1190	448	99.33	0
gene_id_1191	214	97.66	4.00E-147
gene_id_1192	224	99.55	1.00E-148
gene_id_1193	381	99.74	0
gene_id_1194	107	100	7.00E-72
gene_id_1195	188	98.4	3.00E-130
gene_id_1196	200	99.5	3.00E-144
gene_id_1197	254	98.82	1.00E-153
gene_id_1198	352	100	0
gene_id_1199	368	98.64	0
gene_id_1200	291	99.66	0
gene_id_1201	256	99.61	0
gene_id_1202	274	100	0
gene_id_1203	363	93.94	5.00E-137
gene_id_1204	338	100	0
gene_id_1205	209	92.82	7.00E-138
gene_id_1206	280	98.93	0
gene_id_1207	171	100	5.00E-108
gene_id_1208	666	99.55	0
gene_id_1209	152	100	5.00E-105
gene_id_1210	200	98.5	1.00E-140
gene_id_1211	208	97.6	3.00E-144
gene_id_1212	287	100	0
gene_id_1213	229	99.13	3.00E-164
gene_id_1214	69	100	5.00E-43
gene_id_1215	381	99.74	0

gene_id_1216	376	100	0
gene_id_1217	116	100	2.00E-79
gene_id_1218	273	100	1.00E-154
gene_id_1219	253	99.6	1.00E-169
gene_id_1220	290	99.31	0
gene_id_1221	143	98.6	6.00E-98
gene_id_1222	338	98.52	0
gene_id_1223	439	99.32	0
gene_id_1224	449	98	0
gene_id_1225	110	100	4.00E-76
gene_id_1226	853	98.24	0
gene_id_1227	334	99.7	0
gene_id_1228	599	99	0
gene_id_1229	249	100	1.00E-170
gene_id_1230	162	96.91	2.00E-79
gene_id_1231	379	99.21	0
gene_id_1232	240	98.75	1.00E-130
gene_id_1233	178	97.19	8.00E-110
gene_id_1234	75	100	2.00E-31
gene_id_1235	154	99.35	1.00E-105
gene_id_1236	479	100	0
gene_id_1237	312	100	0
gene_id_1238	459	98.47	0
gene_id_1239	224	97.77	2.00E-161
gene_id_1240	147	100	4.00E-87
gene_id_1241	75	100	1.00E-45
gene_id_1242	213	98.59	5.00E-154
gene_id_1243	182	98.9	2.00E-132
gene_id_1244	349	99.71	0
gene_id_1245	1295	99.92	0
gene_id_1246	1255	99.92	0
gene_id_1248	305	99.67	0
gene_id_1249	396	98.99	0
gene_id_1250	362	99.72	0
gene_id_1251	526	99.62	0
gene_id_1252	195	97.95	3.00E-135
gene_id_1253	442	98.87	0
gene_id_1254	677	99.11	0
gene_id_1255	189	100	1.00E-133
gene_id_1256	159	98.11	2.00E-105
gene_id_1257	428	99.53	0
gene_id_1258	336	97.32	0
gene_id_1259	318	99.37	0
gene_id_1260	392	100	0
gene_id_1261	124	98.39	1.00E-84
gene_id_1262	89	97.75	1.00E-40
gene_id_1263	140	100	1.00E-93
gene_id_1264	559	99.28	0
gene_id_1265	99	100	2.00E-61
gene_id_1266	204	99.51	2.00E-147

gene_id_1267	354	99.72	0
gene_id_1268	239	98.74	9.00E-158
gene_id_1269	253	100	0
gene_id_1270	56	98.21	3.00E-17
gene_id_1271	498	98.8	0
gene_id_1272	413	99.76	0
gene_id_1273	383	95.3	0
gene_id_1274	94	100	5.00E-44
gene_id_1275	530	99.43	0
gene_id_1276	222	100	5.00E-155
gene_id_1277	408	99.02	0
gene_id_1278	357	98.88	0
gene_id_1279	221	99.55	9.00E-160
gene_id_1280	82	100	1.00E-51
gene_id_1281	75	100	2.00E-24
gene_id_1282	167	98.8	4.00E-112
gene_id_1283	140	99.29	9.00E-68
gene_id_1284	464	100	0
gene_id_1285	262	100	9.00E-172
gene_id_1286	503	99.6	0
gene_id_1287	180	99.44	3.00E-123
gene_id_1288	169	98.82	5.00E-91
gene_id_1289	76	98.68	6.00E-18
gene_id_1290	314	99.68	0
gene_id_1291	71	98.59	6.00E-25
gene_id_1292	189	100	3.00E-131
gene_id_1293	745	99.6	0
gene_id_1294	326	100	0
gene_id_1295	581	99.66	0
gene_id_1296	520	99.81	0
gene_id_1297	859	97.56	0
gene_id_1298	67	100	1.00E-39
gene_id_1299	183	98.91	4.00E-124
gene_id_1300	946	99.68	0
gene_id_1301	397	99.5	0
gene_id_1302	283	100	0
gene_id_1303	347	100	0
gene_id_1304	306	99.35	0
gene_id_1305	151	98.68	3.00E-87
gene_id_1306	453	100	0
gene_id_1307	236	97.88	1.00E-158
gene_id_1308	426	99.53	0
gene_id_1309	76	100	1.00E-48
gene_id_1310	277	99.28	0
gene_id_1311	339	98.53	0
gene_id_1312	434	100	0
gene_id_1313	234	99.57	2.00E-169
gene_id_1314	150	99.33	1.00E-94
gene_id_1315	593	98.99	0
gene_id_1316	393	100	0

gene_id_1317	400	99	0
gene_id_1318	430	100	0
gene_id_1319	458	99.56	0
gene_id_1320	433	98.38	0
gene_id_1321	276	100	0
gene_id_1322	316	100	0
gene_id_1323	186	98.92	5.00E-121
gene_id_1324	140	99.29	7.00E-96
gene_id_1325	316	100	0
gene_id_1326	365	100	0
gene_id_1327	334	99.7	0
gene_id_1328	294	98.98	0
gene_id_1329	342	100	0
gene_id_1330	520	99.04	0
gene_id_1331	418	99.76	0
gene_id_1332	406	100	0
gene_id_1333	67	98.51	8.00E-35
gene_id_1334	409	99.51	0
gene_id_1335	355	99.44	0
gene_id_1336	64	100	6.00E-26
gene_id_1337	132	100	4.00E-88
gene_id_1338	143	100	2.00E-101
gene_id_1339	246	99.19	6.00E-164
gene_id_1340	100	100	5.00E-64
gene_id_1341	297	100	0
gene_id_1342	197	99.49	1.00E-142
gene_id_1343	108	100	2.00E-58
gene_id_1344	129	100	2.00E-86
gene_id_1345	73	100	6.00E-45
gene_id_1346	251	100	7.00E-180
gene_id_1347	216	99.54	5.00E-153
gene_id_1348	425	100	0
gene_id_1349	151	100	4.00E-103
gene_id_1350	60	98.33	7.00E-33
gene_id_1351	172	99.42	2.00E-104
gene_id_1352	121	100	8.00E-81
gene_id_1353	170	100	2.00E-115
gene_id_1354	131	100	1.00E-87
gene_id_1355	179	100	1.00E-117
gene_id_1356	103	100	7.00E-68
gene_id_1357	122	100	8.00E-81
gene_id_1358	89	100	1.00E-56
gene_id_1359	65	100	2.00E-36
gene_id_1360	137	100	2.00E-78
gene_id_1361	278	100	9.00E-159
gene_id_1362	109	100	8.00E-72
gene_id_1363	78	100	2.00E-49
gene_id_1364	274	99.64	0
gene_id_1365	94	100	4.00E-60
gene_id_1366	210	99.52	1.00E-151

gene_id_1367	190	100	2.00E-133
gene_id_1368	102	100	2.00E-65
gene_id_1369	693	99.86	0
gene_id_1370	135	99.26	1.00E-79
gene_id_1371	131	100	4.00E-90
gene_id_1372	104	100	6.00E-66
gene_id_1373	331	99.4	0
gene_id_1374	80	100	2.00E-50
gene_id_1375	125	97.6	4.00E-82
gene_id_1376	441	99.32	0
gene_id_1377	379	100	0
gene_id_1379	588	98.3	0
gene_id_1380	287	100	3.00E-180
gene_id_1381	130	100	1.00E-83
gene_id_1382	227	99.56	1.00E-160
gene_id_1383	473	98.73	0
gene_id_1384	468	99.57	0
gene_id_1386	232	100	4.00E-166
gene_id_1387	1101	99	0
gene_id_1388	391	97.7	0
gene_id_1389	99	69.7	9.00E-51
gene_id_1389	45	66.67	9.00E-51
gene_id_1390	361	76.18	0
gene_id_1391	522	84.48	0
gene_id_1392	143	70.63	2.00E-69
gene_id_1393	519	81.12	0
gene_id_1394	73	68.49	2.00E-28
gene_id_1395	233	90.13	3.00E-152
gene_id_1396	136	86.03	4.00E-76
gene_id_1397	442	31.22	1.00E-75
gene_id_1399	227	87.67	4.00E-148
gene_id_1400	228	100	6.00E-167
gene_id_1401	177	100	7.00E-111
gene_id_1402	554	99.1	0
gene_id_1403	94	100	1.00E-49
gene_id_1404	85	100	1.00E-55
gene_id_1405	205	100	7.00E-150
gene_id_1406	71	100	4.00E-42
gene_id_1407	459	93.68	0
gene_id_1408	143	58.74	2.00E-24
gene_id_1409	385	70.39	5.00E-179
gene_id_1410	224	99.11	1.00E-163
gene_id_1411	141	97.87	5.00E-96
gene_id_1412	566	99.65	0
gene_id_1413	443	99.77	0
gene_id_1414	112	100	1.00E-72
gene_id_1415	408	100	0
gene_id_1416	223	99.55	3.00E-157
gene_id_1417	256	100	2.00E-178
gene_id_1418	500	100	0

gene_id_1419	253	100	0
gene_id_1420	352	99.72	0
gene_id_1421	435	100	0
gene_id_1422	205	97.56	2.00E-144
gene_id_1423	143	100	8.00E-98
gene_id_1424	178	99.44	3.00E-81
gene_id_1425	320	98.12	0
gene_id_1426	166	97.59	1.00E-112
gene_id_1427	273	99.27	0
gene_id_1428	290	97.24	0
gene_id_1429	182	97.8	6.00E-127
gene_id_1430	258	99.61	0
gene_id_1431	425	99.06	0

Annotation
hypothetical protein X793_06210
pilus assembly protein PilZ
secretion system protein
GspI/GspJ family type II secretion system protein
pilus assembly protein
secretion system protein E
LuxR family DNA-binding response regulator
LuxR family transcriptional regulator
DNA-binding protein
RNA polymerase sigma70
hypothetical protein X793_06165
carbohydrate kinase
tagatose-bisphosphate aldolase
4-hydroxy-3-methylbut-2-enyl diphosphate reductase
tryptophanyl-tRNA synthase
aminotransferase
AsnC family transcriptional regulator
ABC transporter permease
multidrug ABC transporter ATP-binding protein
XRE family transcriptional regulator
hypothetical protein X793_06115
hypothetical protein X793_06110
glutamyl-tRNA(Gln) amidotransferase
glutamyl-tRNA amidotransferase subunit C
hypothetical protein
1-(5-phosphoribosyl)-5- imidazole-4-carboxamide isomerase
N-acetyltransferase GCN5
phosphoribosyl-AMP cyclohydrolase
hypothetical protein
50S ribosomal protein L31
50S ribosomal protein L27
50S ribosomal protein L21
epimerase
dephospho-CoA kinase
hypothetical protein X793_06040
acetyltransferase
ATPase AAA
hypothetical protein X793_06025
hypothetical protein
hypothetical protein
membrane protein
radical SAM protein
hypothetical protein X793_05995
hypothetical protein
hypothetical protein
ATPase AAA
alpha/beta hydrolase
hypothetical protein
hypothetical protein

hypothetical protein
fasciclin
universal stress protein
major facilitator transporter
GTP-binding protein
zinc-binding protein
dienelactone hydrolase
chemotaxis protein CheY
ATPase
competence protein CinA
NUDIX hydrolase
ribonuclease PH
gamma-glutamyl phosphate reductase
MerR family transcriptional regulator
2-alkenal reductase
serine protease
hypothetical protein X793_05875
hypothetical protein
gamma-glutamyl kinase
transcription-repair coupling factor
serine recombinase
1,2-dichloropropane reductive dehalogenase
chemotaxis protein CheY
histidine kinase
histidine kinase
histidine kinase
two component response transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
Uridine kinase
ADP-ribosylglycohydrolase
Phosphohydrolase
NUDIX hydrolase
site-specific recombinase, resolvase family
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
putative reductive dehalogenase subunit A, partial
cobalamin biosynthesis protein CobN
probable ABC transporter, ATP-binding protein
ABC transporter, permease protein
ABC transporter substrate-binding protein
ATPase
dopamine beta hydroxylase
flavodoxin
MerR family transcriptional regulator

ABC transporter
hypothetical protein X793_07040
membrane protein
MarR family transcriptional regulator
dehalogenase
dehalogenase
MarR family transcriptional regulator
radical SAM protein
MFS transporter
MarR family transcriptional regulator
dehalogenase
dehalogenase
ATPase
chemotaxis protein CheY
hypothetical protein X793_07125
hypothetical protein
dehalogenase
dehalogenase
Cro/Cl family transcriptional regulator
hypothetical protein X793_07155
prephenate dehydratase
hypothetical protein X793_07165
preprotein translocase subunit SecG
aspartyl/glutamyl-tRNA amidotransferase subunit B
recombinase
hypothetical protein
hypothetical protein
hypothetical protein
amidase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
RNA methyltransferase fusion protein
hypothetical protein
hypothetical protein
hypothetical protein
phage major tail protein phi13
hypothetical protein
phage protein, HK97, gp10 family
phage head-tail adapter protein
phage protein
hypothetical protein
capsid protein
ATP-dependent Clp protease, proteolytic subunit ClpP
peptidase
terminase
hypothetical protein

hypothetical protein
virulence protein
uncharacterized protein
virulence-related protein
lactate dehydrogenase
S-adenosylmethionine synthetase
terminase
HNH endonuclease
hypothetical protein
hypothetical protein
DEAD/DEAH box helicase
hypothetical protein
Virulence-associated E family protein
hypothetical protein
hypothetical protein
XRE family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
excisionase
hypothetical protein
MULTISPECIES: restriction endonuclease
DEAD/DEAH box helicase
type III restriction protein res subunit
exonuclease SbcD
methionine sulfoxide reductase
uncharacterized protein
hypothetical protein
hypothetical protein
hypothetical protein
MerR family transcriptional regulator
hypothetical protein X793_07210
hypothetical protein
formate hydrogenlyase
hydrogenase
oxidoreductase
hydrogenase subunit
hydrogenase
oxidoreductase
methylglyoxal synthase
hypothetical protein
mechanosensitive ion channel protein
TetR family transcriptional regulator
peroxiredoxin
hypothetical protein X793_07275
hypothetical protein
hypothetical protein
peptidase M28

serine O-acetyltransferase
dihydroorotate dehydrogenase
quinolinate synthetase
SAM-dependent methlyltransferase
AIR synthase
AsnC family transcriptional regulator
thiamine biosynthesis protein ApbE
transcriptional regulator
hypothetical protein
transcriptional regulator
preprotein translocase subunit TatC
preprotein translocase subunit TatA
primosome subunit DnaD
preprotein translocase subunit TatA
dihydropteroate synthase
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
6-pyruvoyl tetrahydrobiopterin synthase
recombinase RecA
RecX family transcriptional regulator
ribonuclease
metallophosphoesterase
phosphotransferase
membrane protein
HhH-GPD family DNA repair protein
hypothetical protein
homocitrate synthase
HIT family hydrolase
AbrB family transcriptional regulator
hypothetical protein X793_07455
hypothetical protein
multidrug ABC transporter ATP-binding protein
ABC transporter permease
cell wall-binding protein
hypothetical protein
desulforedoxin
hypothetical protein
N-acetyl-gamma-glutamyl-phosphate reductase
sodium/hydrogen exchanger
metallo-beta-lactamase
Fe-S oxidoreductase
DNA gyrase subunit A
hypothetical protein
nitrogen-fixing protein NifU
aspartate kinase
hypothetical protein
phosphoglycerate mutase
nucleotide pyrophosphohydrolase
zinc metallopeptidase
30S ribosomal protein S20
LexA family transcriptional regulator

fuculose phosphate aldolase
methionyl-tRNA formyltransferase
chromosomal replication initiator protein DnaA
GTPase CgtA
nicotinic acid mononucleotide adenylyltransferase
DNA gyrase subunit B
GTP pyrophosphokinase
histidyl-tRNA synthetase
saccharopine dehydrogenase
membrane protein
branched-chain amino acid aminotransferase
DNA polymerase IV
hypothetical protein
orotidine 5'-phosphate decarboxylase
hypothetical protein
hypothetical protein X793_00075
folylpolyglutamate synthase
hypothetical protein
hypothetical protein
D-tyrosyl-tRNA(Tyr) deacylase
FUR family transcriptional regulator
hypothetical protein
hypothetical protein X793_00110
hypothetical protein
competence protein ComEC
competence protein ComEA
portal protein
potassium transporter TrkA
universal stress protein
potassium transporter
potassium transporter TrkA
cation transporter
phosphate transport regulator
inorganic phosphate transporter
guanylate kinase
hypothetical protein
ferredoxin-NADP(+) reductase subunit alpha
dihydropyrimidine dehydrogenase subunit A
hypothetical protein
hypothetical protein
SAM-dependent methlyltransferase
hypothetical protein
hypothetical protein X793_00215
hypothetical protein X793_00220
GTP-binding protein YchF
hypothetical protein
DNA polymerase III subunit delta
hypothetical protein
ROK family transcriptional regulator
alanyl-tRNA synthetase

Holliday junction resolvase
queuine tRNA-ribosyltransferase
alcohol dehydrogenase
ATP-dependent Clp protease ATP-binding protein
DNA repair protein RadA
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
cysteinyl-tRNA synthetase
hypothetical protein
hypothetical protein
putative transcription factor, MBF1 like protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
type I restriction-modification protein subunit M
restriction endonuclease
hypothetical protein
hypothetical protein
restriction endonuclease subunit R
metal-dependent hydrolase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein X792_01175
hypothetical protein
DNA polymerase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein X794_03440
integrase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein X794_03415
hypothetical protein X794_03410
histidine kinase
hypothetical protein
peptidase S8
hypothetical protein
hypothetical protein X794_03385
hypothetical protein
hypothetical protein
cytosine permease
hypothetical protein
hypothetical protein X794_03360
hypothetical protein

hypothetical protein
AbrB family transcriptional regulator
hypothetical protein X794_03330
hypothetical protein
hypothetical protein
ATPase AAA
heat shock protein DnaJ domain-containing protein
hypothetical protein
hypothetical protein X792_00980
hypothetical protein X792_00975
XRE family transcriptional regulator
XRE family transcriptional regulator
hypothetical protein
site-specific recombinase, resolvase family
hypothetical protein
hypothetical protein
hypothetical protein
beta-lactamase
Type III restriction enzyme
hypothetical protein
hypothetical protein X792_01175
hypothetical protein, partial
dehalogenase
ATPase
hypothetical protein X793_00475
radical SAM protein
radical SAM protein
hypothetical protein
chemotaxis protein CheY
hypothetical protein X793_00500
iron transporter
feoA family protein
iron dependent repressor
rubrerythrin
molybdopterin-guanine dinucleotide biosynthesis protein MobA
hypothetical protein X793_00530
molybdopterin oxidoreductase
molybdopterin oxidoreductase
(4Fe-4S)-binding protein
ATP-binding protein
hypothetical protein X793_00555
fatty acid-binding protein DegV
LemA family protein
endonuclease
hydrogenase maturation protease
iron hydrogenase
oxidoreductase
Ni/Fe hydrogenase
ABC transporter substrate-binding protein
ABC transporter permease

multidrug ABC transporter ATP-binding protein
TetR family transcriptional regulator
glutamine amidotransferase
pyruvate carboxylase
biotin carboxylase
acetyl-CoA carboxylase
hypothetical protein
pyridine nucleotide-disulfide oxidoreductase
alcohol dehydrogenase
anthranilate phosphoribosyltransferase
ATPase
cobyrinic acid a,c-diamide synthase
hypothetical protein X793_00670
chemotaxis protein CheY
chemotaxis protein CheY
protease
hypothetical protein
general secretion pathway protein H
XRE family transcriptional regulator
ATPase
methylglyoxal synthase
phosphate-binding protein
phosphate ABC transporter permease
phosphate ABC transporter permease
phosphate ABC transporter ATP-binding protein
PhoU family transcriptional regulator
arsenate reductase
acetyltransferase
iron hydrogenase
NADH dehydrogenase subunit F
ferredoxin
iron hydrogenase
hydrolase
hypothetical protein X793_00775
hypothetical protein X793_00780
membrane protein
hypothetical protein
chemotaxis protein CheY
ATPase
dehalogenase
putative reductive dehalogenase anchoring protein
chemotaxis protein CheY
ATPase
hypothetical protein X793_00830
dehalogenase
reductive dehalogenase
dehalogenase
DEAD/DEAH box helicase
membrane protein
formate dehydrogenase accessory protein FdhE

formate dehydrogenase
formate dehydrogenase subunit alpha
hypothetical protein X793_00870
methyltransferase
phosphopantetheine adenylyltransferase
phosphopantetheine adenylyltransferase
colicin V production CvpA
pyrroline-5-carboxylate reductase
leucyl-tRNA synthetase
hypothetical protein
glutaredoxin
ferredoxin-thioredoxin reductase, catalytic subunit, /rubredoxin
hypothetical protein
glycosyl hydrolase
histidinol phosphate phosphatase
glycosyl transferase family 2
epimerase
D-glycero-D-manno-heptose 1-phosphate guanosyltransferase
GHMP kinase
phosphoheptose isomerase
glycosyl transferase family 2
hypothetical protein X793_00970
glycosyltransferase
glycosyl transferase family 1
SAM-dependent methlyltransferase
hypothetical protein
FeS-binding protein
polysaccharide biosynthesis protein
LmbE family protein
aldo/keto reductase
hypothetical protein
PBS lyase
lysine 2,3-aminomutase
serine protease
hemolysin
ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
membrane protein
transcriptional regulator
two component transcriptional regulator, LuxR family
hypothetical protein
hypothetical protein, partial
heat shock protein DnaJ domain protein
hypothetical protein
DNA replication protein DnaC
hypothetical protein
hypothetical protein

MULTISPECIES: RNA polymerase sigma factor RpoD
Cro/Cl family transcriptional regulator
DNA-binding protein
hypothetical protein
patatin
hypothetical protein X793_01320
hypothetical protein
nuclease
amino acid transporter LysE
histone deacetylase
cation transporter
preprotein translocase subunit SecF
preprotein translocase subunit SecD
metal-dependent phosphohydrolase
XRE family transcriptional regulator
primosomal protein N'
50S ribosomal protein L19
tRNA (guanine-N1)-methyltransferase
cell division protein MraZ
16S rRNA methyltransferase
cell division protein FtsA
cell division protein FtsZ
NrdR family transcriptional regulator
ribonucleotide-diphosphate reductase subunit alpha
hypothetical protein
hypothetical protein X793_01420
radical SAM protein
aspartyl-tRNA amidotransferase subunit B
30S ribosomal protein S21
hypothetical protein
hypothetical protein X793_01445
hypothetical protein
hypothetical protein
ribonuclease H
hypothetical protein X793_01495
hypothetical protein X793_01500
peptidase S41
phenylalanyl-tRNA synthetase subunit alpha
phenylalanyl-tRNA synthetase subunit beta
inorganic pyrophosphatase
prolyl-tRNA synthetase
(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
peptidase
1-deoxy-D-xylulose 5-phosphate reductoisomerase
phosphatidate cytidylyltransferase
UDP pyrophosphate synthase
ribosome recycling factor
uridylate kinase
elongation factor Ts
30S ribosomal protein S2

phosphoribosylformylglycinamidine synthase
phosphoribosylformylglycinamidine synthase
pyridoxal biosynthesis protein
(2Fe-2S)-binding protein
hypothetical protein
inosine 5'-monophosphate dehydrogenase
methyltransferase
hypothetical protein
methionyl-tRNA synthetase
heptaprenyl diphosphate synthase
hypothetical protein
cell division protein FtsH
hypothetical protein X793_01645
ribosome-associated protein IOJAP
nucleoside diphosphate kinase
HAD family hydrolase
nucleoid maintenance ATPase YjeE
thiamine-monophosphate kinase
SAM-dependent methlyltransferase
SAM-dependent methlyltransferase
3-dehydroquinate synthase
1,4-dihydroxy-2-naphthoate prenyltransferase
SAM-dependent methlyltransferase
Ser/Thr protein phosphatase
dimethyladenosine transferase
4-diphosphocytidyl-2C-methyl-D-erythritol kinase
rubrerythrin
hypothetical protein
cation transporter
poly(A) polymerase
ABC transporter ATP-binding protein
ABC transporter permease
dephospho-CoA kinase-like protein
cytidine deaminase
diacylglycerol kinase
deoxyuridine 5'-triphosphate nucleotidohydrolase
zinc-binding protein
amino acid ABC transporter ATPase
amino acid ABC transporter permease
ABC transporter substrate-binding protein
fatty acid-binding protein DegV
magnesium transporter
transporter
lactamase
carbohydrate kinase
pantothenate kinase
peptidase ClpP
valyl-tRNA synthase
ATPase
chemotaxis protein CheY

hypothetical protein X793_01845
preprotein translocase subunit SecA
ribose-phosphate pyrophosphokinase
serine hydroxymethyltransferase
uracil-DNA glycosylase
ribonuclease J
DNA segregation ATPase FtsK/SpoIIIE
hypothetical protein
excinuclease ABC subunit B
Holliday junction DNA helicase RuvA
Holliday junction resolvase
transcriptional regulator
4'-phosphopantetheinyl transferase
iron hydrogenase
methylmalonyl-CoA carboxyltransferase
3-isopropylmalate dehydratase large subunit
aconitase/homoaconitase C-terminal domain-containing protein, 3-isopropylmalate dehydratase small sul
isocitrate dehydrogenase
malate dehydrogenase
hypothetical protein
fumarate hydratase subunit alpha
fumarate hydratase
HIT family hydrolase
DNA mismatch repair protein MutT
acetyltransferase
inorganic polyphosphate/ATP-NAD kinase
hypothetical protein
prephenate dehydrogenase
chorismate mutase
chorismate synthase
3-phosphoshikimate 1-carboxyvinyltransferase
shikimate kinase
shikimate 5-dehydrogenase
3-dehydroquinate dehydratase
3-dehydroquinate synthase
3-deoxy-7-phosphoheptulonate synthase
precorrin methylase
multidrug transporter MatE
potassium ABC transporter ATPase
hypothetical protein
hypothetical protein
hypothetical protein
site-specific recombinase, resolvase family
single-stranded DNA-binding protein
Fur family transcriptional regulator
Fe2+ transport system protein A
iron transporter FeoB
MFS transporter
hypothetical protein X793_06845
Crp/Fnr family transcriptional regulator

hypothetical protein X793_06835
camphor resistance protein CrcB
MarR family transcripitonal regulator
SAM-dependent methlyltransferase
thymidylate synthase
tryptophan synthase subunit alpha
tryptophan synthase subunit beta
3-deoxy-7-phosphoheptulonate synthase
N-(5'-phosphoribosyl)anthranilate isomerase
indole-3-glycerol phosphate synthase
anthranilate phosphoribosyltransferase
anthranilate synthase component II
anthranilate synthase component I
hypothetical protein X793_06760
hypothetical protein X793_06730
membrane protein
DNA polymerase III subunit alpha
hypothetical protein
DNA repair protein RadC
hypothetical protein
methylated-DNA--protein-cysteine methyltransferase
ribose ABC transporter permease
competence protein ComF
hypothetical protein
2'-5' RNA ligase
amidohydrolase
50S ribosomal protein L25
hypothetical protein
hypothetical protein
cyclase
MarC family transcriptional regulator
hypothetical protein
MerR family transcriptional regulator
glycerol-3-phosphate acyltransferase
hypothetical protein X793_06625
hypothetical protein X793_06600
TetR family transcriptional regulator
hydrogenase expression/formation protein HypE
hydrogenase expression/formation protein HypD
hydrogenase assembly protein HypC
HAD family hydrolase
hydantoin utilization protein A
hydrogenase nickel incorporation protein HypA
peptidase M16
molecular chaperone GroEL
molecular chaperone GroES
O-sialoglycoprotein endopeptidase
hemolysin
hypothetical protein X793_06535
peptidase M48

phosphoglycerate mutase
tRNA(Ile)-lysidine synthetase
arsenite S-adenosylmethyltransferase
AbrB family transcriptional regulator
nicotinate phosphoribosyltransferase
purine biosynthesis protein purH
phosphoribosylaminoimidazole synthetase
amidophosphoribosyltransferase
hypothetical protein X793_06485
ATP-dependent Clp protease ATP-binding protein
MerR family transcriptional regulator
molecular chaperone DnaJ
CTP synthetase
transaldolase
transcription termination factor Rho
hypothetical protein X792_06595
hypothetical protein
exonuclease
peptidase C14
lactamase
HrcA family transcriptional regulator
CoA-transferase
molecular chaperone DnaK
molecular chaperone DnaJ
glycerol-3-phosphate dehydrogenase
membrane protein
GTPase Der
ornithine carbamoyltransferase
hypothetical protein
sulfurtransferase
DNA-directed DNA polymerase I
phosphatidic acid phosphatase
formamidopyrimidine-DNA glycosylase
hypothetical protein
hypothetical protein
(dimethylallyl)adenosine tRNA methylthiotransferase
preprotein translocase subunit YajC
aspartate oxidase
nicotinate-nucleotide pyrophosphorylase
diguanylate cyclase
auxin-responsive GH3 protein homolog
hypothetical protein X793_06315
hypothetical protein
hypothetical protein
RNA pseudouridine synthase
peptidase A8
molecular chaperone DnaK
diguanylate cyclase
flavodoxin
rRNA maturation factor

hypothetical protein
radical SAM protein
hypothetical protein
glutamyl-tRNA synthetase
hypothetical protein
HAD family hydrolase
peptidase
general secretion pathway protein
twitching motility protein PilT
type IV pilus assembly family protein
hypothetical protein X793_06215
hypothetical protein X793_06210
transcription-repair coupling factor
methyltransferase
acyl carrier protein
nitrogen utilization protein B
3-ketoacyl-ACP reductase
malonyl CoA-ACP transacylase
50S ribosomal protein L32
metal-binding protein
hypothetical protein
enoyl-ACP reductase
hypothetical protein
arginyl-tRNA synthetase
HNH nuclease
ATP-dependent DNA helicase RecG
fatty acid-binding protein DegV
fatty acid-binding protein DegV
fatty acid-binding protein DegV
fatty acid-binding protein DegV
dihydroxyacetone kinase
argininosuccinate lyase
argininosuccinate synthase
hypothetical protein X793_05755
acetylornithine aminotransferase
acetylglutamate kinase
ornithine acetyltransferase
twitching motility protein PilT
hypothetical protein X793_05730
hypothetical protein
flavodoxin
hypothetical protein
hypothetical protein
ArsR family transcriptional regulator
hypothetical protein
competence protein TfoX
FMN reductase
methionine sulfoxide reductase B
methionine sulfoxide reductase A
peptidyl-prolyl cis-trans isomerase

hypothetical protein
hypothetical protein X793_05670
formyltetrahydrofolate deformylase
DNA mismatch repair protein MutS
hypothetical protein
hypothetical protein
transcriptional regulator
ATPase
chemotaxis protein CheY
hypothetical protein X793_05625
DNA polymerase III subunit beta
nucleoside-triphosphate diphosphatase
fructose-1 6-bisphosphatase
cob(I)alamin adenosyltransferase
hypothetical protein
hypothetical protein X793_05540
hypothetical protein
DNA mismatch repair protein MutS
HAD family hydrolase
GNAT family acetyltransferase
excinuclease ABC subunit C
recombinase XerC
hypothetical protein
hypothetical protein
elongation factor G
N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase
peptide chain release factor 1
3-hydroxypropionyl-CoA synthetase
nucleotidyltransferase
protein export protein
homoserine dehydrogenase
threonine synthase
GTP cyclohydrolase
dihydroorotate dehydrogenase
carbamoyl phosphate synthase large subunit
carbamoyl phosphate synthase small subunit
dihydroorotase
aspartate carbamoyltransferase
uracil phosphoribosyltransferase
ATPase AAA
DNA mismatch repair protein MutL
Holliday junction resolvase
orotate phosphoribosyltransferase
signal peptidase
hypothetical protein X793_05385
5-amino-6-(5-phosphoribosylamino)uracil reductase
riboflavin synthase subunit alpha
3,4-dihydroxy-2-butanone 4-phosphate synthase
6,7-dimethyl-8-ribityllumazine synthase
hypothetical protein

hypothetical protein
biotin transporter
ABC transporter
ABC transporter
MarR family transcriptional regulator
alpha/beta hydrolase
iron ABC transporter ATP-binding protein
iron ABC transporter permease
hypothetical protein X793_05305
formylmethanofuran dehydrogenase subunit E
hypothetical protein
FeS-binding protein
MarR family transcriptional regulator
transcriptional regulator
molybdate ABC transporter substrate-binding protein
molybdate ABC transporter permease
molybdenum ABC transporter, ATP-binding protein
nitrogenase reductase
nitrogen fixation nifHD region glnB 1
nitrogen regulatory protein P-II
nitrogenase molybdenum-iron protein alpha chain
nitrogenase molybdenum-iron protein beta chain
nitrogenase iron-molybdenum cofactor biosynthesis protein NifE
nitrogenase
dinitrogenase iron-molybdenum cofactor NifB/Y/X family protein
ferredoxin
acetyltransferase
nitrogenase cofactor biosynthesis protein NifB
Fur family transcriptional regulator
acetyl-CoA synthetase
chemotaxis protein CheY
hypothetical protein X793_05160
hypothetical protein X793_05155
30S ribosomal protein S6
single-stranded DNA-binding protein
30S ribosomal protein S18
ribonuclease P
dehydrogenase
preprotein translocase subunit YidC
SpoIIIJ-associated protein Jag
isoleucyl-tRNA synthetase
serine protease
serine protease
tryptophan synthase subunit beta
long-chain fatty acid--CoA ligase
fatty acid-binding protein DegV
kinase
leucyl aminopeptidase
hypothetical protein
acylphosphatase

hypothetical protein
ribonuclease
serine recombinase
hypothetical protein, partial
hypothetical protein
DNA polymerase
hypothetical protein
DEAD/DEAH box helicase
virulence associated protein
chemotaxis protein CheY
hypothetical protein X793_04815
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
restriction endonuclease subunit R, partial
hypothetical protein
DNA methyltransferase
hypothetical protein
hypothetical protein SD80_36205
chemotaxis protein CheY
phenylacetate-CoA ligase
amino acid-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein X793_04765
redox-active disulfide protein 2
hypothetical protein X793_04755
ArsR family transcriptional regulator
acetyltransferase
glycosyl transferase family 1
hypothetical protein
elongation factor Tu
50S ribosomal protein L33
preprotein translocase subunit SecE
transcription antitermination protein nusG
50S ribosomal protein L11
50S ribosomal protein L1
50S ribosomal protein L10
50S ribosomal protein L7/L12
hypothetical protein
acetyltransferase
acetyltransferase
Fis family transcriptional regulator
transcription termination factor NusA
hypothetical protein
translation initiation factor IF-2
ribosome-binding factor A
tRNA pseudouridine synthase B
hypothetical protein

inositol-3-phosphate synthase
glycosyl transferase family 1
CDP-alcohol phosphatidyltransferase
adenylosuccinate synthetase
acetyltransferase
acetyltransferase
dihydrodipicolinate synthase
semialdehyde dehydrogenase
dihydrodipicolinate reductase
polynucleotide phosphorylase
30S ribosomal protein S15
hypothetical protein X793_04570
DEAD/DEAH box helicase
prolipoprotein diacylglyceryl transferase
membrane protein
recombination protein RecJ
3-oxoacyl-ACP synthase
radical SAM protein
hypothetical protein X793_04535
imidazole glycerol phosphate synthase
DNA mismatch repair protein MutS
superoxide dismutase
bacterioferritin
molecular chaperone Hsp20
ATPase
hypothetical protein
FeS cluster assembly scaffold IscU
hypothetical protein
hypothetical protein
indolepyruvate oxidoreductase
indolepyruvate ferredoxin oxidoreductase
AMP-binding protein
branched-chain amino acid ABC transporter permease
branched-chain amino acid ABC transporter permease
ABC transporter
ABC transporter
branched-chain amino acid ABC transporter ATP-binding protein
AMP-binding protein
hypothetical protein
branched-chain amino acid ABC transporter ATP-binding protein
thioesterase
cobyric acid synthase
endonuclease III
TatD family hydrolase
NADH-quinone oxidoreductase subunit N
oxidoreductase
oxidoreductase
NADH:ubiquinone oxidoreductase subunit K
NADH-quinone oxidoreductase subunit L
(4Fe-4S)-binding protein

NADH:ubiquinone oxidoreductase subunit H
NADH dehydrogenase subunit D
NADH-quinone oxidoreductase subunit C
NADH-quinone oxidoreductase subunit B
NADH-quinone oxidoreductase subunit A
twitching motility protein PilT
hypothetical protein X793_04330
(Fe-S)-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
rubrerythrin
peptidase M29
MFS transporter
arsenic transporter
transcriptional regulator
XRE family transcriptional regulator
membrane protein
MarR family transcriptional regulator
translation elongation factor P
lysyl-tRNA synthetase
hydrogenase
NADH dehydrogenase
hydrogenase
(2Fe-2S)-binding protein
NADH dehydrogenase
hydrogenase
NADH ubiquinone oxidoreductase
ech hydrogenase subunit B
oxidoreductase
elongation factor 4
oxygen-independent coproporphyrinogen III oxidase
ABC transporter ATP-binding protein
ABC transporter substrate-binding protein
hypothetical protein X793_04155
hypothetical protein
sodium extrusion protein NatB
sodium ABC transporter
hypothetical protein
biotin--acetyl-CoA-carboxylase ligase
membrane protein
serine protease
ATP phosphoribosyltransferase
ATP phosphoribosyltransferase
histidinol dehydrogenase
histidinol-phosphate aminotransferase
imidazoleglycerol-phosphate dehydratase

phosphoribosylaminoimidazole-succinocarboxamide synthase
adenylosuccinate lyase
N5-carboxyaminoimidazole ribonucleotide mutase
phosphoribosylamine--glycine ligase
hypothetical protein
GMP synthase (glutamine-hydrolysing)
translation factor Sua5
dihydroxy-acid dehydratase
acetolactate synthase
acetolactate synthase
ketol-acid reductoisomerase
2-isopropylmalate synthase
magnesium transporter MgtC
3-isopropylmalate dehydratase large subunit
3-isopropylmalate dehydratase small subunit
3-isopropylmalate dehydrogenase
alpha-isopropylmalate/homocitrate synthase transferase
nitroreductase
tRNA-splicing ligase RtcB
hypothetical protein X793_03990
hypothetical protein
hypothetical protein
thymidylate synthase
cobalt ABC transporter
hypothetical protein
ABC transporter ATP-binding protein
ABC transporter permease
ABC transporter ATP-binding protein
phosphatidic acid phosphatase
phytoene dehydrogenase
MFS transporter
pantoate--beta-alanine ligase
RecName: Full=3-methyl-2-oxobutanoate hydroxymethyltransferase; AltName: Full=Ketopantoate hydrox
aspartate decarboxylase
pyrroline-5-carboxylate reductase
hypothetical protein X793_03465
stationary phase survival protein SurE
S-adenosylmethionine tRNA ribosyltransferase
ABC transporter permease
ABC transporter
ABC transporter substrate-binding protein
hypoxanthine phosphoribosyltransferase
adenine deaminase
phosphoribosyl transferase
nuclease SbcCD subunit D
glycyl-tRNA synthetase subunit beta
hypothetical protein X793_03405
metallo-beta-lactamase
potassium transporter
haloacid dehalogenase

thiamine-phosphate pyrophosphorylase
endonuclease
ribonuclease HII
thiouridylase
thymidylate kinase
single-stranded DNA-binding protein
RecName: Full=Ribosomal RNA small subunit methyltransferase G; AltName: Full=16S rRNA 7-methylguan
phosphomethylpyrimidine synthase
peptidase M50
CAAX amino terminal protease
monooxygenase FAD-binding protein
transcription elongation factor GreA
protease
membrane protein
ATPase
pyrophosphatase
hypothetical protein
hydrolase
hypothetical protein X793_03290
membrane protein
peptide deformylase
2,3-diketo-5-methylthio-1-phosphopentane phosphatase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein X793_03240
hypothetical protein X793_03240
hypothetical protein X793_03240
threonyl-tRNA synthetase
translation initiation factor IF-3
50S ribosomal protein L35
50S ribosomal protein L20
hypoxanthine-guanine phosphoribosyltransferase
small multi-drug export
1-deoxy-D-xylulose-5-phosphate synthase
phosphoglycerate kinase
phosphoglycerate mutase
triosephosphate isomerase
tRNA dimethylallyltransferase
diaminopimelate epimerase
diaminopimelate aminotransferase
hypothetical protein
GTP-binding proten HflX
short-chain dehydrogenase
FmdB family transcriptional regulator
mercuric reductase
(2Fe-2S)-binding protein
NADH dehydrogenase
hydrogenase

pyruvic-ferredoxin oxidoreductase, beta subunit
2-ketoisovalerate ferredoxin oxidoreductase subunit alpha
pyruvic-ferredoxin oxidoreductase subunit delta
pyruvic-ferredoxin oxidoreductase, gamma subunit
sodium/hydrogen exchanger
DNA processing protein DprA
DNA topoisomerase I
tyrosine recombinase XerC
aminopeptidase
elongation factor P
phosphotransferase
phosphoglycerate transporter
ribokinase
ATP-dependent Clp protease proteolytic subunit
trigger factor
aspartyl-tRNA synthase
hypothetical protein
hypothetical protein
formate--tetrahydrofolate ligase
iron-sulfur cluster-binding protein
carbon monoxide dehydrogenase
bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohyd
acetyl-CoA decarbonylase / synthase complex subunit delta
acetyl-CoA decarbonylase
acetyl-CoA synthase subunit gamma
hypothetical protein
chemotaxis protein CheY
ATPase
thioredoxin
cobinamide kinase
alpha-ribazole-5-phosphate phosphatase
cobalamin 5'-phosphate synthase
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
aspartate aminotransferase
cobalamin biosynthesis protein CobD
hypothetical protein
iron ABC transporter
corrinoid ABC transporter permease
cobalamin ABC transporter substrate-binding protein
hypothetical protein
SAM-dependent methlyltransferase
NADH dehydrogenase
transketolase
ribose 5-phosphate isomerase
ribulose-phosphate 3-epimerase
cyclase
universal stress protein
hypothetical protein
hypothetical protein
cell division protein FtsA

cell division protein FtsZ
hypothetical protein
membrane protein
zinc ABC transporter ATP-binding protein
zinc ABC transporter substrate-binding protein
Fur family transcriptional regulator
D-alanine--D-alanine ligase
lysine 2,3-aminomutase
hypothetical protein
hypothetical protein
ATPase
chemotaxis protein CheY
ribonucleoside-diphosphate reductase
radical SAM protein
hypothetical protein X793_02765
exonuclease
cytochrome C biogenesis protein CcsB
thiol-disulfide oxidoreductase
hypothetical protein X793_02745
hydrogenase maturation protease
hydrogenase, group 3, VhuA subunit
methyl viologen-reducing hydrogenase
radical SAM protein
SAM-dependent methlyltransferase
permease
hypothetical protein
alanine acetyltransferase
hypothetical protein
Holliday junction DNA helicase RuvB
DNA-directed RNA polymerase subunit beta'
DNA-directed RNA polymerase subunit beta
riboflavin biosynthesis protein RibF
tyrosyl-tRNA synthetase
class V aminotransferase
3-phosphoglycerate dehydrogenase
glutamine amidotransferase
hypothetical protein
DNA ligase
peptidyl-tRNA hydrolase
hypothetical protein X793_02640
enolase
2-hydroxyglutaryl-CoA dehydratase
glyceraldehyde-3-phosphate dehydrogenase, type I
cell dividion protein FtsZ
RNA polymerase sigma70
hypothetical protein X793_02605
hypothetical protein
DNA polymerase III subunit gamma/tau
hypothetical protein
recombinase RecR

magnesium transporter
DNA alkylation repair protein
DNA repair protein RecO
hypothetical protein
lysyl-tRNA synthetase
seryl-tRNA synthase
aspartate aminotransferase
hypothetical protein
ABC transporter substrate-binding protein
hypothetical protein X793_02530
hypothetical protein X793_02525
peptide chain release factor 2
endonuclease V
30S ribosomal protein S16
hypothetical protein
ribosome maturation protein RimM
F0F1 ATP synthase subunit epsilon
F0F1 ATP synthase subunit beta
F0F1 ATP synthase subunit gamma
F0F1 ATP synthase subunit alpha
F0F1 ATP synthase subunit delta
ATP synthase subunit B
ATP synthase subunit C
ATP synthase F0 subunit A
hypothetical protein
hypothetical protein X793_02450
phosphoenolpyruvate synthase
deoxyguanosinetriphosphate triphosphohydrolase
DNA primase
RNA polymerase sigma70
exonuclease SbcC
XRE family transcriptional regulator
phosphohydrolase
excinuclease ABC subunit A
peptidase M20
ATPase
phosphate acyltransferase
thioredoxin reductase
50S ribosomal protein L9
replicative DNA helicase
DNA damage-indicible protein DnaD
ATP-binding protein
HNH nuclease
hypothetical protein
DNA polymerase III subunit delta'
diaminopimelate decarboxylase
HAD family hydrolase
phosphatidylethanolamine-binding protein
glutamine--fructose-6-phosphate aminotransferase
glucose-1-phosphate thymidylyltransferase

glucose-1-phosphate thymidylyltransferase
phosphoglucosamine mutase
peptidase U62 modulator of DNA gyrase
peptidase U62 modulator of DNA gyrase
hypothetical protein
PBS lyase
acetyltransferase
hypothetical protein
daunorubicin ABC transporter ATP-binding protein
ABC transporter permease
methylthioribose-1-phosphate isomerase
S-methyl-5'-thioadenosine phosphorylase
methionine synthase
hypothetical protein X793_02245
S-adenosyl-L-homocysteine hydrolase
S-adenosylmethionine synthetase
hypothetical protein
phosphomannomutase
phosphate starvation-inducible protein PsiE
hypothetical protein
30S ribosomal protein S9
50S ribosomal protein L13
tRNA pseudouridine synthase A
50S ribosomal protein L17
DNA-directed RNA polymerase subunit alpha
30S ribosomal protein S4
30S ribosomal protein S11
30S ribosomal protein S13
translation initiation factor IF-1
methionine aminopeptidase
adenylate kinase
preprotein translocase subunit SecY
50S ribosomal protein L15
50S ribosomal protein L30
30S ribosomal protein S5
50S ribosomal protein L18
50S ribosomal protein L6
30S ribosomal protein S8
50S ribosomal protein L5
50S ribosomal protein L24
50S ribosomal protein L14
30S ribosomal protein S17
50S ribosomal protein L29
50S ribosomal protein L16
30S ribosomal protein S3
50S ribosomal protein L22
30S ribosomal protein S19
50S ribosomal protein L2
50S ribosomal protein L23
50S ribosomal protein L4

50S ribosomal protein L3
30S ribosomal protein S10
elongation factor P
30S ribosomal protein S7
30S ribosomal protein S12
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
phosphohydrolase
hypothetical protein
endoribonuclease L-PSP
ATPase
cell dividion protein FtsZ
DNA repair protein RecN
membrane protein
hypothetical protein
XRE family transcriptional regulator
ATPase
metallo-beta-lactamase
LuxR family transcriptional regulator
multi-sensor signal transduction histidine kinase
SAM-dependent methlyltransferase
hypothetical protein scindens]
hypothetical protein scindens]
uncharacterized protein
serine recombinase
recombinase
recombinase
hypothetical protein
amidase
hypothetical protein
hypothetical protein
cytosine methyltransferase, partial
hypothetical protein
hypothetical protein
trichloroethene reductive dehalogenase
trichloroethene reductive dehalogenase anchoring protein
hypothetical protein
resolvase domain-containing protein
hypothetical protein
serine recombinase
chromate resistance protein ChrB
MFS transporter permease
septum formation protein Maf
hypothetical protein
NAD synthetase
glutamine synthetase
nitrogen regulatory protein P-II
ammonium transporter
transcriptional regulator
hypothetical protein
glutamate synthase

imidazole glycerol phosphate synthase
hypothetical protein X793_05095
pyridine nucleotide-disulfide oxidoreductase
imidazole glycerol phosphate synthase
4Fe-4S ferredoxin
hypothetical protein
cysteine synthase
hypothetical protein X793_05125
radical SAM protein
cobalamin biosynthesis protein CobD
cobinamide adenolsyltransferase
carbon-nitrogen hydrolase
glycosyl transferase

osine methyltransferase; Short=16S rRNA m7G methyltransferase

Gene ID	Length (aa)	Identity	e-value
gene_id_3	138	45.65	6.00E-39
gene_id_4	611	42.88	0
gene_id_5	373	61.39	1.00E-149
gene_id_6	512	43.55	3.00E-150
gene_id_7	247	40.89	3.00E-49
gene_id_8	195	25.13	2.00E-09
gene_id_10	148	41.22	6.00E-24
gene_id_11	88	36.36	3.00E-10
gene_id_12	114	73.68	4.00E-55
gene_id_13	287	84.67	1.00E-164
gene_id_14	150	81.33	6.00E-86
gene_id_15	582	86.25	0
gene_id_16	105	80	2.00E-57
gene_id_17	117	56.41	5.00E-34
gene_id_18	206	58.25	1.00E-74
gene_id_19	463	60.91	0
gene_id_20	290	55.17	2.00E-109
gene_id_21	1075	71.16	0
gene_id_22	332	52.41	4.00E-105
gene_id_23	235	72.34	1.00E-128
gene_id_24	39	69.23	4.00E-11
gene_id_25	297	50.17	1.00E-93
gene_id_26	559	39.53	6.00E-102
gene_id_27	433	54.97	5.00E-145
gene_id_28	242	74.38	5.00E-119
gene_id_29	342	84.21	2.00E-179
gene_id_30	64	62.5	1.00E-19
gene_id_31	134	59.7	2.00E-55
gene_id_32	116	55.17	2.00E-37
gene_id_33	100	61	6.00E-34
gene_id_34	174	44.25	1.00E-45
gene_id_35	387	70.8	0
gene_id_36	283	56.18	2.00E-119
gene_id_37	381	34.91	1.00E-46
gene_id_38	609	86.04	0
gene_id_39	445	75.06	0
gene_id_40	522	74.52	0
gene_id_41	299	45.82	6.00E-95
gene_id_42	270	77.04	2.00E-124
gene_id_43	356	69.94	0
gene_id_44	471	82.8	0
gene_id_45	405	87.41	0
gene_id_46	310	78.06	7.00E-165
gene_id_47	394	77.16	0
gene_id_48	289	78.89	5.00E-152
gene_id_49	402	70.4	3.00E-176

gene_id_50	344	75.87	0
gene_id_51	181	35.36	2.00E-32
gene_id_52	329	67.78	4.00E-162
gene_id_53	168	73.81	1.00E-83
gene_id_54	264	72.35	4.00E-141
gene_id_55	238	61.34	4.00E-102
gene_id_56	256	63.28	2.00E-113
gene_id_57	123	37.4	5.00E-22
gene_id_58	215	60.47	9.00E-93
gene_id_59	525	44.95	1.00E-133
gene_id_60	224	42.86	1.00E-59
gene_id_61	130	87.69	3.00E-75
gene_id_62	143	87.41	2.00E-87
gene_id_63	248	64.11	1.00E-117
gene_id_64	265	72.45	2.00E-128
gene_id_65	270	67.41	1.00E-133
gene_id_66	277	70.4	3.00E-141
gene_id_67	112	86.61	6.00E-64
gene_id_68	303	84.49	0
gene_id_69	208	79.81	2.00E-123
gene_id_70	115	93.04	8.00E-61
gene_id_71	123	94.31	3.00E-75
gene_id_72	72	95.83	7.00E-43
gene_id_73	94	58.51	2.00E-26
gene_id_74	236	85.17	1.00E-146
gene_id_75	209	84.21	2.00E-127
gene_id_76	418	87.8	0
gene_id_77	146	87.67	4.00E-69
gene_id_78	61	86.89	1.00E-29
gene_id_79	166	89.16	3.00E-101
gene_id_80	105	77.14	9.00E-54
gene_id_81	166	78.31	4.00E-81
gene_id_82	132	84.09	5.00E-78
gene_id_83	177	87.57	1.00E-109
gene_id_84	109	84.4	2.00E-51
gene_id_85	122	90.16	1.00E-73
gene_id_86	85	88.24	4.00E-47
gene_id_87	64	92.19	4.00E-33
gene_id_88	134	94.78	3.00E-86
gene_id_89	224	84.38	5.00E-137
gene_id_90	110	89.09	3.00E-64
gene_id_91	78	92.31	2.00E-46
gene_id_92	275	88.36	4.00E-179
gene_id_93	94	77.66	8.00E-49
gene_id_94	209	81.82	3.00E-122
gene_id_95	213	81.22	2.00E-94
gene_id_96	103	98.06	3.00E-66

gene_id_97	400	89	0
gene_id_98	677	88.63	0
gene_id_99	156	90.38	8.00E-100
gene_id_100	124	92.74	2.00E-77
gene_id_101	81	62.96	3.00E-26
gene_id_102	1298	86.21	0
gene_id_103	1248	86.06	0
gene_id_104	121	90.91	3.00E-39
gene_id_105	176	83.52	1.00E-100
gene_id_106	234	86.75	1.00E-132
gene_id_107	128	92.97	1.00E-79
gene_id_108	176	85.8	3.00E-99
gene_id_109	71	71.83	3.00E-28
gene_id_110	385	51.43	2.00E-101
gene_id_111	266	75.56	1.00E-140
gene_id_112	234	50.43	8.00E-65
gene_id_113	414	67.39	0
gene_id_114	358	72.07	0
gene_id_115	245	87.76	2.00E-152
gene_id_116	168	62.5	4.00E-68
gene_id_117	414	69.08	0
gene_id_118	248	75.81	3.00E-139
gene_id_119	227	76.21	5.00E-127
gene_id_120	160	67.5	3.00E-73
gene_id_121	481	75.68	0
gene_id_122	220	78.64	6.00E-123
gene_id_123	486	73.25	0
gene_id_124	74	52.7	3.00E-19
gene_id_125	394	65.23	2.00E-157
gene_id_127	368	83.42	0
gene_id_128	153	67.97	3.00E-70
gene_id_130	129	72.09	2.00E-67
gene_id_131	379	57.78	4.00E-148
gene_id_132	104	63.46	8.00E-39
gene_id_133	353	75.35	0
gene_id_134	455	73.85	0
gene_id_135	818	74.69	0
gene_id_136	348	67.53	7.00E-167
gene_id_137	172	63.37	1.00E-73
gene_id_138	147	57.14	1.00E-56
gene_id_139	394	75.63	0
gene_id_140	176	55.11	1.00E-69
gene_id_141	393	69.21	0
gene_id_142	311	76.21	9.00E-146
gene_id_144	149	82.55	2.00E-90
gene_id_145	162	75.93	4.00E-77
gene_id_146	188	74.47	5.00E-98

gene_id_147	88	55.68	4.00E-22
gene_id_148	291	32.3	4.00E-41
gene_id_149	107	62.62	2.00E-40
gene_id_150	214	69.63	1.00E-102
gene_id_151	265	63.4	1.00E-109
gene_id_152	148	75.68	6.00E-80
gene_id_153	758	77.97	0
gene_id_154	428	81.31	0
gene_id_155	263	58.17	1.00E-101
gene_id_156	253	54.94	6.00E-88
gene_id_157	103	66.99	6.00E-37
gene_id_158	251	49.8	6.00E-79
gene_id_159	197	53.3	4.00E-61
gene_id_160	237	62.87	2.00E-90
gene_id_161	179	72.07	2.00E-79
gene_id_162	668	68.11	0
gene_id_163	161	57.14	1.00E-62
gene_id_164	401	54.86	3.00E-150
gene_id_165	338	63.02	9.00E-142
gene_id_166	163	69.94	7.00E-84
gene_id_167	309	73.46	1.00E-156
gene_id_169	122	34.43	6.00E-12
gene_id_170	191	49.21	1.00E-58
gene_id_171	224	75	8.00E-109
gene_id_172	421	60.1	1.00E-168
gene_id_173	348	67.53	9.00E-155
gene_id_174	213	81.69	5.00E-123
gene_id_175	404	78.96	0
gene_id_176	116	50	2.00E-34
gene_id_177	310	63.23	5.00E-115
gene_id_178	490	66.12	0
gene_id_179	392	61.48	6.00E-158
gene_id_179	192	26.04	6.00E-06
gene_id_180	744	32.12	2.00E-44
gene_id_180	649	31.12	1.00E-42
gene_id_180	736	31.52	3.00E-42
gene_id_180	733	30.29	4.00E-39
gene_id_180	950	27.79	1.00E-36
gene_id_180	628	31.53	1.00E-31
gene_id_180	455	30.99	3.00E-20
gene_id_181	337	87.24	0
gene_id_182	311	91.32	0
gene_id_183	233	89.27	5.00E-151
gene_id_184	250	52.8	4.00E-94
gene_id_185	287	72.13	7.00E-146
gene_id_186	187	91.98	1.00E-124
gene_id_187	509	86.25	0

gene_id_189	452	84.73	0
gene_id_190	312	38.78	1.00E-60
gene_id_191	445	72.13	0
gene_id_192	355	55.77	2.00E-130
gene_id_193	295	66.78	4.00E-135
gene_id_194	148	49.32	2.00E-47
gene_id_195	338	55.92	2.00E-130
gene_id_196	283	68.55	2.00E-133
gene_id_197	194	88.66	2.00E-126
gene_id_198	662	87.01	0
gene_id_199	492	88.82	0
gene_id_201	233	57.51	7.00E-82
gene_id_202	503	52.49	0
gene_id_203	283	83.04	1.00E-175
gene_id_204	483	72.88	0
gene_id_205	118	49.15	3.00E-23
gene_id_207	434	67.05	0
gene_id_208	103	65.05	3.00E-43
gene_id_209	112	86.61	4.00E-65
gene_id_210	292	78.42	5.00E-168
gene_id_211	120	73.33	2.00E-57
gene_id_212	329	60.49	1.00E-150
gene_id_213	204	52.45	2.00E-64
gene_id_214	360	50.83	7.00E-111
gene_id_215	419	72.08	0
gene_id_216	232	52.59	1.00E-82
gene_id_217	139	58.27	1.00E-46
gene_id_218	197	45.18	3.00E-55
gene_id_219	368	68.21	2.00E-177
gene_id_220	276	80.07	1.00E-163
gene_id_221	278	78.06	5.00E-164
gene_id_222	392	66.58	0
gene_id_223	198	64.14	2.00E-96
gene_id_224	231	71.43	1.00E-115
gene_id_225	355	57.18	2.00E-129
gene_id_226	254	69.29	2.00E-128
gene_id_227	261	54.02	2.00E-69
gene_id_228	272	67.28	2.00E-95
gene_id_229	269	54.28	2.00E-99
gene_id_230	292	85.62	0
gene_id_231	99	49.49	1.00E-26
gene_id_233	181	65.19	3.00E-81
gene_id_234	123	77.24	5.00E-65
gene_id_235	609	56.98	0
gene_id_236	526	53.99	0
gene_id_237	206	74.27	3.00E-111
gene_id_238	327	68.81	5.00E-160

gene_id_239	302	66.56	1.00E-109
gene_id_240	131	75.57	1.00E-67
gene_id_241	488	75.61	0
gene_id_242	313	84.66	2.00E-154
gene_id_243	311	81.35	7.00E-160
gene_id_244	122	45.9	5.00E-29
gene_id_245	367	52.32	4.00E-102
gene_id_246	175	64	1.00E-74
gene_id_247	346	74.86	4.00E-175
gene_id_248	364	71.98	0
gene_id_249	180	90	1.00E-104
gene_id_250	248	69.35	5.00E-130
gene_id_251	353	48.16	2.00E-109
gene_id_252	81	38.27	7.00E-10
gene_id_253	372	87.1	0
gene_id_254	680	40.29	9.00E-146
gene_id_255	374	45.45	5.00E-109
gene_id_256	135	54.07	2.00E-40
gene_id_257	182	54.95	6.00E-66
gene_id_258	427	52.69	3.00E-118
gene_id_259	199	69.85	1.00E-89
gene_id_260	205	65.37	3.00E-75
gene_id_410	154	68.83	9.00E-71
gene_id_411	257	93.39	4.00E-176
gene_id_412	225	88	2.00E-140
gene_id_413	309	46.93	2.00E-87
gene_id_414	348	87.36	5.00E-172
gene_id_415	398	44.47	6.00E-114
gene_id_416	109	85.32	8.00E-60
gene_id_417	230	83.91	2.00E-142
gene_id_418	200	59.5	2.00E-79
gene_id_419	309	69.58	5.00E-158
gene_id_420	415	79.28	0
gene_id_421	457	73.3	0
gene_id_422	370	71.08	0
gene_id_423	367	82.83	7.00E-164
gene_id_424	427	62.06	7.00E-180
gene_id_425	324	82.41	2.00E-145
gene_id_426	453	59.16	2.00E-180
gene_id_427	496	69.56	0
gene_id_428	700	73.14	0
gene_id_429	150	52.67	1.00E-47
gene_id_430	301	70.76	3.00E-152
gene_id_431	143	79.02	1.00E-65
gene_id_432	151	68.87	8.00E-71
gene_id_433	62	80.65	4.00E-31
gene_id_434	54	53.7	4.00E-11

gene_id_435	642	58.1	0
gene_id_436	179	61.45	4.00E-50
gene_id_437	137	35.77	4.00E-15
gene_id_438	104	72.12	4.00E-50
gene_id_439	127	67.72	8.00E-62
gene_id_440	271	61.62	2.00E-95
gene_id_441	568	75.88	0
gene_id_442	353	77.34	0
gene_id_443	342	74.27	3.00E-180
gene_id_444	381	68.24	0
gene_id_445	274	61.31	9.00E-103
gene_id_446	238	74.37	1.00E-130
gene_id_447	34	88.24	4.00E-11
gene_id_448	49	65.31	8.00E-15
gene_id_449	186	80.11	1.00E-106
gene_id_450	244	88.52	3.00E-158
gene_id_451	214	84.58	4.00E-113
gene_id_452	234	92.74	8.00E-160
gene_id_453	167	40.12	2.00E-29
gene_id_454	118	44.07	2.00E-18
gene_id_455	538	63.2	0
gene_id_456	252	69.44	6.00E-117
gene_id_457	100	39	2.00E-15
gene_id_458	161	85.09	2.00E-87
gene_id_459	206	90.29	2.00E-129
gene_id_460	152	78.29	2.00E-70
gene_id_461	684	76.32	0
gene_id_462	351	71.79	0
gene_id_463	211	48.34	4.00E-66
gene_id_464	295	65.76	1.00E-122
gene_id_465	372	64.78	7.00E-154
gene_id_466	689	81.42	0
gene_id_467	378	67.2	4.00E-174
gene_id_468	256	66.8	8.00E-98
gene_id_469	89	79.78	4.00E-35
gene_id_470	252	77.78	6.00E-113
gene_id_471	165	54.55	4.00E-52
gene_id_472	120	91.67	1.00E-73
gene_id_473	373	73.19	0
gene_id_474	332	80.12	0
gene_id_475	159	74.84	2.00E-80
gene_id_476	64	82.81	2.00E-28
gene_id_477	424	53.54	4.00E-121
gene_id_478	131	63.36	1.00E-43
gene_id_479	182	36.81	4.00E-30
gene_id_480	181	55.25	4.00E-53
gene_id_481	203	46.31	5.00E-42

gene_id_482	172	59.88	2.00E-64
gene_id_483	146	37.67	8.00E-27
gene_id_484	438	81.96	0
gene_id_485	184	53.26	1.00E-61
gene_id_486	335	87.76	0
gene_id_487	514	69.26	0
gene_id_488	99	61.62	2.00E-33
gene_id_489	144	81.25	2.00E-79
gene_id_490	136	60.29	1.00E-51
gene_id_491	245	88.16	5.00E-154
gene_id_492	465	82.58	0
gene_id_493	176	86.36	1.00E-106
gene_id_494	433	75.52	0
gene_id_495	689	75.33	0
gene_id_496	361	60.94	7.00E-154
gene_id_497	354	54.24	4.00E-133
gene_id_498	161	59.01	8.00E-56
gene_id_499	120	66.67	4.00E-54
gene_id_500	397	69.02	0
gene_id_501	349	76.79	0
gene_id_571	130	66.15	3.00E-48
gene_id_572	195	64.62	4.00E-80
gene_id_574	68	77.94	1.00E-32
gene_id_575	363	52.89	5.00E-126
gene_id_576	203	40.39	9.00E-32
gene_id_577	756	31.88	6.00E-121
gene_id_578	370	49.73	3.00E-127
gene_id_579	399	48.37	8.00E-100
gene_id_580	60	68.33	1.00E-20
gene_id_581	639	45.7	0
gene_id_582	677	48.74	0
gene_id_584	258	58.91	4.00E-104
gene_id_587	48	56.25	3.00E-08
gene_id_588	59	64.41	9.00E-19
gene_id_589	74	47.3	1.00E-12
gene_id_590	156	75	1.00E-78
gene_id_591	102	49.02	4.00E-25
gene_id_592	106	43.4	2.00E-18
gene_id_593	53	45.28	3.00E-09
gene_id_594	91	36.26	6.00E-10
gene_id_595	208	65.87	3.00E-77
gene_id_596	393	44.02	3.00E-103
gene_id_598	172	37.21	4.00E-29
gene_id_600	209	80.86	1.00E-121
gene_id_601	221	81.9	5.00E-117
gene_id_602	270	82.59	7.00E-160
gene_id_603	239	80.75	8.00E-139

gene_id_604	635	74.49	0
gene_id_605	150	40	3.00E-26
gene_id_606	323	70.9	3.00E-153
gene_id_607	464	75.43	0
gene_id_608	390	69.49	0
gene_id_609	261	70.88	3.00E-137
gene_id_610	294	76.53	6.00E-166
gene_id_611	214	50.47	2.00E-63
gene_id_612	468	76.71	0
gene_id_613	347	78.1	0
gene_id_614	262	81.68	9.00E-140
gene_id_615	363	60.61	2.00E-141
gene_id_616	227	68.28	3.00E-109
gene_id_617	186	45.16	3.00E-53
gene_id_618	64	43.75	1.00E-09
gene_id_619	310	84.52	3.00E-164
gene_id_620	114	54.39	2.00E-35
gene_id_621	323	43.96	1.00E-69
gene_id_622	376	77.13	0
gene_id_623	253	83.4	4.00E-135
gene_id_624	213	83.1	3.00E-91
gene_id_625	353	80.17	0
gene_id_626	249	81.93	2.00E-147
gene_id_627	374	73.53	0
gene_id_628	326	66.56	8.00E-156
gene_id_629	324	78.7	0
gene_id_630	323	82.66	0
gene_id_631	292	68.15	2.00E-146
gene_id_632	370	57.57	8.00E-150
gene_id_633	291	64.6	7.00E-137
gene_id_634	263	46.77	1.00E-82
gene_id_635	254	70.47	3.00E-102
gene_id_636	390	58.21	5.00E-120
gene_id_637	655	61.37	0
gene_id_638	264	62.88	3.00E-125
gene_id_639	413	83.78	0
gene_id_640	283	63.25	1.00E-133
gene_id_642	565	68.67	0
gene_id_643	326	74.54	8.00E-172
gene_id_644	479	36.12	2.00E-87
gene_id_645	45	55.56	3.00E-09
gene_id_647	590	49.49	1.00E-167
gene_id_648	78	53.85	5.00E-24
gene_id_649	410	78.78	0
gene_id_651	154	42.86	4.00E-30
gene_id_652	188	36.17	1.00E-33
gene_id_653	366	82.51	0

gene_id_654	1039	83.45	0
gene_id_655	730	57.26	0
gene_id_658	56	60.71	5.00E-15
gene_id_659	90	52.22	2.00E-26
gene_id_660	105	67.62	5.00E-46
gene_id_661	124	49.19	5.00E-33
gene_id_662	77	67.53	4.00E-21
gene_id_664	91	54.95	2.00E-17
gene_id_665	148	60.81	4.00E-62
gene_id_690	83	75.9	6.00E-37
gene_id_691	158	36.08	6.00E-24
gene_id_692	152	75	6.00E-70
gene_id_693	670	84.93	0
gene_id_694	167	66.47	5.00E-71
gene_id_695	569	65.55	0
gene_id_696	267	61.05	2.00E-115
gene_id_697	374	83.96	0
gene_id_698	484	72.93	0
gene_id_699	101	82.18	1.00E-54
gene_id_700	362	79.83	0
gene_id_701	137	78.1	3.00E-75
gene_id_702	92	82.61	1.00E-47
gene_id_703	382	87.7	0
gene_id_704	543	86	0
gene_id_705	234	60.68	4.00E-97
gene_id_706	142	77.46	9.00E-70
gene_id_707	269	64.31	2.00E-101
gene_id_708	260	66.54	7.00E-119
gene_id_709	149	79.87	3.00E-84
gene_id_710	81	56.79	6.00E-27
gene_id_711	929	76.21	0
gene_id_712	95	65.26	1.00E-25
gene_id_713	175	77.14	2.00E-101
gene_id_714	193	63.73	2.00E-86
gene_id_715	222	59.01	3.00E-95
gene_id_716	31	87.1	9.00E-10
gene_id_717	136	70.59	4.00E-66
gene_id_718	301	68.11	3.00E-154
gene_id_719	171	83.04	7.00E-94
gene_id_720	586	52.73	0
gene_id_721	915	72.13	0
gene_id_722	277	71.12	1.00E-147
gene_id_723	173	53.76	9.00E-48
gene_id_724	290	72.76	1.00E-150
gene_id_725	88	93.18	1.00E-50
gene_id_726	202	73.76	6.00E-101
gene_id_727	68	83.82	3.00E-32

gene_id_728	395	72.91	0
gene_id_729	396	89.39	0
gene_id_730	70	71.43	5.00E-28
gene_id_731	810	57.9	0
gene_id_732	149	77.85	1.00E-79
gene_id_733	312	64.1	2.00E-144
gene_id_734	252	74.21	2.00E-121
gene_id_735	443	71.11	0
gene_id_736	344	64.83	2.00E-162
gene_id_737	251	56.57	2.00E-95
gene_id_738	136	44.85	2.00E-34
gene_id_739	238	57.56	5.00E-86
gene_id_740	422	61.61	2.00E-149
gene_id_741	440	62.95	0
gene_id_742	626	77.32	0
gene_id_743	291	72.16	1.00E-156
gene_id_744	217	71.89	1.00E-110
gene_id_745	376	67.02	9.00E-167
gene_id_746	217	70.51	1.00E-107
gene_id_747	402	82.34	0
gene_id_748	152	83.55	1.00E-90
gene_id_749	182	60.99	1.00E-81
gene_id_750	284	68.31	1.00E-124
gene_id_751	63	88.89	1.00E-33
gene_id_752	65	61.54	1.00E-21
gene_id_753	670	63.58	0
gene_id_754	65	70.77	1.00E-26
gene_id_755	219	76.26	9.00E-104
gene_id_756	172	27.91	2.00E-06
gene_id_757	60	80	2.00E-26
gene_id_758	119	74.79	9.00E-54
gene_id_759	483	87.37	0
gene_id_760	265	65.66	6.00E-122
gene_id_761	641	73.63	0
gene_id_762	232	65.95	1.00E-111
gene_id_763	210	79.05	5.00E-121
gene_id_764	223	75.34	2.00E-105
gene_id_765	427	84.31	0
gene_id_766	121	65.29	6.00E-54
gene_id_767	244	57.79	1.00E-99
gene_id_768	251	74.1	9.00E-134
gene_id_769	122	52.46	2.00E-22
gene_id_770	265	76.6	6.00E-150
gene_id_771	344	69.48	2.00E-159
gene_id_772	413	80.63	0
gene_id_773	217	60.37	1.00E-86
gene_id_774	426	74.65	0

gene_id_775	387	74.16	0
gene_id_776	115	82.61	2.00E-65
gene_id_777	191	68.59	7.00E-96
gene_id_778	353	75.64	0
gene_id_779	248	72.58	5.00E-139
gene_id_780	176	65.34	9.00E-78
gene_id_781	476	53.78	1.00E-179
gene_id_782	237	69.2	8.00E-119
gene_id_783	293	70.99	4.00E-153
gene_id_784	333	59.76	2.00E-141
gene_id_785	112	50	9.00E-27
gene_id_786	66	59.09	5.00E-21
gene_id_787	185	58.38	6.00E-72
gene_id_788	323	77.71	2.00E-179
gene_id_789	204	73.04	3.00E-99
gene_id_790	417	49.4	2.00E-149
gene_id_791	270	51.48	4.00E-84
gene_id_792	123	48.78	3.00E-37
gene_id_882	192	79.69	3.00E-101
gene_id_883	651	74.5	0
gene_id_884	135	48.15	6.00E-30
gene_id_885	106	78.3	1.00E-56
gene_id_886	194	44.33	1.00E-21
gene_id_887	176	77.27	2.00E-96
gene_id_888	788	63.83	0
gene_id_889	840	63.81	0
gene_id_890	205	66.83	3.00E-77
gene_id_891	78	66.67	3.00E-31
gene_id_892	462	87.45	0
gene_id_893	811	70.41	0
gene_id_894	340	82.65	0
gene_id_895	265	58.87	2.00E-106
gene_id_896	215	77.67	2.00E-118
gene_id_897	447	72.71	0
gene_id_898	277	72.92	6.00E-141
gene_id_899	117	89.74	8.00E-58
gene_id_900	65	89.23	4.00E-33
gene_id_901	154	86.36	1.00E-75
gene_id_902	633	81.36	0
gene_id_903	295	58.31	4.00E-120
gene_id_904	105	63.81	3.00E-41
gene_id_905	176	48.3	2.00E-45
gene_id_906	271	85.61	5.00E-149
gene_id_907	142	40.85	4.00E-26
gene_id_908	356	75.84	4.00E-178
gene_id_909	349	74.79	0
gene_id_910	174	40.23	1.00E-39

gene_id_912	224	80.36	3.00E-107
gene_id_913	148	71.62	2.00E-62
gene_id_914	241	48.96	5.00E-76
gene_id_915	183	69.4	4.00E-76
gene_id_916	215	75.35	4.00E-122
gene_id_917	354	70.06	1.00E-154
gene_id_918	246	58.94	2.00E-96
gene_id_919	403	63.77	0
gene_id_920	222	73.42	3.00E-120
gene_id_921	72	44.44	4.00E-11
gene_id_922	165	64.85	4.00E-67
gene_id_923	154	69.48	3.00E-73
gene_id_924	76	53.95	4.00E-19
gene_id_925	232	51.29	6.00E-83
gene_id_927	340	50.29	1.00E-99
gene_id_928	535	68.22	0
gene_id_929	138	36.23	2.00E-17
gene_id_930	571	44.83	2.00E-94
gene_id_931	100	61	7.00E-33
gene_id_932	342	40.94	4.00E-70
gene_id_933	208	50.48	2.00E-69
gene_id_934	80	65	8.00E-33
gene_id_935	403	48.64	6.00E-123
gene_id_936	284	60.56	3.00E-102
gene_id_937	413	83.54	0
gene_id_938	359	55.15	1.00E-140
gene_id_939	369	74.8	0
gene_id_940	99	74.75	3.00E-49
gene_id_941	66	68.18	1.00E-20
gene_id_942	471	63.91	0
gene_id_943	611	64.98	0
gene_id_944	208	63.94	4.00E-94
gene_id_945	438	73.74	0
gene_id_946	305	75.41	3.00E-163
gene_id_947	497	79.88	0
gene_id_948	319	77.74	9.00E-178
gene_id_949	441	79.37	0
gene_id_950	151	57.62	4.00E-48
gene_id_951	234	70.09	1.00E-113
gene_id_952	430	85.58	0
gene_id_954	710	61.27	0
gene_id_955	279	53.05	3.00E-100
gene_id_956	537	63.31	0
gene_id_957	214	39.25	2.00E-14
gene_id_958	279	74.19	1.00E-158
gene_id_959	723	74.83	0
gene_id_960	432	57.41	1.00E-158

gene_id_961	282	41.13	1.00E-51
gene_id_962	338	44.38	3.00E-84
gene_id_963	562	69.04	0
gene_id_964	252	67.86	1.00E-123
gene_id_965	600	90.5	0
gene_id_966	65	72.31	2.00E-13
gene_id_967	79	72.15	1.00E-33
gene_id_968	139	76.26	3.00E-75
gene_id_969	212	70.28	3.00E-100
gene_id_970	257	63.04	3.00E-123
gene_id_972	445	70.11	0
gene_id_973	259	68.34	1.00E-132
gene_id_974	364	76.65	0
gene_id_975	158	79.11	2.00E-78
gene_id_977	48	54.17	3.00E-10
gene_id_978	157	91.08	6.00E-97
gene_id_979	412	92.48	0
gene_id_981	104	88.46	4.00E-60
gene_id_983	178	92.7	5.00E-118
gene_id_984	284	81.34	1.00E-156
gene_id_985	364	77.2	0
gene_id_986	65	93.85	2.00E-25
gene_id_987	204	82.35	4.00E-122
gene_id_988	175	60.57	2.00E-61
gene_id_989	638	79.62	0
gene_id_990	372	43.82	6.00E-104
gene_id_991	257	81.71	7.00E-154
gene_id_992	246	73.58	6.00E-135
gene_id_993	464	78.45	0
gene_id_994	375	85.33	0
gene_id_995	269	82.53	2.00E-153
gene_id_996	146	41.78	5.00E-17
gene_id_996	68	52.94	5.00E-09
gene_id_996	68	52.94	5.00E-09
gene_id_996	73	50.68	2.00E-07
gene_id_996	60	58.33	5.00E-07
gene_id_998	885	56.27	0
gene_id_999	403	43.42	7.00E-110
gene_id_1000	58	48.28	8.00E-13
gene_id_1001	418	57.89	1.00E-141
gene_id_1002	566	55.3	2.00E-174
gene_id_1003	295	58.64	4.00E-127
gene_id_1004	257	72.76	3.00E-139
gene_id_1005	350	67.43	4.00E-164
gene_id_1006	300	63.67	9.00E-126
gene_id_1007	67	65.67	1.00E-25
gene_id_1008	355	80	0

gene_id_1009	245	85.31	2.00E-150
gene_id_1010	175	68.57	2.00E-85
gene_id_1011	227	66.08	1.00E-91
gene_id_1012	359	34.26	8.00E-69
gene_id_1013	1178	80.73	0
gene_id_1014	116	65.52	5.00E-13
gene_id_1015	66	39.39	1.00E-10
gene_id_1016	119	57.98	5.00E-23
gene_id_1016	127	49.61	9.00E-14
gene_id_1017	155	70.32	7.00E-74
gene_id_1018	327	80.12	3.00E-179
gene_id_1019	510	76.86	0
gene_id_1020	418	80.14	0
gene_id_1021	163	76.07	3.00E-87
gene_id_1022	349	74.21	0
gene_id_1023	552	61.05	0
gene_id_1024	75	60	2.00E-22
gene_id_1026	277	78.7	5.00E-161
gene_id_1027	369	79.95	0
gene_id_1028	515	40.97	1.00E-114
gene_id_1029	170	67.65	3.00E-62
gene_id_1030	438	76.71	0
gene_id_1031	129	59.69	3.00E-42
gene_id_1034	158	42.41	5.00E-32
gene_id_1035	61	54.1	4.00E-14
gene_id_1036	404	47.77	1.00E-114
gene_id_1128	389	64.78	9.00E-154
gene_id_1129	412	61.89	3.00E-174
gene_id_1130	362	78.45	0
gene_id_1131	239	82.43	2.00E-142
gene_id_1132	215	60.47	4.00E-94
gene_id_1133	187	54.01	6.00E-65
gene_id_1134	266	68.42	3.00E-127
gene_id_1135	181	67.4	1.00E-83
gene_id_1136	322	82.92	3.00E-174
gene_id_1137	274	84.67	5.00E-171
gene_id_1138	242	76.86	1.00E-132
gene_id_1139	377	72.41	0
gene_id_1140	429	65.73	0
gene_id_1141	574	77.7	0
gene_id_1142	383	71.54	0
gene_id_1143	267	73.03	4.00E-129
gene_id_1144	273	86.45	1.00E-174
gene_id_1145	140	80	4.00E-78
gene_id_1146	270	75.93	5.00E-138
gene_id_1147	257	77.04	9.00E-132
gene_id_1148	754	68.97	0

gene_id_1149	243	60.08	1.00E-109
gene_id_1150	186	80.11	1.00E-104
gene_id_1151	339	73.45	2.00E-174
gene_id_1152	121	79.34	7.00E-61
gene_id_1153	313	46.65	2.00E-59
gene_id_1154	157	75.8	4.00E-58
gene_id_1155	407	56.27	1.00E-176
gene_id_1156	588	76.36	0
gene_id_1157	196	50	5.00E-48
gene_id_1158	213	68.08	7.00E-101
gene_id_1159	1423	47.22	0
gene_id_1160	429	61.31	0
gene_id_1160	194	24.23	1.00E-11
gene_id_1161	423	68.79	0
gene_id_1162	252	73.81	5.00E-127
gene_id_1163	256	75.78	5.00E-107
gene_id_1164	572	61.19	0
gene_id_1165	81	59.26	3.00E-12
gene_id_1166	438	56.62	2.00E-169
gene_id_1167	125	54.4	1.00E-32
gene_id_1168	343	70.55	2.00E-153
gene_id_1169	199	63.32	2.00E-76
gene_id_1170	303	42.24	5.00E-81
gene_id_1171	262	82.44	9.00E-161
gene_id_1172	247	62.75	1.00E-97
gene_id_1173	342	89.77	0
gene_id_1174	87	83.91	1.00E-45
gene_id_1175	229	38.86	1.00E-45
gene_id_1176	291	70.45	3.00E-147
gene_id_1177	419	82.1	0
gene_id_1178	253	39.92	5.00E-48
gene_id_1179	91	73.63	1.00E-42
gene_id_1180	455	90.99	0
gene_id_1181	283	74.56	5.00E-142
gene_id_1182	500	85.8	0
gene_id_1183	184	61.96	5.00E-76
gene_id_1184	167	77.25	1.00E-70
gene_id_1185	53	96.23	6.00E-11
gene_id_1186	226	74.78	6.00E-86
gene_id_1187	116	45.69	1.00E-29
gene_id_1188	70	50	1.00E-19
gene_id_1189	388	78.35	0
gene_id_1190	342	85.96	0
gene_id_1191	218	70.64	2.00E-95
gene_id_1192	531	41.81	2.00E-140
gene_id_1193	187	67.91	1.00E-81
gene_id_1194	337	43.62	4.00E-82

gene_id_1195	791	63.34	0
gene_id_1196	76	68.42	8.00E-30
gene_id_1197	148	70.27	5.00E-76
gene_id_1198	219	67.58	3.00E-97
gene_id_1199	279	72.76	2.00E-140
gene_id_1200	266	60.9	2.00E-107
gene_id_1201	332	76.2	3.00E-139
gene_id_1202	302	57.28	8.00E-123
gene_id_1203	231	71	1.00E-116
gene_id_1204	305	64.26	3.00E-134
gene_id_1206	79	63.29	2.00E-29
gene_id_1207	249	73.9	2.00E-133
gene_id_1208	469	75.48	0
gene_id_1209	130	63.85	4.00E-50
gene_id_1210	246	39.84	9.00E-39
gene_id_1211	132	77.27	2.00E-65
gene_id_1212	215	65.12	5.00E-99
gene_id_1213	630	54.6	0
gene_id_1214	342	74.56	2.00E-151
gene_id_1215	360	63.33	7.00E-158
gene_id_1216	253	52.57	7.00E-85
gene_id_1217	297	57.58	1.00E-112
gene_id_1218	320	60	4.00E-145
gene_id_1219	418	50.24	2.00E-131
gene_id_1220	194	44.85	5.00E-49
gene_id_1221	77	53.25	1.00E-21
gene_id_1222	268	73.13	2.00E-140
gene_id_1223	347	65.99	8.00E-161
gene_id_1224	397	64.74	0
gene_id_1225	319	80.88	4.00E-131
gene_id_1226	1230	67.56	0
gene_id_1227	278	66.91	3.00E-128
gene_id_1228	699	44.92	0
gene_id_1229	665	46.02	0
gene_id_1230	371	70.89	0
gene_id_1231	728	83.65	0
gene_id_1232	708	53.25	0
gene_id_1233	177	74.58	3.00E-93
gene_id_1234	1251	66.27	0
gene_id_1236	563	57.37	0
gene_id_1237	140	70.71	9.00E-61
gene_id_1238	85	60	6.00E-29
gene_id_1239	95	72.63	5.00E-46
gene_id_1241	222	75.68	8.00E-111
gene_id_1242	888	60.81	0
gene_id_1243	167	62.28	1.00E-66
gene_id_1244	673	80.53	0

gene_id_1245	569	69.42	0
gene_id_1246	254	66.93	6.00E-114
gene_id_1247	208	79.33	4.00E-119
gene_id_1248	411	80.78	0
gene_id_1249	185	66.49	3.00E-66
gene_id_1250	144	83.33	3.00E-71
gene_id_1251	137	56.2	2.00E-46
gene_id_1252	174	68.39	1.00E-48
gene_id_1253	348	66.95	3.00E-161
gene_id_1254	286	66.43	8.00E-132
gene_id_1255	355	80	0
gene_id_1256	284	78.87	2.00E-160
gene_id_1257	65	86.15	3.00E-35
gene_id_1258	411	71.29	0
gene_id_1259	277	71.48	1.00E-125
gene_id_1260	293	43.69	1.00E-84
gene_id_1261	276	73.19	3.00E-144
gene_id_1262	257	59.14	3.00E-101
gene_id_1263	186	68.28	2.00E-90
gene_id_1264	274	68.61	6.00E-128
gene_id_1265	208	67.79	1.00E-99
gene_id_1266	316	84.49	0
gene_id_1267	453	76.16	0
gene_id_1268	396	75	0
gene_id_1269	269	76.58	2.00E-133
gene_id_1270	360	60.83	2.00E-166
gene_id_1271	301	65.12	4.00E-139
gene_id_1272	320	78.75	0
gene_id_1273	251	68.92	1.00E-128
gene_id_1274	223	82.96	1.00E-112
gene_id_1275	288	62.85	3.00E-98
gene_id_1276	148	76.35	2.00E-74
gene_id_1277	861	66.55	0
gene_id_1278	269	72.86	5.00E-140
gene_id_1279	258	56.98	6.00E-103
gene_id_1280	281	71.89	9.00E-139
gene_id_1281	230	71.3	6.00E-78
gene_id_1282	36	80.56	3.00E-10
gene_id_1283	78	38.46	4.00E-08
gene_id_1284	36	58.33	5.00E-06
gene_id_1288	149	41.61	1.00E-27
gene_id_1289	292	79.45	1.00E-173
gene_id_1290	262	83.59	1.00E-164
gene_id_1291	279	74.91	2.00E-148
gene_id_1292	174	74.71	2.00E-94
gene_id_1293	327	60.86	7.00E-135
gene_id_1294	253	75.49	1.00E-138

gene_id_1295	643	82.12	0
gene_id_1296	84	88.1	2.00E-45
gene_id_1297	261	67.05	5.00E-121
gene_id_1298	236	65.25	1.00E-98
gene_id_1299	261	78.54	4.00E-150
gene_id_1300	326	54.91	7.00E-109
gene_id_1301	147	66.67	2.00E-63
gene_id_1302	217	71.43	2.00E-112
gene_id_1303	477	79.45	0
gene_id_1305	280	36.07	3.00E-42
gene_id_1306	309	54.69	9.00E-107
gene_id_1307	311	57.88	5.00E-113
gene_id_1308	241	69.29	2.00E-110
gene_id_1309	240	51.67	3.00E-71
gene_id_1310	197	48.73	2.00E-60
gene_id_1311	1420	63.45	0
gene_id_1312	115	70.43	2.00E-52
gene_id_1313	373	70.78	8.00E-159
gene_id_1314	381	57.22	1.00E-131
gene_id_1315	378	76.72	0
gene_id_1316	457	58.86	2.00E-174
gene_id_1317	183	54.1	2.00E-52
gene_id_1319	52	63.46	7.00E-12
gene_id_1320	319	60.19	2.00E-143
gene_id_1322	77	50.65	1.00E-19
gene_id_1324	222	88.29	4.00E-143
gene_id_1325	395	49.87	3.00E-135
gene_id_1326	244	82.38	3.00E-150
gene_id_1327	141	77.3	1.00E-77
gene_id_1328	61	68.85	4.00E-21
gene_id_1769	302	62.91	2.00E-140
gene_id_1770	244	38.93	2.00E-44
gene_id_1771	106	65.09	8.00E-44
gene_id_1772	86	82.56	4.00E-44
gene_id_1773	123	62.6	4.00E-50
gene_id_1774	600	60.67	0
gene_id_1775	301	57.14	2.00E-110
gene_id_1777	151	62.91	1.00E-64
gene_id_1778	78	44.87	4.00E-16
gene_id_1780	627	49.6	0
gene_id_1781	559	82.65	0
gene_id_1782	151	80.13	5.00E-88
gene_id_1783	537	78.77	0
gene_id_1784	95	76.84	2.00E-48
gene_id_1785	407	64.62	0
gene_id_1786	102	56.86	1.00E-41
gene_id_1788	130	50.77	6.00E-24

gene_id_1789	94	54.26	5.00E-25
gene_id_1790	174	69.54	7.00E-84
gene_id_1791	312	67.95	7.00E-140
gene_id_1792	433	39.03	9.00E-86
gene_id_1793	305	65.9	3.00E-135
gene_id_1794	68	64.71	4.00E-10
gene_id_1795	271	70.85	4.00E-105
gene_id_1795	303	56.11	3.00E-91
gene_id_1795	126	34.13	8.00E-08
gene_id_1796	263	78.33	2.00E-148
gene_id_1797	293	81.91	5.00E-168
gene_id_1798	292	83.22	4.00E-178
gene_id_1799	173	42.2	1.00E-40
gene_id_1800	63	38.1	6.00E-09
gene_id_1801	261	33.72	4.00E-24
gene_id_1802	115	73.91	6.00E-53
gene_id_1803	77	59.74	3.00E-22
gene_id_1804	117	38.46	8.00E-23
gene_id_1805	60	63.33	2.00E-17
gene_id_1806	444	50.9	5.00E-157
gene_id_1807	218	59.63	5.00E-76
gene_id_1808	661	62.03	0
gene_id_1809	182	57.14	1.00E-70
gene_id_1810	371	40.7	1.00E-80
gene_id_1811	419	83.53	0
gene_id_1813	205	43.41	1.00E-40
gene_id_1814	200	62.5	7.00E-85
gene_id_1815	293	59.04	1.00E-125
gene_id_1816	156	58.33	7.00E-47
gene_id_1817	779	86.26	0
gene_id_1818	603	66.5	0
gene_id_1819	119	77.31	5.00E-60
gene_id_1821	228	63.6	1.00E-100
gene_id_1822	89	76.4	1.00E-35
gene_id_1823	245	53.06	1.00E-78
gene_id_1824	420	55.48	6.00E-156
gene_id_1825	349	55.3	7.00E-129
gene_id_1826	68	77.94	1.00E-29
gene_id_1827	215	56.74	3.00E-74
gene_id_1828	83	57.83	4.00E-13
gene_id_1829	77	54.55	8.00E-21
gene_id_1830	483	70.6	0
gene_id_1831	185	78.92	3.00E-101
gene_id_1833	61	49.18	2.00E-10
gene_id_1834	774	78.04	0
gene_id_1835	120	68.33	1.00E-52
gene_id_1836	35	65.71	4.00E-07

gene_id_1837	209	75.6	4.00E-98
gene_id_1838	50	58	1.00E-10
gene_id_1839	460	68.26	0
gene_id_1840	803	75.47	0
gene_id_1841	83	50.6	1.00E-23
gene_id_1842	226	66.81	1.00E-83
gene_id_1843	477	81.34	0
gene_id_1844	487	82.96	0
gene_id_1845	96	78.12	2.00E-46
gene_id_1846	89	66.29	2.00E-27
gene_id_1847	571	46.58	4.00E-170
gene_id_1848	689	61.54	0
gene_id_1850	287	47.04	3.00E-84
gene_id_1851	742	61.73	0
gene_id_1852	129	64.34	3.00E-49
gene_id_1853	748	71.39	0
gene_id_1854	293	49.49	5.00E-94
gene_id_1855	541	65.43	0
gene_id_1856	237	54.85	4.00E-86
gene_id_1857	310	69.35	9.00E-152
gene_id_1859	145	79.31	2.00E-76
gene_id_1860	411	54.01	6.00E-144
gene_id_1861	244	62.7	1.00E-100
gene_id_1862	217	76.96	9.00E-122
gene_id_1863	252	88.1	8.00E-163
gene_id_1864	241	77.18	9.00E-118
gene_id_1865	200	73.5	1.00E-100
gene_id_1866	195	72.31	1.00E-92
gene_id_1867	349	61.89	2.00E-144
gene_id_1868	446	74.66	0
gene_id_1869	220	85.45	1.00E-132
gene_id_1870	315	66.03	4.00E-152
gene_id_1871	175	60	4.00E-74
gene_id_1872	393	70.23	0
gene_id_1873	99	81.82	5.00E-54
gene_id_1874	702	92.59	0
gene_id_1875	513	72.9	0
gene_id_1876	352	64.77	7.00E-116
gene_id_1877	195	67.18	3.00E-93
gene_id_1878	318	60.69	2.00E-137
gene_id_1879	191	67.02	2.00E-88
gene_id_1880	220	52.27	3.00E-56
gene_id_1881	966	64.6	0
gene_id_1882	170	52.94	8.00E-30
gene_id_1883	423	69.27	0
gene_id_1884	515	74.17	0
gene_id_1885	200	63	3.00E-94

gene_id_1886	355	76.9	0
gene_id_1887	474	78.06	0
gene_id_1888	236	80.51	8.00E-136
gene_id_1889	160	73.12	2.00E-69
gene_id_1890	456	86.18	0
gene_id_1892	402	68.91	0
gene_id_1893	152	70.39	7.00E-62
gene_id_1894	513	84.02	0
gene_id_1895	273	81.68	9.00E-168
gene_id_1896	339	76.11	0
gene_id_1897	279	57.71	2.00E-107
gene_id_1898	363	73.83	0
gene_id_1899	246	83.74	9.00E-155
gene_id_1900	203	43.35	6.00E-62
gene_id_1901	513	62.77	0
gene_id_1902	526	90.3	0
gene_id_1903	94	89.36	1.00E-51
gene_id_1904	193	86.53	2.00E-109
gene_id_1905	472	72.67	0
gene_id_1906	344	77.33	3.00E-177
gene_id_1907	66	86.36	1.00E-34
gene_id_1908	144	66.67	2.00E-55
gene_id_1909	212	62.74	3.00E-99
gene_id_1910	159	61.64	9.00E-66
gene_id_1911	330	67.58	6.00E-147
gene_id_1912	433	76.44	0
gene_id_1913	180	63.33	5.00E-69
gene_id_1914	361	59.56	7.00E-143
gene_id_1914	122	48.36	4.00E-24
gene_id_1915	73	50.68	1.00E-16
gene_id_1916	278	58.99	2.00E-119
gene_id_1917	116	83.62	7.00E-67
gene_id_1918	84	83.33	3.00E-40
gene_id_1919	515	63.69	0
gene_id_1920	106	66.04	2.00E-41
gene_id_1921	664	58.58	0
gene_id_1922	271	63.1	2.00E-120
gene_id_1923	902	47.23	0
gene_id_1924	237	65.4	1.00E-92
gene_id_1925	235	78.3	2.00E-108
gene_id_1926	190	56.32	1.00E-75
gene_id_1927	339	67.85	2.00E-168
gene_id_1928	342	74.27	0
gene_id_1929	170	56.47	9.00E-38
gene_id_1930	323	79.26	0
gene_id_1931	303	80.2	0
gene_id_1932	233	77.68	1.00E-122

gene_id_1933	466	67.6	0
gene_id_1934	267	75.66	3.00E-152
gene_id_1935	342	73.1	0
gene_id_1935	122	32.79	3.00E-10
gene_id_1936	569	90.16	0
gene_id_1937	61	68.85	2.00E-22
gene_id_1938	163	71.78	2.00E-72
gene_id_1939	691	60.78	0
gene_id_1940	146	58.9	2.00E-48
gene_id_1941	126	78.57	2.00E-66
gene_id_1942	315	73.65	2.00E-155
gene_id_1943	1217	86.2	0
gene_id_1944	472	66.74	0
gene_id_1946	381	62.47	0
gene_id_1947	188	63.83	1.00E-83
gene_id_1948	552	88.95	0
gene_id_1949	307	68.73	2.00E-145
gene_id_1950	267	44.57	8.00E-60
gene_id_1951	343	83.09	0
gene_id_1952	224	70.09	4.00E-112
gene_id_1953	270	87.78	1.00E-179
gene_id_1954	481	82.95	0
gene_id_1957	680	89.71	0
gene_id_1958	520	76.54	0
gene_id_1959	339	75.22	0
gene_id_1960	342	72.22	0
gene_id_1961	308	66.56	1.00E-100
gene_id_1962	186	72.04	2.00E-90
gene_id_1963	170	80.59	1.00E-100
gene_id_1964	123	54.47	3.00E-49
gene_id_1965	295	40.34	3.00E-76
gene_id_1966	388	87.11	0
gene_id_1967	291	53.95	2.00E-110
gene_id_1968	265	73.96	5.00E-142
gene_id_1969	155	86.45	3.00E-83
gene_id_1970	703	84.5	0
gene_id_1971	199	67.34	5.00E-97
gene_id_1972	851	88.95	0
gene_id_1973	296	80.41	5.00E-175
gene_id_1974	206	53.4	2.00E-76
gene_id_1975	354	51.41	6.00E-118
gene_id_1976	204	69.61	5.00E-107
gene_id_1977	199	53.27	4.00E-63
gene_id_1978	293	84.98	1.00E-171
gene_id_1979	78	42.31	3.00E-16
gene_id_1980	218	49.08	4.00E-47
gene_id_1981	211	70.62	3.00E-92

gene_id_1982	195	51.28	3.00E-59
gene_id_1983	510	55.69	0
gene_id_1984	244	68.85	6.00E-123
gene_id_1985	144	52.78	2.00E-37
gene_id_1986	401	62.09	2.00E-173
gene_id_1988	464	62.5	0
gene_id_1989	159	77.36	6.00E-89
gene_id_1990	150	70.67	6.00E-63
gene_id_1992	384	62.5	1.00E-168
gene_id_1994	495	74.75	0
gene_id_1995	136	65.44	6.00E-63
gene_id_1996	323	66.56	3.00E-156
gene_id_1997	265	32.45	2.00E-34
gene_id_1998	131	75.57	4.00E-66
gene_id_1999	250	58	4.00E-86
gene_id_2000	165	61.82	9.00E-43
gene_id_2001	184	58.7	1.00E-63
gene_id_2002	255	61.57	3.00E-95
gene_id_2003	165	64.85	4.00E-65
gene_id_2004	163	70.55	1.00E-84
gene_id_2005	556	77.7	0
gene_id_2006	89	84.27	4.00E-47
gene_id_2007	153	67.32	6.00E-61
gene_id_2008	248	81.05	6.00E-147
gene_id_2009	250	79.6	5.00E-142
gene_id_2010	317	75.71	7.00E-178
gene_id_2012	237	42.19	3.00E-09
gene_id_2013	462	55.41	1.00E-157
gene_id_2014	393	70.48	0
gene_id_2015	490	65.1	0
gene_id_2016	136	55.15	1.00E-48
gene_id_2017	213	52.11	5.00E-72
gene_id_2018	253	71.15	7.00E-125
gene_id_2019	636	70.75	0
gene_id_2020	160	50	6.00E-51
gene_id_2021	136	63.97	3.00E-51
gene_id_2022	159	47.17	3.00E-34
gene_id_2023	631	78.13	0
gene_id_2025	451	63.19	0
gene_id_2026	293	78.16	2.00E-170
gene_id_2027	291	80.07	6.00E-172
gene_id_2028	42	71.43	4.00E-11
gene_id_2029	212	36.32	3.00E-36
gene_id_2030	166	62.65	3.00E-67
gene_id_2031	66	59.09	4.00E-16
gene_id_2033	220	45.91	4.00E-63
gene_id_2034	546	85.16	0

gene_id_2035	521	74.47	0
gene_id_2036	373	69.97	0
gene_id_2037	372	66.4	1.00E-154
gene_id_2038	297	72.39	4.00E-159
gene_id_2040	385	32.99	1.00E-49
gene_id_2041	331	59.52	8.00E-150
gene_id_2042	295	40	1.00E-64
gene_id_2044	190	48.95	1.00E-60
gene_id_2045	290	41.03	1.00E-58
gene_id_2046	314	90.45	0
gene_id_2047	134	90.3	6.00E-84
gene_id_2048	341	43.11	1.00E-85
gene_id_2049	106	83.96	6.00E-58
gene_id_2050	88	75	1.00E-39
gene_id_2051	99	35.35	3.00E-07
gene_id_2052	409	61.86	0
gene_id_2054	261	30.27	3.00E-24
gene_id_2061	280	49.29	1.00E-82
gene_id_2062	68	44.12	2.00E-11
gene_id_2063	82	48.78	5.00E-17
gene_id_2065	66	56.06	9.00E-17
gene_id_2066	163	62.58	3.00E-70
gene_id_2067	225	74.67	3.00E-114
gene_id_2068	264	76.89	8.00E-147
gene_id_2069	164	75.61	5.00E-80
gene_id_2070	152	75.66	3.00E-49
gene_id_2071	1064	88.53	0
gene_id_2072	381	80.84	0
gene_id_2073	426	79.58	0
gene_id_2074	137	67.88	8.00E-53
gene_id_2075	754	61.27	0
gene_id_2076	106	76.42	1.00E-52
gene_id_2077	115	83.48	4.00E-65
gene_id_2078	242	57.02	2.00E-92
gene_id_2079	144	59.72	3.00E-47
gene_id_2080	391	48.34	6.00E-113
gene_id_2081	290	61.03	7.00E-129
gene_id_2082	196	72.96	1.00E-90
gene_id_2083	247	79.76	3.00E-141
gene_id_2084	217	44.7	1.00E-49
gene_id_2085	389	67.61	0
gene_id_2086	228	85.09	2.00E-116
gene_id_2087	121	72.73	1.00E-57
gene_id_2089	775	72.39	0
gene_id_2090	114	75.44	2.00E-56
gene_id_2091	347	84.44	0
gene_id_2092	188	65.96	3.00E-85

gene_id_2093	80	62.5	8.00E-25
gene_id_2094	78	65.38	8.00E-27
gene_id_2095	126	51.59	9.00E-35
gene_id_2096	302	61.26	6.00E-113
gene_id_2097	165	67.27	1.00E-77
gene_id_2098	224	68.3	3.00E-85
gene_id_2099	379	60.95	1.00E-169
gene_id_2100	393	73.79	0
gene_id_2101	462	69.05	0
gene_id_2102	295	71.53	2.00E-147
gene_id_2103	256	86.33	2.00E-161
gene_id_2104	220	50.45	1.00E-78
gene_id_2105	794	70.15	0
gene_id_2106	308	61.69	8.00E-132
gene_id_2107	238	66.81	2.00E-114
gene_id_2108	624	75.16	0
gene_id_2109	458	66.81	0
gene_id_2110	208	69.71	4.00E-87
gene_id_2111	208	75	5.00E-84
gene_id_2112	68	76.47	2.00E-32
gene_id_2113	115	66.96	2.00E-45
gene_id_2114	515	71.65	0
gene_id_2115	369	75.34	0
gene_id_2116	68	64.71	1.00E-22
gene_id_2117	365	71.78	0
gene_id_2118	277	46.21	2.00E-79
gene_id_2119	79	68.35	3.00E-29
gene_id_2120	628	84.08	0
gene_id_2121	111	37.84	3.00E-19
gene_id_2122	202	62.87	1.00E-92
gene_id_2123	96	75	2.00E-39
gene_id_2124	80	48.75	2.00E-16
gene_id_2125	188	53.72	7.00E-31
gene_id_2126	148	68.92	3.00E-69
gene_id_2128	133	52.63	2.00E-40
gene_id_2129	198	48.99	2.00E-57
gene_id_2130	303	62.38	7.00E-136
gene_id_2131	295	64.41	4.00E-140
gene_id_2132	296	65.88	2.00E-134
gene_id_2133	374	72.46	0
gene_id_2134	259	58.69	3.00E-113
gene_id_2135	176	63.07	2.00E-73
gene_id_2136	80	48.75	4.00E-19
gene_id_2137	119	68.91	2.00E-55
gene_id_2138	704	63.49	0
gene_id_2139	132	46.21	4.00E-32
gene_id_2140	261	72.41	5.00E-135

gene_id_2141	233	57.51	2.00E-69
gene_id_2142	298	69.8	8.00E-154
gene_id_2143	163	71.17	9.00E-71
gene_id_2144	248	62.1	1.00E-109
gene_id_2145	363	65.29	8.00E-161
gene_id_2146	238	66.81	2.00E-113
gene_id_2147	462	70.78	0
gene_id_2148	479	63.88	0
gene_id_2149	317	37.22	4.00E-65
gene_id_2150	290	56.9	3.00E-121
gene_id_2151	225	54.22	3.00E-84
gene_id_2152	569	57.12	0
gene_id_2153	373	37.53	2.00E-65
gene_id_2154	551	51.36	0
gene_id_2155	904	60.73	0
gene_id_2156	100	74	1.00E-43
gene_id_2157	350	54.86	4.00E-141
gene_id_2158	812	33.13	1.00E-120
gene_id_2159	490	55.71	0
gene_id_2160	222	68.47	1.00E-103
gene_id_2161	419	44.15	1.00E-126
gene_id_2162	143	82.52	9.00E-70
gene_id_2163	254	70.08	4.00E-96
gene_id_2164	640	81.88	0
gene_id_2165	406	66.26	0
gene_id_2166	432	74.31	0
gene_id_2167	197	60.91	2.00E-63
gene_id_2168	199	73.87	6.00E-82
gene_id_2169	811	84.83	0
gene_id_2170	376	59.84	6.00E-157
gene_id_2171	1028	71.01	0
gene_id_2172	360	41.39	1.00E-68
gene_id_2173	396	69.95	0
gene_id_2174	283	76.68	1.00E-146
gene_id_2175	518	84.75	0
gene_id_2176	402	46.02	3.00E-114
gene_id_2177	283	67.84	3.00E-136
gene_id_2178	333	69.97	8.00E-167
gene_id_2318	101	63.37	1.00E-26
gene_id_2319	148	61.49	1.00E-62
gene_id_2320	374	63.1	2.00E-146
gene_id_2321	438	41.32	2.00E-108
gene_id_2322	583	71.7	0
gene_id_2323	66	83.33	2.00E-33
gene_id_2324	192	69.79	1.00E-77
gene_id_2325	1134	74.43	0
gene_id_2326	277	63.9	9.00E-126

gene_id_2327	656	65.4	0
gene_id_2328	410	83.41	0
gene_id_2329	94	54.26	9.00E-25
gene_id_2330	86	72.09	3.00E-41
gene_id_2331	448	64.29	0
gene_id_2332	495	73.54	0
gene_id_2333	342	66.08	7.00E-163
gene_id_2334	243	68.72	2.00E-95
gene_id_2335	262	67.18	4.00E-116
gene_id_2336	331	73.11	0
gene_id_2337	213	75.59	3.00E-118
gene_id_2338	556	56.47	0
gene_id_2339	339	66.08	6.00E-170
gene_id_2340	340	75	0
gene_id_2341	218	72.02	5.00E-111
gene_id_2342	197	62.44	7.00E-87
gene_id_2343	159	74.84	6.00E-72
gene_id_2344	117	64.96	5.00E-39
gene_id_2345	238	55.46	5.00E-89
gene_id_2346	563	62.7	0
gene_id_2347	160	79.38	2.00E-88
gene_id_2348	430	84.88	0
gene_id_2349	147	58.5	1.00E-58
gene_id_2350	66	63.64	2.00E-20
gene_id_2351	209	45.45	2.00E-55
gene_id_2352	429	74.13	0
gene_id_2353	101	52.48	1.00E-30
gene_id_2354	368	72.83	0
gene_id_2355	319	71.16	2.00E-164
gene_id_2356	330	75.45	0
gene_id_2357	259	86.49	1.00E-165
gene_id_2358	314	82.17	3.00E-155
gene_id_2360	364	77.75	0
gene_id_2361	275	89.82	1.00E-180
gene_id_2362	219	62.56	2.00E-95
gene_id_2363	392	54.34	3.00E-149
gene_id_2364	467	58.46	1.00E-175
gene_id_2365	293	75.43	4.00E-156
gene_id_2366	309	86.73	6.00E-173
gene_id_2367	502	83.07	0
gene_id_2368	433	80.14	0
gene_id_2369	355	70.7	1.00E-173
gene_id_2370	170	61.76	4.00E-74
gene_id_2371	280	73.93	1.00E-138
gene_id_2372	390	79.74	0
gene_id_2373	67	61.19	2.00E-22
gene_id_2374	506	55.93	0

gene_id_2377	278	52.88	6.00E-95
gene_id_2378	255	66.67	3.00E-126
gene_id_2379	234	58.97	4.00E-85
gene_id_2380	438	81.51	0
gene_id_2381	488	84.84	0
gene_id_2382	341	73.02	2.00E-145
gene_id_2383	307	70.03	1.00E-136
gene_id_2384	285	67.37	2.00E-117
gene_id_2385	256	74.61	3.00E-117
gene_id_2386	420	71.19	0
gene_id_2387	291	90.72	1.00E-164
gene_id_2388	220	64.09	2.00E-80
gene_id_2389	101	57.43	1.00E-33
gene_id_2390	291	62.2	5.00E-124
gene_id_2391	140	58.57	7.00E-27
gene_id_2394	477	41.3	3.00E-92
gene_id_2395	139	66.19	2.00E-51
gene_id_2396	98	70.41	2.00E-45
gene_id_2397	146	48.63	6.00E-37
gene_id_2398	569	64.85	0
gene_id_2399	601	82.53	0
gene_id_2400	531	72.69	0
gene_id_2401	301	66.45	5.00E-145
gene_id_2402	115	66.96	4.00E-48
gene_id_2403	285	70.53	6.00E-153
gene_id_2404	151	80.13	5.00E-85
gene_id_2405	385	64.16	0
gene_id_2406	550	79.45	0
gene_id_2407	302	47.02	5.00E-81
gene_id_2408	276	71.74	3.00E-152
gene_id_2410	93	68.82	4.00E-35
gene_id_2411	470	75.11	0
gene_id_2412	330	82.12	1.00E-179
gene_id_2413	507	68.24	0
gene_id_2413	225	32	4.00E-15
gene_id_2414	337	83.98	0
gene_id_2415	222	72.52	4.00E-119
gene_id_2416	150	72.67	1.00E-76
gene_id_2417	207	77.29	3.00E-117
gene_id_2418	452	89.6	0
gene_id_2419	89	82.02	3.00E-33
gene_id_2421	302	66.89	7.00E-151
gene_id_2422	247	57.49	3.00E-103
gene_id_2424	287	68.99	2.00E-144
gene_id_2425	54	68.52	1.00E-15
gene_id_2426	384	59.64	3.00E-117
gene_id_2427	125	66.4	7.00E-58

gene_id_2428	77	57.14	3.00E-24
gene_id_2429	757	55.75	0
gene_id_2430	433	72.06	6.00E-178
gene_id_2431	454	67.4	0
gene_id_2432	451	82.48	0
gene_id_2433	554	71.12	0
gene_id_2434	330	81.21	7.00E-169
gene_id_2435	208	70.67	7.00E-111
gene_id_2436	59	50.85	1.00E-12
gene_id_2437	414	71.26	0
gene_id_2438	430	78.6	0
gene_id_2439	67	88.06	2.00E-35
gene_id_2440	264	45.83	3.00E-70
gene_id_2441	409	78	0
gene_id_2442	130	81.54	3.00E-70
gene_id_2443	374	43.32	1.00E-102
gene_id_2444	416	84.86	0
gene_id_2445	164	75.61	3.00E-74
gene_id_2446	107	63.55	9.00E-41
gene_id_2447	57	68.42	5.00E-09
gene_id_2448	123	60.16	1.00E-38
gene_id_2449	132	74.24	9.00E-51
gene_id_2450	311	66.88	5.00E-143
gene_id_2451	293	60.07	1.00E-125
gene_id_2452	818	79.46	0
gene_id_2453	421	78.15	0
gene_id_2454	110	76.36	2.00E-56
gene_id_2455	582	85.74	0
gene_id_2456	179	36.87	8.00E-38
gene_id_2457	622	80.23	0
gene_id_2458	330	70.3	2.00E-165
gene_id_2459	328	78.35	1.00E-179
gene_id_2460	560	50.54	1.00E-141
gene_id_2461	157	56.05	5.00E-62
gene_id_2462	113	61.06	2.00E-43
gene_id_2463	109	68.81	4.00E-52
gene_id_2465	416	81.97	0
gene_id_2466	99	72.73	5.00E-45
gene_id_2467	275	68	2.00E-85
gene_id_2468	293	67.24	2.00E-144
gene_id_2469	480	67.29	0
gene_id_2470	192	64.58	1.00E-78
gene_id_2471	310	60.65	8.00E-105
gene_id_2472	136	59.56	8.00E-39
gene_id_2472	134	35.82	1.00E-12
gene_id_2473	156	63.46	2.00E-63
gene_id_2474	198	66.67	5.00E-94

gene_id_2475	331	59.52	3.00E-146
gene_id_2476	785	69.04	0
gene_id_2477	254	82.28	2.00E-154
gene_id_2478	99	61.62	1.00E-35
gene_id_2479	257	59.14	2.00E-105
gene_id_2480	396	81.06	0
gene_id_2481	408	73.53	0
gene_id_2482	211	75.36	1.00E-115
gene_id_2483	106	69.81	5.00E-45
gene_id_2484	363	63.64	5.00E-174
gene_id_2485	98	77.55	5.00E-26
gene_id_2486	234	70.94	3.00E-110
gene_id_2487	184	64.67	2.00E-84
gene_id_2488	145	60.69	2.00E-55
gene_id_2489	1180	79.49	0
gene_id_2490	248	66.13	3.00E-119
gene_id_2491	308	67.21	6.00E-146
gene_id_2492	332	77.41	1.00E-138
gene_id_2493	340	70.59	1.00E-153
gene_id_2494	268	72.76	1.00E-136
gene_id_2495	244	64.75	1.00E-111
gene_id_2496	687	62.59	0
gene_id_2497	332	83.73	6.00E-172
gene_id_2498	209	76.08	2.00E-99
gene_id_2499	132	68.94	3.00E-39
gene_id_2500	87	67.82	4.00E-24
gene_id_2501	575	57.22	0
gene_id_2502	230	75.22	6.00E-121
gene_id_2503	205	41.46	9.00E-40
gene_id_2504	354	63.84	4.00E-167
gene_id_2505	139	58.27	2.00E-59
gene_id_2506	271	42.07	3.00E-65
gene_id_2507	76	52.63	6.00E-19
gene_id_2508	215	64.19	3.00E-88
gene_id_2509	136	73.53	1.00E-67
gene_id_2510	206	36.89	7.00E-22
gene_id_2511	358	66.2	1.00E-139
gene_id_2512	180	77.78	2.00E-102
gene_id_2513	421	52.02	6.00E-130
gene_id_2514	429	75.06	0
gene_id_2515	376	76.6	7.00E-172
gene_id_2516	209	79.43	2.00E-123
gene_id_2517	113	67.26	2.00E-47
gene_id_2518	140	43.57	1.00E-20
gene_id_2519	129	56.59	3.00E-39
gene_id_2520	303	57.43	3.00E-123
gene_id_2521	1170	77.35	0

gene_id_2522	281	28.11	4.00E-25
gene_id_2523	268	67.16	1.00E-121
gene_id_2524	548	66.24	0
gene_id_2525	316	59.81	3.00E-138
gene_id_2526	213	83.57	4.00E-130
gene_id_2527	426	82.16	0
gene_id_2528	364	80.22	0
gene_id_2529	497	69.62	0
gene_id_2530	343	74.05	0
gene_id_2531	265	47.17	2.00E-79
gene_id_2532	511	84.54	0
gene_id_2533	63	65.08	9.00E-21
gene_id_2536	55	89.09	6.00E-24
gene_id_2537	437	77.35	0
gene_id_2538	108	60.19	1.00E-22
gene_id_2539	462	65.58	8.00E-156
gene_id_2540	495	57.78	0
gene_id_2541	512	59.38	0
gene_id_2542	352	57.39	6.00E-130
gene_id_2543	610	59.34	0
gene_id_2544	134	42.54	4.00E-21
gene_id_2545	112	51.79	8.00E-35
gene_id_2546	538	63.01	0
gene_id_2548	45	57.78	8.00E-09
gene_id_2550	124	75	2.00E-58
gene_id_2551	77	31.17	1.00E-06
gene_id_2552	440	55.68	2.00E-134
gene_id_2553	223	69.51	3.00E-98
gene_id_2554	358	67.04	2.00E-155
gene_id_2555	184	57.61	5.00E-46
gene_id_2556	165	60.61	1.00E-66
gene_id_2557	491	57.64	5.00E-171
gene_id_2558	857	77.25	0
gene_id_2559	111	68.47	1.00E-42
gene_id_2560	614	73.45	0
gene_id_2561	128	64.06	6.00E-50
gene_id_2562	344	70.06	6.00E-151
gene_id_2563	178	56.74	8.00E-64
gene_id_2564	252	66.67	3.00E-103
gene_id_2565	393	81.93	0
gene_id_2566	261	64.75	1.00E-111
gene_id_2567	497	59.36	0
gene_id_2568	185	72.97	3.00E-98
gene_id_2569	530	79.25	0
gene_id_2570	251	62.95	2.00E-112
gene_id_2571	526	67.49	0
gene_id_2572	293	59.39	2.00E-125

gene_id_2573	407	55.77	8.00E-149
gene_id_2575	410	78.78	0
gene_id_2576	145	59.31	1.00E-47
gene_id_2577	329	59.88	2.00E-136
gene_id_2577	120	40	3.00E-11
gene_id_2578	521	72.74	0
gene_id_2579	153	71.9	1.00E-73
gene_id_2580	194	34.54	2.00E-24
gene_id_2581	193	38.34	7.00E-31
gene_id_2582	184	63.04	3.00E-79
gene_id_2583	252	46.83	2.00E-76
gene_id_2584	287	48.78	4.00E-100
gene_id_2585	283	51.24	4.00E-94
gene_id_2586	787	48.41	0
gene_id_2587	317	56.47	6.00E-120
gene_id_2588	419	48.69	6.00E-114
gene_id_2589	174	59.2	3.00E-65
gene_id_2590	195	51.28	6.00E-48
gene_id_2591	351	54.13	8.00E-122
gene_id_2592	357	66.67	1.00E-167
gene_id_2593	149	64.43	2.00E-63
gene_id_2594	251	58.17	2.00E-100
gene_id_2595	220	70	2.00E-86
gene_id_2596	185	64.32	3.00E-80
gene_id_2597	392	72.45	0
gene_id_2598	277	77.62	8.00E-148
gene_id_2599	296	76.01	5.00E-158
gene_id_2600	342	63.45	2.00E-155
gene_id_2601	165	49.09	6.00E-40
gene_id_2602	277	57.76	8.00E-103
gene_id_2603	659	66.77	0
gene_id_2604	137	76.64	2.00E-78
gene_id_2605	299	51.17	2.00E-106
gene_id_2606	331	54.08	6.00E-124
gene_id_2607	268	64.55	4.00E-132
gene_id_2608	454	49.34	5.00E-156
gene_id_2609	139	45.32	2.00E-32
gene_id_2610	462	73.81	0
gene_id_2611	306	58.82	1.00E-131
gene_id_2612	271	49.08	1.00E-90
gene_id_2613	577	60.31	0
gene_id_2614	283	69.96	3.00E-131
gene_id_2615	536	65.67	0
gene_id_2616	227	34.36	2.00E-31
gene_id_2617	226	37.61	1.00E-38
gene_id_2618	121	71.9	7.00E-57
gene_id_2619	1091	57.75	0

gene_id_3705	129	80.62	2.00E-68
gene_id_3706	175	36.57	4.00E-21
gene_id_3707	305	55.08	6.00E-106
gene_id_3708	471	51.38	1.00E-172
gene_id_3709	332	68.37	7.00E-155
gene_id_3710	152	69.08	3.00E-73
gene_id_3711	432	46.06	3.00E-134
gene_id_3712	309	40.45	4.00E-84
gene_id_3713	457	46.17	1.00E-130
gene_id_3714	247	40.08	6.00E-46
gene_id_3715	321	86.92	0
gene_id_3716	389	78.41	0
gene_id_3717	333	80.18	0
gene_id_3718	209	67.46	1.00E-94
gene_id_3719	331	80.06	0
gene_id_3720	385	67.27	0
gene_id_3721	296	55.41	1.00E-113
gene_id_3722	218	52.29	7.00E-74
gene_id_3723	310	75.48	4.00E-176
gene_id_3724	302	77.48	4.00E-163
gene_id_3725	253	77.87	4.00E-130
gene_id_3726	76	52.63	6.00E-15
gene_id_3727	460	64.78	0
gene_id_3728	451	72.28	0
gene_id_3729	542	55.17	2.00E-168
gene_id_3729	219	50.68	2.00E-40
gene_id_3729	168	56.55	4.00E-36
gene_id_3729	263	47.53	9.00E-33
gene_id_3729	106	53.77	5.00E-10
gene_id_3735	78	67.95	9.00E-32
gene_id_3736	565	57.52	0
gene_id_3737	385	67.53	2.00E-166
gene_id_3738	77	57.14	9.00E-26
gene_id_3739	496	70.36	0
gene_id_3740	405	79.51	0
gene_id_3741	245	77.96	2.00E-138
gene_id_4259	51	92.16	1.00E-26
gene_id_4260	283	59.72	5.00E-127
gene_id_4261	320	75.62	1.00E-142
gene_id_4262	305	64.92	2.00E-138
gene_id_4263	517	70.41	0
gene_id_4264	530	57.55	0
gene_id_4265	228	83.77	1.00E-126
gene_id_4266	430	70.47	0
gene_id_4267	206	77.67	2.00E-116
gene_id_4268	171	58.48	7.00E-69
gene_id_4269	332	73.8	0

gene_id_4270	268	41.79	2.00E-61
gene_id_4271	172	43.6	3.00E-43
gene_id_4272	557	36.62	4.00E-92
gene_id_4273	135	72.59	3.00E-71
gene_id_4274	258	75.19	2.00E-128
gene_id_4275	144	67.36	7.00E-65
gene_id_4276	470	59.79	0
gene_id_4277	299	55.85	3.00E-118
gene_id_4278	786	71.88	0
gene_id_4279	268	66.79	2.00E-140
gene_id_4280	426	77	0
gene_id_4281	322	75.78	0
gene_id_4282	248	62.1	3.00E-113
gene_id_4283	111	81.08	2.00E-60
gene_id_4284	185	76.22	3.00E-102
gene_id_4285	345	41.74	6.00E-65
gene_id_4286	232	75	2.00E-121
gene_id_4287	369	69.92	0
gene_id_4288	560	67.32	0
gene_id_4289	774	74.81	0
gene_id_4291	374	59.09	2.00E-156
gene_id_4292	517	52.03	0
gene_id_4293	230	52.17	2.00E-73
gene_id_4294	498	63.45	0
gene_id_4295	107	89.72	3.00E-62
gene_id_4296	76	90.79	8.00E-39
gene_id_4297	373	77.48	0
gene_id_4298	294	70.75	8.00E-148
gene_id_4299	275	40.73	2.00E-50
gene_id_4300	318	88.99	0
gene_id_4302	117	74.36	6.00E-57
gene_id_4303	686	66.18	0
gene_id_4304	614	54.23	2.00E-164
gene_id_4305	160	73.75	6.00E-77
gene_id_4306	579	68.05	0
gene_id_4307	271	70.11	2.00E-144
gene_id_4308	333	77.78	0
gene_id_4309	412	37.38	5.00E-73
gene_id_4309	422	36.97	1.00E-69
gene_id_4309	402	35.57	4.00E-67
gene_id_4309	395	33.16	6.00E-52
gene_id_4309	272	36.76	1.00E-42
gene_id_4310	343	79.88	0
gene_id_4311	293	79.18	5.00E-149
gene_id_4312	324	76.85	8.00E-122
gene_id_4313	252	71.83	1.00E-128
gene_id_4314	235	75.32	1.00E-112

gene_id_4315	165	61.21	1.00E-69
gene_id_4316	417	58.03	3.00E-158
gene_id_4317	260	86.15	3.00E-152
gene_id_4318	215	86.05	9.00E-120
gene_id_4319	252	86.11	2.00E-149
gene_id_4320	83	56.63	4.00E-23
gene_id_4321	89	77.53	8.00E-34
gene_id_4322	793	74.02	0
gene_id_4323	235	66.81	6.00E-109
gene_id_4324	225	40.89	3.00E-48
gene_id_4325	252	76.98	7.00E-138
gene_id_4326	806	78.41	0
gene_id_4327	298	70.13	2.00E-135
gene_id_4328	537	51.4	0
gene_id_4329	214	58.88	2.00E-95
gene_id_4330	158	69.62	7.00E-70
gene_id_4331	387	67.18	1.00E-165
gene_id_4332	858	70.16	0
gene_id_4333	251	57.37	3.00E-95
gene_id_4334	211	55.92	4.00E-71
gene_id_4335	321	75.08	6.00E-177
gene_id_4336	323	89.78	2.00E-149
gene_id_4337	429	82.28	0
gene_id_4338	379	63.32	2.00E-126
gene_id_4339	602	69.27	0
gene_id_4340	356	72.47	6.00E-169
gene_id_4341	256	73.05	2.00E-139
gene_id_4342	345	60.87	4.00E-146
gene_id_4343	209	71.77	1.00E-98
gene_id_4344	232	40.52	2.00E-42
gene_id_4345	136	67.65	2.00E-62
gene_id_4346	215	64.19	6.00E-83
gene_id_4347	213	75.59	9.00E-91
gene_id_4348	216	60.19	5.00E-97
gene_id_4349	197	81.22	1.00E-113
gene_id_4351	468	79.27	0
gene_id_4352	139	65.47	8.00E-53
gene_id_4353	247	80.16	9.00E-140
gene_id_4354	314	67.52	8.00E-141
gene_id_4355	87	67.82	2.00E-24
gene_id_4356	571	60.25	0
gene_id_4357	417	83.21	0
gene_id_4358	640	80.16	0
gene_id_4359	390	69.74	0
gene_id_4360	417	67.87	0
gene_id_4361	289	49.83	5.00E-96
gene_id_4362	539	43.97	4.00E-89

gene_id_4363	395	48.86	2.00E-138
gene_id_4365	350	47.43	3.00E-103
gene_id_4366	171	77.78	8.00E-95
gene_id_4367	535	51.59	0
gene_id_4369	192	64.06	3.00E-88
gene_id_4370	257	71.6	1.00E-136
gene_id_4371	214	68.69	9.00E-106
gene_id_4372	119	61.34	9.00E-44
gene_id_4373	253	71.54	1.00E-136
gene_id_4374	649	75.65	0
gene_id_4375	297	57.58	5.00E-115
gene_id_4376	138	83.33	4.00E-80
gene_id_4377	224	70.54	1.00E-116
gene_id_4378	543	42.73	9.00E-126
gene_id_4379	402	62.94	1.00E-161
gene_id_4380	72	77.78	2.00E-33
gene_id_4381	191	79.58	1.00E-98
gene_id_4382	307	70.68	2.00E-151
gene_id_4383	188	58.51	1.00E-81
gene_id_4384	294	79.59	1.00E-162
gene_id_4385	190	60	2.00E-69
gene_id_4386	448	72.99	0
gene_id_4387	299	56.19	2.00E-120
gene_id_4388	164	64.63	1.00E-69
gene_id_4389	711	86.22	0
gene_id_4390	547	47.53	6.00E-116
gene_id_4394	275	96.36	3.00E-164
gene_id_4395	108	86.11	2.00E-58
gene_id_4396	135	91.11	2.00E-80
gene_id_4397	521	90.6	0
gene_id_4398	116	83.62	7.00E-68
gene_id_4399	462	87.88	0
gene_id_4400	124	72.58	1.00E-58
gene_id_4401	401	63.34	0
gene_id_4402	236	42.37	7.00E-50
gene_id_4403	261	58.24	4.00E-103
gene_id_4404	237	83.54	2.00E-146
gene_id_4405	177	70.06	3.00E-91
gene_id_4406	300	55.33	3.00E-113
gene_id_4407	294	72.11	3.00E-155
gene_id_4408	244	66.8	3.00E-113
gene_id_4409	314	62.1	1.00E-138
gene_id_4410	252	76.19	2.00E-142
gene_id_4411	411	79.32	0
gene_id_4412	257	85.6	6.00E-167
gene_id_4413	248	62.1	4.00E-108
gene_id_4414	334	63.47	7.00E-149

gene_id_4415	170	48.24	2.00E-43
gene_id_4416	445	75.28	0
gene_id_4417	282	75.53	2.00E-144
gene_id_4418	137	51.09	5.00E-40
gene_id_4705	204	59.8	5.00E-77
gene_id_4706	374	91.71	0
gene_id_4707	33	78.79	3.00E-07
gene_id_4708	305	72.13	5.00E-160
gene_id_4709	289	70.59	1.00E-152
gene_id_4710	109	69.72	1.00E-53
gene_id_4711	311	67.52	7.00E-149
gene_id_4712	183	55.74	9.00E-70
gene_id_4713	83	83.13	1.00E-43
gene_id_4714	204	82.84	1.00E-121
gene_id_4715	404	79.46	1.00E-174
gene_id_4716	223	81.61	4.00E-128
gene_id_4717	361	64.54	1.00E-129
gene_id_4718	417	76.74	0
gene_id_4719	375	78.13	0
gene_id_4720	95	77.89	8.00E-37
gene_id_4721	422	75.36	0
gene_id_4722	70	61.43	1.00E-22
gene_id_4723	96	89.58	2.00E-55
gene_id_4724	106	67.92	4.00E-40
gene_id_4725	103	81.55	1.00E-53
gene_id_4726	481	71.1	0
gene_id_4727	233	60.94	1.00E-87
gene_id_4728	617	74.39	0
gene_id_4729	290	56.55	4.00E-93
gene_id_4730	243	60.49	3.00E-102
gene_id_4731	368	82.61	0
gene_id_4732	87	82.76	6.00E-45
gene_id_4733	263	92.78	1.00E-151
gene_id_4734	202	57.43	1.00E-73
gene_id_4735	620	78.39	0
gene_id_4736	155	54.84	4.00E-49
gene_id_4737	307	67.1	1.00E-135
gene_id_4738	344	90.99	0
gene_id_4739	232	75.43	2.00E-122
gene_id_4740	189	64.55	1.00E-82
gene_id_4741	80	68.75	3.00E-30
gene_id_4742	426	71.36	0
gene_id_4743	428	72.2	0
gene_id_4744	72	83.33	4.00E-33
gene_id_4746	509	86.64	0
gene_id_4747	135	93.33	3.00E-70
gene_id_4748	312	79.17	2.00E-173

gene_id_4749	130	89.23	5.00E-78
gene_id_4750	548	88.69	0
gene_id_4751	500	84	0
gene_id_4752	212	76.42	2.00E-112
gene_id_4753	573	79.58	0
gene_id_4754	595	83.36	0
gene_id_4755	119	79.83	4.00E-61
gene_id_4756	187	58.82	3.00E-67
gene_id_4757	165	75.15	5.00E-88
gene_id_4758	246	54.47	3.00E-90
gene_id_4759	112	50	1.00E-27
gene_id_4760	445	66.29	0
gene_id_4761	136	73.53	6.00E-68
gene_id_4762	84	70.24	1.00E-34
gene_id_4763	408	67.89	7.00E-175
gene_id_4764	428	60.28	7.00E-172
gene_id_4765	882	79.14	0
gene_id_4766	183	57.92	4.00E-64
gene_id_4767	291	70.1	4.00E-102
gene_id_4768	220	65.45	6.00E-101
gene_id_4769	279	55.2	2.00E-96
gene_id_4770	467	64.67	0
gene_id_4771	188	77.13	4.00E-106
gene_id_4772	460	80.87	0
gene_id_4773	284	77.82	7.00E-156
gene_id_4774	245	66.53	2.00E-119
gene_id_4775	555	84.14	0
gene_id_4776	285	75.09	1.00E-152
gene_id_4777	282	72.7	3.00E-146
gene_id_4778	486	86.83	0
gene_id_4779	242	72.73	8.00E-115
gene_id_4780	64	64.06	3.00E-09
gene_id_4781	551	81.49	0
gene_id_4782	240	50.42	7.00E-79
gene_id_4783	322	65.22	2.00E-150
gene_id_4784	82	81.71	1.00E-41
gene_id_4785	238	84.03	1.00E-134
gene_id_4786	252	87.3	3.00E-168
gene_id_4787	357	78.99	0
gene_id_4788	543	77.72	0
gene_id_4789	545	80.37	0
gene_id_4790	156	70.51	5.00E-78
gene_id_4791	149	71.14	6.00E-72
gene_id_4792	202	67.82	2.00E-102
gene_id_4793	769	85.57	0
gene_id_4794	176	49.43	4.00E-54
gene_id_4795	496	67.54	0

gene_id_4796	561	78.79	0
gene_id_4797	420	91.19	0
gene_id_4798	199	87.94	5.00E-113
gene_id_4799	425	69.18	0
gene_id_4800	413	62.47	0
gene_id_4801	300	62	6.00E-129
gene_id_4802	140	56.43	1.00E-53
gene_id_4803	441	59.41	5.00E-152
gene_id_4804	342	49.71	2.00E-112
gene_id_4805	604	58.77	2.00E-178
gene_id_4806	382	78.53	0
gene_id_4807	190	76.84	1.00E-101
gene_id_4808	284	86.62	2.00E-162
gene_id_4809	260	87.69	5.00E-142
gene_id_4811	215	65.58	4.00E-106
gene_id_4813	252	86.9	3.00E-165
gene_id_4814	582	93.13	0
gene_id_4815	185	68.11	9.00E-78
gene_id_4816	185	84.32	7.00E-102
gene_id_4817	280	82.14	7.00E-163
gene_id_4818	348	70.4	0
gene_id_4819	510	83.14	0
gene_id_4820	282	76.24	3.00E-155
gene_id_4821	97	68.04	7.00E-31
gene_id_4822	309	80.26	1.00E-178
gene_id_4823	415	81.45	0
gene_id_4824	482	86.72	0
gene_id_4825	460	72.39	0
gene_id_4826	136	85.29	2.00E-79
gene_id_4827	319	58.62	6.00E-122
gene_id_4828	144	48.61	3.00E-34
gene_id_4829	157	57.32	1.00E-47
gene_id_4830	195	64.62	3.00E-87
gene_id_4831	237	82.28	1.00E-143
gene_id_4832	437	72.54	0
gene_id_4833	545	56.15	0
gene_id_4834	254	73.62	9.00E-118
gene_id_4835	325	78.77	0
gene_id_4836	217	81.11	9.00E-120
gene_id_4837	151	66.23	2.00E-67
gene_id_4838	266	59.02	6.00E-114
gene_id_4839	129	72.87	2.00E-65
gene_id_4841	252	54.37	8.00E-91
gene_id_4842	212	70.28	1.00E-107
gene_id_4843	85	34.12	9.00E-09
gene_id_4844	515	67.77	0
gene_id_4845	348	66.95	6.00E-144

gene_id_4846	137	82.48	7.00E-70
gene_id_4848	243	60.91	3.00E-100
gene_id_4849	121	41.32	4.00E-19
gene_id_4851	70	54.29	1.00E-16
gene_id_4852	183	59.02	1.00E-74
gene_id_4853	70	35.71	2.00E-10
gene_id_4854	60	75	2.00E-26
gene_id_4855	346	50.29	3.00E-114
gene_id_4856	964	29.46	9.00E-92
gene_id_4857	92	32.61	3.00E-06
gene_id_4858	515	28.35	1.00E-49
gene_id_5334	178	37.64	3.00E-25
gene_id_5335	551	85.66	0
gene_id_5336	127	37.8	2.00E-20
gene_id_5337	293	75.77	2.00E-164
gene_id_5338	187	66.84	5.00E-91
gene_id_5339	284	53.87	3.00E-110
gene_id_5340	191	54.97	1.00E-71
gene_id_5341	457	45.3	1.00E-132
gene_id_5342	217	76.5	2.00E-124
gene_id_5343	337	68.25	6.00E-171
gene_id_5344	140	50.71	8.00E-48
gene_id_5345	735	85.44	0
gene_id_5346	196	46.43	1.00E-20
gene_id_5348	601	41.1	3.00E-96
gene_id_5349	913	55.2	0
gene_id_5350	259	52.12	7.00E-82
gene_id_5350	148	60.81	9.00E-51
gene_id_5351	307	54.4	6.00E-110
gene_id_5353	329	51.37	4.00E-119
gene_id_5354	115	75.65	3.00E-56
gene_id_5355	152	61.18	4.00E-68
gene_id_5356	104	77.88	1.00E-52
gene_id_5357	72	68.06	2.00E-26
gene_id_5358	112	72.32	2.00E-51
gene_id_5359	209	86.12	1.00E-130
gene_id_5360	227	73.13	5.00E-108
gene_id_5361	273	43.96	1.00E-72
gene_id_5362	111	80.18	5.00E-59
gene_id_5363	83	55.42	1.00E-21
gene_id_5364	206	38.35	1.00E-44
gene_id_5365	185	67.03	1.00E-83
gene_id_5366	193	84.46	4.00E-106
gene_id_5367	873	88.55	0
gene_id_5368	317	74.45	6.00E-177
gene_id_5369	299	82.61	0
gene_id_5371	242	50.41	8.00E-82

gene_id_5372	261	61.3	2.00E-104
gene_id_5373	123	56.91	3.00E-44
gene_id_5374	88	95.45	2.00E-42
gene_id_5375	115	94.78	4.00E-73
gene_id_5376	82	42.68	4.00E-19
gene_id_5377	51	74.51	9.00E-16
gene_id_5378	308	40.91	7.00E-60
gene_id_5381	96	32.29	5.00E-07
gene_id_5382	383	31.59	8.00E-40
gene_id_5383	371	64.69	4.00E-175
gene_id_5416	456	91.23	0
gene_id_5417	511	93.74	0
gene_id_5418	634	90.06	0
gene_id_5419	102	89.22	4.00E-59
gene_id_5420	168	85.71	7.00E-79
gene_id_5421	147	82.31	2.00E-87
gene_id_5422	346	95.95	0
gene_id_5423	355	92.39	0
gene_id_5424	156	83.33	1.00E-90
gene_id_5425	173	92.49	4.00E-115
gene_id_5426	118	89.83	1.00E-70
gene_id_5427	101	60.4	9.00E-22
gene_id_5428	400	66.25	7.00E-160
gene_id_5429	265	47.92	2.00E-76
gene_id_5430	229	49.78	4.00E-51
gene_id_5431	236	57.2	2.00E-63
gene_id_5432	421	81.24	0
gene_id_5433	318	54.72	3.00E-122
gene_id_5435	342	53.8	7.00E-80
gene_id_5436	286	72.73	5.00E-157
gene_id_5437	335	74.63	9.00E-172
gene_id_5438	417	72.42	0
gene_id_5439	527	71.16	0
gene_id_5440	361	78.95	3.00E-178
gene_id_5441	166	74.1	1.00E-87
gene_id_5442	189	85.19	2.00E-116
gene_id_5443	223	55.16	2.00E-74
gene_id_5444	224	59.38	6.00E-91
gene_id_5445	571	57.27	0
gene_id_5446	574	65.51	0
gene_id_5447	113	40.71	5.00E-18
gene_id_5448	954	66.35	0
gene_id_5449	334	83.53	1.00E-146
gene_id_5450	462	69.7	0
gene_id_5451	141	51.77	3.00E-46
gene_id_5452	95	41.05	3.00E-09
gene_id_5453	263	43.35	1.00E-64

gene_id_5454	108	92.59	6.00E-66
gene_id_5455	148	75	5.00E-50
gene_id_5456	102	40.2	2.00E-21
gene_id_5457	525	69.14	0
gene_id_5458	490	67.55	0
gene_id_5459	195	63.59	8.00E-65
gene_id_5460	272	67.65	8.00E-90
gene_id_5461	661	54.61	0
gene_id_5462	165	78.18	3.00E-77
gene_id_5463	561	72.37	0
gene_id_5464	183	75.96	2.00E-82
gene_id_5465	443	72.23	0
gene_id_5466	478	80.13	0
gene_id_5467	343	67.64	7.00E-123
gene_id_5468	96	75	2.00E-43
gene_id_5469	267	56.18	1.00E-85
gene_id_5470	219	64.84	8.00E-76
gene_id_5471	91	87.91	7.00E-49
gene_id_5472	192	55.73	4.00E-28
gene_id_5473	145	51.72	9.00E-45
gene_id_5474	606	83.99	0
gene_id_5475	174	69.54	1.00E-80
gene_id_5476	212	85.85	2.00E-130
gene_id_5477	556	90.65	0
gene_id_5478	264	86.74	1.00E-161
gene_id_5479	85	84.71	5.00E-29
gene_id_5480	148	69.59	1.00E-57
gene_id_5481	113	76.99	1.00E-54
gene_id_5482	538	63.57	0
gene_id_5483	403	68.98	0
gene_id_5484	334	73.35	0
gene_id_5485	248	59.68	2.00E-84
gene_id_5486	394	76.65	0
gene_id_5488	125	80	1.00E-69
gene_id_5489	102	92.16	4.00E-60
gene_id_5490	76	90.79	6.00E-43
gene_id_5491	159	49.06	2.00E-47
gene_id_5492	232	31.03	5.00E-16
gene_id_5493	129	41.09	2.00E-27
gene_id_5494	282	52.84	6.00E-103
gene_id_5495	128	50.78	4.00E-42
gene_id_5496	386	65.8	0
gene_id_5498	159	64.78	4.00E-61
gene_id_5499	453	45.03	2.00E-130
gene_id_5500	1153	59.41	0
gene_id_5501	807	57.99	0
gene_id_5502	478	66.11	0

gene_id_5503	371	59.03	1.00E-160
gene_id_5504	377	70.56	0
gene_id_5505	630	68.57	0
gene_id_5506	808	64.73	0
gene_id_5507	102	37.25	6.00E-20
gene_id_5508	808	70.17	0
gene_id_5509	475	56.21	0
gene_id_5510	372	65.32	0
gene_id_5511	395	72.15	0
gene_id_5512	103	73.79	2.00E-46
gene_id_5513	348	62.93	5.00E-157
gene_id_5514	196	71.43	4.00E-84
gene_id_5515	252	70.24	4.00E-115
gene_id_5516	885	80.79	0
gene_id_5518	214	47.66	5.00E-46
gene_id_5519	194	62.37	5.00E-68
gene_id_5520	851	45.83	0
gene_id_5521	221	65.61	2.00E-103
gene_id_5522	318	78.62	0
gene_id_5523	189	66.14	1.00E-73
gene_id_5524	340	56.47	4.00E-128
gene_id_5525	173	45.09	2.00E-37
gene_id_5526	169	55.03	3.00E-58
gene_id_5527	208	75	3.00E-93
gene_id_5528	256	29.69	4.00E-30
gene_id_5561	54	53.7	1.00E-10
gene_id_5562	339	77.58	0
gene_id_5563	116	56.03	1.00E-43
gene_id_5564	379	70.71	0
gene_id_5565	381	56.43	2.00E-161
gene_id_5566	875	64.8	0
gene_id_5567	273	68.86	9.00E-135
gene_id_5568	202	51.49	5.00E-61
gene_id_5569	183	66.12	4.00E-78
gene_id_5570	532	68.61	0
gene_id_5571	312	85.26	0
gene_id_5572	428	75	0
gene_id_5573	354	76.27	0
gene_id_5574	1072	82.84	0
gene_id_5575	251	66.14	2.00E-119
gene_id_5576	301	81.73	2.00E-172
gene_id_5577	232	65.52	2.00E-97
gene_id_5578	190	81.58	1.00E-109
gene_id_5579	47	61.7	2.00E-12
gene_id_5580	260	75.77	9.00E-137
gene_id_5581	257	81.71	2.00E-134
gene_id_5582	357	78.71	0

gene_id_5583	220	51.82	3.00E-70
gene_id_5584	265	70.94	7.00E-110
gene_id_5585	120	75	4.00E-63
gene_id_5586	38	68.42	4.00E-09
gene_id_5587	300	36	1.00E-56
gene_id_5588	125	63.2	2.00E-53
gene_id_5589	432	70.14	0
gene_id_5866	442	89.59	0
gene_id_5867	767	74.05	0
gene_id_5868	390	76.15	0
gene_id_5869	370	68.65	0
gene_id_5870	367	85.56	0
gene_id_5871	294	82.99	2.00E-153
gene_id_5872	317	81.07	2.00E-150
gene_id_5873	254	86.22	5.00E-161
gene_id_5874	234	87.18	2.00E-144
gene_id_5875	214	67.29	8.00E-90
gene_id_5876	295	69.15	5.00E-139
gene_id_5877	129	62.79	3.00E-42
gene_id_5878	196	57.65	2.00E-75
gene_id_5879	90	50	3.00E-24
gene_id_5880	267	68.16	2.00E-107
gene_id_5881	63	79.37	8.00E-31
gene_id_5882	740	72.84	0
gene_id_5883	239	59.41	9.00E-98
gene_id_5884	366	82.79	0
gene_id_5885	313	51.44	1.00E-114
gene_id_5886	94	70.21	1.00E-42
gene_id_5887	132	75	2.00E-64
gene_id_5888	76	89.47	4.00E-42
gene_id_5890	90	71.11	2.00E-42
gene_id_5891	309	63.43	3.00E-125
gene_id_5892	668	63.02	0
gene_id_5893	147	77.55	2.00E-78
gene_id_5894	644	79.5	0
gene_id_5895	444	85.59	0
gene_id_5896	221	25.34	2.00E-10
gene_id_5897	381	39.9	4.00E-81
gene_id_5898	229	44.1	7.00E-67
gene_id_5899	465	39.35	1.00E-103
gene_id_5900	296	56.08	3.00E-116
gene_id_5901	601	44.09	3.00E-131
gene_id_6189	490	64.49	0
gene_id_6190	468	62.39	0
gene_id_6191	174	74.71	1.00E-86
gene_id_6192	415	72.53	0
gene_id_6193	149	64.43	1.00E-70

gene_id_6194	390	63.08	5.00E-136
gene_id_6195	130	52.31	1.00E-31
gene_id_6197	539	86.64	0
gene_id_6198	164	53.05	1.00E-40
gene_id_6199	201	37.31	6.00E-27
gene_id_6201	365	70.41	0
gene_id_6202	128	67.97	7.00E-20
gene_id_6253	220	80.91	9.00E-130
gene_id_6254	81	72.84	3.00E-30
gene_id_6255	82	65.85	1.00E-27
gene_id_6256	198	79.29	8.00E-102
gene_id_6257	96	86.46	4.00E-51
gene_id_6258	578	63.49	0
gene_id_6260	148	82.43	1.00E-87
gene_id_6261	283	46.29	2.00E-71
gene_id_6262	107	42.06	8.00E-20
gene_id_6263	279	30.47	2.00E-29
gene_id_6264	137	81.02	9.00E-74
gene_id_6265	145	59.31	5.00E-55
gene_id_6266	292	73.97	1.00E-161
gene_id_6267	191	78.53	2.00E-102
gene_id_6268	199	75.38	1.00E-109
gene_id_6269	607	64.58	0
gene_id_6270	117	48.72	2.00E-30
gene_id_6271	167	39.52	9.00E-33
gene_id_6273	35	68.57	4.00E-06
gene_id_6274	150	62	2.00E-46
gene_id_6275	577	71.58	0
gene_id_6276	577	67.59	0
gene_id_6277	59	50.85	3.00E-17
gene_id_6278	192	41.67	2.00E-48
gene_id_6279	163	54.6	6.00E-61
gene_id_6280	461	73.54	0
gene_id_6281	195	74.87	7.00E-91
gene_id_6282	279	33.33	2.00E-57
gene_id_6283	734	69.89	0
gene_id_6284	330	86.06	0
gene_id_6285	336	88.69	0
gene_id_6286	208	60.58	5.00E-76
gene_id_6287	140	71.43	3.00E-40
gene_id_6288	365	69.59	0
gene_id_6289	142	62.68	9.00E-57
gene_id_6290	387	81.14	0
gene_id_6291	277	66.79	1.00E-135
gene_id_6292	467	85.65	0
gene_id_6293	123	82.93	4.00E-65
gene_id_6296	193	64.25	2.00E-87

gene_id_6297	174	62.64	5.00E-68
gene_id_6299	212	46.7	4.00E-53
gene_id_6301	52	44.23	9.00E-08
gene_id_6302	191	48.69	5.00E-61
gene_id_6303	403	70.22	6.00E-159
gene_id_6304	521	77.35	0
gene_id_6305	332	67.17	5.00E-130
gene_id_6306	106	71.7	6.00E-50
gene_id_6308	241	65.98	6.00E-116
gene_id_6309	381	58.53	5.00E-156
gene_id_6310	359	57.94	3.00E-146
gene_id_6311	297	79.46	2.00E-175
gene_id_6312	148	31.76	4.00E-15
gene_id_6313	484	57.23	0
gene_id_6314	302	71.85	9.00E-151
gene_id_6315	188	71.81	3.00E-100
gene_id_6316	99	60.61	4.00E-35
gene_id_6319	279	55.2	7.00E-103
gene_id_6320	98	36.73	1.00E-08
gene_id_6321	172	56.98	2.00E-62
gene_id_6322	463	60.04	0
gene_id_6323	125	82.4	5.00E-72
gene_id_6324	603	86.07	0
gene_id_6325	517	65.38	0
gene_id_6326	182	80.77	2.00E-104
gene_id_6327	163	77.3	8.00E-81
gene_id_6328	70	90	5.00E-40
gene_id_6329	168	58.93	9.00E-65
gene_id_6330	119	71.43	2.00E-49
gene_id_6331	314	50	2.00E-108
gene_id_6332	158	39.24	4.00E-36
gene_id_6334	52	40.38	2.00E-07
gene_id_6335	106	37.74	1.00E-13
gene_id_6336	195	86.15	2.00E-123
gene_id_6337	77	72.73	9.00E-38
gene_id_6338	40	82.5	1.00E-15
gene_id_6339	88	64.77	4.00E-34
gene_id_6340	380	63.42	2.00E-121
gene_id_6341	318	49.69	1.00E-96
gene_id_6342	384	72.92	0
gene_id_6343	457	46.17	1.00E-124
gene_id_6344	216	73.15	2.00E-109
gene_id_6345	341	46.63	2.00E-97
gene_id_6346	635	71.18	0
gene_id_6347	121	75.21	4.00E-59
gene_id_6348	598	69.06	0
gene_id_6349	217	73.27	1.00E-117

gene_id_6350	314	67.83	4.00E-156
gene_id_6351	436	39.22	1.00E-87
gene_id_6352	220	67.27	3.00E-111
gene_id_6353	382	71.47	0
gene_id_6354	449	58.57	1.00E-170
gene_id_6355	141	60.99	2.00E-60
gene_id_6357	76	36.84	9.00E-08
gene_id_6359	151	66.89	1.00E-68
gene_id_6361	562	57.12	0
gene_id_6400	519	52.02	0
gene_id_6401	186	62.37	3.00E-80
gene_id_6402	159	77.36	1.00E-86
gene_id_6403	135	63.7	4.00E-44
gene_id_6404	399	73.43	0
gene_id_6405	256	73.83	2.00E-129
gene_id_6406	412	56.55	1.00E-168
gene_id_6407	378	77.25	0
gene_id_6408	166	51.81	5.00E-54
gene_id_6409	58	86.21	8.00E-30
gene_id_6410	164	82.32	7.00E-96
gene_id_6411	337	83.38	4.00E-178
gene_id_6412	334	77.25	2.00E-173
gene_id_6413	307	82.41	1.00E-175
gene_id_6414	314	74.52	5.00E-172
gene_id_6415	247	80.57	1.00E-128
gene_id_6416	78	92.31	1.00E-40
gene_id_6417	315	84.13	8.00E-175
gene_id_6418	412	81.31	0
gene_id_6419	237	69.2	5.00E-100
gene_id_6420	353	55.24	2.00E-137
gene_id_6421	86	91.86	2.00E-34
gene_id_6422	1184	51.86	0
gene_id_6423	305	79.34	3.00E-164
gene_id_6424	119	62.18	1.00E-41
gene_id_6425	450	84.67	0
gene_id_6426	93	89.25	1.00E-53
gene_id_6427	75	82.67	7.00E-35
gene_id_6428	135	82.22	2.00E-73
gene_id_6429	164	60.98	9.00E-70
gene_id_6430	246	73.58	4.00E-134
gene_id_6431	187	74.33	7.00E-104
gene_id_6432	113	88.5	1.00E-65
gene_id_6433	175	91.43	2.00E-114
gene_id_6434	282	78.01	6.00E-158
gene_id_6435	257	68.09	4.00E-114
gene_id_6436	223	31.84	5.00E-30
gene_id_6437	81	75.31	2.00E-37

gene_id_6438	341	50.15	8.00E-117
gene_id_6439	117	62.39	1.00E-44
gene_id_6440	167	70.06	9.00E-86
gene_id_6441	505	71.09	0
gene_id_6442	166	63.25	4.00E-74
gene_id_6443	65	46.15	6.00E-11
gene_id_6444	231	25.97	5.00E-19
gene_id_6445	72	54.17	2.00E-20
gene_id_6448	279	55.2	2.00E-90
gene_id_6449	557	73.43	0
gene_id_6450	349	74.21	0
gene_id_6451	368	62.23	5.00E-161
gene_id_6452	74	63.51	1.00E-14
gene_id_6453	224	52.68	1.00E-55
gene_id_6454	151	37.75	6.00E-14
gene_id_6455	127	37.8	8.00E-17
gene_id_6457	374	30.21	3.00E-25
gene_id_6458	85	63.53	4.00E-35
gene_id_6459	356	45.22	3.00E-114
gene_id_6460	179	45.81	4.00E-52
gene_id_6461	175	42.29	3.00E-45
gene_id_6462	381	69.03	5.00E-173
gene_id_6463	175	66.29	7.00E-75
gene_id_6464	360	60.56	3.00E-154
gene_id_6465	374	63.1	1.00E-164
gene_id_6466	1017	78.96	0
gene_id_6467	318	72.96	3.00E-162
gene_id_6468	145	53.79	7.00E-35
gene_id_6469	245	75.1	1.00E-134
gene_id_6470	381	62.73	2.00E-148
gene_id_6471	358	54.75	1.00E-136
gene_id_6472	221	72.85	1.00E-116
gene_id_6473	260	78.85	5.00E-141
gene_id_6474	579	52.5	0
gene_id_6475	281	57.65	2.00E-112
gene_id_6476	327	73.09	1.00E-131
gene_id_6477	303	64.03	9.00E-142
gene_id_6478	514	59.34	0
gene_id_6479	379	70.98	0
gene_id_6480	274	76.64	4.00E-158
gene_id_6481	178	68.54	2.00E-69
gene_id_6482	120	40	9.00E-23
gene_id_6483	723	78.28	0
gene_id_6484	204	62.25	5.00E-87
gene_id_6485	361	69.25	2.00E-166
gene_id_6486	206	59.22	2.00E-84
gene_id_6487	192	60.42	3.00E-80

gene_id_6488	236	67.37	4.00E-106
gene_id_6489	251	81.67	3.00E-149
gene_id_6490	352	58.24	4.00E-134
gene_id_6491	229	74.67	4.00E-127
gene_id_6492	252	60.32	4.00E-103
gene_id_6493	205	78.05	3.00E-113
gene_id_6494	462	67.1	0
gene_id_6495	191	65.45	1.00E-75
gene_id_6496	505	77.43	0
gene_id_6497	311	65.92	5.00E-117
gene_id_6498	235	62.13	1.00E-88
gene_id_6499	293	56.31	1.00E-112
gene_id_6500	360	56.11	1.00E-151
gene_id_6501	202	71.78	5.00E-106
gene_id_6502	110	69.09	5.00E-44
gene_id_6503	1226	72.1	0
gene_id_6504	149	66.44	3.00E-70
gene_id_6505	342	89.47	0
gene_id_6506	69	76.81	2.00E-30
gene_id_6507	99	67.68	1.00E-39
gene_id_6508	575	83.3	0
gene_id_6508	169	42.6	2.00E-21
gene_id_6509	115	78.26	4.00E-61
gene_id_6510	314	61.78	1.00E-130
gene_id_6511	291	63.57	1.00E-126
gene_id_6512	305	57.05	8.00E-121
gene_id_6513	88	88.64	3.00E-49
gene_id_6514	697	84.22	0
gene_id_6515	234	73.93	1.00E-115
gene_id_6516	286	67.48	6.00E-117
gene_id_6517	408	65.93	0
gene_id_6518	150	62.67	3.00E-65
gene_id_6519	95	52.63	9.00E-24
gene_id_6520	97	72.16	1.00E-44
gene_id_6521	164	67.07	3.00E-28
gene_id_6522	259	80.69	6.00E-154
gene_id_6523	343	83.09	0
gene_id_6524	406	75.62	0
gene_id_6525	290	75.17	1.00E-157
gene_id_6526	555	83.42	0
gene_id_6527	261	79.69	1.00E-142
gene_id_6528	69	56.52	5.00E-20
gene_id_6529	733	67.12	0
gene_id_6530	76	76.32	2.00E-31
gene_id_6530	80	60	2.00E-24
gene_id_6531	620	78.23	0
gene_id_6532	108	39.81	1.00E-14

gene_id_6533	345	61.74	7.00E-162
gene_id_6534	442	69.46	0
gene_id_6535	413	65.62	0
gene_id_6536	524	79.01	0
gene_id_6537	67	79.1	2.00E-33
gene_id_6538	343	83.09	2.00E-178
gene_id_6539	128	42.19	2.00E-22
gene_id_6540	492	90.85	0
gene_id_6541	172	67.44	3.00E-80
gene_id_6542	259	69.88	2.00E-134
gene_id_6543	86	97.67	6.00E-42
gene_id_6544	496	56.65	0
gene_id_6545	268	61.57	4.00E-111
gene_id_6546	89	62.92	1.00E-19
gene_id_6547	276	81.16	2.00E-148
gene_id_6548	100	70	1.00E-44
gene_id_6549	114	60.53	7.00E-29
gene_id_6550	93	47.31	8.00E-24
gene_id_6551	436	75.92	0
gene_id_6552	864	68.29	0
gene_id_6553	618	62.94	0
gene_id_6554	257	59.14	7.00E-105
gene_id_6555	308	62.34	2.00E-136
gene_id_6556	79	89.87	3.00E-45
gene_id_6557	256	63.28	7.00E-119
gene_id_6558	184	79.35	2.00E-101
gene_id_6559	94	70.21	5.00E-40
gene_id_6560	266	66.92	5.00E-126
gene_id_6561	186	80.11	9.00E-86
gene_id_6562	215	57.67	1.00E-78
gene_id_6563	112	54.46	2.00E-36
gene_id_6564	160	69.38	3.00E-71
gene_id_6565	250	80.4	1.00E-145
gene_id_6566	221	77.83	3.00E-110
gene_id_6567	244	60.66	2.00E-97
gene_id_6568	377	56.23	3.00E-140
gene_id_6569	248	81.85	6.00E-148
gene_id_6570	269	68.77	4.00E-115
gene_id_6571	346	78.61	4.00E-164
gene_id_6572	159	61.01	3.00E-66
gene_id_6573	368	66.58	2.00E-159
gene_id_6574	455	78.46	0
gene_id_6576	256	68.75	7.00E-122
gene_id_6577	274	69.71	2.00E-140
gene_id_6578	251	78.09	3.00E-142
gene_id_6579	318	84.28	1.00E-164
gene_id_6580	312	71.47	2.00E-148

gene_id_6581	213	64.79	2.00E-100
gene_id_6582	67	71.64	3.00E-25
gene_id_6583	684	68.27	0
gene_id_6584	173	49.13	6.00E-56
gene_id_6585	164	47.56	2.00E-39
gene_id_6586	445	73.71	0
gene_id_6587	391	82.1	0
gene_id_6588	201	59.2	2.00E-76
gene_id_6589	117	51.28	3.00E-35
gene_id_6591	247	55.87	2.00E-97
gene_id_6592	181	51.93	4.00E-66
gene_id_6593	221	77.38	3.00E-124
gene_id_6594	225	78.67	5.00E-113
gene_id_6595	249	77.91	1.00E-144
gene_id_6596	289	83.74	3.00E-173
gene_id_6597	372	75.81	0
gene_id_6598	316	70.89	2.00E-153
gene_id_6599	510	81.76	0
gene_id_6600	258	63.57	9.00E-117
gene_id_6601	324	69.75	1.00E-171
gene_id_6602	330	74.85	0
gene_id_6603	303	82.18	1.00E-162
gene_id_6604	310	82.26	0
gene_id_6605	267	68.16	7.00E-130
gene_id_6606	261	49.81	3.00E-78
gene_id_6607	94	43.62	9.00E-11
gene_id_6608	218	55.96	5.00E-75
gene_id_6609	518	56.56	0
gene_id_6610	226	61.95	4.00E-99
gene_id_6611	407	83.54	0
gene_id_6612	350	39.14	6.00E-59
gene_id_6614	260	60.77	5.00E-112
gene_id_6615	78	65.38	1.00E-31
gene_id_6616	202	69.31	6.00E-81
gene_id_6617	233	53.65	3.00E-84
gene_id_6618	164	73.17	5.00E-79
gene_id_6619	265	60.75	4.00E-100
gene_id_6620	842	58.55	0
gene_id_6621	189	42.33	2.00E-43
gene_id_6623	378	44.97	6.00E-122
gene_id_6624	316	75.32	3.00E-160
gene_id_6625	334	86.83	0
gene_id_6626	414	83.09	0
gene_id_6627	430	81.4	0
gene_id_6628	587	62.69	0
gene_id_6629	405	66.67	0
gene_id_6630	1066	61.82	0

gene_id_6631	441	74.6	0
gene_id_6632	112	36.61	5.00E-09
gene_id_6636	228	66.23	8.00E-103
gene_id_6637	570	62.11	0
gene_id_6638	443	81.26	0
gene_id_6639	448	65.4	0
gene_id_6640	356	68.54	0
gene_id_6641	273	42.86	3.00E-70
gene_id_6642	285	52.63	9.00E-102
gene_id_6643	283	72.79	1.00E-131
gene_id_6644	157	26.75	2.00E-07
gene_id_6645	478	35.98	7.00E-86
gene_id_6648	716	73.46	0
gene_id_6649	450	48.89	1.00E-142
gene_id_6650	570	38.42	2.00E-102
gene_id_6652	575	73.39	0
gene_id_6653	266	91.35	0
gene_id_6654	104	73.08	4.00E-52
gene_id_6655	563	75.84	0
gene_id_6657	141	68.79	2.00E-67
gene_id_6658	95	50.53	7.00E-25
gene_id_6659	385	77.4	0
gene_id_6660	91	53.85	5.00E-28
gene_id_6661	752	52.53	0
gene_id_6662	474	63.08	0
gene_id_6663	305	66.23	4.00E-134
gene_id_6664	219	67.12	4.00E-78
gene_id_6666	407	72.73	0
gene_id_6667	462	71	2.00E-175
gene_id_6668	92	82.61	1.00E-50
gene_id_6669	153	56.86	5.00E-21
gene_id_6670	293	64.85	9.00E-130
gene_id_6671	286	66.08	3.00E-125
gene_id_6672	464	73.28	0
gene_id_6673	99	45.45	3.00E-12
gene_id_6674	178	75.84	6.00E-100
gene_id_6675	173	41.62	6.00E-38
gene_id_6676	317	77.92	0
gene_id_6677	62	83.87	2.00E-28
gene_id_6678	292	68.84	5.00E-115
gene_id_6679	310	73.23	8.00E-115
gene_id_6680	355	78.03	7.00E-168
gene_id_6681	495	65.25	0
gene_id_6682	372	79.84	0
gene_id_6683	202	51.49	2.00E-64
gene_id_6684	261	73.18	4.00E-130
gene_id_6685	285	76.14	7.00E-161

gene_id_6686	393	79.13	0
gene_id_6687	108	41.67	1.00E-20
gene_id_6688	193	36.79	9.00E-42
gene_id_6689	413	76.03	0
gene_id_6690	102	44.12	2.00E-21
gene_id_6691	90	54.44	9.00E-32
gene_id_6692	472	88.35	0
gene_id_6693	470	89.79	0
gene_id_6694	453	70.64	0
gene_id_6695	358	67.88	1.00E-160
gene_id_6696	290	66.9	3.00E-126
gene_id_6697	270	72.96	5.00E-130
gene_id_6698	340	69.71	1.00E-167
gene_id_6700	214	80.84	1.00E-112
gene_id_6701	662	42.6	6.00E-144
gene_id_6702	206	59.71	3.00E-83
gene_id_6703	491	55.6	0
gene_id_6704	334	64.97	7.00E-152
gene_id_6705	228	74.56	7.00E-125
gene_id_6706	407	54.05	4.00E-150
gene_id_6707	335	45.07	7.00E-77
gene_id_6847	507	54.24	0
gene_id_6849	100	39	3.00E-15
gene_id_6850	543	36.46	2.00E-84
gene_id_6851	70	48.57	5.00E-15
gene_id_6852	178	60.67	2.00E-69
gene_id_6853	91	89.01	3.00E-53
gene_id_6854	220	93.18	4.00E-136
gene_id_6855	306	74.51	9.00E-174
gene_id_6857	195	43.59	9.00E-48
gene_id_6858	194	88.66	3.00E-110
gene_id_6859	200	71.5	2.00E-89
gene_id_6860	150	82.67	5.00E-85
gene_id_6862	107	36.45	2.00E-17
gene_id_6863	395	75.7	6.00E-179
gene_id_6864	126	61.11	7.00E-49
gene_id_6866	62	66.13	8.00E-22
gene_id_6868	272	27.21	3.00E-13
gene_id_7665	224	79.46	6.00E-128
gene_id_7666	95	83.16	5.00E-54
gene_id_7667	447	60.18	0
gene_id_7668	216	75.93	2.00E-114
gene_id_7669	230	71.74	6.00E-122
gene_id_7670	361	69.53	0
gene_id_7671	768	42.97	0
gene_id_7672	132	64.39	3.00E-59
gene_id_7673	956	46.97	0

gene_id_7674	318	51.57	3.00E-113
gene_id_7675	417	37.17	2.00E-72
gene_id_7676	217	57.14	9.00E-83
gene_id_7677	455	32.53	1.00E-71
gene_id_7678	522	39.27	6.00E-120
gene_id_7679	354	38.7	3.00E-65
gene_id_7680	471	49.26	2.00E-161
gene_id_7681	355	39.15	2.00E-69
gene_id_7682	269	71.38	3.00E-142
gene_id_7683	243	60.08	2.00E-104
gene_id_7684	444	79.5	0
gene_id_7685	442	58.82	0
gene_id_7686	310	66.77	7.00E-147
gene_id_7687	334	35.33	4.00E-66
gene_id_7688	422	35.55	1.00E-56
gene_id_7689	387	64.34	8.00E-126
gene_id_7690	107	45.79	1.00E-20
gene_id_7691	130	63.85	1.00E-54
gene_id_7692	516	52.33	1.00E-158
gene_id_7693	128	46.88	1.00E-29
gene_id_7694	74	68.92	1.00E-18
gene_id_7695	151	52.98	3.00E-52
gene_id_7696	186	43.01	5.00E-45
gene_id_7697	307	61.24	1.00E-130
gene_id_7698	602	52.99	0
gene_id_7699	162	45.68	4.00E-41
gene_id_7700	99	61.62	5.00E-36
gene_id_7701	133	53.38	1.00E-32
gene_id_7702	194	80.93	6.00E-119
gene_id_7703	214	54.21	9.00E-80
gene_id_7704	718	72.56	0
gene_id_7705	79	67.09	1.00E-29
gene_id_7706	47	74.47	1.00E-16
gene_id_7707	70	67.14	5.00E-26
gene_id_7708	74	51.35	6.00E-20
gene_id_7709	194	52.58	2.00E-62
gene_id_7710	628	71.34	0
gene_id_7711	278	82.73	9.00E-165
gene_id_7712	116	68.97	5.00E-49
gene_id_7713	189	53.44	7.00E-41
gene_id_7714	141	48.94	2.00E-44
gene_id_7715	224	71.43	3.00E-113
gene_id_7716	432	52.78	4.00E-139
gene_id_7717	117	49.57	5.00E-25
gene_id_7718	489	75.46	0
gene_id_7719	276	63.04	3.00E-126
gene_id_7720	321	71.34	5.00E-170

gene_id_7721	151	77.48	3.00E-82
gene_id_7722	291	73.88	8.00E-157
gene_id_7723	509	54.03	0
gene_id_7724	90	36.67	7.00E-11
gene_id_7725	631	70.36	0
gene_id_7726	347	64.27	1.00E-167
gene_id_7727	78	71.79	6.00E-35
gene_id_7728	156	67.95	2.00E-72
gene_id_7729	199	69.85	2.00E-98
gene_id_7730	487	63.45	0
gene_id_7731	514	77.24	0
gene_id_7732	412	74.76	0
gene_id_7733	317	52.37	3.00E-122
gene_id_7734	292	67.47	1.00E-146
gene_id_7735	260	62.69	2.00E-125
gene_id_7736	325	60.62	3.00E-133
gene_id_7737	104	72.12	2.00E-43
gene_id_7738	626	67.73	0
gene_id_7739	262	64.5	3.00E-111
gene_id_7740	583	60.72	0
gene_id_7741	312	74.36	0
gene_id_7856	240	76.67	8.00E-125
gene_id_7857	221	90.05	8.00E-143
gene_id_7858	239	87.45	1.00E-128
gene_id_7859	66	90.91	6.00E-36
gene_id_7860	173	80.35	2.00E-95
gene_id_7861	49	67.35	3.00E-15
gene_id_7862	505	67.33	0
gene_id_7863	235	59.57	5.00E-114
gene_id_7864	382	68.06	0
gene_id_7865	419	72.32	0
gene_id_7866	102	82.35	7.00E-56
gene_id_7867	224	59.82	6.00E-85
gene_id_7868	837	81.48	0
gene_id_7869	307	80.13	0
gene_id_7870	212	65.09	7.00E-88
gene_id_7871	684	67.25	0
gene_id_7872	365	73.7	0
gene_id_7873	280	72.14	4.00E-120
gene_id_7874	273	73.99	3.00E-130
gene_id_7875	277	79.06	5.00E-167
gene_id_7876	310	81.94	5.00E-176
gene_id_7877	218	64.68	2.00E-95
gene_id_7878	225	80.89	2.00E-131
gene_id_7879	295	78.64	1.00E-142
gene_id_7880	352	74.72	0
gene_id_7881	382	80.89	0

gene_id_7882	422	42.42	1.00E-112
gene_id_7883	243	52.26	2.00E-84
gene_id_7884	411	63.99	0
gene_id_7886	671	83.61	0
gene_id_7887	942	83.44	0
gene_id_7888	440	80	0
gene_id_7889	598	78.93	0
gene_id_7890	164	84.76	3.00E-85
gene_id_7891	210	70.48	3.00E-103
gene_id_7892	51	92.16	1.00E-25
gene_id_7893	179	75.42	8.00E-90
gene_id_7894	442	62.22	0
gene_id_7895	288	81.94	1.00E-169
gene_id_7897	337	72.11	1.00E-151
gene_id_7898	150	60	1.00E-52
gene_id_7899	114	66.67	3.00E-21
gene_id_7900	248	59.27	2.00E-102
gene_id_7901	382	76.18	2.00E-178
gene_id_7902	192	67.71	7.00E-88
gene_id_7903	239	68.2	4.00E-121
gene_id_7904	291	82.82	3.00E-172
gene_id_7905	450	82.22	0
gene_id_7906	280	80.36	4.00E-158
gene_id_7907	252	57.14	2.00E-102
gene_id_7909	293	67.58	2.00E-143
gene_id_7910	407	71.25	0
gene_id_7911	430	89.07	0
gene_id_7912	381	81.63	0
gene_id_7913	478	88.7	0
gene_id_7914	375	85.87	0
gene_id_7915	157	59.24	6.00E-61
gene_id_7916	410	76.1	0
gene_id_7917	356	60.67	7.00E-152
gene_id_7918	447	76.06	0
gene_id_7919	153	43.79	3.00E-40
gene_id_7920	241	54.77	2.00E-96
gene_id_7922	339	66.37	1.00E-138
gene_id_7923	335	83.28	0
gene_id_7924	394	74.87	0
gene_id_7925	249	75.1	2.00E-125
gene_id_7926	516	73.45	0
gene_id_7927	427	81.73	0
gene_id_7928	639	53.99	0
gene_id_7929	544	81.07	0
gene_id_7930	414	59.9	8.00E-175
gene_id_7931	364	70.6	0
gene_id_7933	584	70.55	0

gene_id_7934	64	79.69	2.00E-08
gene_id_7935	665	89.92	0
gene_id_7936	240	50	4.00E-74
gene_id_7937	158	65.19	9.00E-68
gene_id_7938	244	67.21	1.00E-114
gene_id_7939	128	70.31	4.00E-62
gene_id_7940	724	75.55	0
gene_id_7941	155	82.58	8.00E-90
gene_id_7942	146	35.62	6.00E-23
gene_id_7943	409	65.53	0
gene_id_7944	599	51.25	0
gene_id_7945	715	39.58	1.00E-138
gene_id_7945	168	35.71	2.00E-14
gene_id_7946	257	63.42	7.00E-92
gene_id_7947	242	30.99	2.00E-30
gene_id_7949	129	78.29	8.00E-69
gene_id_7950	372	72.85	2.00E-159
gene_id_7951	368	87.5	0
gene_id_7952	216	75.46	1.00E-116
gene_id_7953	96	81.25	2.00E-53
gene_id_7954	140	79.29	2.00E-75
gene_id_7955	141	59.57	9.00E-44
gene_id_7956	249	81.93	4.00E-126
gene_id_7957	871	85.76	0
gene_id_7958	665	62.11	0
gene_id_7959	171	76.02	5.00E-93
gene_id_7960	426	83.8	0
gene_id_7961	744	69.09	0
gene_id_7962	329	48.33	3.00E-97
gene_id_7963	119	65.55	9.00E-48
gene_id_7964	206	79.61	2.00E-108
gene_id_7966	201	82.09	1.00E-115
gene_id_7967	684	88.74	0
gene_id_7968	182	81.87	2.00E-106
gene_id_7969	168	72.02	1.00E-83
gene_id_7970	125	80.8	1.00E-67
gene_id_7971	173	72.83	1.00E-89
gene_id_7972	177	90.96	6.00E-98
gene_id_7973	106	77.36	8.00E-55
gene_id_7974	49	77.55	1.00E-18
gene_id_7975	205	28.29	5.00E-13
gene_id_7976	108	69.44	3.00E-48
gene_id_7977	182	71.43	4.00E-77
gene_id_7978	207	57.49	4.00E-75
gene_id_7979	375	69.07	5.00E-165
gene_id_7980	1026	74.46	0
gene_id_7981	143	70.63	6.00E-50

gene_id_7982	386	59.07	1.00E-162
gene_id_7983	377	60.74	3.00E-159
gene_id_7984	441	80.73	0
gene_id_7985	375	54.4	4.00E-135
gene_id_7986	286	51.05	2.00E-83
gene_id_7987	356	49.44	1.00E-111
gene_id_7988	246	58.54	1.00E-105
gene_id_7989	231	58.01	7.00E-86
gene_id_7990	463	54.86	2.00E-164
gene_id_7991	388	63.92	0
gene_id_7992	435	74.25	0
gene_id_7993	242	81.4	1.00E-139
gene_id_7994	327	87.77	0
gene_id_7995	327	82.87	0
gene_id_7996	72	81.94	8.00E-33
gene_id_7997	449	76.17	0
gene_id_7998	248	82.26	1.00E-144
gene_id_7999	167	74.85	6.00E-55
gene_id_8001	361	81.44	0
gene_id_8002	277	74.01	1.00E-152
gene_id_8003	499	77.76	0
gene_id_8004	444	88.74	0
gene_id_8005	281	73.31	5.00E-148
gene_id_8007	239	84.52	2.00E-147
gene_id_8008	229	86.46	1.00E-122
gene_id_8009	296	83.45	3.00E-179
gene_id_8010	443	80.36	0
gene_id_8011	254	81.89	8.00E-137
gene_id_8012	472	83.05	0
gene_id_8013	410	81.22	0
gene_id_8014	434	91.47	0
gene_id_8015	287	51.92	1.00E-85
gene_id_8016	363	77.13	0
gene_id_8017	129	71.32	4.00E-61
gene_id_8018	448	75.45	0
gene_id_8019	481	81.08	0
gene_id_8020	275	75.27	7.00E-143
gene_id_8021	314	73.25	8.00E-162
gene_id_8022	270	67.04	1.00E-133
gene_id_8023	466	74.89	0
gene_id_8024	301	77.41	1.00E-172
gene_id_8025	577	70.36	0
gene_id_8026	461	78.96	0
gene_id_8027	445	81.12	0
gene_id_8028	258	69.77	2.00E-122
gene_id_8029	562	80.6	0
gene_id_8030	249	54.22	5.00E-98

gene_id_8031	582	83.51	0
gene_id_8032	238	49.58	2.00E-65
gene_id_8034	132	75.76	1.00E-60
gene_id_8035	290	79.66	3.00E-176
gene_id_8036	115	73.04	4.00E-57
gene_id_8037	274	71.53	2.00E-127
gene_id_8038	219	64.84	4.00E-101
gene_id_8039	164	53.05	2.00E-57
gene_id_8040	403	62.53	0
gene_id_8041	191	65.45	1.00E-91
gene_id_8043	118	83.9	4.00E-66
gene_id_8044	171	94.15	1.00E-115
gene_id_8045	153	67.97	2.00E-60
gene_id_8046	365	86.3	0
gene_id_8047	345	83.19	6.00E-165
gene_id_8048	146	72.6	3.00E-74
gene_id_8049	142	76.76	7.00E-61
gene_id_8050	102	83.33	1.00E-40
gene_id_8051	610	76.39	0
gene_id_8052	490	78.57	0
gene_id_8053	470	71.28	0
gene_id_8054	400	65.75	2.00E-157
gene_id_8055	336	83.04	0
gene_id_8056	33	66.67	2.00E-06
gene_id_8057	386	41.71	4.00E-92
gene_id_8058	122	54.1	6.00E-36
gene_id_8059	587	65.93	0
gene_id_8060	382	70.42	7.00E-176
gene_id_8061	387	55.3	5.00E-129
gene_id_8063	651	54.22	0
gene_id_8064	301	38.21	1.00E-60
gene_id_8065	431	42.92	5.00E-109
gene_id_8066	749	63.28	0
gene_id_8067	71	63.38	6.00E-26
gene_id_8068	359	64.35	2.00E-162
gene_id_8069	334	69.76	1.00E-169
gene_id_8070	207	30.43	8.00E-17
gene_id_8071	572	56.64	6.00E-163
gene_id_8072	384	52.86	2.00E-145
gene_id_8073	210	55.71	7.00E-70
gene_id_8074	407	67.32	0
gene_id_8075	119	80.67	3.00E-63
gene_id_8076	477	54.51	3.00E-165
gene_id_8077	389	66.84	7.00E-162
gene_id_8078	699	47.93	0
gene_id_8079	271	66.42	4.00E-122
gene_id_8080	427	83.37	0

gene_id_8081	225	55.11	1.00E-74
gene_id_8082	439	72.44	0
gene_id_8083	460	83.04	0
gene_id_8084	142	64.08	5.00E-60
gene_id_8085	258	51.16	3.00E-91
gene_id_8086	374	86.1	0
gene_id_8087	196	66.33	4.00E-81
gene_id_8088	87	66.67	2.00E-31
gene_id_8089	289	64.36	2.00E-136
gene_id_8090	351	48.72	9.00E-100
gene_id_8091	425	80.24	0
gene_id_8092	157	87.9	6.00E-92
gene_id_8093	723	58.92	0
gene_id_8094	123	69.11	1.00E-51
gene_id_8095	216	69.44	3.00E-68
gene_id_8096	225	68.44	3.00E-86
gene_id_8097	201	57.71	4.00E-75
gene_id_8098	94	62.77	1.00E-35
gene_id_8099	276	68.84	2.00E-147
gene_id_8198	91	39.56	4.00E-14
gene_id_8200	347	55.62	1.00E-143
gene_id_8201	322	57.76	8.00E-134
gene_id_8202	176	35.23	2.00E-27
gene_id_8203	184	32.61	6.00E-18
gene_id_8204	531	52.35	0
gene_id_8205	115	43.48	3.00E-21
gene_id_8205	95	45.26	8.00E-18
gene_id_8206	421	29.69	3.00E-52
gene_id_8207	1175	32.26	0
gene_id_8208	199	35.18	3.00E-35
gene_id_8209	468	33.12	7.00E-51
gene_id_8210	115	46.09	8.00E-27
gene_id_8211	394	38.07	1.00E-74
gene_id_8212	290	33.45	3.00E-33
gene_id_8213	617	33.39	9.00E-89
gene_id_8214	562	41.28	1.00E-140
gene_id_8694	154	57.79	1.00E-47
gene_id_8695	283	78.45	5.00E-160
gene_id_8696	422	62.8	0
gene_id_8697	331	82.48	0
gene_id_8698	320	72.5	3.00E-144
gene_id_8699	376	50.53	8.00E-124
gene_id_8700	255	56.08	3.00E-94
gene_id_8701	334	55.69	8.00E-136
gene_id_8702	269	71.38	7.00E-129
gene_id_8703	470	49.36	7.00E-161
gene_id_8704	332	79.52	0

gene_id_8705	302	42.38	1.00E-64
gene_id_8706	427	65.11	0
gene_id_8707	106	79.25	3.00E-48
gene_id_8708	381	50.92	2.00E-84
gene_id_8709	550	78.73	0
gene_id_8710	190	54.74	1.00E-66
gene_id_8711	422	55.21	3.00E-154
gene_id_8712	311	70.42	2.00E-169
gene_id_8713	379	58.05	2.00E-147
gene_id_8714	306	55.23	8.00E-126
gene_id_8715	395	66.58	5.00E-170
gene_id_8716	343	81.05	0
gene_id_8717	505	80.4	0
gene_id_8718	307	85.34	5.00E-143
gene_id_8719	255	46.27	3.00E-74
gene_id_8720	455	72.97	0
gene_id_8721	111	58.56	5.00E-15
gene_id_8722	725	39.72	8.00E-159
gene_id_8723	119	62.18	1.00E-42
gene_id_8725	406	64.04	3.00E-155
gene_id_8726	385	66.75	4.00E-175
gene_id_8727	325	38.46	4.00E-51
gene_id_8728	719	68.57	0
gene_id_8729	89	53.93	3.00E-30
gene_id_8730	377	55.7	6.00E-148
gene_id_8731	696	70.83	0
gene_id_8732	380	63.16	3.00E-149
gene_id_8733	66	65.15	5.00E-22
gene_id_8734	486	68.52	0
gene_id_8735	298	32.55	7.00E-31
gene_id_8736	635	68.5	0
gene_id_8737	272	68.75	7.00E-135
gene_id_8738	203	72.41	3.00E-104
gene_id_8739	122	75.41	3.00E-61
gene_id_8740	108	68.52	5.00E-41
gene_id_8742	446	56.28	2.00E-170
gene_id_8743	303	45.87	8.00E-78
gene_id_8745	236	49.58	2.00E-74
gene_id_8745	117	35.9	2.00E-10
gene_id_8746	455	75.16	0
gene_id_8747	159	47.17	3.00E-41
gene_id_8748	460	55.22	2.00E-168
gene_id_8749	370	56.22	9.00E-152
gene_id_8750	391	43.22	3.00E-108
gene_id_8751	181	46.96	2.00E-51
gene_id_8752	311	42.12	2.00E-68
gene_id_8753	132	70.45	5.00E-49

gene_id_8754	136	75	3.00E-69
gene_id_8755	182	86.81	5.00E-104
gene_id_8756	460	55	5.00E-172
gene_id_8757	314	66.24	7.00E-122
gene_id_8758	259	57.53	2.00E-108
gene_id_8759	547	55.94	0
gene_id_8760	154	64.94	1.00E-45
gene_id_8761	178	67.42	2.00E-80
gene_id_8762	94	39.36	1.00E-18
gene_id_8763	203	52.71	1.00E-73
gene_id_8764	153	67.32	1.00E-62
gene_id_8765	466	72.53	0
gene_id_8766	301	38.21	1.00E-40
gene_id_8767	448	69.87	0
gene_id_8769	318	67.3	5.00E-167
gene_id_8770	294	55.44	4.00E-104
gene_id_8771	235	42.55	1.00E-58
gene_id_8772	271	88.93	2.00E-176
gene_id_8773	108	80.56	2.00E-40
gene_id_8774	135	67.41	3.00E-61
gene_id_8775	533	79.17	0
gene_id_8776	462	80.95	0
gene_id_8777	436	77.98	0
gene_id_8778	452	68.58	0
gene_id_8779	405	66.91	0
gene_id_8780	102	74.51	1.00E-37
gene_id_8781	202	50.99	4.00E-59
gene_id_8782	349	41.83	5.00E-77
gene_id_8783	222	57.21	3.00E-85
gene_id_9474	475	62.32	0
gene_id_9475	77	54.55	2.00E-20
gene_id_9480	176	28.98	3.00E-16
gene_id_9481	137	27.01	6.00E-06
gene_id_9484	141	56.74	6.00E-45
gene_id_9486	145	46.9	1.00E-39
gene_id_9487	55	60	6.00E-14
gene_id_9488	216	35.19	1.00E-31
gene_id_9488	170	34.71	1.00E-21
gene_id_9488	184	34.24	4.00E-20
gene_id_9489	106	40.57	1.00E-13
gene_id_9491	193	56.99	4.00E-65
gene_id_9492	285	50.53	2.00E-69
gene_id_9494	49	79.59	1.00E-22
gene_id_9496	43	60.47	9.00E-09
gene_id_9497	318	60.06	1.00E-130
gene_id_9503	128	76.56	3.00E-64
gene_id_9504	201	64.68	8.00E-95

gene_id_9505	194	50	3.00E-42
gene_id_9507	597	65.83	0
gene_id_9508	410	77.56	0
gene_id_9509	131	36.64	9.00E-09
gene_id_9707	28	75	7.00E-06
gene_id_9708	425	92.24	0
gene_id_9709	475	34.32	1.00E-83
gene_id_9710	301	63.79	2.00E-100
gene_id_9711	130	70.77	3.00E-59
gene_id_9712	276	56.52	3.00E-97
gene_id_9713	91	92.31	2.00E-54
gene_id_9714	61	68.85	2.00E-21
gene_id_9715	331	85.8	0
gene_id_9716	208	80.29	3.00E-114
gene_id_9717	541	87.62	0
gene_id_9718	306	52.94	7.00E-91
gene_id_9719	171	40.35	1.00E-41
gene_id_9720	296	91.89	0
gene_id_9722	439	77.68	0
gene_id_9723	516	92.25	0
gene_id_9724	327	87.77	0
gene_id_9725	288	87.5	3.00E-158
gene_id_9726	311	93.57	0
gene_id_9727	203	90.15	4.00E-132
gene_id_9728	230	86.96	7.00E-139
gene_id_9729	309	64.72	4.00E-102
gene_id_9730	531	60.08	0
gene_id_9731	230	56.52	2.00E-87
gene_id_9732	298	54.7	9.00E-103
gene_id_9733	44	59.09	2.00E-06
gene_id_9734	42	90.48	6.00E-17
gene_id_9735	163	38.04	3.00E-27
gene_id_9736	132	55.3	3.00E-44
gene_id_9737	50	64	2.00E-16
gene_id_9738	294	32.65	9.00E-24
gene_id_9739	96	66.67	4.00E-28
gene_id_9740	327	73.09	1.00E-160
gene_id_9741	272	65.07	3.00E-127
gene_id_9743	386	91.19	0
gene_id_9744	99	66.67	3.00E-40
gene_id_9745	424	68.4	0
gene_id_9746	392	56.63	1.00E-144
gene_id_9748	190	48.42	2.00E-58
gene_id_9749	157	80.25	5.00E-56
gene_id_9750	172	76.74	7.00E-92
gene_id_9751	210	70.48	4.00E-93
gene_id_9752	86	81.4	2.00E-41

gene_id_9753	143	77.62	5.00E-71
gene_id_9754	252	68.25	7.00E-116
gene_id_9755	124	65.32	3.00E-53
gene_id_9756	86	52.33	9.00E-13
gene_id_9757	278	67.27	5.00E-118
gene_id_9758	291	70.1	5.00E-133
gene_id_9759	79	72.15	4.00E-32
gene_id_9760	122	60.66	1.00E-48
gene_id_9761	382	75.39	0
gene_id_9762	275	61.82	2.00E-112
gene_id_9763	262	60.69	2.00E-105
gene_id_9764	297	68.69	5.00E-148
gene_id_9765	198	73.23	2.00E-70
gene_id_9766	375	64.27	8.00E-167
gene_id_9767	224	67.86	8.00E-40
gene_id_9931	318	79.25	2.00E-179
gene_id_9932	178	75.28	2.00E-85
gene_id_9933	197	77.66	1.00E-106
gene_id_9934	358	76.54	0
gene_id_9935	61	83.61	1.00E-28
gene_id_9937	136	74.26	1.00E-49
gene_id_9938	217	44.24	2.00E-63
gene_id_9939	173	58.38	3.00E-65
gene_id_9940	238	66.39	6.00E-97
gene_id_9941	328	84.45	0
gene_id_9942	206	65.53	2.00E-91
gene_id_9943	438	62.79	0
gene_id_9944	228	64.91	1.00E-110
gene_id_9945	494	77.13	0
gene_id_9946	195	76.92	1.00E-87
gene_id_9947	112	50.89	9.00E-13
gene_id_9948	130	58.46	1.00E-46
gene_id_9949	113	79.65	2.00E-50
gene_id_9950	334	77.25	4.00E-179
gene_id_9951	149	72.48	3.00E-77
gene_id_9952	64	90.62	4.00E-34
gene_id_9954	244	77.46	4.00E-139
gene_id_9955	137	76.64	8.00E-62
gene_id_9956	111	69.37	2.00E-48
gene_id_9957	387	74.16	0
gene_id_9958	438	63.7	0
gene_id_9959	389	66.84	0
gene_id_9960	295	92.2	0
gene_id_9962	214	64.95	2.00E-87
gene_id_9963	395	58.23	5.00E-160
gene_id_9964	166	65.66	3.00E-74
gene_id_9966	255	87.06	6.00E-163

gene_id_9967	446	73.99	0
gene_id_9968	569	57.12	0
gene_id_9969	150	76	7.00E-80
gene_id_9970	187	55.08	3.00E-69
gene_id_9971	284	60.21	9.00E-122
gene_id_9972	265	72.08	2.00E-125
gene_id_9973	628	72.61	0
gene_id_9974	151	75.5	3.00E-77
gene_id_9975	291	68.73	2.00E-130
gene_id_9976	82	57.32	3.00E-19
gene_id_9977	393	65.9	0
gene_id_9978	317	57.73	2.00E-125
gene_id_9979	136	65.44	1.00E-59
gene_id_9980	75	77.33	2.00E-23
gene_id_9981	145	65.52	4.00E-53
gene_id_9982	129	90.7	3.00E-62
gene_id_9983	168	62.5	2.00E-65
gene_id_9984	201	64.68	3.00E-75
gene_id_9985	200	44	6.00E-38
gene_id_9986	372	72.31	2.00E-165
gene_id_9987	128	89.84	2.00E-66
gene_id_9988	63	95.24	9.00E-33
gene_id_9989	108	53.7	1.00E-32
gene_id_9990	334	60.48	3.00E-144
gene_id_9991	153	53.59	4.00E-43
gene_id_9992	185	80.54	1.00E-110
gene_id_9993	339	61.06	3.00E-147
gene_id_9994	130	70	1.00E-58
gene_id_9995	545	68.26	0
gene_id_9996	66	45.45	5.00E-18
gene_id_9997	405	74.32	0
gene_id_9998	193	55.96	3.00E-68
gene_id_9999	329	62.61	3.00E-149
gene_id_10000	102	60.78	3.00E-24
gene_id_10001	136	78.68	1.00E-69
gene_id_10002	85	80	4.00E-31
gene_id_10003	870	69.43	0
gene_id_10004	341	57.77	5.00E-126
gene_id_10005	68	58.82	4.00E-06
gene_id_10006	60	65	7.00E-20
gene_id_10007	168	55.95	5.00E-62
gene_id_10008	364	76.65	0
gene_id_10009	121	90.91	1.00E-75
gene_id_10010	401	79.8	0
gene_id_10011	131	83.97	2.00E-72
gene_id_10012	424	66.04	0
gene_id_10013	342	62.87	5.00E-141

gene_id_10014	594	78.45	0
gene_id_10015	421	72.45	0
gene_id_10016	489	52.35	7.00E-178
gene_id_10017	149	79.87	3.00E-85
gene_id_10018	345	54.2	3.00E-103
gene_id_10019	205	64.39	1.00E-93
gene_id_10020	734	78.2	0
gene_id_10021	170	76.47	5.00E-91
gene_id_10022	1200	45.17	0
gene_id_10023	597	49.25	4.00E-172
gene_id_10024	478	50.21	9.00E-153
gene_id_10025	143	48.25	1.00E-33
gene_id_10026	331	47.73	6.00E-101
gene_id_10027	299	73.58	1.00E-159
gene_id_10028	401	78.05	0
gene_id_10029	221	78.28	5.00E-125
gene_id_10030	110	71.82	3.00E-50
gene_id_10031	234	76.92	5.00E-118
gene_id_10032	198	46.46	8.00E-51
gene_id_10033	98	62.24	8.00E-38
gene_id_10034	368	89.95	0
gene_id_10035	340	73.53	0
gene_id_10036	415	58.07	4.00E-162
gene_id_10037	76	68.42	7.00E-11
gene_id_10038	173	61.27	1.00E-80
gene_id_10039	337	84.87	0
gene_id_10040	199	62.31	4.00E-84
gene_id_10041	156	81.41	8.00E-91
gene_id_10042	191	67.02	1.00E-91
gene_id_10389	615	35.45	3.00E-108
gene_id_10389	443	33.18	7.00E-62
gene_id_10389	566	31.63	7.00E-62
gene_id_10389	588	26.36	4.00E-36
gene_id_10389	536	24.81	6.00E-31
gene_id_10389	156	39.74	1.00E-22
gene_id_10390	161	58.39	1.00E-42
gene_id_10390	56	58.93	5.00E-10
gene_id_10390	65	55.38	7.00E-10
gene_id_10391	362	25.69	1.00E-20
gene_id_10395	110	70.91	3.00E-52
gene_id_10397	176	70.45	2.00E-79
gene_id_10398	61	75.41	4.00E-26
gene_id_10400	193	48.19	2.00E-57
gene_id_10401	127	72.44	8.00E-60
gene_id_10402	311	47.91	1.00E-105
gene_id_10403	150	57.33	2.00E-55
gene_id_10404	627	67.46	0

gene_id_10405	412	52.91	6.00E-139
gene_id_10406	68	86.76	2.00E-35
gene_id_10407	113	57.52	3.00E-39
gene_id_10408	218	65.14	4.00E-90
gene_id_10409	44	61.36	4.00E-08
gene_id_10410	367	62.13	1.00E-143
gene_id_10411	371	83.56	0
gene_id_10412	257	77.82	2.00E-151
gene_id_10413	365	69.59	0
gene_id_10414	207	68.12	3.00E-92
gene_id_10415	209	60.77	3.00E-90
gene_id_10416	127	69.29	5.00E-63
gene_id_10417	321	42.06	3.00E-86
gene_id_10419	619	57.03	0
gene_id_10420	363	50.69	3.00E-88
gene_id_10421	401	40.65	2.00E-100
gene_id_10422	52	40.38	2.00E-06
gene_id_10423	577	46.97	9.00E-84
gene_id_10424	301	74.09	2.00E-170
gene_id_10425	527	60.72	0
gene_id_10426	275	71.64	6.00E-118
gene_id_10427	384	63.54	3.00E-178
gene_id_10428	1010	47.72	0
gene_id_10429	1144	61.8	0
gene_id_10430	1248	63.78	0
gene_id_10432	239	81.59	1.00E-135
gene_id_10433	475	86.53	0
gene_id_10434	238	73.11	4.00E-125
gene_id_10435	72	61.11	1.00E-18
gene_id_10436	247	54.25	5.00E-94
gene_id_10437	317	71.29	3.00E-147
gene_id_10438	73	65.75	1.00E-25
gene_id_10439	381	61.42	3.00E-168
gene_id_10441	357	72.83	0
gene_id_10443	200	57	2.00E-77
gene_id_10444	65	81.54	2.00E-30
gene_id_10445	503	67	0
gene_id_10446	229	75.55	2.00E-103
gene_id_10447	97	74.23	4.00E-41
gene_id_10448	356	62.36	8.00E-158
gene_id_10450	204	61.27	2.00E-74
gene_id_10451	359	76.32	3.00E-178
gene_id_10452	531	47.65	8.00E-165
gene_id_10453	373	55.23	4.00E-141
gene_id_10454	451	82.93	0
gene_id_10455	456	63.16	0
gene_id_10456	851	64.51	0

gene_id_10457	409	70.42	0
gene_id_10458	503	61.63	0
gene_id_10459	517	62.09	0
gene_id_10460	698	68.48	0
gene_id_10461	130	57.69	6.00E-16
gene_id_10462	426	68.08	0
gene_id_10463	94	54.26	2.00E-33
gene_id_10464	222	43.24	4.00E-55
gene_id_10465	318	35.85	1.00E-52
gene_id_10466	78	52.56	2.00E-19
gene_id_10467	482	61.2	0
gene_id_10468	904	63.83	0
gene_id_10469	308	53.57	1.00E-102
gene_id_10470	690	62.32	0
gene_id_10471	514	61.48	0
gene_id_10472	136	59.56	3.00E-55
gene_id_10473	193	68.91	4.00E-89
gene_id_10474	163	56.44	3.00E-41
gene_id_10475	267	82.4	3.00E-121
gene_id_10476	112	62.5	1.00E-41
gene_id_10477	92	66.3	7.00E-28
gene_id_10914	76	53.95	2.00E-19
gene_id_10915	107	69.16	1.00E-48
gene_id_10916	218	70.64	3.00E-97
gene_id_10917	211	71.56	8.00E-103
gene_id_10918	207	65.7	8.00E-90
gene_id_10919	365	70.41	0
gene_id_10920	256	82.81	6.00E-116
gene_id_10921	66	43.94	5.00E-15
gene_id_10922	363	60.61	2.00E-157
gene_id_10923	222	50.9	2.00E-74
gene_id_10924	370	93.51	0
gene_id_10925	601	69.88	0
gene_id_10926	329	78.12	0
gene_id_10927	130	58.46	6.00E-48
gene_id_10928	685	69.05	0
gene_id_10929	280	91.79	0
gene_id_10930	136	69.12	5.00E-60
gene_id_10931	245	56.73	4.00E-90
gene_id_10932	422	77.01	0
gene_id_10933	192	67.19	2.00E-74
gene_id_10934	293	82.94	6.00E-180
gene_id_10935	128	71.09	1.00E-58
gene_id_10936	116	52.59	2.00E-24
gene_id_10937	137	71.53	6.00E-57
gene_id_10938	714	75.63	0
gene_id_10939	321	73.52	2.00E-165

gene_id_10940	403	56.08	4.00E-152
gene_id_10941	91	81.32	8.00E-44
gene_id_10942	495	82.42	0
gene_id_10943	150	79.33	1.00E-72
gene_id_10944	43	100	5.00E-22
gene_id_10945	115	72.17	7.00E-55
gene_id_10946	428	67.76	0
gene_id_10947	231	56.71	2.00E-88
gene_id_10948	311	71.06	1.00E-145
gene_id_10949	379	78.63	0
gene_id_10950	616	86.53	0
gene_id_10951	176	59.09	5.00E-68
gene_id_10952	529	81.1	0
gene_id_10953	339	71.68	0
gene_id_10954	376	54.52	4.00E-145
gene_id_10955	598	85.79	0
gene_id_10956	103	34.95	3.00E-11
gene_id_10957	325	61.54	5.00E-149
gene_id_10958	323	82.97	8.00E-178
gene_id_10959	87	83.91	2.00E-19
gene_id_10960	345	55.65	4.00E-135
gene_id_10961	792	45.2	0
gene_id_10962	198	47.98	4.00E-50
gene_id_10964	174	41.38	6.00E-24
gene_id_10965	826	79.42	0
gene_id_10966	130	72.31	6.00E-56
gene_id_10967	161	50.31	9.00E-56
gene_id_10968	261	85.06	1.00E-153
gene_id_10969	218	80.28	5.00E-124
gene_id_10970	460	81.74	0
gene_id_10971	439	72.21	0
gene_id_10972	351	65.81	4.00E-139
gene_id_10973	464	81.25	0
gene_id_10974	314	53.5	1.00E-102
gene_id_10975	365	40	2.00E-69
gene_id_10976	253	45.45	2.00E-68
gene_id_10977	215	62.79	1.00E-50
gene_id_10978	121	61.16	6.00E-44
gene_id_10979	428	69.63	0
gene_id_10980	491	65.17	0
gene_id_10981	498	83.53	0
gene_id_10982	222	76.58	5.00E-113
gene_id_10983	182	67.03	7.00E-83
gene_id_10985	66	51.52	1.00E-11
gene_id_10986	184	58.7	1.00E-64
gene_id_10987	132	89.39	5.00E-76
gene_id_10988	85	95.29	3.00E-46

gene_id_10989	93	76.34	6.00E-34
gene_id_10990	289	51.56	6.00E-63
gene_id_10991	203	75.86	4.00E-82
gene_id_10993	124	54.84	1.00E-46
gene_id_10996	229	74.67	8.00E-127
gene_id_10997	450	63.33	0
gene_id_10998	265	79.62	2.00E-142
gene_id_10999	473	86.05	0
gene_id_11000	82	89.02	8.00E-43
gene_id_11001	147	70.07	2.00E-71
gene_id_11002	960	70	0
gene_id_11003	83	48.19	5.00E-18
gene_id_11028	383	52.22	6.00E-141
gene_id_11029	361	76.45	0
gene_id_11031	578	70.93	0
gene_id_11032	412	45.63	2.00E-119
gene_id_11033	429	39.63	4.00E-101
gene_id_11034	109	77.06	8.00E-54
gene_id_11036	269	25.28	2.00E-17
gene_id_11037	205	57.07	7.00E-63
gene_id_11038	82	53.66	9.00E-25
gene_id_11039	1672	57.18	0
gene_id_11040	168	42.26	3.00E-19
gene_id_11041	226	62.83	8.00E-83
gene_id_11042	293	89.42	0
gene_id_11043	189	78.84	3.00E-103
gene_id_11044	656	40.4	1.00E-120
gene_id_11045	199	66.83	6.00E-96
gene_id_11046	247	25.91	5.00E-11
gene_id_11047	211	68.72	9.00E-106
gene_id_11048	124	56.45	3.00E-39
gene_id_11049	250	86.4	4.00E-139
gene_id_11050	151	82.12	2.00E-83
gene_id_11051	286	66.78	3.00E-143
gene_id_11052	70	87.14	2.00E-38
gene_id_11053	187	70.05	4.00E-73
gene_id_11054	196	72.96	7.00E-104
gene_id_11055	113	58.41	9.00E-40
gene_id_11056	79	69.62	8.00E-31
gene_id_11057	96	30.21	6.00E-06
gene_id_11058	284	28.17	6.00E-16
gene_id_11059	115	57.39	1.00E-38
gene_id_11060	166	54.22	3.00E-42
gene_id_11061	620	45.48	0
gene_id_11061	278	33.81	8.00E-29
gene_id_11061	380	28.68	7.00E-20
gene_id_11061	326	25.15	2.00E-16

gene_id_11125	497	79.07	0
gene_id_11126	135	82.22	2.00E-76
gene_id_11127	344	80.81	0
gene_id_11128	299	69.9	3.00E-149
gene_id_11129	173	74.57	4.00E-91
gene_id_11130	317	66.88	3.00E-161
gene_id_11131	317	72.87	6.00E-174
gene_id_11132	254	83.46	3.00E-143
gene_id_11133	324	66.36	4.00E-149
gene_id_11134	126	79.37	2.00E-67
gene_id_11135	283	68.55	1.00E-142
gene_id_11136	223	76.68	1.00E-112
gene_id_11137	465	52.04	3.00E-145
gene_id_11138	95	52.63	3.00E-25
gene_id_11139	331	66.47	2.00E-154
gene_id_11140	588	86.22	0
gene_id_11141	178	83.15	2.00E-105
gene_id_11142	457	53.17	1.00E-149
gene_id_11143	151	60.26	4.00E-55
gene_id_11144	250	68.8	2.00E-99
gene_id_11145	815	54.11	0
gene_id_11146	61	65.57	1.00E-20
gene_id_11147	462	67.1	0
gene_id_11148	410	67.8	0
gene_id_11149	454	72.69	0
gene_id_11150	91	63.74	3.00E-37
gene_id_11151	271	31	8.00E-25
gene_id_11152	127	74.8	7.00E-49
gene_id_11153	91	53.85	5.00E-29
gene_id_11154	138	46.38	5.00E-30
gene_id_11155	231	54.11	9.00E-84
gene_id_11156	93	78.49	2.00E-43
gene_id_11157	78	50	4.00E-17
gene_id_11158	389	53.21	9.00E-132
gene_id_11159	367	45.78	1.00E-94
gene_id_11160	547	66	0
gene_id_11161	303	77.23	5.00E-164
gene_id_11162	678	54.28	0
gene_id_11163	286	81.12	3.00E-142
gene_id_11164	262	83.21	3.00E-158
gene_id_11165	284	80.99	3.00E-168
gene_id_11166	576	67.19	0
gene_id_11167	219	47.95	6.00E-72
gene_id_11168	380	46.05	2.00E-104
gene_id_11169	592	62.67	0
gene_id_11170	461	74.84	0
gene_id_11171	132	75.76	2.00E-43

gene_id_11172	62	82.26	5.00E-28
gene_id_11173	213	61.03	2.00E-73
gene_id_11174	458	53.71	9.00E-164
gene_id_11175	306	56.86	6.00E-125
gene_id_11176	54	46.3	3.00E-08
gene_id_11177	220	77.27	3.00E-111
gene_id_11178	251	89.24	3.00E-168
gene_id_11179	516	63.76	0
gene_id_11180	462	77.49	0
gene_id_11181	371	80.59	0
gene_id_11183	230	79.13	2.00E-132
gene_id_11184	91	89.01	2.00E-50
gene_id_11185	481	70.06	0
gene_id_11186	520	77.5	0
gene_id_11187	190	85.26	6.00E-110
gene_id_11188	1091	72.5	0
gene_id_11189	80	61.25	5.00E-24
gene_id_11190	126	57.14	9.00E-36
gene_id_11191	237	63.29	4.00E-88
gene_id_11193	160	38.12	4.00E-30
gene_id_11195	365	73.7	1.00E-178
gene_id_11196	479	74.74	0
gene_id_11197	259	69.5	1.00E-98
gene_id_11198	258	73.64	2.00E-139
gene_id_11199	324	60.19	8.00E-140
gene_id_11200	274	59.12	2.00E-117
gene_id_11201	272	73.53	5.00E-143
gene_id_11203	184	51.09	2.00E-66
gene_id_11204	344	73.26	4.00E-179
gene_id_11205	622	79.58	0
gene_id_11206	603	84.74	0
gene_id_11207	864	70.49	0
gene_id_11208	440	77.95	0
gene_id_11209	337	63.8	5.00E-144
gene_id_11210	402	83.58	0
gene_id_11211	269	60.59	6.00E-98
gene_id_11212	206	66.02	8.00E-83
gene_id_11213	324	95.06	0
gene_id_11214	293	77.13	2.00E-151
gene_id_11216	340	78.24	3.00E-170
gene_id_11217	655	48.85	0
gene_id_11218	169	53.85	2.00E-53
gene_id_11219	283	51.24	5.00E-86
gene_id_11220	148	46.62	8.00E-19
gene_id_11221	223	55.16	8.00E-69
gene_id_11222	164	48.17	4.00E-46
gene_id_11223	207	60.87	6.00E-74

gene_id_11224	320	84.06	0
gene_id_11225	214	82.24	2.00E-116
gene_id_11226	207	43.96	3.00E-59
gene_id_11227	134	72.39	6.00E-62
gene_id_11228	765	55.82	0
gene_id_11229	193	43.01	2.00E-47
gene_id_11230	309	72.17	2.00E-165
gene_id_11231	535	86.54	0
gene_id_11232	121	59.5	9.00E-42
gene_id_11233	556	77.16	0
gene_id_11234	136	54.41	9.00E-47
gene_id_11235	287	64.11	6.00E-112
gene_id_11236	158	72.15	7.00E-79
gene_id_11237	286	75.52	7.00E-161
gene_id_11238	274	51.82	3.00E-91
gene_id_11239	452	55.53	9.00E-153
gene_id_11240	424	80.9	0
gene_id_11241	258	57.75	7.00E-106
gene_id_11242	289	52.25	6.00E-88
gene_id_11243	520	56.54	0
gene_id_11244	224	70.98	4.00E-101
gene_id_11267	68	66.18	3.00E-22
gene_id_11268	110	59.09	4.00E-19
gene_id_11269	147	47.62	7.00E-40
gene_id_11270	225	43.56	8.00E-46
gene_id_11272	116	51.72	2.00E-34
gene_id_11274	483	48.86	2.00E-150
gene_id_11331	228	67.98	4.00E-104
gene_id_11332	135	48.15	5.00E-35
gene_id_11333	162	50.62	7.00E-52
gene_id_11334	628	42.68	6.00E-169
gene_id_11335	254	34.25	6.00E-35
gene_id_11336	119	45.38	7.00E-25
gene_id_11337	441	24.72	3.00E-20
gene_id_11338	1457	24.85	8.00E-83
gene_id_11339	392	28.83	1.00E-37
gene_id_11340	428	26.87	9.00E-37
gene_id_11341	241	28.63	2.00E-15
gene_id_11343	578	39.45	3.00E-137
gene_id_11539	273	53.48	3.00E-99
gene_id_11540	233	88.41	5.00E-138
gene_id_11541	491	58.66	0
gene_id_11543	278	65.83	3.00E-107
gene_id_11544	137	77.37	7.00E-70
gene_id_11545	511	57.14	0
gene_id_11546	339	74.93	8.00E-163
gene_id_11628	301	66.45	1.00E-120

gene_id_11629	404	75.74	0
gene_id_11630	148	91.22	3.00E-90
gene_id_11631	492	88.41	0
gene_id_11632	342	62.87	2.00E-144
gene_id_11633	194	74.74	8.00E-90
gene_id_11634	440	80.91	0
gene_id_11635	434	67.74	0
gene_id_11636	387	66.93	6.00E-180
gene_id_11637	258	74.81	5.00E-89
gene_id_11638	352	58.81	7.00E-136
gene_id_11639	655	61.98	0
gene_id_11641	618	82.2	0
gene_id_11642	195	58.97	5.00E-80
gene_id_11643	221	67.42	3.00E-93
gene_id_11644	426	67.84	0
gene_id_11645	333	66.67	7.00E-155
gene_id_11646	173	48.55	8.00E-47
gene_id_11647	412	72.09	0
gene_id_11648	229	69.87	4.00E-113
gene_id_11649	279	58.78	1.00E-118
gene_id_11650	75	76	9.00E-33
gene_id_11768	1256	69.35	0
gene_id_11769	293	64.51	5.00E-137
gene_id_11770	270	86.3	1.00E-151
gene_id_11771	295	45.42	9.00E-82
gene_id_11772	120	59.17	5.00E-42
gene_id_11773	157	43.95	1.00E-44
gene_id_11774	159	71.07	5.00E-77
gene_id_11775	385	80.78	0
gene_id_11776	152	67.11	3.00E-72
gene_id_11777	283	49.47	1.00E-98
gene_id_11778	119	84.03	9.00E-65
gene_id_11779	417	77.46	0
gene_id_11780	307	69.38	5.00E-126
gene_id_11781	104	73.08	5.00E-52
gene_id_11782	65	64.62	3.00E-22
gene_id_11783	372	68.55	0
gene_id_11784	335	78.51	0
gene_id_11785	298	65.77	1.00E-144
gene_id_11786	153	71.24	1.00E-77
gene_id_11787	199	58.29	3.00E-71
gene_id_11788	247	65.18	3.00E-95
gene_id_11789	377	62.6	6.00E-172
gene_id_11790	61	62.3	4.00E-18
gene_id_11791	162	69.14	4.00E-74
gene_id_11792	151	41.06	4.00E-34
gene_id_11793	460	78.7	0

gene_id_11794	391	71.61	1.00E-162
gene_id_11795	179	60.89	5.00E-59
gene_id_11796	130	66.15	3.00E-56
gene_id_11797	102	53.92	2.00E-19
gene_id_11798	561	73.8	0
gene_id_11799	247	51.42	1.00E-86
gene_id_11800	79	64.56	2.00E-11
gene_id_11801	211	75.83	5.00E-115
gene_id_11802	197	61.42	4.00E-50
gene_id_11820	689	71.55	0
gene_id_11821	163	65.64	1.00E-73
gene_id_11822	137	59.12	8.00E-57
gene_id_11823	160	69.38	7.00E-77
gene_id_11824	357	78.71	0
gene_id_11825	259	69.11	8.00E-124
gene_id_11826	143	80.42	4.00E-81
gene_id_11827	417	72.9	0
gene_id_11829	608	65.46	0
gene_id_11830	184	39.13	1.00E-22
gene_id_11833	45	80	6.00E-17
gene_id_12842	92	55.43	1.00E-19
gene_id_12843	282	58.16	2.00E-112
gene_id_12844	309	87.7	0
gene_id_12845	66	75.76	2.00E-25
gene_id_12846	210	64.29	2.00E-89
gene_id_12847	218	66.51	8.00E-100
gene_id_12848	267	67.42	2.00E-122
gene_id_12849	315	67.62	9.00E-156
gene_id_12850	267	36.33	1.00E-48
gene_id_12851	202	47.03	4.00E-59
gene_id_12853	188	62.23	7.00E-80
gene_id_12854	119	77.31	3.00E-60
gene_id_12868	761	28.65	4.00E-43
gene_id_12868	729	29.9	4.00E-39
gene_id_12868	500	32.8	5.00E-34
gene_id_12868	707	27.86	2.00E-33
gene_id_12868	530	30.19	3.00E-33
gene_id_12868	518	30.31	7.00E-33
gene_id_12868	495	31.11	9.00E-33
gene_id_12868	475	30.74	6.00E-31
gene_id_12868	669	29	2.00E-24
gene_id_12868	647	27.82	1.00E-21
gene_id_12869	718	60.03	0
gene_id_12870	452	69.69	0
gene_id_12871	703	67.85	0
gene_id_12872	290	83.45	3.00E-177
gene_id_13800	121	37.19	5.00E-13

gene_id_13801	311	42.44	9.00E-74
gene_id_13802	69	53.62	3.00E-09
gene_id_13803	185	75.68	1.00E-96
gene_id_13804	153	70.59	4.00E-69
gene_id_13805	1061	89.73	0
gene_id_13806	409	84.6	0
gene_id_13807	432	85.19	0
gene_id_13808	381	69.82	2.00E-167
gene_id_13809	230	76.52	8.00E-123
gene_id_13810	184	80.43	3.00E-92
gene_id_13811	62	51.61	3.00E-08
gene_id_13812	127	74.02	6.00E-61
gene_id_13813	676	62.28	0
gene_id_13814	69	50.72	4.00E-16
gene_id_13815	211	72.51	1.00E-95
gene_id_13816	227	82.82	1.00E-110
gene_id_13818	63	71.43	1.00E-14
gene_id_13819	43	51.16	7.00E-06
gene_id_13820	392	39.54	9.00E-82
gene_id_13821	234	72.65	3.00E-105
gene_id_13823	409	34.47	1.00E-50
gene_id_13826	217	54.84	3.00E-77
gene_id_13827	213	63.85	2.00E-78
gene_id_13830	86	53.49	3.00E-20
gene_id_13831	80	70	3.00E-21
gene_id_13832	563	60.57	4.00E-159
gene_id_13833	799	69.21	0
gene_id_13834	413	67.07	0
gene_id_13836	64	62.5	1.00E-18
gene_id_13837	294	63.95	2.00E-130
gene_id_13838	156	35.26	2.00E-18
gene_id_13838	125	32.8	3.00E-08
gene_id_14425	329	48.33	8.00E-78
gene_id_14426	485	40.41	5.00E-69
gene_id_14427	132	56.06	1.00E-38
gene_id_14462	225	67.56	3.00E-45
gene_id_14463	169	50.89	2.00E-45
gene_id_14464	71	74.65	2.00E-31
gene_id_14465	535	78.88	0
gene_id_14466	455	88.35	0
gene_id_14467	463	90.28	0
gene_id_14468	126	63.49	1.00E-53
gene_id_14469	615	74.8	0
gene_id_14470	235	84.68	1.00E-124
gene_id_14471	79	74.68	9.00E-37
gene_id_14473	188	63.83	2.00E-84
gene_id_14474	416	48.56	5.00E-118

gene_id_14475	250	70.4	3.00E-124
gene_id_14476	251	80.48	2.00E-137
gene_id_14477	294	50.34	7.00E-98
gene_id_14478	445	72.58	0
gene_id_14479	349	61.32	1.00E-142
gene_id_14480	162	56.79	3.00E-61
gene_id_14607	156	58.97	8.00E-61
gene_id_14608	119	70.59	6.00E-54
gene_id_14609	310	73.55	2.00E-144
gene_id_14610	209	69.38	6.00E-100
gene_id_14611	299	58.19	2.00E-78
gene_id_14612	188	70.74	5.00E-98
gene_id_14613	183	65.03	3.00E-79
gene_id_14614	142	88.73	3.00E-87
gene_id_17115	358	89.66	0
gene_id_17116	211	83.41	5.00E-114
gene_id_17117	1111	86.05	0
gene_id_17118	354	92.09	0
gene_id_17119	288	85.42	1.00E-171
gene_id_17120	239	48.12	5.00E-63
gene_id_17121	135	87.41	2.00E-81
gene_id_17122	215	79.53	6.00E-105
gene_id_17123	500	71.8	0
gene_id_17124	108	59.26	9.00E-28
gene_id_17125	743	67.16	0
gene_id_17126	275	68.36	7.00E-140
gene_id_17127	183	70.49	1.00E-83
gene_id_17128	428	64.72	0
gene_id_17129	322	48.14	1.00E-99
gene_id_17130	556	60.25	0
gene_id_17131	89	37.08	4.00E-11
gene_id_17298	694	89.91	0
gene_id_19607	57	40.35	1.00E-08
gene_id_19608	54	55.56	3.00E-11
gene_id_19609	56	44.64	1.00E-06
gene_id_19611	513	62.18	0
gene_id_21159	196	41.33	1.00E-39
gene_id_21160	214	88.79	5.00E-139
gene_id_21161	154	83.77	1.00E-81
gene_id_21164	156	34.62	5.00E-17

Annotation
hypothetical protein
dinucleotide-utilizing enzyme possibly involved in molybdopterin or thiamin biosynthesis
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
DNA-binding protein
GCN5-related N-acetyltransferase
MULTISPECIES: zinc-binding protein
MULTISPECIES: hypothetical protein
regulatory protein MarR
MULTISPECIES: arsenic transporter ATPase
arsenic resistance operon repressor
hypothetical protein
hisitidine kinase
integral membrane sensor signal transduction histidine kinase
phosphonate ABC transporter, periplasmic phosphonate-binding protein
molybdopterin oxidoreductase
Polysulphide reductase, NrfD
(4Fe-4S)-binding protein
preprotein translocase subunit TatA
molybdenum cofactor biosynthesis protein MoaA
von Willebrand factor A
magnesium chelatase
major intrinsic protein
arsenic transporter
hypothetical protein, partial
ArsC family transcriptional regulator
protein tyrosine phosphatase
ArsR family transcriptional regulator
RNA polymerase sigma-H factor
cysteine desulfurase
hypothetical protein
MULTISPECIES: hypothetical protein
glutamine amidotransferase
phosphoglucosamine mutase
hypothetical protein
hypothetical protein
hypothetical protein
branched-chain amino acid aminotransferase
MULTISPECIES: argininosuccinate lyase
argininosuccinate synthase
ornithine carbamoyltransferase
acetylornithine aminotransferase
acetylglutamate kinase
ornithine acetyltransferase

N-acetyl-gamma-glutamyl-phosphate reductase
DedA family protein
pyruvate-formate lyase
hypothetical protein
extradiol ring-cleavage dioxygenase
cell wall hydrolase
glycosyl transferase family 51
nitrite reductase
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: 30S ribosomal protein S9
50S ribosomal protein L13
tRNA pseudouridine synthase A
transporter
cobalt transporter ATP-binding subunit
MULTISPECIES: cobalt ABC transporter ATP-binding protein
50S ribosomal protein L17
DNA-directed RNA polymerase subunit alpha
30S ribosomal protein S4
30S ribosomal protein S11
30S ribosomal protein S13
translation initiation factor IF-1
50S ribosomal protein L14
MULTISPECIES: methionine aminopeptidase
adenylate kinase
preprotein translocase subunit SecY
50S ribosomal protein L15
MULTISPECIES: 50S ribosomal protein L30
MULTISPECIES: 30S ribosomal protein S5
50S ribosomal protein L18
50S ribosomal protein L6
30S ribosomal protein S8
50S ribosomal protein L5
50S ribosomal protein L24
50S ribosomal protein L14
30S ribosomal protein S17
MULTISPECIES: 50S ribosomal protein L29
50S ribosomal protein L16
30S ribosomal protein S3
50S ribosomal protein L22
ribosomal protein S19
50S ribosomal protein L2
50S ribosomal protein L23
50S ribosomal protein L4
50S ribosomal protein L3
MULTISPECIES: 30S ribosomal protein S10

elongation factor Tu
elongation factor P
30S ribosomal protein S7
MULTISPECIES: 30S ribosomal protein S12
50S ribosomal protein L7ae
DNA-directed RNA polymerase subunit beta'
DNA-directed RNA polymerase subunit beta
50S ribosomal protein L7/L12
50S ribosomal protein L10
50S ribosomal protein L1
50S ribosomal protein L11
transcription termination/antitermination factor NusG
preprotein translocase subunit SecE
arabinose ABC transporter permease
undecaprenyl-diphosphatase 2
hypothetical protein
6-phosphofructokinase
6-phosphofructokinase 2
MULTISPECIES: RNA polymerase sigma70 factor
hypothetical protein
vanomycin resistance protein VanB
RNA methyltransferase
thymidylate synthase ThyX
MULTISPECIES: ribonuclease III
MULTISPECIES: cysteinyl-tRNA synthetase
serine acetyltransferase
glutamate--tRNA ligase
hypothetical protein
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
PilT protein domain protein
CarD family transcriptional regulator
MULTISPECIES: hypothetical protein
stage II sporulation protein P
stage II sporulation protein P
protein of unknown function DUF147
DNA repair protein RadA
negative regulator of genetic competence ClpC/MecB
ATP:guanido phosphotransferase
hypothetical protein
CtsR family transcriptional regulator
SAM-dependent methyltransferase
hypothetical protein
lactamase
2-nitropropane dioxygenase
S-adenosylmethionine decarboxylase
rubrerythrin
carbonic anhydrase

hypothetical protein
hypothetical protein
iron-binding protein, hemerythrin
5'-nucleotidase
molybdopterin dehydrogenase FAD-binding
(2Fe-2S)-binding protein
aldehyde oxidase
xanthine permease
selenium-dependent molybdenum hydroxylase system protein, YqeB family
xanthine dehydrogenase
putative sulfurylase small subunit, molybdopterin cytosine dinucleotide biosynthesis
Conserved hypothetical protein CHP03172
hypothetical protein
inositol monophosphatase, partial
membrane protein, partial
formate dehydrogenase
molybdopterin-guanine dinucleotide biosynthesis protein MobB
molybdenum cofactor biosynthesis protein
molybdopterin-binding protein
molybdenum cofactor biosynthesis protein C
molybdenum cofactor biosynthesis protein
hypothetical protein HPO_09985
hypothetical protein
transcriptional regulator
histidine kinase
hemolysin D
ABC-type antimicrobial peptide transport system, ATPase component
multidrug ABC transporter substrate-binding protein
PadR family transcriptional regulator
secretion protein HlyD
multidrug transporter, partial
transporter
transporter
Alkaline phosphatase
Alkaline phosphatase
Alkaline phosphatase
Alkaline phosphatase
Alkaline phosphatase
Alkaline phosphatase
Alkaline phosphatase
L-lactate dehydrogenase
LysR family transcriptional regulator
MULTISPECIES: aspartate racemase
hypothetical protein
zinc transporter ZitB
MULTISPECIES: alkyl hydroperoxide reductase subunit C
NADH dehydrogenase

adenylosuccinate lyase
MULTISPECIES: N-acetylglucosamine kinase
permease
membrane protein
N-acetylmuramic acid-6-phosphate etherase
PTS glucose transporter subunit IIA
N-acetylglucosamine-6-phosphate deacetylase, partial
hypothetical protein
XRE family transcriptional regulator
2-isopropylmalate synthase
glycosyl transferase family 1
hypothetical protein, partial
hypothetical protein
hypothetical protein
RNA helicase
adhesin
FAD/FMN-containing dehydrogenase
hypothetical protein
alkylphosphonate utilization protein
Fe-S oxidoreductase
MULTISPECIES: ArsC family transcriptional regulator
sugar isomerase
peptidase M23
MULTISPECIES: RND transporter
amidohydrolase
transcriptional regulator
phosphonate C-P lyase
phosphonate metabolism protein
carbon-phosphorus lyase
carbon-phosphorus lyase complex subunit PhnJ
phosphonate C-P lyase system protein PhnK
phosphonate metabolism protein PhnM
phosphonate metabolim protein, transferase hexapeptide repeat family
phosphonate ABC transporter ATP-binding protein
phosphonate ABC transporter phosphate-binding protein
phosphonate ABC transporter ATP-binding protein
phosphonate ABC transporter permease
ABC-type phosphate/phosphonate transport system, permease component
phosphoesterase
dihydrodipicolinate synthase
hydrogenase expression protein HypC
MULTISPECIES: hypothetical protein
hypothetical protein
protein serine/threonine phosphatase
cyclic di-GMP phosphodiesterase response regulator RpfG
metal dependent phosphohydrolase
LacI family transcriptional regulator

ribokinase
D-ribose pyranase
D-ribose transporter ATP-binding protein
ribose ABC transporter permease
D-ribose transporter subunit RbsB
hypothetical protein
arabinose efflux permease
rubrerythrin
amino acid lyase
glycerophosphoryl diester phosphodiesterase
rubrerythrin
beta-lactamase
hypothetical protein
hypothetical protein
ethanolamine utilization protein EutJ
hypothetical protein
nitroreductase
regulatory protein MarR
hypothetical protein
hypothetical protein
MULTISPECIES: cobalt transporter
ABC transporter
stage II sporulation protein R
RNA polymerase sigma-G factor
RNA polymerase sigma-E factor
MULTISPECIES: peptidase
cell division protein FtsZ
MULTISPECIES: cell division protein FtsA
hypothetical protein
hypothetical protein
Polypeptide-transport-associated domain protein, FtsQ-type
D-alanine--D-alanine ligase
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
UDP-N-acetylmuramate--alanine ligase
UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
stage V sporulation protein E
UDP-N-acetylmuramoylalanine ligase
phospho-N-acetylmuramoyl-pentapeptide-transferase
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
UDP-N-acetylmuramyl peptide synthase
putative PASTA sensor protein
hypothetical protein TcarDRAFT_0190
16S rRNA methyltransferase
protein MraZ
prolyl-tRNA synthetase
MULTISPECIES: disulfide oxidoreductase
iron-dependent repressor, putative

iron transporter FeoB
MULTISPECIES: hypothetical protein
hypothetical protein
thioredoxin
CoA-binding protein
hypothetical protein
prolyl-tRNA synthetase
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
MULTISPECIES: peptidase
1-deoxy-D-xylulose 5-phosphate reductoisomerase
phosphatidate cytidylyltransferase
UDP pyrophosphate synthase
hypothetical protein
hypothetical protein
ribosome recycling factor
uridylate kinase
elongation factor Ts
30S ribosomal protein S2
hypothetical protein
hypothetical protein
protein of unknown function DUF342
MULTISPECIES: RNA polymerase sigma 70
hypothetical protein
chemotaxis protein CheD
chemotaxis protein CheY
MULTISPECIES: chemotaxis protein CheW
MULTISPECIES: chemotaxis protein CheA
chemotaxis protein CheY
hypothetical protein
cobyrinic acid a,c-diamide synthase
GTP-binding protein
flagellar biosynthesis protein FlhA
flagellar biosynthesis protein FlhB
MULTISPECIES: flagellar biosynthesis protein FliR
flagellar biosynthesis protein FliQ
flagellar biosynthesis protein flip
flagellar biosynthetic protein FliO
chemotaxis protein CheY
flagellar motor switch protein FliN
MULTISPECIES: flagellar motor switch protein FliM
MULTISPECIES: flagellar basal body protein FliL
MULTISPECIES: flagellar protein
fagellar hook-basal body protein
flagellar operon protein
flagellar hook capping protein
MULTISPECIES: flagellar hook-length control protein
magnesium transporter MgtE

lytic transglycosylase
flagellar export protein FliJ
MULTISPECIES: ATP synthase
flagellar assembly protein FliH
flagellar motor switch protein FliG
MULTISPECIES: flagellar M-ring protein FliF
flagellar hook-basal body protein FliE
flagellar basal body rod protein FlgC
flagellar basal body rod protein
transcriptional regulator
ATP-dependent protease
ATP-dependent protease subunit HslV
tRNA (uracil-5-)-methyltransferase
DNA topoisomerase I
DNA processing protein DprA
processive diacylglycerol glucosyltransferase
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
MULTISPECIES: dienelactone hydrolase
dihydropteroate synthase
quinolinate phosphoribosyl transferase
hypothetical protein
N-acetylmuramoyl-L-alanine amidase
integrase family protein
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
phospholipase, patatin family
hypothetical protein
DNA helicase
DNA helicase
oxalate:formate antiporter
hypothetical protein DESME_09635
hypothetical protein
hypothetical protein
N-acetylmuramoyl-L-alanine amidase
single-stranded DNA-binding protein
phage replication protein
hypothetical protein
transcriptional regulator, XRE family
homoserine lactone transporter
phage integrase family protein
hypothetical protein
MULTISPECIES: hypothetical protein
polar amino acid ABC transporter permease
hypothetical protein
macrolide ABC transporter ATP-binding protein

C4-dicarboxylate ABC transporter
hypothetical protein
tRAP transporter solute receptor TAXI family
glycolate oxidase subunit GlcD
Electron transfer flavoprotein, alpha subunit
electron transfer flavoprotein subunit beta
LysR family transcriptional regulator
protein of unknown function DUF1624
FAD-binding protein
electron transfer flavoprotein subunit alpha
MULTISPECIES: electron transfer flavoprotein subunit beta
histidine kinase
PhoP family transcriptional regulator
hypothetical protein
hypothetical protein
cysteine synthase
hypothetical protein
cystathionine beta-lyase
cystathionine gamma-synthase
ABC transporter substrate-binding protein
methionine ABC transporter permease
ABC transporter related
methionine ABC transporter substrate-binding protein
hypothetical protein
MULTISPECIES: biotin synthase
biotin synthase
glyoxylate reductase
LysR family transcriptional regulator
MFS transporter
LysR family transcriptional regulator
alpha/beta hydrolase
nitrite transporter NirC
arabinose ABC transporter permease
sulfatase
MULTISPECIES: potassium-transporting ATPase subunit A
O-acetylhomoserine aminocarboxypropyltransferase
hypothetical protein
ABC transporter ATP-binding protein
UDP-galactose-4-epimerase
diguanylate cyclase
hypothetical protein
heavy metal transport/detoxification protein
hypothetical protein
C4-dicarboxylate ABC transporter
MULTISPECIES: hypothetical protein
MULTISPECIES: TetR family transcriptional regulator
efflux pump periplasmic linker BepF

efflux pump membrane transporter BepE
MULTISPECIES: diguanylate cyclase
hypothetical protein ALO_05308
hypothetical protein
carboxymuconolactone decarboxylase
YmaF family protein
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: sporulation protein, YlmC/YmxH family
hypothetical protein
NrdR family transcriptional regulator
ribonucleoside-triphosphate reductase
ribonucleoside-triphosphate reductase activating protein
radical SAM protein
laccase domain containing protein YlmD
ethanolamine utilization protein EutJ
MULTISPECIES: Fis family transcriptional regulator
pyridine nucleotide-disulfide oxidoreductase
MULTISPECIES: Pyridine nucleotide-disulfide oxidoreductase, FAD/NAD(P)-binding domain-containing protein
4Fe-4S ferredoxin
BFD domain protein (2Fe-2S)-binding domain protein
FAD-dependent oxidoreductase
1-pyrroline-5-carboxylate dehydrogenase
alanine racemase
cell division protein SepF
pyrroline-5-carboxylate reductase
RNA-binding protein S4
septum formation initiator
hypothetical protein
isoleucyl-tRNA synthetase
hypothetical protein
NADH dehydrogenase
transcriptional regulator
alkaline phosphatase
ferredoxin
peptidase A8
pseudouridine synthase, RluA family
uracil phosphoribosyltransferase
fibronectin-binding protein
ATPase
diaminopimelate epimerase
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
guanylate kinase
DNA-directed RNA polymerase subunit omega

peptidase ClpP
S-adenosylmethionine synthetase
Heavy metal transport/detoxification protein
MULTISPECIES: primosomal protein N'
peptide deformylase
methionyl-tRNA formyltransferase
hypothetical protein
16S rRNA methyltransferase
ribosomal RNA large subunit methyltransferase N
signal peptide protein
forkhead-associated protein
protein phosphatase PrpC
cell cycle protein
cell division protein FtsI
serine/threonine protein kinase
ribosome biogenesis GTPase RsgA
ribulose-phosphate 3-epimerase
5-amino-6-(5-phosphoribosylamino)uracil reductase
riboflavin synthase subunit alpha
3,4-dihydroxy-2-butanone 4-phosphate synthase
6,7-dimethyl-8-ribityllumazine synthase
phosphodiesterase YfcE
molecular chaperone Hsp33
MULTISPECIES: 50S ribosomal protein L28
disulfide oxidoreductase
MULTISPECIES: ATP-dependent DNA helicase RecG
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
3D domain protein
inosine-5'-monophosphate dehydrogenase
polysaccharide deacetylase
MULTISPECIES: penicillin-binding protein 1A
N-acetylmannosaminyltransferase
phosphatidylserine decarboxylase
MULTISPECIES: CDP-diacylglycerol--serine O-phosphatidyltransferase
glycosyl transferase family 2
6-carboxy-5,6,7,8-tetrahydropterin synthase QueD
radical SAM protein
stationary phase survival protein SurE
hypothetical protein
5'-methylthioadenosine phosphorylase
methylthioribose-1-phosphate isomerase
S-adenosyl-L-homocysteine hydrolase
aldolase
N-ethylammeline chlorohydrolase

diaminopimelate aminotransferase
ASCH domain protein
propanediol utilization phosphotransacylase
2-ketoisovalerate ferredoxin reductase
2-oxoglutarate oxidoreductase
2-oxoglutarate ferredoxin oxidoreductase subunit gamma
diguanylate cyclase
type 11 methyltransferase
putative esterase of the alpha-beta hydrolase superfamily
conserved hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
XRE family transcriptional regulator
vanomycin resistance protein VanB
photosystem reaction center subunit H
hypothetical protein, partial
hypothetical protein
MULTISPECIES: penicillin-binding protein 1A
hypothetical protein
hypothetical protein
hypothetical protein
ferredoxin
DNA mismatch repair protein MutS
peptidase U32
MULTISPECIES: hypothetical protein
hypothetical protein
amino acid permease
phenylalanyl-tRNA synthetase subunit beta
phenylalanyl-tRNA synthetase subunit alpha
MULTISPECIES: RNA methyltransferase
MULTISPECIES: potassium uptake system protein
MULTISPECIES: potassium uptake protein, TrkH family
D-tagatose-1,6-bisphosphate aldolase subunit KbaY
50S ribosomal protein L20
50S ribosomal protein L35
translation initiation factor IF-3
threonyl-tRNA synthetase
sporulation protein
hypothetical protein
MULTISPECIES: deacetylase
MULTISPECIES: ethanolamine utilization protein
hypothetical protein
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
hypothetical protein

MULTISPECIES: hypothetical protein
hypothetical protein
alpha/beta superfamily hydrolase
hypothetical protein
MULTISPECIES: hypothetical protein
YibE/F family protein
3D domain protein
amidase
sulfite reductase
glutaredoxin
MULTISPECIES: rubrerythrin
peroxidase
transposase
MULTISPECIES: ubiquinone/menaquinone biosynthesis methyltransferase
MULTISPECIES: mechanosensitive ion channel protein MscS
gamma-glutamyltransferase
anti-sigma regulatory factor, serine/threonine protein kinase
hypothetical protein
anti-anti-sigma factor
diguanylate cyclase
NUDIX hydrolase
hypothetical protein UFO1_0009
histidine kinase
transcriptional regulatory protein GlnL
proton glutamate symport protein
metal dependent phosphohydrolase
glycoside hydrolase family 18
hypothetical protein
copper ion binding protein, putative
transcriptional regulator
penicillin-binding protein 2
siroheme synthase
serine carboxypeptidase
hydroxymethylbilane synthase
HemD protein
MULTISPECIES: delta-aminolevulinic acid dehydratase
glutamate-1-semialdehyde aminotransferase
hypothetical protein
MULTISPECIES: cAMP-binding protein
hybrid cluster protein
cell division protein FtsA
MULTISPECIES: fatty acid-binding protein DegV
MULTISPECIES: dihydroxyacetone kinase
Formiminotransferase-cyclodeaminase
short-chain dehydrogenase
hypothetical protein
putative efflux protein, MATE family

hypothetical protein
metal dependent phosphohydrolase
histidine kinase
MULTISPECIES: LytTR family transcriptional regulator
MULTISPECIES: carbon starvation protein CstA
hypothetical protein
Coat F domain protein
transcriptional regulator
deoxyribose-phosphate aldolase
hypothetical protein
phosphomannomutase
beta-lactamase
peptidase S1
50S rRNA methyltransferase
hypothetical protein, partial
MarR family transcriptional regulator
MFS transporter
hypothetical protein UFO1_3517
MULTISPECIES: hypothetical protein
LysR family transcriptional regulator
major facilitator transporter
tautomerase
3-methyladenine DNA glycosylase
GCN5 family acetyltransferase
TonB-dependent receptor
membrane protein
glutamate racemase 2
MULTISPECIES: methionine aminopeptidase
hypothetical protein
ATPase AAA
hypothetical protein
Hemolysin-type calcium-binding region protein
Hemolysin-type calcium-binding region protein
Hemolysin-type calcium-binding region protein
Hemolysin-type calcium-binding region protein
Hemolysin-type calcium-binding region protein
phosphoenolpyruvate synthase
threonyl-tRNA synthetase
hypothetical protein
amino acid permease
chemotaxis protein
arginase
transcriptional regulator, IclR family
butyrate kinase
phosphate butyryltransferase
2-oxoacid:acceptor oxidoreductase
2-ketoisovalerate ferredoxin oxidoreductase

MFS transporter
2-oxoacid:ferredoxin oxidoreductase subunit gamma
hypothetical protein
hypothetical protein
pyruvate-flavodoxin oxidoreductase
membrane protein
hypothetical protein
hypothetical protein, partial
hypothetical protein, partial
acetolactate synthase
ketol-acid reductoisomerase
2-isopropylmalate synthase
3-isopropylmalate dehydratase large subunit
3-isopropylmalate dehydratase small subunit
3-isopropylmalate dehydrogenase
hypothetical protein
MULTISPECIES: hypothetical protein
spermidine synthase
aminopeptidase
histidine kinase
transcriptional regulator
major facilitator transporter
hypothetical protein
relaxase/mobilization nuclease domain protein
hypothetical protein
site-specific recombinase, phage integrase family
S-layer protein
hypothetical protein
permease
MULTISPECIES: ABC transporter ATP-binding protein
organic solvent tolerance protein OstA
hypothetical protein
lipid A biosynthesis acyltransferase
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
KpsF/GutQ family protein
2-dehydro-3-deoxyphosphooctonate aldolase
3-deoxy-manno-octulosonate cytidylyltransferase
tetraacyldisaccharide 4'-kinase
3-deoxy-D-manno-octulosonic acid transferase
lipid A export ATP-binding/permease protein MsbA
lipid-A-disaccharide synthase
hypothetical protein
acyl-(acyl-carrier-protein)--UDP-N-acetylglucosamine O-acyltransferase
3-hydroxyacyl-ACP dehydratase
3-hydroxyacyl-ACP dehydratase
ABC transporter
hypothetical protein

lipid A biosynthesis acyltransferase
hypothetical protein
UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase
molecular chaperone Skp
periplasmic chaperone for outer membrane protein Skp
molecular chaperone Skp
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: RNA polymerase subunit sigma-70
hypothetical protein
transporter
transporter
mammalian cell entry protein
ABC transporter
membrane protein
peptidase S55 SpoIVB
hypothetical protein
exopolysaccharide biosynthesis protein
flagellar rod assembly protein FlgJ
flagellar basal body P-ring biosynthesis protein FlgA
MULTISPECIES: flagellar L-ring protein
MULTISPECIES: flagella basal body P-ring formation protein FlgA
flagellar basal body rod protein FlgG
flagellar basal-body rod protein FlgF
MULTISPECIES: rod shape-determining protein Mbl
stage III sporulation protein D
MULTISPECIES: peptidase M23
stage II sporulation protein SpoIID
MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase
hypothetical protein
F-type ATP synthase F1complex subunit epsilon
F0F1 ATP synthase subunit beta
F0F1 ATP synthase subunit gamma
ATP F0F1 synthase subunit alpha
F-type ATP synthase F1 complex subunit delta
F-type ATP synthase F0 complex subunit beta
MULTISPECIES: ATP synthase F0 subunit C
ATP synthase F0 subunit A
ATP synthase I
ATP synthase
UDP-N-acetylglucosamine 2-epimerase
UDP-phosphate N-acetylglucosaminyl 1-phosphate transferase
MULTISPECIES: nucleotide pyrophosphohydrolase
hypothetical protein
metal dependent phosphohydrolase
MULTISPECIES: diguanylate cyclase

iron transporter
iron transporter FeoA
cytidine deaminase
multidrug ABC transporter permease
ABC-type multidrug transport system, ATPase component
iron ABC transporter ATP-binding protein
putative iron(3+)-hydroxamate import system permease protein FhuB
ABC transporter substrate-binding protein
precorrin-2 C20-methyltransferase
sirohydrochlorin cobaltochelatase
ferrous iron transport protein A
ferrous iron transport protein B
ferrous iron transport protein B
Iron dependent repressor
MULTISPECIES: biopolymer transporter TonB
MULTISPECIES: biopolymer transportern ExbD
flagellar motor protein MotA
MULTISPECIES: magnesium chelatase
MULTISPECIES: magnesium chelatase
adenosylcobinamide amidohydrolase CbiZ
carbon-nitrogen hydrolase
ABC transporter substrate-binding protein
xylose isomerase
nitrogenase molybdenum-iron protein, alpha and beta subunit
nitrogenase molybdenum-iron protein, alpha and beta subunit
nitrogenase molybdenum-iron protein, alpha and beta subunit
nitrogenase iron protein 4
radical SAM protein
cobalamin import ATP-binding protein BtuD
hemin transport system permease protein HmuU
cobaltochelatase
Sirohydrochlorin cobaltochelatase
tonB-dependent receptor
hypothetical protein
transporter
methylmalonyl-CoA mutase
hypothetical protein, partial
Cob(I)yrinic acid a,c-diamide adenosyltransferase
MULTISPECIES: cobalamin biosynthesis protein
hypothetical protein, partial
flavodoxin
sulfate transporter
dihydroorotate dehydrogenase
Fis family transcriptional regulator
hypothetical protein
ATPase
potassium-transporting ATPase subunit B

potassium-transporting ATPase subunit A
Silent information regulator protein Sir2
uracil phosphoribosyltransferase
serine hydroxymethyltransferase
hypothetical protein
ribose 5-phosphate isomerase B
protein tyrosine phosphatase, partial
hypothetical protein
translation factor SUA5
modification methylase HemK
peptide chain release factor 1
MULTISPECIES: membrane protein
MULTISPECIES: 50S ribosomal protein L31
hypothetical protein
methyl-accepting chemotaxis sensory transducer
hypothetical protein
hypothetical protein
polysaccharide deacetylase
peptidyl-tRNA hydrolase
polysaccharide deacetylase
GCN5 family acetyltransferase
ribose-phosphate pyrophosphokinase
bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase
threonine dehydratase
LacI family transcriptional regulator
hypothetical protein
hypothetical protein
2-hydroxyglutaryl-CoA dehydratase
4-diphosphocytidyl-2C-methyl-D-erythritol kinase
MULTISPECIES: GntR family transcriptional regulator
MULTISPECIES: 4-diphosphocytidyl-2C-methyl-D-erythritol kinase
chemotaxis protein CheW
cyanophycin synthetase
cyanophycinase
hypothetical protein
hypothetical protein SOV_2c08030
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
sporulation protein
hypothetical protein
peptidase
glycosyl transferase, family 2
dimethyladenosine transferase
MULTISPECIES: ribonuclease M5
hypothetical protein
hydrolase TatD

methionyl-tRNA synthetase
MULTISPECIES: AbrB family transcriptional regulator
Ribosomal RNA small subunit methyltransferase I
methyltransferase
hypothetical protein
MULTISPECIES: DNA polymerase III subunit delta'
hypothetical protein
thymidylate kinase
arginine decarboxylase
hypothetical protein
permease
ABC-type metal ion transport system, periplasmic component/surface adhesin
metal ABC transporter permease
iron ABC transporter permease
regulatory protein TetR
putative CoA-substrate-specific enzyme activase
hypothetical protein
histidine kinase
response regulator receiver protein
lysine/ornithine decarboxylase
MULTISPECIES: hypothetical protein
hypothetical protein JBW_0872
MULTISPECIES: hypothetical protein
hypothetical protein UFO1_1271
hypothetical protein
MULTISPECIES: manganese catalase
alcohol dehydrogenase
hypothetical protein
transcriptional regulator
hypothetical protein
hypothetical protein F502_02627
hypothetical protein
translation repressor RelE
prevent-host-death protein
hypothetical protein, partial
reverse transcriptase
adenine methyltransferase
hypothetical protein
hypothetical protein
DNA primase
DNA polymerase elongation subunit family B
hypothetical protein
PD-(D/E)XK nuclease superfamily
VRR-NUC domain containing protein
helicase SNF2
hypothetical protein
RNA polymerase sigma factor, sigma-70 family

putative transcriptional regulator
hypothetical protein
sirohydrochlorin cobaltochelatase
Na+/H+ antiporter
YIEGIA protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein, partial
RNA polymerase, sigma-24 subunit, ECF subfamily
putative transmembrane anti-sigma factor
hypothetical protein
transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
vanomycin resistance protein VanB
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
glycosyl transferase, family 2
cytochrome c-type biogenesis protein CcdA
NLP/P60 protein
aminodeoxychorismate lyase
peptidase A8
cadmium-transporting ATPase
zinc-transporting ATPase
transcriptional regulator, ArsR family
MULTISPECIES: hypothetical protein
MULTISPECIES: small basic protein
polysaccharide deacetylase
stage IV sporulation protein B
peptidase M23B
hypothetical protein
chitooligosaccharide deacetylase
conserved hypothetical protein
iron transporter FeoA
ferrous iron transporter B
iron transporter
siderophore-interacting protein
copper/silver-translocating P-type ATPase,heavy metal-translocating P-type ATPase, Cd/Co/Hg/Pb/Zn-transporti
ArsR family transcriptional regulator
hypothetical protein ALO_12895

hypothetical protein
DNA polymerase III, epsilon subunit
MULTISPECIES: RNA methyltransferase
ATP-dependent protease
hypothetical protein
abortive infection protein
aspartyl/glutamyl-tRNA amidotransferase subunit B
MULTISPECIES: glutamyl-tRNA(Gln) amidotransferase
MULTISPECIES: glutamyl-tRNA amidotransferase subunit C
NAD-dependent DNA ligase LigA
MULTISPECIES: DNA helicase UvrD
putative ATP-dependent endonuclease of the OLD family
DNA polymerase III subunit epsilon
NAD-dependent DNA ligase LigA
MULTISPECIES: NAD-dependent DNA ligase LigA
ATP-dependent DNA helicase PcrA
LysR family transcriptional regulator
inorganic diphosphatase
hypothetical protein TcarDRAFT_2685
glyoxylate reductase
cytochrome oxidase biogenesis protein Surf12C
MULTISPECIES: hypothetical protein
conserved hypothetical protein
histidine biosynthesis bifunctional protein HisIE
imidazole glycerol phosphate synthase
1-(5-phosphoribosyl)-5- imidazole-4-carboxamide isomerase
imidazole glycerol phosphate synthase
MULTISPECIES: imidazoleglycerol-phosphate dehydratase
histidinol phosphate aminotransferase
histidinol dehydrogenase
ATP phosphoribosyltransferase HisG
hydroxyacid dehydrogenase
phosphohydrolase
nitrile hydratase subunit alpha
hypothetical protein
carbon-monoxide dehydrogenase, catalytic subunit
drug resistance transporter, EmrB/QacA subfamily
secretion protein HlyD family protein
TetR family transcriptional regulator
Zn-dependent dipeptidase, microsomal dipeptidase
cell wall hydrolase
glycoside hydrolase
peptidase M16
hypothetical protein
phosphoribosylamine--glycine ligase
MULTISPECIES: purine biosynthesis protein purH
phosphoribosylglycinamide formyltransferase

phosphoribosylaminoimidazole synthetase
amidophosphoribosyltransferase
phosphoribosylaminoimidazole-succinocarboxamide synthase
N5-carboxyaminoimidazole ribonucleotide mutase
permease
FAD-dependent oxidoreductase
endoribonuclease L-PSP family protein
GMP synthase
phosphorylase
hypothetical protein
hypothetical protein
radical SAM protein
polysaccharide deacetylase
hypothetical protein
sensor protein
MULTISPECIES: molecular chaperone GroEL
MULTISPECIES: molecular chaperone GroES
response regulator receiver and ANTAR domain protein
histidine kinase
O-sialoglycoprotein endopeptidase
small acid-soluble spore protein alpha/beta type
alanine acetyltransferase
peptidase M22
ATPase
thiamine-monophosphate kinase
phosphomethylpyrimidine synthase
MULTISPECIES: spore germination protein
Fis family transcriptional regulator
Fis family transcriptional regulator
MULTISPECIES: hypothetical protein
MULTISPECIES: beta-lactamase
mRNA interferase endoA
putative transcriptional regulator, CopG family protein
carbohydrate kinase
4'-phosphopantetheinyl transferase
histidine kinase
chemotaxis protein CheR
hypothetical protein
flagellar motor protein MotB
flagellar motor protein MotA
hypothetical protein
MULTISPECIES: radical SAM protein
biotin synthase
hypothetical protein
glycerate dehydrogenase
xylose isomerase
MULTISPECIES: GntR family transcriptional regulator

aminotransferase
pyridoxal kinase
putative decarboxylase
putative decarboxylase
MULTISPECIES: hydroxylamine reductase
spore protein
ferritin
MULTISPECIES: hypothetical protein
hypothetical protein
transcriptional regulator, LytTR family
hypothetical protein
Dynamin family protein
histidine kinase
cyclic nucleotide-binding protein
hypothetical protein
ABC transporter
hypothetical protein
hypothetical protein
histidine kinase, partial
response regulator
amidohydrolase
catalase
MULTISPECIES: peptide transporter
hypothetical protein HMPREF0083_01523
putative oxidoreductase of aldo/keto reductase family
MULTISPECIES: Fe-S oxidoreductase
Bile acid:sodium symporter
MULTISPECIES: NADPH-dependent FMN reductase
N-acyltransferase YncA
cupin
transcriptional regulator
major facilitator transporter
beta-lactamase
MULTISPECIES: molybdopterin dehydrogenase
(2Fe-2S)-binding protein
aldehyde oxidase
molybdopterin-guanine dinucleotide biosynthesis protein MobA
aldehyde oxidoreductase
LysR family transcriptional regulator
membrane protein
N-acetylmuramyl-L-alanine amidase, negative regulator of AmpC, AmpD
hypothetical protein
MULTISPECIES: membrane protein
tartronate semialdehyde reductase
hypothetical protein
hypothetical protein
hypothetical protein

hypothetical protein ALO_13005
PMT family glycosyltransferase
glycosyl transferase family 2
GtrA family protein
response regulator PleD
GntR family transcriptional regulator
transcriptional regulator
transcriptional regulator
benzoate transporter, partial
hypothetical protein
glyoxalase
molybdenum cofactor biosynthesis protein MoaA
hypothetical protein
MULTISPECIES: pyridoxamine 5-phosphate oxidase
MULTISPECIES: hypothetical protein
MULTISPECIES: membrane protein
3D domain-containing protein
MULTISPECIES: beta-lactamase
MULTISPECIES: rubrerythrin
MULTISPECIES: N-acetyltransferase GCN5
pyridine nucleotide-disulfide oxidoreductase
ArsR family transcriptional regulator
MULTISPECIES: pyridoxamine 5'-phosphate oxidase
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component
taurine ABC transporter ATPase
ABC transporter substrate-binding protein
hypothetical protein
PAS modulated sigma54 specific transcriptional regulator, Fis family
aminotransferase
nitric-oxide reductase
cytochrome C
transcriptional regulator
carbon monoxide dehydrogenase
carbon monoxide dehydrogenase
iron-sulfur protein
hypothetical protein ALO_16202
hypothetical protein, partial
threonyl-tRNA synthetase
Cysteine desulfurase
3-demethylubiquinone-9 3-methyltransferase
LysR family transcriptional regulator
hypothetical protein UFO1_0288
hypothetical protein
flavin-nucleotide-binding protein
hypothetical protein
hypothetical protein
hydroxylamine reductase

histidine kinase
cyclic nucleotide-binding protein
MFS transporter
LysR family transcriptional regulator
hypothetical protein
MULTISPECIES: hypothetical protein
alpha/beta hydrolase
hypothetical protein
transcription regulator
phosphoglycerate dehydrogenase
MULTISPECIES: fosmidomycin resistance protein
histidine kinase
hypothetical protein
MazF family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
XRE family transcriptional regulator
phosphohydrolase
4Fe-4S ferredoxin
hypothetical protein
glycoside hydrolase
hypothetical protein
metal transporter
RND transporter
transporter
hypothetical protein
phosphoenolpyruvate synthase
camphor resistance protein CrcB
hypothetical protein
ferredoxin
transcriptional regulator
metallophosphoesterase
hypothetical protein
hypothetical protein
3-ketoacyl-ACP reductase
MULTISPECIES: hypothetical protein
MULTISPECIES: histidine kinase
MULTISPECIES: transcriptional regulator
ArsR family transcriptional regulator
heavy metal translocating P-type ATPase
glutamate synthase GltB
glutamine amidotransferase GlxB
sporulation protein

protein of unknown function UPF0180
hypothetical protein
integral membrane protein CcmA involved in cell shape determination
peptidase M23B
hypothetical protein
membrane protein
cysteine desulfurase
iron-only hydrogenase maturation protein HydF
aspartate ammonia-lyase
plasmid stablization protein ParB
MULTISPECIES: sporulation initiation inhibitor Soj
hypothetical protein
methionine synthase
parB-like partition protein
16S rRNA methyltransferase
tRNA uridine 5-carboxymethylaminomethyl modification protein
tRNA modification GTPase MnmE
DNA-binding protein
membrane protein
MULTISPECIES: membrane protein
ribonuclease P
chromosomal replication initiator protein DnaA
DNA polymerase III subunit beta
hypothetical protein
MULTISPECIES: recombinase RecF
hypothetical protein
hypothetical protein
DNA gyrase subunit B
hypothetical protein, partial
lactate utilization protein C
HxlR family transcriptional regulator
LysM domain containing protein
lysine transporter LysE
MULTISPECIES: AsnC family transcriptional regulator
alkylhydroperoxidase
TetR family transcriptional regulator
membrane protein
multidrug ABC transporter ATPase
multidrug ABC transporter ATP-binding protein
transporter
Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase
guanylate kinase
hypothetical protein
ArsR family transcriptional regulator
cadmium-transporting ATPase
AIG2 family protein
protease HtpX

hypothetical protein
LysR family transcriptional regulator
BioX
6-carboxyhexanoate--CoA ligase
2-amino-3-ketobutyrate CoA ligase
dethiobiotin synthase
hypothetical protein
hypothetical protein
hypothetical protein
transglutaminase
haloacid dehalogenase
radical SAM domain protein
putative transcriptional regulator, Crp/Fnr family
hypothetical protein
calcium-transporting ATPase
hypothetical protein
magnesium transporter
histidine kinase
hypothetical protein
beta-lactamase
ErfK/YbiS/YcfS/YnhG family protein
MULTISPECIES: peptidylprolyl isomerase
MULTISPECIES: membrane protein
protein PrkA
sporulation protein YhbH
MULTISPECIES: stage V sporulation protein R
putative sporulation protein YtaF
conserved hypothetical protein
DNA gyrase subunit A
RND transporter
acriflavin resistance protein
xanthine permease
hypothetical protein
hypothetical protein
heme ABC transporter ATP-binding protein
signal transduction protein
Prephenate dehydratase
3-deoxy-7-phosphoheptulonate synthase
hypothetical protein
alkyl hydroperoxide reductase
acyltransferase
hypothetical protein
pyruvate kinase
hypothetical protein
hypothetical protein
DNA polymerase III subunit alpha
ABC-type uncharacterized transport system, periplasmic component

peptidase U32
acetylornithine aminotransferase
hypothetical protein
fosmidomycin resistance protein
hypothetical protein
nitrogenase
MULTISPECIES: uroporphyrinogen decarboxylase
ABC-type transporter permease component
sulfonate ABC transporter ATP-binding protein
ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic component
hypothetical protein
ferredoxin
methylcobamide:CoM methyltransferase straminisolvens]
methyltransferase MtaA/CmuA family
cobalamin-binding protein clariflavum]
MULTISPECIES: radical SAM protein
putative methyltransferase, YaeB family
MULTISPECIES: dinitrogenase iron-molybdenum cofactor biosynthesis protein
hypothetical protein
MULTISPECIES: amidohydrolase
CoA-binding domain-containing protein
O-acetylhomoserine aminocarboxypropyltransferase
cupin
haloacid dehalogenase
haloacid dehalogenase
putative aminotransferase
putative translation initiation inhibitor, yjgF family clariflavum]
aryldialkylphosphatase
auxin efflux carrier
MULTISPECIES: ABC transporter substrate-binding protein
ABC transporter ATP-binding protein
MULTISPECIES: ABC transporter permease
TonB-denpendent receptor
nitrogenase iron protein
MULTISPECIES: hypothetical protein
cystathionine beta-lyase
MULTISPECIES: FAD-linked oxidase
MULTISPECIES: ABC transporter ATP-binding protein
MULTISPECIES: cysteine synthase
MULTISPECIES: nitrogenase
MULTISPECIES: oxidoreductase/nitrogenase component 1
Uroporphyrinogen decarboxylase (URO-D)
2-oxoacid:ferredoxin oxidoreductase, gamma subunit
2-oxoacid:ferredoxin oxidoreductase, beta subunit
2-oxoacid:ferredoxin oxidoreductase, alpha subunit
hypothetical protein
acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II

hypothetical protein
ABC transporter ATP-binding protein
ABC transporter permease
hydrogenase
MULTISPECIES: nitrogenase
MULTISPECIES: nitrate ABC transporter substrate-binding protein
nitrate ABC transporter substrate-binding protein
MULTISPECIES: ABC transporter permease
ABC transporter permease
MULTISPECIES: hypothetical protein
nitrogenase iron protein
ABC transporter
protein of unknown function DUF214
MULTISPECIES: hypothetical protein
Protein of unknown function DUF4418
S-layer domain protein domain protein
Protein of unknown function DUF2292
MULTISPECIES: dihydroorotate dehydrogenase
cell division protein SepF
ribonucleoside-diphosphate reductase
MULTISPECIES: GTP-binding protein
metallo-beta-lactamase
UDP-N-acetylenolpyruvoylglucosamine reductase
hypothetical protein
endonuclease IV
tRNA methyltransferase
peptidase M20
dihydroxy-acid dehydratase
2-dehydropantoate 2-reductase
hypothetical protein
hypothetical protein
thiamine biosynthesis protein ThiH
phosphotransacetylase
hydrolase GDSL
hydrolase GDSL
3-deoxy-7-phosphoheptulonate synthase
metal-dependent hydrolase
acetyltransferase
endonuclease III
MULTISPECIES: hypothetical protein
hypothetical protein
thioredoxin-disulfide reductase
flavin reductase
amino acid aminotransferase
hypothetical protein
major facilitator superfamily MFS_1
hypothetical protein

hypothetical protein
diguanylate cyclase
MULTISPECIES: serine/threonine exchanger SteT
MULTISPECIES: hydrogenase assembly protein HupF
oxaloacetate decarboxylase
ATPase AAA
inorganic phosphate transporter
phosphate transport regulator
hypothetical protein
aspartate/tyrosine/aromatic aminotransferase
asparaginyl-tRNA synthetase
MULTISPECIES: spore protein
hypothetical protein
aspartate kinase
Superoxide dismutase
hypothetical protein
uracil transporter
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein ALO_16202
hypothetical protein, partial
MarR family transcriptional regulator
pyruvate formate lyase-activating protein
formate acetyltransferase
major facilitator transporter
arsenic resistance operon repressor
MULTISPECIES: arsenic transporter ATPase
MULTISPECIES: hypothetical protein
methyl-accepting chemotaxis protein
Dimethylmenaquinone methyltransferase
bile acid:sodium symporter
chemotaxis protein
RNA polymerase subunit sigma24
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: membrane protein
MULTISPECIES: methylated-DNA--protein-cysteine methyltransferase
MULTISPECIES: multidrug transporter
MULTISPECIES: LysR family transcriptional regulator
hypothetical protein
metal dependent phosphohydrolase
hypothetical protein
hypothetical protein ALO_16202
hypothetical protein ALO_16202
methylated-DNA--protein-cysteine methyltransferase
HhH-GPD superfamily base excision DNA repair protein

MULTISPECIES: hypothetical protein
hypothetical protein
ABC transporter
ArsR family transcriptional regulator
NUDIX hydrolase
anaerobic nitric oxide reductase flavorubredoxin
hypothetical protein
flavodoxin
HTH-type transcriptional regulator
D-alanine--D-alanine ligase
branched-chain amino acid transporter
autotransporter
DNA-binding protein
hypothetical protein
pyruvate-flavodoxin oxidoreductase
AraC family transcriptional regulator
iron-uptake system-binding protein
ferrichrome ABC transporter permease
iron ABC transporter permease
ABC transporter related protein
MULTISPECIES: esterase
Fis family transcriptional regulator
dihydroxyacetone kinase subunit K
dihydroxyacetone kinase, L subunit DhaL
dihydroxyacetone kinase phosphotransfer subunit DhaM
phosphocarrier protein hpr
phosphoenolpyruvate-protein phosphotransferase
hypothetical protein
MULTISPECIES: cytochrome C biogenesis protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
MULTISPECIES: hypothetical protein
flagellar motor protein MotA
biopolymer transporter ExbD
biopolymer transporter TonB
MULTISPECIES: iron permease FTR1
Ferrous iron transport protein
membrane protein
ABC transporter permease
ABC transporter permease
GTPase
FMN-binding protein
Heptaprenyl diphosphate synthase component I
hypothetical protein
MULTISPECIES: thiamine biosynthesis protein ApbE
pyruvate-flavodoxin oxidoreductase

MULTISPECIES: hypothetical protein
MULTISPECIES: RpiR family transcriptional regulator
dihydroxy-acid dehydratase
hypothetical protein
ketohydroxyglutarate aldolase
MULTISPECIES: permease
MULTISPECIES: alcohol dehydrogenase
xylulose kinase
MULTISPECIES: 3-phosphoglycerate dehydrogenase
hydrolase Cof
gluconokinase
carbon storage regulator
carbon storage regulator
hypothetical protein
hypothetical protein, partial
flagellar hook protein FlgE
flagellar hook-associated protein FlgK
flagellar hook-associated protein FlgK
flagellar hook-associated protein FlgL
hypothetical protein
hypothetical protein
hypothetical protein
cyclic di-GMP phosphodiesterase response regulator RpfG
hypothetical protein UFO1_4428
Allergen V5/Tpx-1 family protein
hypothetical protein
sensor histidine kinase ResE
transcriptional regulator
hemolysin D
SNARE associated protein
bacterioferritin
methyl-accepting chemotaxis protein McpB
MULTISPECIES: ATP-dependent Clp protease ATP-binding protein
cupin
asparagine synthase
hypothetical protein
anthranilate phosphoribosyltransferase
phosphoribosylanthranilate isomerase
indole-3-glycerol phosphate synthase
tryptophan synthase subunit beta
tryptophan synthase subunit alpha
anthranilate synthase
anthranilate synthase
peptide chain release factor 3
galactose-1-phosphate uridylyltransferase
polysaccharide biosynthesis protein
MULTISPECIES: diacylglycerol kinase

protein of unknown function DUF815
L,L-diaminopimelate aminotransferase
hypothetical protein
spore peptidoglycan hydrolase (N-acetylglucosaminidase)
spore peptidoglycan hydrolase (N-acetylglucosaminidase)
ribonuclease J
hypothetical protein
hypothetical protein
hypothetical protein
RNA polymerase sigma-70 factor
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
methyltransferase
hypothetical protein
alanine racemase
acetyltransferase
oxidoreductase
channel protein, hemolysin III family
acetyltransferase, GNAT family
MULTISPECIES: glycine/betaine ABC transporter ATP-binding protein
MULTISPECIES: ABC transporter permease
MULTISPECIES: glycine/betaine ABC transporter
segregation protein A
heterodisulfide reductase
heterodisulfide reductase subunit B
heterodisulfide reductase subunit
heterodisulfide reductase subunit MvhD
4Fe-4S ferredoxin
4Fe-4S protein
hydrogenase
ATP-binding protein, partial
transporter
hypothetical protein
hypothetical protein
hypothetical protein
pyruvate ferredoxin oxidoreductase
2-oxoacid ferredoxin oxidoreductase subunit beta
hypothetical protein
hypothetical protein
hypothetical protein IX84_31550
integrase
Type I restriction-modification system, DNA-methyltransferase subunit M

hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: organic solvent tolerance protein OstA
PfkB domain protein
ADP-heptose synthase
nucleotide sugar dehydrogenase
putative glycosyltransferase
hypothetical protein LI82_11840
glycosyl transferase family 25
NAD-dependent dehydratase
aminotransferase DegT cellulosi]
nucleotidyltransferase
serine acetyltransferase
hypothetical protein
UDP-N-acetylglucosamine 2-epimerase cellulosi]
hypothetical protein
GlcNAc-PI de-N-acetylase
oxidoreductase
oxidoreductase
CMP-N-acetylneuraminic acid synthetase
membrane protein
mannose-1-phosphate guanyltransferase
phosphomannomutase
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein, partial
NADH dehydrogenase
hydrogenase assembly protein HupF
serine phosphatase
NADH dehydrogenase I chain G
hydrogenase expression protein HupE
tyrosyl-tRNA synthetase
transcriptional regulator
hypothetical protein
MULTISPECIES: hypothetical protein
glycosyl transferase family 2
UDP-glucose 4-epimerase
glycosyl transferase family 39
glycosyl transferase family 39
regulator
histidine kinase
AAA ATPase
methyltransferase family protein
hypothetical protein

MULTISPECIES: LysR family transcriptional regulator
hypothetical protein
hypothetical protein
ubiquinol-cytochrome C reductase
hypothetical protein
MarR family transcriptional regulator
hypothetical protein
pyruvate formate-lyase
formate acetyltransferase
MULTISPECIES: alpha/beta hydrolase
diaminopimelate decarboxylase
GDP-mannose 4,6-dehydratase
hypothetical protein C173_08376
hypothetical protein
RNA polymerase sigma-70 factor
MULTISPECIES: hypothetical protein
membrane protein
metal dependent phosphohydrolase
sulfate transporter
ribonucleoside-triphosphate reductase
polynucleotide adenylyltransferase, partial
hypothetical protein
hypothetical protein, partial
diguanylate cyclase
dihydroxy-acid dehydratase
dihydroxy-acid dehydratase
dihydroxy-acid dehydratase
dihydrodipicolinate synthase
hypothetical protein, partial
homoserine O-succinyltransferase
histidine kinase
chemotaxis protein CheA
chemotaxis protein cellobioparum]
chemotaxis protein CheW
chemotaxis protein
chemotaxis protein CheR
chemotaxis protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: branched-chain amino acid ABC transporter substrate-binding protein
MULTISPECIES: ABC transporter permease
amino acid ABC transporter
MULTISPECIES: ABC transporter
amino acid ABC transporter ATPase

acetyltransferase
MULTISPECIES: lipase
amino acid ABC transporter substrate-binding protein
amino acid ABC transporter permease
amino acid ABC transporter ATPase
hypothetical protein
MULTISPECIES: transcriptional regulator
ATPase P
2-phosphosulfolactate phosphatase
two component transcriptional regulator, winged helix family protein
ABC-type antimicrobial peptide transport system, ATPase component
ABC-type transport system, involved in lipoprotein release, permease component
RND family efflux transporter, MFP subunit
glycosyl transferase family 2
hypothetical protein, partial
hypothetical protein
MULTISPECIES: MFS transporter
hypothetical protein
aromatic ring-cleaving dioxygenase
peptidase M50
MULTISPECIES: lactate dehydrogenase
MULTISPECIES: sodium transporter
hypothetical protein
multidrug transporter
TonB-dependent receptor
ABC transporter
ABC transporter
MULTISPECIES: ABC transporter
MULTISPECIES: TetR family transcriptional regulator
hypothetical protein
biopolymer transport protein ExbD/TolR
flagellar motor protein MotA
hypothetical protein
hypothetical protein
30S ribosomal protein S4
PTS mannitol transporter subunit IIB
phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA 2
Cro/Cl family transcriptional regulator
1-phosphofructokinase
PTS sugar transporter subunit IIA
phosphoenolpyruvate-protein phosphotransferase
L-sorbose 1-phosphate reductase
protein PrkA
MULTISPECIES: hypothetical protein
MULTISPECIES: stage V sporulation protein R
hypothetical protein
hypothetical protein, partial

diguanylate phosphodiesterase
HD-GYP domain-containing protein
MULTISPECIES: 4-vinyl reductase 4VR
MULTISPECIES: histidine kinase
transcriptional regulator (TetR family protein)
crotonase
hypothetical protein
Excinuclease ABC C subunit domain protein
hypothetical protein
chaperone protein HtpG
MULTISPECIES: transporter
hypothetical protein
methyltransferase type 11
hypothetical protein
hypothetical protein
hypothetical protein
FMN reductase
NADH oxidase
nitroreductase
LysR substrate-binding protein
MULTISPECIES: oxidoreductase
hydrogenase, Fe-only
MULTISPECIES: molybdenum cofactor biosynthesis protein MoeA
MULTISPECIES: effector protein
MULTISPECIES: formate dehydrogenase
chemotaxis protein
MULTISPECIES: nitrogenase iron protein
nitrogen fixation protein NifHD
MULTISPECIES: nitrogen regulatory protein P-II
nitrogenase iron-iron protein alpha chain
nitrogenase iron-iron protein delta chain
nitrogenase iron-iron protein beta chain
hypothetical protein
FeMo cofactor biosynthesis protein NifB
MULTISPECIES: pyruvate carboxyltransferase
homocitrate synthase
MULTISPECIES: amidotransferase
MULTISPECIES: pyridoxamine 5-phosphate oxidase
transporter
LysR family transcriptional regulator
allophanate hydrolase
urea amidolyase
LamB/YcsF family protein
MULTISPECIES: membrane protein
hypothetical protein
kinase A inhibitor
urea amidolyase related protein

acetyl-CoA carboxylase
acetyl-CoA carboxylase
methyl-accepting chemotaxis protein
hypothetical protein ALO_19632
hypothetical protein
radical SAM domain-containing protein
hypothetical protein AAS4A_0931
MULTISPECIES: chemotaxis protein CheV
MULTISPECIES: RNA-binding protein
ribosomal silencing factor RsfS
transcriptional regulator
phosphohydrolase
RNP-1 like RNA-binding protein
nicotinic acid mononucleotide adenylyltransferase
multidrug ABC transporter substrate-binding protein
macrolide ABC transporter ATP-binding protein
hemolysin D
gamma-glutamyl phosphate reductase
gamma-glutamyl kinase
putative RNA-binding protein, YhbY family
GTPase CgtA
histidine kinase
MULTISPECIES: 50S ribosomal protein L27
ribosomal protein
50S ribosomal protein L21
ribonuclease G
MULTISPECIES: hypothetical protein
Fe-S oxidoreductase
MULTISPECIES: peptidase M50
peptidase M23
rod shape-determining protein RodA
cell division topological specificity factor
septum site-determining protein MinD
septum site-determining protein MinC
peptidoglycan glycosyltransferase
rod shape-determining protein MreD
rod shape-determining protein MreC
rod shape-determining protein MreB
DNA repair protein RadC
septum formation protein Maf
hypothetical protein
MULTISPECIES: membrane protein
MULTISPECIES: membrane protein
acetyl/propionyl-CoA carboxylase, alpha subunit
MULTISPECIES: methylmalonyl-CoA carboxyltransferase
hypothetical protein
GTPase

B12 binding domain protein
methylmalonyl-CoA mutase
MULTISPECIES: acetyl-CoA hydrolase
REX family transcriptional regulator
ferredoxin
NADH dehydrogenase
NADH dehydrogenase
histidine kinase
NADH dehydrogenase subunit E
PHP domain-containing protein
hypothetical protein
ferredoxin
anti-sigma regulatory factor
hypothetical protein
polymerase
folylpolyglutamate synthase
valyl-tRNA synthetase
Exonuclease RNase T and DNA polymerase III
serine dehydratase
MULTISPECIES: serine dehydratase
MULTISPECIES: aminotransferase class IV
MULTISPECIES: para-aminobenzoate synthase
anthranilate synthase component II
dihydropyrimidine dehydrogenase
ferredoxin-NADP reductase
methylenetetrahydrofolate reductase
formate--tetrahydrofolate ligase
5,10-methylene-tetrahydrofolate cyclohydrolase
4-hydroxybenzoate nonaprenyltransferase UbiA
3-octaprenyl-4-hydroxybenzoate carboxylyase UbiD
preprotein translocase subunit TatC
twin-arginine translocation protein TatA
lactate permease
GntR family transcriptional regulator
Polyprenyl synthetase
4Fe-4S ferredoxin iron-sulfur binding domain-containing protein
2 -oxoacid:ferredoxin oxidoreductase, gamma subunit OorC
2-oxoglutarate synthase
2-oxoglutarate synthase subunit KorA
lactate permease
lactate permease
transcriptional regulator
transcriptional regulator
GTP-binding protein
peptidase
hypothetical protein
microtubule-severing ATPase

Lon protease
ATP-dependent protease
ATP-dependent Clp protease proteolytic subunit
trigger factor
putative Fe-S oxidoreductase
ABC transporter substrate-binding protein
MULTISPECIES: Fur family transcriptional regulator
hypothetical protein
A/G-specific DNA-adenine glycosylase
methyl-accepting chemotaxis protein
aldo/keto reductase
TetR family transcriptional regulator
permease
AraC family transcriptional regulator
hypothetical protein
succinate dehydrogenase
succinate dehydrogenase flavoprotein subunit
hypothetical protein
fumarate hydratase
MULTISPECIES: fumarate hydratase
MULTISPECIES: citrate lyase ligase
citrate lyase subunit alpha
citrate lyase
MULTISPECIES: citrate lyase subunit gamma
conserved hypothetical protein
Methylaspartate ammonia-lyase
MULTISPECIES: glutamate mutase
mutL
MULTISPECIES: methylaspartate mutase
GntR family transcriptional regulator
hypothetical protein SOV_1c04960
phosphodiesterase
xanthosine triphosphate pyrophosphatase
ribonuclease PH
histone deacetylase superfamily
hydantoinase
MULTISPECIES: 2-hydroxyglutaryl-CoA dehydratase
MULTISPECIES: 2-hydroxyglutaryl-CoA dehydratase
hypothetical protein
hypothetical protein
glutamate racemase
MULTISPECIES: thioesterase
hypothetical protein
O-methyltransferase
MULTISPECIES: hypothetical protein
multidrug resistance protein B
secretion protein HlyD

hypothetical protein HMPREF1207_05568
hypothetical protein
hypothetical protein
DNA-binding protein
hypothetical protein
excisionase
hypothetical protein
RNA-directed DNA polymerase
hypothetical protein
hypothetical protein
hypothetical protein
XRE family transcriptional regulator
glycolate permease GlcA
MULTISPECIES: peptidase
LysR family transcriptional regulator
DNA-3-methyladenine glycosylase
metallo-beta-lactamase
histidine kinase
amino acid decarboxylase
hypothetical protein
NADH-flavin oxidoreductase/NADH oxidase NADH
Fur family transcriptional regulator
catalase-peroxidase
hypothetical protein cellobioparum]
methyl-accepting chemotaxis protein McpB
chemotaxis protein CheA
chemotaxis protein CheY
chemotaxis protein CheY
response regulator receiver modulated diguanylate cyclase
hypothetical protein
membrane protein
pyridoxamine 5'-phosphate oxidase
cupin
Protein of unknown function DUF2798
MarR family transcriptional regulator
methyltransferase
ArsR family transcriptional regulator
nitrite reductase
MULTISPECIES: hypothetical protein
DNA-binding protein
hypothetical protein M918_06300
hypothetical protein
MULTISPECIES: TetR family transcriptional regulator
MULTISPECIES: phosphoenolpyruvate synthase
2-hydroxyacid dehydrogenase
LysR family transcriptional regulator
hypothetical protein

protein of unknown function DUF218
amino acid-binding protein
glutaredoxin
MULTISPECIES: cupin
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
RES domain-containing protein
(Fe-S)-binding protein
MULTISPECIES: NADH-quinone oxidoreductase subunit N
MULTISPECIES: NADH dehydrogenase subunit M
MULTISPECIES: NADH dehydrogenase subunit L
MULTISPECIES: NADH:ubiquinone oxidoreductase subunit K
MULTISPECIES: NADH-ubiquinone oxidoreductase
MULTISPECIES: 4Fe-4S ferredoxin
MULTISPECIES: NADH:ubiquinone oxidoreductase subunit H
MULTISPECIES: NAD(P)H-quinone oxidoreductase subunit H
MULTISPECIES: NADH dehydrogenase
MULTISPECIES: NADH-quinone oxidoreductase subunit B
NADH-ubiquinone/plastoquinone oxidoreductase chain 3
hypothetical protein
ammonia channel protein
hypothetical protein
cobalt ABC transporter, inner membrane subunit CbiQ
cobalt transporter CbiM
seryl-tRNA synthetase
metal-dependent phosphohydrolase
hypothetical protein
thioredoxin-disulfide reductase
aldo/keto reductase
hypothetical protein SOV_3c01470
3-phosphoglycerate dehydrogenase
Phosphoserine aminotransferase
flavin reductase
intracellular protease 1
hypothetical protein
hypothetical protein
cysteine ABC transporter permease
cysteine ABC transporter permease
hypothetical protein
4Fe-4S ferredoxin
cytochrome d ubiquinol oxidase subunit 2
cytochrome D ubiquinol oxidase subunit I
transcriptional regulator
hypothetical protein
hypothetical protein

ArsR family transcriptional regulator
oxidoreductase
formate hydrogenlyase complex iron-sulfur subunit, partial
hypothetical protein
hydrogenase 4, membrane subunit
hypothetical protein
hypothetical protein
hypothetical protein
acetolactate synthase
acetolactate synthase large subunit
propanediol utilization: polyhedral bodies pduT
MULTISPECIES: Respiratory-chain NADH dehydrogenase domain 51 kDa subunit
aldehyde dehydrogenase
cobalamin adenosyltransferase
Ethanolamine utilization protein EutN/carboxysome structural protein Ccml
flavoprotein
propanediol utilization phosphotransacylase
carboxysome structural protein EutM
microcompartment protein
MULTISPECIES: dehydratase
glycerol dehydratase
propanediol dehydratase
propanediol dehydratase
propanediol dehydratase
ethanolamine utilization protein eutL
carboxysome structural protein EutM
ethanolamine utilization protein EutP
propanediol utilization protein PduU
AraC family transcriptional regulator
histidine kinase
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
cobalamin biosynthesis protein CobS
MULTISPECIES: aspartate aminotransferase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
alcohol dehydrogenase
putative DNA-binding protein
PAS sensor protein
hypothetical protein
glycogen phosphorylase
glycogen synthase

glucose-1-phosphate adenylyltransferase
glucose-1-phosphate adenylyltransferase
glycogen branching protein
maltodextrin phosphorylase
hypothetical protein
maltodextrin phosphorylase
glycogen synthase
glucose-1-phosphate adenylyltransferase
glucose-1-phosphate adenylyltransferase
hypothetical protein
peptidase M48
hypothetical protein
phosphotransferase
pyruvate phosphate dikinase
MULTISPECIES: metal-chelation protein CHAD
lysine exporter protein LysE/YggA
hypothetical protein
MULTISPECIES: hypothetical protein
nitrite reductase
hypothetical protein
hypothetical protein, partial
alkaline phosphatase
acetyltransferase
homoserine lactone transporter
hypothetical protein
hypothetical protein UFO1_2324
MULTISPECIES: recombinase RecA
hypothetical protein
histidine kinase
ErfK/YbiS/YcfS/YnhG family protein
DNA polymerase I
formamidopyrimidine-DNA glycosylase
MULTISPECIES: dephospho-CoA kinase
transglycosylase
ABC transporter substrate-binding protein
aspartate carbamoyltransferase
dihydroorotase
carbamoyl phosphate synthase small subunit
MULTISPECIES: carbamoyl phosphate synthase large subunit
oxidoreductase
dihydroorotate dehydrogenase
hypothetical protein
orotate phosphoribosyltransferase
hypothetical protein DUF1540
nitrate ABC transporter ATP-binding protein
taurine ABC transporter permease
metal ABC transporter substrate-binding protein

hypothetical protein
hypothetical protein
response regulator receiver protein
hypothetical protein
hypothetical protein
secondary thiamine-phosphate synthase
MULTISPECIES: DNA recombination protein RmuC
glutamate synthase
4Fe-4S ferredoxin
ethanolamine utilization protein EutJ
ethanolamine utilization protein EutJ
ethanolamine utilization protein EutJ
ABC transporter permease
MULTISPECIES: ABC transporter
leucine/isoleucine/valine transporter ATP-binding subunit
amino acid ABC transporter ATPase
signal-transduction protein
cation transporter
hypothetical protein, partial
hypothetical protein
Protein of unknown function DUF3343
mechanosensitive ion channel protein MscS
hypothetical protein
formate acetyltransferase
pyruvate formate lyase-activating protein
GTP-binding protein YchF
flagellar protein FliB
30S ribosomal protein S6
single-stranded DNA-binding protein 3
30S ribosomal protein S18
MULTISPECIES: hypothetical protein
MULTISPECIES: membrane protein
phosphoesterase
50S ribosomal protein L9
anti-sigma H factor
DNA helicase
hypothetical protein
hypothetical protein
hydrolase
diguanylate cyclase
chemotaxis protein CheV
chemotaxis protein
long-chain fatty acid--CoA ligase
6-phosphogluconate dehydrogenase
mannosyl-glycoprotein endo-beta-N-acetylglucosamidase
pyridine nucleotide-disulfide oxidoreductase
hypothetical protein

MFS transporter
transcriptional regulator, XRE family
putative ABC transport system ATP-binding protein
MULTISPECIES: hypothetical protein
hypothetical protein
beta 1,4 glucosyltransferase
collagen triple helix repeat-containing protein, partial
ATP synthase
pro-sigmaK processing inhibitor BofA
hypothetical protein
recombinase RecR
DNA-binding protein, YbaB/EbfC family
MULTISPECIES: DNA polymerase III subunit gamma/tau
tRNA-specific adenosine deaminase
MULTISPECIES: hypothetical protein
chemotaxis protein CheY
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: transcriptional regulator
ATP-dependent Clp protease ClpP
oxidoreductase/nitrogenase
heavy metal translocating P-type ATPase
ArsR family transcriptional regulator
hypothetical protein, partial
hypothetical protein UFO1_4426
hypothetical protein
MULTISPECIES: multidrug ABC transporter ATP-binding protein
ABC transporter
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: ferredoxin-dependent glutamate synthase
cobinamide adenolsyltransferase
diguanylate cyclase
DNA helicase
Fe-S oxidoreductase
putative mycofactocin radical SAM maturase MftC
hypothetical protein
MULTISPECIES: membrane protein
oxidoreductase
hypothetical protein
ethanolamine utilization protein EutJ
pirin
symporter
HutP family protein
MULTISPECIES: hypothetical protein

MULTISPECIES: hypothetical protein
hypothetical protein
DNA-binding protein
TetR family transcriptional regulator
MULTISPECIES: MFS transporter
MULTISPECIES: multidrug transporter
MULTISPECIES: secretion protein HlyD
MULTISPECIES: PadR family transcriptional regulator
Nucleotidyl transferase
hypothetical protein
hypothetical protein
MULTISPECIES: dehydrogenase
chemotaxis protein CheW
Fis family transcriptional regulator
transcriptional regulator
hypothetical protein
antibiotic biosynthesis monooxygenase
transposase
transposase
hypothetical protein
GntR family transcriptional regulator
FMN-binding protein
cell division protein FtsH
MFS transporter
glutathione peroxidase
hypothetical protein, partial
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
Sigma-70 region 4 type 2
CotJC
Spore coat assembly protein CotJB, domain-containing protein
hypothetical protein, partial
phage shock protein C
stage V sporulation protein E
hypothetical protein
homoserine O-acetyltransferase
MULTISPECIES: hypothetical protein
tRNA (guanine-N7)-methyltransferase
signal transduction histidine kinase, nitrogen specific, NtrB
Fis family transcriptional regulator
methylglyoxal synthase
methyl-accepting chemotaxis protein
nitrite reductase

transporter
PAS domain S-box/diguanylate cyclase (GGDEF) domain-containing protein
peroxiredoxin
cyclic di-GMP phosphodiesterase response regulator RpfG
ACP synthase
acyl-CoA hydrolase
hypothetical protein
protein of unknown function DUF1003
chemotaxis protein
hypothetical protein
methyltransferase
phosphopantetheine adenylyltransferase
ATPase
sporulation integral membrane protein YlbJ
Patatin
hypothetical protein
acetate kinase
MULTISPECIES: hypothetical protein
50S ribosomal protein L32
DeoR family transcriptional regulator
phosphate acyltransferase
3-oxoacyl-ACP synthase
2-nitropropane dioxygenase
malonyl CoA-ACP transacylase
3-oxoacyl-ACP reductase
acyl carrier protein
2-nitropropane dioxygenase
3-oxoacyl-ACP synthase
MULTISPECIES: ribonuclease III
radical SAM protein
stage V sporulation protein S
chromosome segregation protein SMC
cell division protein FtsY
putative transcriptional regulator with HTH domain containing protein
signal recognition particle protein
MULTISPECIES: 30S ribosomal protein S16
hypothetical protein
16S rRNA processing protein RimM
16S rRNA processing protein RimM
tRNA (guanine-N1)-methyltransferase
hypothetical protein
50S ribosomal protein L19
signal peptidase I
GTPase YlqF
ribonuclease HII
hypothetical protein
MULTISPECIES: flagellar biosynthesis

phosphohydrolase
endonuclease
hypothetical protein
Fis family transcriptional regulator
HAD family hydrolase
hypothetical protein
flagellar motor protein MotB
MULTISPECIES: hypothetical protein
shikimate dehydrogenase
type II secretion system protein E
twitching motility protein PilT
secretion system protein
hypothetical protein, partial
peptidase A24
hypothetical protein
hypothetical protein JBW_3305
hypothetical protein
competence protein ComF
pilus assembly protein PilM
Fimbrial assembly family protein
hypothetical protein
hypothetical protein
MULTISPECIES: shikimate kinase
3-dehydroquinate synthase
RND transporter
acriflavin resistance protein
6-phosphofructokinase
hypothetical protein
1-(5-phosphoribosyl)-5-amino-4-imidazole-carboxylate carboxylase
MULTISPECIES: hypothetical protein
HD-GYP domain-containing protein
7-cyano-7-deazaguanine synthase
GTP cyclohydrolase
N-6 DNA methylase
hypothetical protein
lysylphosphatidylglycerol synthetase
UDP-glucose 4-epimerase
glycosyl transferase family 39
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
glyoxalase/bleomycin resistance protein/dioxygenase
(Fe-S)-binding protein
MULTISPECIES: hypothetical protein
cobalt-precorrin-6A synthase
hypothetical protein
nucleotide-binding protein

precorrin-2 C20-methyltransferase
MULTISPECIES: cobalt-precorrin-4 C(11)-methyltransferase
cobalamin biosynthesis protein CbiG
cobalt-precorrin-3B C(17)-methyltransferase
MULTISPECIES: precorrin-6x reductase
precorrin isomerase
cobyrinic acid a,c-diamide synthase
bifunctional adenosylcobalamin biosynthesis protein CobU
cobalamin biosynthesis protein CobQ
cobalamin biosynthesis protein
MULTISPECIES: cobalamin 5'-phosphate synthase
GHMP kinase
L-threonine-O-3-phosphate decarboxylase
phosphoglycerate mutase
ArsC family transcriptional regulator
DNA polymerase III subunit alpha
ribosome maturation factor RimP
transcription termination factor NusA
hypothetical protein
50S ribosomal protein L7ae
MULTISPECIES: translation initiation factor IF-2
MULTISPECIES: translation initiation factor IF-2
ribosome-binding factor A
phosphoesterase
MULTISPECIES: tRNA pseudouridine synthase B
riboflavin biosynthesis protein RibF
30S ribosomal protein S15
polyribonucleotide nucleotidyltransferase
polysaccharide deacetylase
germination-specific N-acetylmuramoyl-L-alanine amidase CwlD
zinc protease
deoxyuridine 5'-triphosphate nucleotidohydrolase
hypothetical protein
YlmC/YmxH family sporulation protein
membrane protein
dihydrodipicolinate reductase
aspartate-semialdehyde dehydrogenase
aspartokinase 1
dihydrodipicolinate synthase
ribonuclease J
translocation-enhancing protein TepA
hypothetical protein
DNA translocase FtsK
XRE family transcriptional regulator
XRE family transcriptional regulator
hypothetical protein
hypothetical protein

MULTISPECIES: iron ABC transporter substrate-binding protein
hypothetical protein
damage-inducible protein CinA
RNA helicase
50S ribosomal protein L31
recA protein
hypothetical protein
2,3 cyclic-nucleotide 2-phosphodiesterase
hypothetical protein
metallophosphoesterase
MULTISPECIES: stage V sporulation protein S
cytosol aminopeptidase
histidinol phosphatase
conserved hypothetical protein
hypothetical protein
hypothetical protein
permease
hypothetical protein
(dimethylallyl)adenosine tRNA methylthiotransferase
DNA mismatch repair protein MutS
DNA mismatch repair protein MutL
hypothetical protein
tRNA delta(2)-isopentenylpyrophosphate transferase
RNA-binding protein Hfq
histidinol-phosphatase
stage V sporulation protein K
ABC transporter, partial
ABC transporter
MULTISPECIES: ABC transporter
membrane protein
LrgA
hypothetical protein
MULTISPECIES: amino acid ABC transporter substrate-binding protein
amino acid ABC transporter permease
Cystine ABC transporter, ATP-binding protein
MULTISPECIES: cystathionine gamma-synthase
cobalt ABC transporter ATP-binding protein
MULTISPECIES: cobalt ABC transporter permease
cobalamin biosynthesis protein CbiM
hypothetical protein
MULTISPECIES: mechanosensitive ion channel protein
amidohydrolase
hypothetical protein
5-keto-4-deoxyuronate isomerase
2-deoxy-D-gluconate 3-dehydrogenase
2-keto-3-deoxygluconate permease
2-dehydro-3-deoxygluconokinase

ketohydroxyglutarate aldolase
MULTISPECIES: hypothetical protein
MULTISPECIES: ATPase
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: membrane protein
MULTISPECIES: cystathionine gamma-lyase
hypothetical protein, partial
transcriptional regulator
hypothetical protein
gamma-glutamyl cyclotransferase
polar amino acid ABC transporter permease
MULTISPECIES: amino acid ABC transporter permease
glutamine ABC transporter ATP-binding protein
MULTISPECIES: amino acid ABC transporter substrate-binding protein
amidohydrolase
peptidase U61
ABC transporter substrate-binding protein
hypothetical protein UFO1_4750
MULTISPECIES: peptide ABC transporter ATP-binding protein
MULTISPECIES: peptide ABC transporter ATP-binding protein
diguanylate cyclase
peptide ABC transporter permease
D-Ala-D-Ala carboxypeptidase
response regulator
hypothetical protein
hypothetical protein, partial
histidine kinase
MULTISPECIES: transcriptional regulator
C4-dicarboxylate transporter
ankyrin repeat-containing domain-containing protein
hypothetical protein
hypothetical protein CSBG_00124
hypothetical protein
hypothetical protein
thiW protein
hydroxyethylthiazole kinase
ATP-dependent helicase HrpB
protein of unknown function DUF3298-containing protein
metallophosphoesterase
carbamate kinase
ornithine carbamoyltransferase
peptidase M20
uracil permease
Fis family transcriptional regulator
diaminopropionate ammonia-lyase
selenate reductase

chlorohydrolase/aminohydrolase
abortive infection protein
hypothetical protein
MULTISPECIES: adenine deaminase
Xanthine/uracil/vitamin C permease
hydroxydechloroatrazine ethylaminohydrolase
hypothetical protein
MULTISPECIES: DNA-formamidopyrimidine glycosylase
hypothetical protein, partial
hypothetical protein
hypothetical protein
hypothetical protein, partial
DNA topoisomerase III
magnesium chelatase
von Willebrand factor A
sulfate adenylyltransferase
MULTISPECIES: sulfate adenylyltransferase
adenylylsulfate reductase subunit beta
MULTISPECIES: adenylylsulfate reductase subunit alpha
hypothetical protein
hypothetical protein SOV_4c03090
MULTISPECIES: lactaldehyde reductase
hypothetical protein
heavy metal resistance protein CzcA
multidrug MFS transporter
Nod factor export ATP-binding protein I
ABC transporter permease
peptidase M29
symporter
hypothetical protein
hypothetical protein
pseudouridine synthase
membrane protein
membrane protein
hypothetical protein UFO1_2741
thioredoxin peroxidase
hypothetical protein
hypothetical protein
hypothetical protein
protein of unknown function DUF6 transmembrane
ABC transporter permease
ABC transporter permease
ABC transporter
ABC transporter substrate-binding protein
Molybdopterin-guanine dinucleotide biosynthesis protein A
crotonase
3-hydroxybutyryl-CoA dehydrogenase

acetyl-CoA acetyltransferase
hypothetical protein HMPREF1250_0759
MULTISPECIES: hypothetical protein
4-hydroxybutyrate CoA transferase
hypothetical protein
nitrogen-fixing protein NifU
4-hydroxybutyryl-CoA dehydratase
membrane protein
transcriptional regulator, partial
sulfate ABC transporter
sulfate ABC transporter permease
sulfate/thiosulfate transporter subunit
hypothetical protein
3,4-dihydroxy-2-butanone 4-phosphate synthase
hypothetical protein
putative metal-dependent hydrolase
glucose 6-phosphate dehydrogenase
ABC-type antimicrobial peptide transport system, ATPase component
Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase
hypothetical protein
cyclic di-GMP phosphodiesterase response regulator RpfG
putative DNA recombinase
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hydrolase GDSL, partial
hisitidine kinase
MULTISPECIES: methyltransferase
exopolyphosphatase
integrase
hypothetical protein
enolase
enolase
hypothetical protein
sodium/hydrogen exchanger
universal stress protein UspA
integrase core domain protein
hypothetical protein
glutamine-binding periplasmic protein
zinc-binding protein
glycosyl transferase
(Fe-S)-binding protein
MULTISPECIES: transcriptional regulator
uDP-galactopyranose mutase
hypothetical protein
glycerol-3-phosphate cytidylyltransferase
hypothetical protein

hypothetical protein obeum]
glycosyl transferase family 2
conserved hypothetical protein
hypothetical protein
glycosyl transferase family 2/glycosyl transferase family 8
putative O-methyltransferase
hypothetical protein
putative O-methyltransferase
hypothetical protein
hypothetical protein
glycerol-3-phosphate cytidylyltransferase
hypothetical protein
hypothetical protein, partial
Methyltransferase type 12
hypothetical protein
Flagellin (Fragment)
hypothetical protein SOV_3c02440
flagellar protein FliS
flagellar hook protein FliD
flagellar protein FlaG protein
carbon storage regulator
flagellar assembly protein FliW
hypothetical protein
flagellar hook protein
flagellar hook protein FlgK
FlgN family protein
anti-sigma-28 factor FlgM
MULTISPECIES: flagellar protein
phosphohydrolase
competence protein ComF
helicase RecD
hypothetical protein
Protein of unknown function YvrJ
hypothetical protein
hypothetical protein
RNA polymerase sigma-70 factor
ABC transporter
MULTISPECIES: bacteriocin
rubrerythrin
hypothetical protein
hypothetical protein
chemotaxis protein CheY
hypothetical protein
hypothetical protein
glucose-6-phosphate isomerase
MULTISPECIES: dTDP-4-dehydrorhamnose reductase
spore coat protein

spore coat protein
glucose-1-phosphate thymidylyltransferase
hypothetical protein
hypothetical protein
NAD+ synthetase
metal dependent phosphohydrolase
hypothetical protein
cysteinyl-tRNA(Pro) deacylase
hypothetical protein
threonine synthase
phosphoenolpyruvate carboxykinase
C4-dicarboxylate transporter
UV damage repair endonuclease
ATP-dependent DNA ligase
DNA repair protein
DNA ligase
putative zinc-binding protein
oligopeptidase PepB
N-acetylmuramoyl-L-alanine amidase
radical SAM protein
radical SAM protein
glutamine ABC transporter substrate-binding protein
glutamine transport system permease protein GlnP
glutamine ABC transporter ATP-binding protein
cold-shock protein
hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: hydrogenase
MULTISPECIES: (4Fe-4S)-binding protein
hydrogenase
periplasmic hydrogenase large subunit
putative periplasmic hydrogenase small subunit
cytochrome b subunit of formate dehydrogenase
preprotein translocase subunit SecA
peptide chain release factor 2
hypothetical protein
membrane protein
polysaccharide pyruvyl transferase
hypothetical protein
hypothetical protein
transketolase
transketolase
peptidase M50
ABC transporter
cell division protein FtsX
peptidase M23
peptidase S41

hydrolase GDSL
transposase
trypsin
excinuclease ABC subunit B
excinuclease ABC subunit A
acetyl-CoA carboxylase
excinuclease ABC subunit C
LemA family protein
hypothetical protein
MULTISPECIES: rubredoxin
MULTISPECIES: hypothetical protein
multidrug transporter MatE
malate dehydrogenase
FMN-dependent alpha-hydroxy acid dehydrogenase
methylated-DNA-protein-cysteine methyltransferase
conserved hypothetical protein
hydrolase Cof
glycerate kinase
hypothetical protein
MULTISPECIES: hydrolase
glmZ(sRNA)-inactivating NTPase
MULTISPECIES: hypothetical protein
sporulation regulator WhiA
polysaccharide deacetylase
hypothetical protein
MULTISPECIES: malate dehydrogenase
MULTISPECIES: C4-dicarboxylate ABC transporter
MULTISPECIES: carboxypeptidase
MULTISPECIES: tannase
hypothetical protein
cytochrome C nitrite reductase
cytochrome C552
copper amine oxidase
radical SAM protein
Pyridoxamine 5'-phosphate oxidase-related protein
hypothetical protein
DeoR family transcriptional regulator
glyceraldehyde-3-phosphate dehydrogenase
phosphoglycerate kinase
triosephosphate isomerase
phosphoglyceromutase
enolase
phosphonate ABC transporter substrate-binding protein
glycerol-3-phosphate dehydrogenase, anaerobic, A subunit
glycerol-3-phosphate dehydrogenase
glycerol-3-phosphate dehydrogenase
pyruvate kinase

MULTISPECIES: preprotein translocase subunit SecG
MULTISPECIES: potassium transporter
glutamine amidotransferase
hypothetical protein
carboxylesterase
thioesterase
MULTISPECIES: ribonuclease R
single-stranded DNA-binding protein
hypothetical protein
N-glycosyltransferase
polysaccharide deacetylase
Tetratricopeptide TPR_2 repeat protein
Tetratricopeptide TPR_2 repeat protein
MULTISPECIES: membrane protein
hypothetical protein
transcriptional regulator
MFS transporter
4Fe-4S ferredoxin
carboxymuconolactone decarboxylase
hypothetical protein
cupin
membrane protein
membrane protein
phosphoenolpyruvate synthase
Na+ antiporter
glutamine amidotransferase
MULTISPECIES: Cys/Met metabolism pyridoxal-phosphate-dependent protein
TonB-denpendent receptor
MULTISPECIES: AraC family transcriptional regulator
TonB domain-containing protein
HAD family hydrolase
SAM-dependent methyltransferase
MULTISPECIES: catalase
flavodoxin
nitroreductase
glyoxalase
nitroreductase
MULTISPECIES: membrane protein
hypothetical protein
small acid-soluble spore P family protein
cell envelope biogenesis protein OmpA
quaternary ammonium transporter
TetR family transcriptional regulator
MULTISPECIES: TetR family transcriptional regulator
efflux transporter, RND family, MFP subunit
multidrug transporter AcrB
UspA domain-containing protein

hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
inner-membrane translocator
urea ABC transporter permease
urea ABC transporter ATP-binding protein
urea ABC transporter ATP-binding protein
hypothetical protein
peptidase dimerization protein
peptidase dimerization protein
hypothetical protein
allophanate hydrolase
allophanate hydrolase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
3-phosphoglycerate dehydrogenase
tagatose-bisphosphate aldolase
carbohydrate kinase
permease
transcriptional regulator, RpiR family
ABC transporter
MULTISPECIES: polar amino acid ABC transporter permease
MULTISPECIES: ABC transporter substrate-binding protein
MULTISPECIES: aminotransferase class III
MULTISPECIES: 2-deoxy-D-gluconate 3-dehydrogenase
aldehyde dehydrogenase
MULTISPECIES: purine catabolism protein PurC
4-aminobutyrate aminotransferase
hypothetical protein
aminomethyltransferase
MULTISPECIES: glycine cleavage system protein H
glycine dehydrogenase subunit 1
glycine dehydrogenase subunit 2
elongator protein 3/MiaB/NifB
radical SAM protein, partial
octanoyltransferase LipM
dihydrolipoyl dehydrogenase
transcriptional regulator
peptidoglycan glycosyltransferase
fumarate hydratase
MULTISPECIES: biotin synthase
DNA metabolism protein
MULTISPECIES: chemotaxis sensory transducer
methyltransferase type 11

thiamine ABC transporter permease
hypothetical protein ETSY2_21090
MULTISPECIES: inosine-5-monophosphate dehydrogenase
AraC family transcriptional regulator
hypothetical protein
MULTISPECIES: AraC family transcriptional regulator
MULTISPECIES: tRNA synthetase subunit beta
hypothetical protein
hypothetical protein
5'-nucleotidase
MULTISPECIES: NADH-quinone oxidoreductase subunit A
NADH dehydrogenase
NADH dehydrogenase
NAD(P)H-quinone oxidoreductase subunit H
NADH:ubiquinone oxidoreductase subunit H
NADH-quinone oxidoreductase subunit I
NADH-ubiquinone oxidoreductase
NADH:ubiquinone oxidoreductase subunit K
NADH dehydrogenase
NADH dehydrogenase subunit M
NADH-quinone oxidoreductase subunit N
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
chemotaxis protein CheY
pyruvate kinase
glycerate kinase, partial
hypothetical protein, partial
chemotaxis protein
hypothetical protein
diguanylate cyclase
HAD family hydrolase
MULTISPECIES: hypothetical protein
hydrogenase isoenzymes formation protein HypD
hydrogenase expression/formation protein HypE
MULTISPECIES: TetR family transcriptional regulator
hypothetical protein
alcohol dehydrogenase
hypothetical protein
membrane protein
hypothetical protein, partial
hypothetical protein
hypothetical protein, partial
PTS system, lactose/cellobiose family IIC component
membrane protein
adenylosuccinate synthetase

membrane protein
hypothetical protein
FAD-binding protein
MarR family transcriptional regulator
hypothetical protein
MULTISPECIES: 4Fe-4S ferredoxin
membrane protein
MULTISPECIES: hypothetical protein
LysR family transcriptional regulator
putative ammonia monooxygenase
cytochrome c-552
respiratory nitrite reductase specific menaquinol--cytochrome-c reductase (NrfH) precursor
cytochrome c-type biogenesis protein CycK
cytochrome c-type biogenesis protein CcmE
cytochrome C biogenesis protein
cytochrome c-type biogenesis protein CcmB
cytochrome c biogenesis ATP-binding export protein CcmA
MULTISPECIES: stress protein
ferredoxin
hypothetical protein
fe-S oxidoreductase
hypothetical protein
PAS domain S-box/diguanylate cyclase (GGDEF) domain-containing protein
hypothetical protein
hypothetical protein BN1050_02423
hypothetical protein BN1050_02424
hypothetical protein BN1050_02424
hypothetical protein
SMC domain-containing protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: RpiR family transcriptional regulator
MULTISPECIES: type III effector
MULTISPECIES: 4-hydroxythreonine-4-phosphate dehydrogenase
2-keto-3-deoxygluconate permease
2-hydroxyglutarate dehydrogenase
electron transfer flavoprotein subunit beta
MULTISPECIES: electron transfer flavoprotein subunit alpha
membrane protein
PAS/PAC sensor-containing diguanylate cyclase
methyl-accepting chemotaxis sensory transducer with cache sensor

hypothetical protein
RNA helicase
zinc-binding protein
major facilitator superfamily protein
phosphoglucomutase
hypothetical protein
Hexokinase
galactose-1-phosphate uridylyltransferase
Galactokinase
hypothetical protein ALO_04918
transcriptional regulator
sugar ABC transporter substrate-binding protein
D-ribose transporter ATP binding protein
hypothetical protein
hypothetical protein
transporter
DoxX family protein
hypothetical protein
hypothetical protein
Mg2+/Co2+ transporter
major facilitator superfamily MFS_1
hypothetical protein
ATP-dependent DNA helicase RecQ
hypothetical protein
glycoside hydrolase family 18
DNA topoisomerase
helicase
hypothetical protein
amino acid permease
hypothetical protein
multidrug ABC transporter ATP-binding protein
dihydrodipicolinate reductase
GntR family transcriptional regulator
lactoylglutathione lyase
hypothetical protein
cytochrome D ubiquinol oxidase subunit I
cytochrome d ubiquinol oxidase subunit 2, partial
hypothetical protein
hypothetical protein
DEAD-box ATP-dependent RNA helicase CshA
MULTISPECIES: hypothetical protein
RNA polymerase subunit sigma-54
acyltransferase 3
hydrolase GDSL
phosphohydrolase
hypothetical protein
C_GCAxxG_C_C family redox protein, partial

glyoxalase
reverse rubrerythrin-1
diguanylate cyclase
bile acid:sodium symporter
exodeoxyribonuclease III
diguanylate cyclase/phosphodiesterase with PAS/PAC sensor
DNA mismatch repair protein MutT
hypothetical protein
hypothetical protein
Xaa-Pro dipeptidase
thioesterase superfamily protein
aspartate ammonia-lyase
hypothetical protein
MULTISPECIES: amino acid permease
methionine-R-sulfoxide reductase
hypothetical protein
AraC family transcriptional regulator
nitrogenase iron protein
nitrogen fixation protein NifHD
nitrogen regulatory protein-PII
nitrogenase molybdenum-iron protein alpha chain
nitrogenase molybdenum-iron protein beta chain
nitrogenase iron-molybdenum cofactor biosynthesis protein NifE
nitrogenase
FeMo cofactor biosynthesis protein NifB
ferredoxin
Nitrogenase iron-iron accessory protein AnfO
pyruvate carboxyltransferase, partial
homocitrate synthase
resolvase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
MULTISPECIES: hypothetical protein
hypothetical protein SOV_2c02330
exported hypothetical protein
exported hypothetical protein
exported hypothetical protein
RDD domain-containing protein
glycosyl hydrolase family 25
hypothetical protein SOV_5c02610
hypothetical protein
4-oxalocrotonate tautomerase
aldo/keto reductase
ATPase AAA
hypothetical protein

hypothetical protein
GTP-binding protein
hypothetical protein
hypothetical protein TcarDRAFT_2045
hypothetical protein FB4_0023
DNA polymerase
Na+/H+ antiporter
hypothetical protein
hypothetical protein
membrane protein
hypothetical protein
hypothetical protein
cobalamin biosynthesis protein P47K
hypothetical protein
ABC transporter substrate-binding protein
Protein of unknown function DUF318, transmembrane
hypothetical protein
transcriptional regulator
S-layer domain protein
ABC transporter substrate-binding protein
ABC transporter permease
binding-protein-dependent transporters inner membrane component
peptide ABC transporter ATP-binding protein
ABC transporter
Methyltransferase type 11
hypothetical protein
hypothetical protein
hypothetical protein
3-hydroxybutyryl-CoA dehydrogenase
hypothetical protein
transposase
resolvase josui]
MULTISPECIES: hypothetical protein
iron-sulfur cluster-binding protein
hypothetical protein
hypothetical protein
membrane protein
transcriptional regulator, LysR family
altronate dehydratase
D-galactarate dehydratase
hypothetical protein
sugar diacid utilization regulator
methylase involved in ubiquinone/menaquinone biosynthesis
sulfur transport
putative transporter component
4Fe-4S ferredoxin iron-sulfur binding domain-containing protein
hypothetical protein

hypothetical protein
cation diffusion facilitator family transporter
MULTISPECIES: FeS cluster assembly scaffold IscU
hypothetical protein
cobyrinic acid a,c-diamide synthase
cobyrinic acid ac-diamide synthase
hypothetical protein
dinitrogenase iron-molybdenum cofactor biosynthesis protein
ATPase-like, ParA/MinD
MULTISPECIES: beta-lactamase
ATPase-like, ParA/MinD
MULTISPECIES: glycine/betaine ABC transporter substrate-binding protein
choline ABC transporter permease
glycine/betaine ABC transporter ATPase
H(+)/Cl(-) exchange transporter ClcA
MULTISPECIES: FAD-dependent oxidoreductase
spore maturation protein
MULTISPECIES: nucleoside recognition protein
D-Ala-D-Ala carboxypeptidase
hypothetical protein
sporulation protein YtfJ
hypothetical protein
hypothetical protein
aromatic-ring-hydroxylating dioxygenase
tryptophan--tRNA ligase
peptidase
diaminopimelate decarboxylase
hypothetical protein
stage V sporulation protein AF
stage V sporulation protein AE
hypothetical protein, partial
hypothetical protein
SpoVA protein
stage V sporulation protein AD
MULTISPECIES: stage V sporulation protein AC
hypothetical protein
sporulation sigma factor SigG
ATPase
anti-sigma F factor antagonist
MULTISPECIES: D-Ala-D-Ala carboxypeptidase
MULTISPECIES: pyrimidine-nucleoside phosphorylase
phosphopentomutase
tyrosine recombinase XerD
stage II sporulation protein P
hypothetical protein
ADP-ribose pyrophosphatase
MULTISPECIES: chemotaxis protein CheY

serine peptidase
DNA recombination protein RecN
arginine repressor ArgR
rRNA methyltransferase
inorganic polyphosphate/ATP-NAD kinase PpnK
putative ribosomal RNA methyltransferase
deoxyxylulose-5-phosphate synthase
MULTISPECIES: acid phosphatase
geranyltranstransferase CrtE
exodeoxyribonuclease VII small subunit
exodeoxyribonuclease VII large subunit
O-sialoglycoprotein endopeptidase
transcription antitermination protein NusB
hypothetical protein
MULTISPECIES: hypothetical protein
alkaline shock protein
stage III sporulation protein D
hypothetical protein
MULTISPECIES: stage III sporulation protein AF
stage III sporulation protein AE
MULTISPECIES: stage III sporulation protein AD
stage III sporulation protein AC
MULTISPECIES: stage III sporulation protein AB
stage III sporulation protein AA
MULTISPECIES: hypothetical protein
elongation factor P
hypothetical protein
3-dehydroquinate dehydratase
Peptidoglycan glycosyltransferase
peptidase
peptidase U32
MULTISPECIES: O-methyltransferase
aminodeoxychorismate lyase
hypothetical protein
RNAse H-fold protein YqgF
hypothetical protein
alanyl-tRNA synthetase
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
PRC-barrel domain-containing protein
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
NifU-like protein
cysteine desulfurase
AsnC family transcriptional regulator
ATPase AAA
threonine aldolase

MULTISPECIES: aspartyl-tRNA synthetase
histidyl-tRNA synthetase
Radical SAM domain protein
Fur family transcriptional regulator
MULTISPECIES: hypothetical protein
beta-lactamase domain-containing protein
(p)ppGpp synthetase
adenine phosphoribosyltransferase
single-stranded-DNA-specific exonuclease RecJ
von Willebrand factor A
magnesium chelatase
hypothetical protein
hypothetical protein
protein translocase subunit SecF
preprotein translocase subunit SecD
phosphohydrolase
hypothetical protein
serine/threonine protein phosphatase
5-formyltetrahydrofolate cyclo-ligase
preprotein translocase subunit YajC
queuine tRNA-ribosyltransferase
S-adenosylmethionine tRNA ribosyltransferase
stage II sporulation protein SpoIID
hypothetical protein
hypothetical protein
MULTISPECIES: Holliday junction DNA helicase RuvB
MULTISPECIES: Holliday junction DNA helicase RuvA
crossover junction endodeoxyribonuclease
hypothetical protein
Fibronectin type III domain-containing protein
Fibronectin type III domain-containing protein
Fibronectin type III domain-containing protein
Fibronectin type III domain-containing protein
Fibronectin type III domain-containing protein
Fibronectin type III domain-containing protein
phage tail protein, partial
phage tail protein, partial
phage tail protein, partial
radical SAM protein
hypothetical protein
MULTISPECIES: cell wall hydrolase
hypothetical protein
putative metal-dependent phosphoesterase
hypothetical protein
MULTISPECIES: metal-dependent phosphohydrolase
mannosyl-glycoprotein endo-beta-N-acetylglucosamidase
peptidoglycan glycosyltransferase

PHP C-terminal domain protein
MULTISPECIES: spore protein
hydrogenase expression protein HypC
hydantoin utilization protein A
sporulation protein
alanine racemase
alanine dehydrogenase
MULTISPECIES: chemotaxis protein CheR
D-Ala-D-Ala carboxypeptidase
polysaccharide deacetylase
polysaccharide deacetylase
hypothetical protein
phenylacetate--CoA ligase
spore germination protein
Spore germination protein
hypothetical protein
hypothetical protein UFO1_0482
chemotaxis sensory transducer
Quinolinate synthase A
aspartate oxidase
MULTISPECIES: nicotinate-nucleotide pyrophosphorylase
exonuclease SbcD
chromosome segregation protein SMC
ATP-dependent nuclease subunit B
DNA helicase UvrD
Fe-S oxidoreductase
amino acid dehydrogenase
MULTISPECIES: lactate utilization protein C
hypothetical protein
polysaccharide deacetylase
Mg2+ transporter protein, CorA family protein
hypothetical protein SOV_2c04180
DNA polymerase IV
hypothetical protein
hypothetical protein
small acid-soluble spore protein, H-type
GntR family transcriptional regulator
AzlC family protein
branched-chain amino acid ABC transporter
hypothetical protein
hypothetical protein
hypothetical protein
D-aminoacylase
peptidase
pyridoxal-5'-phosphate-dependent protein subunit beta
hypothetical protein
aldehyde oxidoreductase

threonine synthase
exopolyphosphatase Ppx
exopolyphosphatase Ppx
polyphosphate kinase
membrane protein
hypothetical protein
hypothetical protein
hypothetical protein M918_06300
hypothetical protein MPLB_1510007
hypothetical protein
ATP-binding protein
endonuclease symbiosum]
hypothetical protein
hypothetical protein symbiosum]
cytosine methyltransferase, partial
very short patch repair endonuclease, putative
cyclase
MarR family transcriptional regulator
MULTISPECIES: short-chain dehydrogenase
hypothetical protein
MULTISPECIES: ArsR family transcriptional regulator
transposase
thioredoxin
hypothetical protein
thiamine-phosphate pyrophosphorylase
thiamine biosynthesis protein ThiF
thiamine biosynthesis protein ThiH
thiazole synthase
thiamine biosynthesis protein ThiS
MULTISPECIES: NGG1p interacting factor 3 protein, NIF3
hypothetical protein
RNA polymerase sigma factor RpoD
MULTISPECIES: DNA primase
deoxyguanosinetriphosphate triphosphohydrolase
organic solvent tolerance protein OstA
glycyl-tRNA synthetase subunit beta
glycyl-tRNA synthetase subunit alpha
ubiquitin
DNA recombination protein RecO
membrane protein
hypothetical protein
MULTISPECIES: GTPase Era
cytidine deaminase
diacylglycerol kinase
16S rRNA maturation RNase YbeY
phosphohydrolase
PhoH family protein

stage IV sporulation protein
sporulation protein YqfC
protein of unknown function DUF87
hypothetical protein
30S ribosomal protein S21
HIT family hydrolase
RNA modification enzyme MiaB
16S rRNA methyltransferase
ribosomal protein L11 methyltransferase
molecular chaperone DnaJ
chaperone protein DnaK
co-chaperone GrpE
chaperonin
HrcA family transcriptional regulator
coproporphyrinogen III oxidase
elongation factor 4
hypothetical protein
stage II sporulation protein P
germination protein
30S ribosomal protein S20
DNA polymerase III subunit delta
competence protein ComEC
competence protein ComEA helix-hairpin-helix repeat protein
resolvase
leucyl-tRNA synthetase
hypothetical protein
Redoxin domain protein
diacylglyceryl transferase
MULTISPECIES: histidine kinase
FAD-binding protein
hypothetical protein
sugar diacid recognition domain protein
amino acid transporter
membrane protein
serine protease
hypothetical protein
membrane protein
NAD(FAD)-dependent dehydrogenase
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
FAD-dependent oxidoreductase
MULTISPECIES: glycerol kinase
glycerol transporter
glycerol uptake operon antiterminator regulatory protein
hypothetical protein C883_3381
N-acetylmuramoyl-L-alanine amidase family 2
symporter
symporter

Na+/solute symporter
hypothetical protein
membrane protein
NUDIX hydrolase
ribulose 5-phosphate epimerase
glycerol-1-phosphate dehydrogenase
MULTISPECIES: HAD family hydrolase
MULTISPECIES: PTS galactitol transporter subunit IIC
PTS fructose transporter subunit IIB
PTS fructose transporter subunit IIA
PTS sugar transporter
membrane protein
amidohydrolase, imidazolonepropionase
radical SAM protein
hypothetical protein
hypothetical protein
hypothetical protein
membrane protein
hypothetical protein
hypothetical protein UFO1_2605
hypothetical protein UFO1_2604
heavy metal translocating P-type ATPase
hypothetical protein
6-phosphogluconate dehydrogenase
pyridoxal biosynthesis protein
glutamine amidotransferase
chemotaxis sensory transducer
hypothetical protein
hypothetical protein CCAN12_660017
MULTISPECIES: hypothetical protein
membrane protein
MULTISPECIES: permease
AsnC family transcriptional regulator
5-carboxymethyl-2-hydroxymuconate isomerase
hypothetical protein
MULTISPECIES: hypothetical protein
N-acetylmuramoyl-L-alanine amidase
hypothetical protein
hypothetical protein
hypothetical protein
radical SAM protein
L-aspartate 1-decarboxylase
hypothetical protein GCWU000246_00711
MULTISPECIES: fibronectin
MULTISPECIES: fibronectin
MULTISPECIES: fibronectin
MULTISPECIES: fibronectin

lysyl-tRNA synthetase
transcription elongation factor GreA
shikimate 5-dehydrogenase
quinate 5-dehydrogenase
transcriptional regulator
hypothetical protein
hypothetical protein
MULTISPECIES: pantothenate kinase
MULTISPECIES: biotin-(acetyl-CoA carboxylase) ligase
aspartate decarboxylase
pantoate--beta-alanine ligase
transcriptional regulator
MULTISPECIES: ATP-binding protein
hypothetical protein SOV_3c04380
hypothetical protein
cell division protein FtsH
hypoxanthine phosphoribosyltransferase
tRNA(Ile)-lysidine synthetase
hypothetical protein
protein of unknown function DUF1212
MULTISPECIES: serine phosphatase
iron hydrogenase
cytochrome B
hydrogenase
FAD-dependent oxidoreductase
4Fe-4S ferredoxin
hypothetical protein, partial
hypothetical protein
septum formation inhibitor
spore cortex biosynthesis protein YabQ
lytic transglycosylase
sporulation protein YabP/YqfC
hypothetical protein
spore germination protein
MULTISPECIES: spore germination protein
spore germination protein
MULTISPECIES: stage II sporulation protein SpoIID
chemotaxis sensory transducer
phosphate ABC transporter permease
phosphate ABC transporter permease protein PstC
phosphate ABC transporter substrate-binding protein
MULTISPECIES: diguanylate cyclase
hypothetical protein, partial
hypothetical protein
MULTISPECIES: histidine kinase
phosphate starvation protein PhoH
hypothetical protein

RNA-binding protein
histidine kinase
histidine kinase
phosphonate ABC transporter substrate-binding protein
hypothetical protein FB4_3784
MULTISPECIES: PhoU family transcriptional regulator
phosphate ABC transporter ATP-binding protein
hypothetical protein
amino acid permease
alanine dehydrogenase
PhoP family transcriptional regulator
DNA-binding protein
MULTISPECIES: nucleotide pyrophosphohydrolase
MULTISPECIES: polysaccharide biosynthesis protein
stage V sporulation protein T
transcription-repair coupling factor
hypothetical protein
MULTISPECIES: hypothetical protein
peptidase M23
conserved hypothetical protein
YibE/F family protein
alkaline phosphatase 4
MULTISPECIES: ABC transporter permease
MULTISPECIES: ABC transporter ATP-binding protein
myristoyl transferase
4Fe-4S ferredoxin, iron-sulpur binding domain-containing protein
(Fe-S)-binding protein
AraC family transcriptional regulator
hypothetical protein
glycoside hydrolase
glycosyl transferase family 2
polysaccharide deacetylase
MULTISPECIES: UDP-N-acetyl-D-galactosamine dehydrogenase
MULTISPECIES: S-layer protein
serine/threonine transporter SstT
hypothetical protein, partial
3-isopropylmalate dehydrogenase
phosphate acetyltransferase
transcriptional regulator LysR family
MscS Mechanosensitive ion channel
TonB-denpendent receptor
hypothetical protein
hydrogenase assembly protein HupF
MULTISPECIES: hypothetical protein
cyclic nucleotide-binding protein
hypothetical protein
hypothetical protein UFO1_3595

fructose-1,6-bisphosphatase, class II
transaldolase
hypothetical protein
chemotaxis protein CheY
MULTISPECIES: hypothetical protein
hypothetical protein
serine protease ClpP
CTP synthase
RNA polymerase
arginyl-tRNA synthetase
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
SpoIID/LytB domain-containing protein
VanW family protein
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
MULTISPECIES: hypothetical protein
lysylphosphatidylglycerol synthetase
multi-sensor signal transduction histidine kinase
hypothetical protein
transporter
DNA-directed RNA polymerase subunit omega
hypothetical protein
universal stress protein
hypothetical protein
hypothetical protein
Resolvase domain-containing protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
DNA-binding helix-turn-helix protein
hypothetical protein gnavus]
hypothetical protein
hypothetical protein
hypothetical protein LR68_03029
hypothetical protein
MULTISPECIES: Tn7 transposition protein D
hypothetical protein
XRE family transcriptional regulator
histidine kinase celerecrescens]
MULTISPECIES: NADH:flavin oxidoreductase
GreA/GreB family elongation factor
ArsR family transcriptional regulator
rod shape-determining protein MreB
homoserine kinase

MULTISPECIES: homoserine dehydrogenase
ACT domain-containing protein
stage IV sporulation protein A
glycerol-3-phosphate dehydrogenase
membrane protein
ribosome-associated GTPase EngA
peptide-binding protein
stage II sporulation protein P
MULTISPECIES: hypothetical protein
isopentenyl-diphosphate delta-isomerase
4-hydroxy-3-methylbut-2-enyl diphosphate reductase
carbon starvation protein CstA
1-acyl-sn-glycerol-3-phosphate acyltransferase
cytidylate kinase
3-phosphoshikimate 1-carboxyvinyltransferase
3-deoxy-7-phosphoheptulonate synthase
hypothetical protein
FAD-dependent oxidoreductase
ribosomal large subunit pseudouridine synthase B
hypothetical protein
glucose-inhibited division protein A
phosphoribosylformylglycinamidine synthase
LysR family transcriptional regulator
S-adenosylmethionine decarboxylase
hypothetical protein
chemotaxis protein CheY
hypothetical protein
AsnC family transcriptional regulator
aspartate aminotransferase AspC
chemotaxis protein CheX
MULTISPECIES: hypothetical protein
nitrogen regulatory PII
MULTISPECIES: ammonia channel protein, partial
hypothetical protein
hypothetical protein
hypothetical protein
RubisCO-like protein
transketolase clariflavum]
transketolase clariflavum]
hypothetical protein
membrane protein
3-ketoacyl-ACP reductase
hypothetical protein
hypothetical protein
G/U mismatch-specific DNA glycosylase
hypothetical protein
FAD-dependent oxidoreductase

membrane protein
coat protein F
hypothetical protein
hypothetical protein, partial
MULTISPECIES: glutaminyl-tRNA synthetase
hypothetical protein
transglycosylase
DNA polymerase
membrane protein
MULTISPECIES: elongation factor G
ATP:cob(I)alamin adenosyltransferase
MULTISPECIES: nucleoside diphosphate kinase
carbonic anhydrases/acetyltransferase, isoleucine patch superfamily
peptidase M28
protease
oligoketide cyclase/lipid transport protein
putrescine--2-oxoglutarate aminotransferase
amino acid transporter
hypothetical protein
transposase, IS200 family, partial
hypothetical protein, partial
pseudouridine synthase
fructose-bisphosphate aldolase
molybdenum-pterin-binding protein
molybdenum import ATP-binding protein ModC
MULTISPECIES: molybdate ABC transporter, inner membrane subunit
molybdate ABC transporter substrate-binding protein
metal-binding protein
MULTISPECIES: hypothetical protein
nitrogenase iron-iron accessory protein AnfO
nitroreductase
MarR family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
toxin RTX-I translocation ATP-binding protein
type I secretion membrane fusion protein, HlyD family
peptidase C39
UTP--glucose-1-phosphate uridylyltransferase
hypothetical protein

hypothetical protein
hypothetical protein
glycoside hydrolase
hypothetical protein
MULTISPECIES: metal transporter
RND transporter
transporter
histidine kinase
PhoP family transcriptional regulator
LemA family protein
hypothetical protein
SCP-like extracellular protein
ATPase
hypothetical protein
isoprenylcysteine carboxyl methyltransferase
diacylglyceryl transferase
hypothetical protein
hypothetical protein FB4_0791
hypothetical protein
S-layer domain protein domain protein
S-layer protein
hypothetical protein
protein of unknown function DUF477
PhoP family transcriptional regulator
PhoP family transcriptional regulator
chemotaxis protein
ATPase P
hypothetical protein
hypothetical protein
multicopper oxidase
Chain A, Crystal Structure Of Engineered Protein. Northeast Structural Genomics Consortium Target Or265.
Chain A, Crystal Structure Of Engineered Protein. Northeast Structural Genomics Consortium Target Or265.
hypothetical protein
S-layer protein
resolvase
H(+)/Cl(-) exchange transporter ClcA
diguanylate cyclase domain protein sordellii]
hypothetical protein
sigma54 specific transcriptional regulator
amino acid permease
L-cysteine desulfhydrase
endoribonuclease L-PSP
amino acid/polyamine/organocation transporter, APC superfamily
Collagen triple helix repeat (20 copies) termitidis]
hypothetical protein
signal peptidase
metallophosphoesterase

radical SAM protein
thiamine biosynthesis protein ThiF
Putative alpha/beta hydrolase superfamily protein
glutamate synthase, partial
stilbene synthase
hypothetical protein
MULTISPECIES: hydrogenase expression/formation protein
MULTISPECIES: chorismate mutase
glycosyltransferase
glycoside hydrolase
sodium:phosphate symporter
HAD family hydrolase
protein of unknown function DUF1256
MULTISPECIES: RNA polymerase sigma 70, partial
MULTISPECIES: UDP-N-acetylglucosamine 2-epimerase
glycosyltransferase
MULTISPECIES: glycosyltransferase family 2
MULTISPECIES: polysaccharide biosynthesis protein
dTDP-4-dehydrorhamnose reductase
energy transducer TonB
MULTISPECIES: biopolymer transportern ExbD
flagellar motor protein MotA
MULTISPECIES: peptidase
hypothetical protein
MULTISPECIES: TonB-denpendent receptor
MULTISPECIES: AraC family transcriptional regulator
biotin biosynthesis protein BioY
peptidase M20
acetyltransferase
acetolactate synthase
MULTISPECIES: acetolactate synthase
glutamine synthetase
hypothetical protein
sporulation protein
hypothetical protein
serine recombinase
hypothetical protein
hypothetical protein
ATPase
Chain A, Crystal Structure Of Engineered Protein. Northeast Structural Genomics Consortium Target Or265.

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Gene ID	Length (aa)	Identity	e-value
gene_id_667	661	96.52	0
gene_id_668	282	100	0
gene_id_669	157	100	2.00E-107
gene_id_670	130	98.46	8.00E-90
gene_id_671	358	98.6	0
gene_id_672	122	97.54	1.00E-83
gene_id_673	208	95.19	4.00E-144
gene_id_674	101	97.03	2.00E-62
gene_id_675	407	93.86	0
gene_id_676	277	98.56	0
gene_id_677	488	99.39	0
gene_id_678	141	94.33	3.00E-87
gene_id_679	846	97.64	0
gene_id_680	292	94.18	0
gene_id_681	61	91.8	5.00E-19
gene_id_682	29	96.55	8.00E-12
gene_id_683	405	95.8	0
gene_id_684	229	93.45	1.00E-120
gene_id_685	177	93.22	6.00E-116
gene_id_686	396	98.99	0
gene_id_687	645	99.38	0
gene_id_688	381	98.69	0
gene_id_689	529	93.19	0
gene_id_1037	44	95.45	4.00E-21
gene_id_1038	779	97.82	0
gene_id_1039	181	99.45	6.00E-98
gene_id_1040	252	98.81	8.00E-174
gene_id_1041	230	97.39	3.00E-133
gene_id_1043	140	95	9.00E-89
gene_id_1044	390	98.21	0
gene_id_1045	223	97.31	9.00E-142
gene_id_1046	478	74.48	0
gene_id_1047	189	56.08	1.00E-20
gene_id_1049	266	88.72	7.00E-145
gene_id_1050	102	54.9	1.00E-31
gene_id_1052	121	31.4	9.00E-16
gene_id_1054	96	52.08	6.00E-25
gene_id_1055	427	50.59	7.00E-128
gene_id_1055	252	28.17	9.00E-21
gene_id_1057	79	51.9	2.00E-15
gene_id_1059	81	58.02	2.00E-22
gene_id_1062	582	66.67	0
gene_id_1063	456	83.77	0
gene_id_1064	170	45.88	1.00E-41
gene_id_1066	548	96.72	0
gene_id_1067	1070	98.69	0

gene_id_1068	373	98.93	1.00E-174
gene_id_1069	278	99.64	2.00E-170
gene_id_1070	729	99.04	0
gene_id_1071	278	98.92	0
gene_id_1072	146	91.78	9.00E-87
gene_id_1073	135	65.93	6.00E-63
gene_id_1074	338	91.42	0
gene_id_1075	485	97.73	0
gene_id_1075	243	34.16	2.00E-24
gene_id_1076	115	96.52	2.00E-74
gene_id_1077	99	80.81	1.00E-52
gene_id_1078	433	98.15	0
gene_id_1079	236	97.88	5.00E-141
gene_id_1080	129	96.9	9.00E-73
gene_id_1081	65	93.85	9.00E-34
gene_id_1082	119	96.64	3.00E-76
gene_id_1083	77	98.7	9.00E-32
gene_id_1086	166	51.2	4.00E-49
gene_id_1087	141	60.99	1.00E-51
gene_id_1088	716	51.12	0
gene_id_1089	53	58.49	1.00E-07
gene_id_1090	162	45.68	1.00E-36
gene_id_1091	603	63.68	0
gene_id_1092	342	50.88	5.00E-95
gene_id_1093	346	59.83	3.00E-146
gene_id_1094	122	52.46	4.00E-26
gene_id_1095	343	54.23	5.00E-118
gene_id_1096	157	46.5	2.00E-41
gene_id_1097	351	47.01	5.00E-93
gene_id_1098	515	56.12	0
gene_id_1100	423	26.95	2.00E-40
gene_id_1101	520	49.42	2.00E-164
gene_id_1102	87	60.92	4.00E-25
gene_id_1103	275	52.73	1.00E-85
gene_id_1104	235	48.09	4.00E-73
gene_id_1105	214	42.06	5.00E-37
gene_id_1106	198	38.89	2.00E-42
gene_id_1107	803	56.41	0
gene_id_1109	179	66.48	2.00E-74
gene_id_1110	89	55.06	1.00E-27
gene_id_1111	81	58.02	3.00E-25
gene_id_1112	317	61.51	6.00E-135
gene_id_1113	132	39.39	1.00E-12
gene_id_1114	242	55.79	2.00E-94
gene_id_1116	43	55.81	2.00E-07
gene_id_1117	240	97.5	5.00E-161
gene_id_1118	129	58.14	2.00E-06

gene_id_1119	242	96.69	2.00E-114
gene_id_1120	660	96.67	0
gene_id_1121	484	74.79	0
gene_id_1122	185	99.46	1.00E-126
gene_id_1123	331	97.58	0
gene_id_1124	448	96.65	0
gene_id_1125	1133	88.79	0
gene_id_1126	1100	90.64	0
gene_id_1127	373	98.93	0
gene_id_2179	73	98.63	4.00E-44
gene_id_2181	126	41.27	2.00E-24
gene_id_2184	103	66.99	1.00E-36
gene_id_2188	226	34.96	2.00E-27
gene_id_2622	146	85.62	2.00E-47
gene_id_2623	60	90	3.00E-12
gene_id_2624	145	97.93	1.00E-97
gene_id_2625	752	94.55	0
gene_id_2625	118	88.98	3.00E-23
gene_id_2626	77	100	1.00E-32
gene_id_2628	533	96.06	0
gene_id_2629	453	95.14	0
gene_id_2630	136	100	9.00E-95
gene_id_2631	273	97.8	2.00E-175
gene_id_2632	292	93.49	0
gene_id_2633	242	82.23	3.00E-104
gene_id_5384	235	95.74	6.00E-125
gene_id_5385	185	99.46	1.00E-128
gene_id_5386	160	94.38	2.00E-101
gene_id_5387	238	96.22	3.00E-151
gene_id_5388	321	94.08	0
gene_id_5389	364	96.7	0
gene_id_5390	65	100	7.00E-30
gene_id_5391	265	97.36	5.00E-165
gene_id_5392	171	88.3	4.00E-61
gene_id_5393	503	97.81	0
gene_id_5394	227	98.24	1.00E-161
gene_id_5395	160	98.12	4.00E-105
gene_id_5396	64	100	4.00E-29
gene_id_5397	130	85.38	2.00E-42
gene_id_5398	208	95.19	1.00E-123
gene_id_5399	573	85.69	0
gene_id_5400	518	87.07	0
gene_id_5401	294	69.73	2.00E-141
gene_id_5402	1055	81.33	0
gene_id_5404	301	50.5	5.00E-93
gene_id_5405	240	38.33	3.00E-39
gene_id_5406	180	61.11	4.00E-66

gene_id_5407	478	41	1.00E-108
gene_id_5408	37	86.49	5.00E-08
gene_id_5409	211	93.84	1.00E-110
gene_id_5410	278	93.53	4.00E-169
gene_id_5411	350	96.86	3.00E-161
gene_id_5412	218	99.08	9.00E-157
gene_id_5413	762	95.93	0
gene_id_5529	171	99.42	2.00E-87
gene_id_5530	113	97.35	3.00E-50
gene_id_5531	1070	92.8	0
gene_id_5532	721	92.51	0
gene_id_5533	689	87.81	0
gene_id_5534	155	98.06	6.00E-106
gene_id_5535	73	98.63	1.00E-31
gene_id_5536	186	80.11	2.00E-54
gene_id_5537	163	97.55	7.00E-85
gene_id_5538	204	99.51	3.00E-134
gene_id_5539	110	100	1.00E-58
gene_id_5540	372	95.97	0
gene_id_5541	62	98.39	4.00E-34
gene_id_5542	169	97.04	9.00E-105
gene_id_5543	125	100	3.00E-86
gene_id_5544	331	91.54	4.00E-155
gene_id_5635	660	98.64	0
gene_id_5636	145	87.59	1.00E-81
gene_id_5637	124	100	3.00E-73
gene_id_5638	349	99.43	0
gene_id_5639	313	98.72	0
gene_id_5640	375	97.33	0
gene_id_5642	501	98	0
gene_id_5643	121	98.35	3.00E-82
gene_id_5644	360	99.72	0
gene_id_5645	531	99.44	0
gene_id_5646	766	98.56	0
gene_id_5647	230	93.91	6.00E-126
gene_id_5648	133	90.23	3.00E-65
gene_id_5649	551	97.1	0
gene_id_5650	335	84.18	1.00E-171
gene_id_5651	729	90.95	0
gene_id_5653	219	91.78	4.00E-113
gene_id_5653	45	95.56	4.00E-113
gene_id_5654	69	97.1	3.00E-36
gene_id_5656	841	89.06	0
gene_id_5657	336	97.32	0
gene_id_5658	38	97.37	3.00E-15
gene_id_5659	384	95.57	0
gene_id_5660	171	98.83	2.00E-104

gene_id_5661	545	98.53	0
gene_id_5662	201	100	4.00E-144
gene_id_5663	376	98.67	0
gene_id_5664	254	94.09	2.00E-169
gene_id_5665	231	95.24	8.00E-145
gene_id_5666	378	97.88	0
gene_id_5667	3511	93.9	0
gene_id_5667	984	30.59	1.00E-66
gene_id_5667	417	26.14	3.00E-07
gene_id_5667	563	24.51	5.00E-07
gene_id_6873	147	81.63	7.00E-50
gene_id_6874	406	97.04	0
gene_id_6876	581	88.12	0
gene_id_6877	152	96.05	5.00E-90
gene_id_6878	644	98.29	0
gene_id_6879	161	95.03	1.00E-96
gene_id_6880	433	98.15	0
gene_id_6881	589	90.83	0
gene_id_6882	317	98.42	0
gene_id_6883	126	84.13	2.00E-06
gene_id_6884	98	96.94	1.00E-26
gene_id_6885	601	99.17	0
gene_id_6886	198	98.99	7.00E-125
gene_id_6887	237	92.83	1.00E-95
gene_id_6888	180	61.67	3.00E-66
gene_id_6891	55	50.91	5.00E-12
gene_id_6892	116	73.28	3.00E-46
gene_id_6895	104	51.92	2.00E-26
gene_id_6898	110	65.45	5.00E-42
gene_id_6900	314	88.22	0
gene_id_6901	179	83.24	4.00E-50
gene_id_6902	810	94.07	0
gene_id_6903	162	99.38	2.00E-112
gene_id_6904	387	98.71	0
gene_id_6905	152	99.34	6.00E-79
gene_id_6906	370	95.41	0
gene_id_6907	326	98.47	1.00E-173
gene_id_6908	321	99.69	0
gene_id_6909	432	99.31	0
gene_id_8261	398	90.2	0
gene_id_8262	612	97.71	0
gene_id_8263	72	100	2.00E-44
gene_id_8264	239	99.16	2.00E-163
gene_id_8510	93	98.92	5.00E-53
gene_id_8511	364	82.97	0
gene_id_8512	423	72.81	0
gene_id_8513	358	68.99	5.00E-151

gene_id_8514	352	66.48	4.00E-128
gene_id_8515	383	63.45	5.00E-138
gene_id_8516	360	98.61	0
gene_id_8517	555	94.05	0
gene_id_8518	251	98.8	0
gene_id_8519	111	95.5	7.00E-68
gene_id_8520	170	93.53	1.00E-83
gene_id_8521	267	96.63	1.00E-130
gene_id_8522	497	89.74	0
gene_id_8523	151	94.04	2.00E-99
gene_id_8524	388	97.68	0
gene_id_8525	281	99.29	0
gene_id_8526	266	98.5	2.00E-174
gene_id_8527	154	98.7	5.00E-90
gene_id_8528	327	98.17	0
gene_id_8529	175	100	3.00E-103
gene_id_8530	816	93.01	0
gene_id_8531	884	98.64	0
gene_id_8532	224	98.66	3.00E-154
gene_id_8533	425	93.88	0
gene_id_8534	501	100	0
gene_id_9302	30	90	5.00E-06
gene_id_9303	164	99.39	1.00E-116
gene_id_9304	820	94.76	0
gene_id_9305	274	82.12	3.00E-131
gene_id_9306	245	99.59	9.00E-175
gene_id_9307	149	94.63	1.00E-93
gene_id_9308	248	98.79	4.00E-180
gene_id_9309	698	91.69	0
gene_id_9310	142	87.32	3.00E-83
gene_id_9311	74	94.59	3.00E-21
gene_id_9312	319	98.43	0
gene_id_9313	209	99.52	1.00E-146
gene_id_9314	178	100	5.00E-100
gene_id_9315	128	96.09	1.00E-81
gene_id_9316	368	98.64	0
gene_id_9317	192	93.75	2.00E-128
gene_id_9318	228	94.3	4.00E-131
gene_id_9319	146	100	6.00E-100
gene_id_9320	291	98.28	9.00E-179
gene_id_9321	1264	97.55	0
gene_id_9322	128	88.28	1.00E-52
gene_id_9323	295	90.85	2.00E-161
gene_id_9324	114	98.25	2.00E-75
gene_id_9325	130	92.31	2.00E-79
gene_id_9498	149	98.66	2.00E-53
gene_id_9499	210	89.52	5.00E-120

gene_id_9500	226	96.46	4.00E-126
gene_id_9501	500	97	0
gene_id_9502	382	98.95	0
gene_id_10360	180	98.89	1.00E-125
gene_id_10361	263	99.24	0
gene_id_10362	361	98.89	0
gene_id_10363	79	98.73	6.00E-48
gene_id_10365	403	96.03	0
gene_id_10366	188	98.4	5.00E-118
gene_id_10367	417	93.29	0
gene_id_10368	356	60.96	8.00E-104
gene_id_10369	229	98.25	1.00E-111
gene_id_10371	335	99.1	0
gene_id_10373	251	99.6	8.00E-180
gene_id_10374	136	97.79	5.00E-95
gene_id_10375	310	98.06	0
gene_id_10376	341	94.13	0
gene_id_10377	134	91.04	3.00E-81
gene_id_10378	518	73.75	0
gene_id_10379	298	94.63	0
gene_id_10380	351	93.16	0
gene_id_10381	173	97.69	9.00E-112
gene_id_10382	619	98.22	0
gene_id_10383	431	97.22	0
gene_id_10869	337	88.43	2.00E-160
gene_id_10870	363	92.29	0
gene_id_10871	250	78.4	3.00E-119
gene_id_10872	306	91.5	2.00E-157
gene_id_10873	263	95.82	3.00E-134
gene_id_10874	286	97.2	7.00E-162
gene_id_10875	418	98.33	0
gene_id_10876	997	97.19	0
gene_id_10876	199	37.69	3.00E-20
gene_id_10877	228	99.56	1.00E-139
gene_id_10878	172	96.51	5.00E-116
gene_id_10879	556	37.95	7.00E-105
gene_id_10880	392	38.27	3.00E-62
gene_id_10882	222	40.09	2.00E-31
gene_id_10883	613	48.94	0
gene_id_10884	67	47.76	7.00E-12
gene_id_10885	64	43.75	3.00E-07
gene_id_10886	468	49.36	7.00E-129
gene_id_10887	774	36.82	2.00E-130
gene_id_10888	114	51.75	4.00E-24
gene_id_10889	94	61.7	7.00E-25
gene_id_10890	156	60.9	7.00E-54
gene_id_10891	110	52.73	2.00E-26

gene_id_10893	39	56.41	7.00E-07
gene_id_10896	122	35.25	1.00E-06
gene_id_10897	65	63.08	5.00E-19
gene_id_10899	469	43.5	5.00E-124
gene_id_10902	719	57.44	0
gene_id_10904	152	39.47	5.00E-27
gene_id_10905	129	44.96	2.00E-18
gene_id_10906	940	33.83	8.00E-105
gene_id_10907	156	49.36	4.00E-25
gene_id_10908	48	54.17	2.00E-06
gene_id_10910	69	71.01	2.00E-19
gene_id_10911	107	49.53	2.00E-13
gene_id_11291	254	98.43	6.00E-153
gene_id_11292	414	86.47	0
gene_id_11293	108	91.67	1.00E-52
gene_id_11294	371	100	0
gene_id_11295	426	98.12	0
gene_id_11746	454	86.56	0
gene_id_11747	364	76.1	0
gene_id_11748	231	62.34	2.00E-81
gene_id_11749	522	85.06	0
gene_id_11750	286	86.36	1.00E-156
gene_id_11751	286	85.31	3.00E-163
gene_id_11752	370	68.92	5.00E-150
gene_id_11753	366	62.57	2.00E-136
gene_id_11754	302	68.54	2.00E-133
gene_id_11755	904	92.04	0
gene_id_11756	328	93.6	0
gene_id_11757	717	93.72	0
gene_id_11758	480	95.62	0
gene_id_11759	127	93.7	3.00E-69
gene_id_11760	319	98.75	0
gene_id_11762	119	98.32	9.00E-78
gene_id_11763	526	95.44	0
gene_id_11805	268	80.6	1.00E-131
gene_id_11806	330	94.24	4.00E-142
gene_id_11807	139	98.56	3.00E-96
gene_id_11808	100	97	1.00E-60
gene_id_11809	518	77.22	0
gene_id_11810	155	92.9	1.00E-85
gene_id_11811	299	91.97	1.00E-154
gene_id_11812	535	87.1	0
gene_id_11813	63	100	3.00E-37
gene_id_11814	381	98.43	0
gene_id_11815	437	99.77	0
gene_id_11816	85	95.29	2.00E-52
gene_id_11817	188	90.43	5.00E-85

gene_id_11834	233	89.7	2.00E-98
gene_id_11835	131	94.66	2.00E-81
gene_id_11836	150	99.33	1.00E-106
gene_id_11837	128	97.66	6.00E-74
gene_id_11838	463	99.57	0
gene_id_11839	226	99.56	5.00E-156
gene_id_11840	45	100	6.00E-24
gene_id_11841	388	99.23	0
gene_id_11842	372	98.66	0
gene_id_11843	531	98.87	0
gene_id_11844	271	98.52	0
gene_id_11845	338	95.86	0
gene_id_11846	453	99.56	0
gene_id_11847	925	91.89	0
gene_id_11848	369	99.73	0
gene_id_11849	131	95.42	3.00E-81
gene_id_11850	147	99.32	9.00E-99
gene_id_11851	148	97.97	6.00E-87
gene_id_11852	372	98.92	0
gene_id_11853	302	98.68	0
gene_id_11854	397	98.99	0
gene_id_11855	259	97.68	0
gene_id_11856	234	99.15	4.00E-155
gene_id_11858	412	88.83	6.00E-173
gene_id_11859	276	100	0
gene_id_11860	116	100	4.00E-74
gene_id_11861	124	99.19	3.00E-68
gene_id_11862	544	99.26	0
gene_id_11863	458	98.47	0
gene_id_11864	346	92.49	0
gene_id_11865	100	99	8.00E-67
gene_id_13390	257	96.89	4.00E-170
gene_id_13391	540	82.41	0
gene_id_13392	227	91.19	1.00E-130
gene_id_13393	277	94.95	7.00E-161
gene_id_13394	247	85.02	8.00E-119
gene_id_13395	225	96	1.00E-151
gene_id_13399	95	43.16	7.00E-17
gene_id_13401	242	56.2	1.00E-94
gene_id_13402	134	38.06	7.00E-13
gene_id_13403	317	60.88	6.00E-134
gene_id_13404	82	59.76	2.00E-24
gene_id_13405	84	54.76	1.00E-26
gene_id_13406	180	70.56	2.00E-77
gene_id_13408	803	58.53	0
gene_id_13409	205	38.54	2.00E-43
gene_id_13410	265	42.64	4.00E-41

gene_id_13411	231	49.35	1.00E-72
gene_id_13412	275	52.73	3.00E-85
gene_id_13413	87	60.92	6.00E-26
gene_id_13414	515	49.71	7.00E-164
gene_id_13415	426	28.17	8.00E-46
gene_id_13417	515	56.5	0
gene_id_13418	351	46.72	4.00E-92
gene_id_13419	157	47.77	6.00E-43
gene_id_13420	344	54.65	1.00E-111
gene_id_13421	145	47.59	7.00E-37
gene_id_13422	346	59.54	4.00E-146
gene_id_13423	310	54.19	7.00E-94
gene_id_13424	602	64.29	0
gene_id_13425	162	46.3	4.00E-37
gene_id_13426	39	71.79	1.00E-09
gene_id_13427	787	43.46	0
gene_id_13428	136	59.56	6.00E-53
gene_id_13429	203	42.36	6.00E-37
gene_id_13430	280	78.57	3.00E-162
gene_id_13431	122	84.43	3.00E-57
gene_id_13433	306	55.23	6.00E-111
gene_id_13433	216	29.17	1.00E-11
gene_id_13434	59	64.41	4.00E-11
gene_id_13435	66	74.24	7.00E-24
gene_id_13436	330	41.52	4.00E-83
gene_id_13437	669	61.29	0
gene_id_13438	186	53.76	2.00E-52
gene_id_13774	154	96.75	2.00E-85
gene_id_13775	474	95.78	0
gene_id_13776	153	98.69	4.00E-105
gene_id_13777	591	98.48	0
gene_id_13778	98	95.92	1.00E-59
gene_id_13779	259	98.07	2.00E-172
gene_id_13780	252	97.62	7.00E-151
gene_id_13781	117	97.44	9.00E-76
gene_id_13782	241	94.19	9.00E-123
gene_id_13783	115	98.26	9.00E-74
gene_id_13784	431	96.98	0
gene_id_13785	192	96.35	4.00E-116
gene_id_13786	77	100	2.00E-44
gene_id_13787	79	100	1.00E-49
gene_id_13788	438	99.54	0
gene_id_13790	365	97.81	0
gene_id_13791	326	98.77	0
gene_id_13792	293	98.63	0
gene_id_13793	340	96.18	0
gene_id_13794	275	97.09	0

gene_id_13795	304	93.42	1.00E-172
gene_id_13796	69	100	1.00E-30
gene_id_13797	611	92.8	0
gene_id_13798	125	92	2.00E-55
gene_id_14019	371	95.15	8.00E-128
gene_id_14020	155	97.42	3.00E-80
gene_id_14021	312	91.67	3.00E-128
gene_id_14022	58	100	3.00E-34
gene_id_14023	202	93.07	1.00E-118
gene_id_14024	59	98.31	4.00E-28
gene_id_14025	346	98.84	0
gene_id_14026	314	97.13	2.00E-174
gene_id_14027	247	100	2.00E-153
gene_id_14028	76	100	4.00E-43
gene_id_14029	415	99.28	0
gene_id_14030	412	99.76	0
gene_id_14032	154	98.7	7.00E-106
gene_id_14033	417	88.97	0
gene_id_14034	230	97.39	2.00E-131
gene_id_14035	409	99.51	0
gene_id_14036	156	99.36	2.00E-106
gene_id_14037	165	97.58	8.00E-114
gene_id_14038	833	97.6	0
gene_id_14039	193	92.23	1.00E-109
gene_id_14040	338	98.52	0
gene_id_14041	225	99.11	2.00E-147
gene_id_14042	111	94.59	4.00E-68
gene_id_14043	877	96.01	0
gene_id_14044	1041	97.02	0
gene_id_14045	397	97.73	0
gene_id_14046	60	100	4.00E-37
gene_id_14047	68	98.53	2.00E-38
gene_id_14048	380	87.11	2.00E-153
gene_id_14049	276	93.12	3.00E-168
gene_id_14050	158	100	1.00E-79
gene_id_14051	408	97.79	0
gene_id_14052	301	97.34	3.00E-169
gene_id_14053	376	96.54	0
gene_id_14054	74	94.59	5.00E-41
gene_id_14055	666	96.85	0
gene_id_14056	498	91.97	0
gene_id_14057	163	98.16	1.00E-99
gene_id_14058	187	97.33	3.00E-116
gene_id_14238	406	94.33	0
gene_id_14239	323	96.59	0
gene_id_14240	265	99.25	0
gene_id_14241	172	89.53	3.00E-66

gene_id_14242	433	96.77	0
gene_id_14243	332	99.4	0
gene_id_14244	269	93.68	2.00E-151
gene_id_14245	49	100	7.00E-27
gene_id_14246	671	95.83	0
gene_id_14246	499	95.39	0
gene_id_14247	293	82.25	2.00E-95
gene_id_14248	605	96.69	0
gene_id_14249	314	98.73	0
gene_id_14250	375	42.13	2.00E-73
gene_id_14251	233	30.9	4.00E-29
gene_id_14252	335	28.06	1.00E-45
gene_id_14253	290	47.59	7.00E-91
gene_id_14254	288	31.25	8.00E-42
gene_id_14255	230	31.3	1.00E-34
gene_id_14256	151	53.64	2.00E-41
gene_id_14257	395	64.81	0
gene_id_14258	323	32.51	1.00E-28
gene_id_14259	210	33.33	1.00E-38
gene_id_14260	319	58.93	4.00E-136
gene_id_14261	349	46.13	2.00E-103
gene_id_14262	387	29.72	2.00E-33
gene_id_14263	500	38.8	6.00E-90
gene_id_14264	344	62.5	3.00E-157
gene_id_14265	282	35.46	1.00E-52
gene_id_14266	420	36.9	3.00E-82
gene_id_14267	485	36.7	4.00E-84
gene_id_14268	412	72.57	0
gene_id_14269	296	38.18	8.00E-49
gene_id_14270	255	29.02	6.00E-15
gene_id_14271	247	64.37	2.00E-96
gene_id_14272	252	69.05	3.00E-102
gene_id_14273	207	58.45	2.00E-77
gene_id_14274	374	75.4	0
gene_id_14275	226	61.5	5.00E-102
gene_id_14276	339	74.04	5.00E-162
gene_id_14277	492	32.93	1.00E-70
gene_id_14278	364	66.76	1.00E-155
gene_id_14279	323	71.52	2.00E-161
gene_id_14280	266	41.73	2.00E-69
gene_id_14281	696	37.21	1.00E-99
gene_id_14282	191	49.74	5.00E-54
gene_id_14283	336	54.46	8.00E-118
gene_id_14284	392	92.86	0
gene_id_14285	310	98.06	5.00E-127
gene_id_14286	139	98.56	2.00E-92
gene_id_14287	542	90.59	0

gene_id_14288	115	100	2.00E-75
gene_id_14289	576	99.65	0
gene_id_14290	107	99.07	2.00E-67
gene_id_14291	243	93.83	4.00E-135
gene_id_14292	96	91.67	4.00E-34
gene_id_14293	151	100	9.00E-102
gene_id_14294	84	100	2.00E-36
gene_id_14344	96	98.96	3.00E-62
gene_id_14345	647	99.07	0
gene_id_14345	86	98.84	2.00E-35
gene_id_14345	68	97.06	2.00E-20
gene_id_14346	407	100	0
gene_id_14347	230	90.43	6.00E-124
gene_id_14348	259	98.84	0
gene_id_14349	260	100	0
gene_id_14350	346	97.11	0
gene_id_14351	238	98.74	3.00E-132
gene_id_14352	374	100	0
gene_id_14353	201	97.01	4.00E-127
gene_id_14353	139	99.28	3.00E-88
gene_id_14353	98	96.94	4.00E-36
gene_id_14354	154	98.05	7.00E-75
gene_id_14355	702	99.43	0
gene_id_14356	498	98.59	0
gene_id_14357	79	100	5.00E-33
gene_id_14358	140	98.57	3.00E-92
gene_id_14359	556	97.3	0
gene_id_14438	681	98.83	0
gene_id_14439	238	98.32	1.00E-169
gene_id_14440	154	98.7	2.00E-92
gene_id_14441	104	91.35	1.00E-58
gene_id_14442	92	97.83	2.00E-58
gene_id_14443	64	98.44	1.00E-36
gene_id_14444	209	98.09	3.00E-127
gene_id_14445	87	86.21	2.00E-16
gene_id_14446	262	99.24	4.00E-151
gene_id_14447	425	98.59	0
gene_id_14448	287	99.3	0
gene_id_14450	501	95.41	0
gene_id_14451	310	97.74	2.00E-175
gene_id_14452	133	97.74	4.00E-88
gene_id_14453	204	96.57	4.00E-140
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gene_id_14455	172	97.67	9.00E-115
gene_id_14456	318	96.23	3.00E-175
gene_id_14457	646	96.9	0
gene_id_14458	110	90	1.00E-31

gene_id_14583	289	96.89	9.00E-149
gene_id_14584	160	100	2.00E-111
gene_id_14585	156	94.23	5.00E-86
gene_id_14586	78	100	6.00E-50
gene_id_14587	706	97.59	0
gene_id_14588	874	98.63	0
gene_id_14589	120	100	4.00E-77
gene_id_14590	105	81.9	5.00E-33
gene_id_14591	431	98.14	0
gene_id_14592	368	94.84	0
gene_id_14593	343	99.71	0
gene_id_14594	879	98.52	0
gene_id_14595	255	92.94	9.00E-148
gene_id_14596	432	94.68	0
gene_id_14597	72	97.22	3.00E-41
gene_id_14598	226	99.56	5.00E-149
gene_id_14599	255	99.22	3.00E-179
gene_id_14600	230	100	1.00E-160
gene_id_14601	201	99	6.00E-140
gene_id_14602	405	93.58	4.00E-157
gene_id_14603	267	98.88	1.00E-170
gene_id_14604	519	92.29	0
gene_id_14605	175	99.43	5.00E-116
gene_id_14606	37	91.89	7.00E-11
gene_id_14844	163	95.71	1.00E-76
gene_id_14845	252	96.43	2.00E-147
gene_id_14846	686	99.13	0
gene_id_14847	424	98.35	0
gene_id_14848	261	84.29	8.00E-120
gene_id_14849	292	96.92	0
gene_id_14850	191	98.43	1.00E-123
gene_id_14851	800	97	0
gene_id_14852	235	99.15	3.00E-172
gene_id_14853	236	97.46	1.00E-161
gene_id_14855	321	96.88	0
gene_id_14856	550	99.27	0
gene_id_14857	504	92.86	0
gene_id_14858	108	98.15	9.00E-68
gene_id_14859	142	93.66	2.00E-76
gene_id_14860	105	96.19	2.00E-65
gene_id_14861	610	83.28	0
gene_id_15029	353	84.99	4.00E-132
gene_id_15031	756	96.43	0
gene_id_15032	748	96.12	0
gene_id_15034	191	96.86	1.00E-114
gene_id_15035	281	100	0
gene_id_15036	241	99.59	2.00E-176

gene_id_15037	171	97.66	2.00E-120
gene_id_15038	92	91.3	5.00E-54
gene_id_15039	67	98.51	1.00E-41
gene_id_15040	213	88.26	3.00E-80
gene_id_15041	91	81.32	5.00E-18
gene_id_15042	178	98.31	2.00E-48
gene_id_15043	313	97.44	8.00E-133
gene_id_15044	43	83.72	4.00E-14
gene_id_15045	118	97.46	2.00E-55
gene_id_15061	175	73.71	2.00E-67
gene_id_15062	330	87.88	0
gene_id_15063	135	98.52	4.00E-73
gene_id_15064	259	81.08	3.00E-99
gene_id_15064	67	94.03	4.00E-30
gene_id_15064	123	79.67	1.00E-25
gene_id_15065	421	100	0
gene_id_15066	197	97.46	2.00E-78
gene_id_15067	283	85.16	2.00E-139
gene_id_15068	191	99.48	4.00E-135
gene_id_15069	357	92.16	0
gene_id_15070	594	95.45	0
gene_id_15153	1019	97.25	0
gene_id_15154	322	91.3	3.00E-168
gene_id_15155	365	100	0
gene_id_15156	306	99.35	7.00E-162
gene_id_15157	358	98.6	0
gene_id_15158	255	98.43	0
gene_id_15159	241	100	3.00E-172
gene_id_15160	1606	92.96	0
gene_id_15162	270	86.67	9.00E-130
gene_id_15163	287	94.43	0
gene_id_15164	197	54.82	1.00E-65
gene_id_15166	164	36.59	7.00E-32
gene_id_15168	285	36.14	1.00E-45
gene_id_15169	96	61.46	9.00E-32
gene_id_15170	427	49.41	9.00E-124
gene_id_15170	255	27.06	2.00E-19
gene_id_15171	155	45.16	2.00E-34
gene_id_15172	53	45.28	3.00E-07
gene_id_15175	86	68.6	1.00E-36
gene_id_15179	625	54.08	0
gene_id_15180	231	49.35	5.00E-48
gene_id_15224	411	96.84	0
gene_id_15225	304	79.28	1.00E-97
gene_id_15226	698	96.56	0
gene_id_15227	187	74.33	9.00E-71
gene_id_15228	270	94.07	2.00E-168

gene_id_15229	90	100	8.00E-54
gene_id_15230	62	100	1.00E-36
gene_id_15231	70	98.57	1.00E-25
gene_id_15232	148	99.32	2.00E-81
gene_id_15233	360	92.22	0
gene_id_15237	249	99.6	8.00E-158
gene_id_15238	343	91.84	0
gene_id_15239	309	96.76	0
gene_id_15240	248	97.98	3.00E-167
gene_id_15241	147	98.64	7.00E-102
gene_id_15242	334	98.5	0
gene_id_15243	64	100	9.00E-28
gene_id_15244	160	98.75	1.00E-108
gene_id_15245	941	97.02	0
gene_id_15246	200	90.5	7.00E-78
gene_id_15247	83	97.59	7.00E-40
gene_id_15248	166	99.4	2.00E-114
gene_id_15249	567	99.47	0
gene_id_15250	317	99.05	0
gene_id_15251	159	98.74	5.00E-110
gene_id_15252	58	93.1	5.00E-09
gene_id_15253	177	98.31	3.00E-106
gene_id_15254	113	100	4.00E-61
gene_id_15255	147	96.6	9.00E-85
gene_id_15256	234	98.72	2.00E-142
gene_id_15257	339	97.64	0
gene_id_15258	234	94.87	5.00E-139
gene_id_15259	169	96.45	3.00E-84
gene_id_15260	287	98.26	4.00E-173
gene_id_15261	397	92.44	0
gene_id_15262	370	97.03	0
gene_id_15263	101	99.01	3.00E-64
gene_id_15264	90	97.78	8.00E-56
gene_id_15265	105	100	1.00E-70
gene_id_15266	395	89.37	6.00E-180
gene_id_15267	911	94.84	0
gene_id_15268	815	93.01	0
gene_id_15269	787	88.56	0
gene_id_15270	155	89.03	1.00E-61
gene_id_15271	696	97.56	0
gene_id_15272	174	97.13	3.00E-103
gene_id_15273	189	95.24	1.00E-129
gene_id_15274	393	99.49	0
gene_id_15275	232	97.84	2.00E-150
gene_id_15276	128	93.75	3.00E-57
gene_id_15277	228	99.12	3.00E-150
gene_id_15278	391	98.72	0

gene_id_15279	383	97.65	0
gene_id_15280	275	85.45	1.00E-151
gene_id_15281	401	97.26	0
gene_id_15282	59	98.31	1.00E-35
gene_id_15283	291	57.04	5.00E-73
gene_id_15284	408	76.23	2.00E-176
gene_id_15285	66	98.48	1.00E-33
gene_id_15286	242	98.76	8.00E-175
gene_id_15287	256	99.22	7.00E-173
gene_id_15288	233	98.28	1.00E-164
gene_id_15289	229	99.56	4.00E-135
gene_id_15290	286	97.9	0
gene_id_15291	223	96.86	3.00E-144
gene_id_15292	417	94.24	0
gene_id_15293	433	96.77	0
gene_id_15294	544	94.12	0
gene_id_15295	139	100	5.00E-98
gene_id_15296	258	96.51	2.00E-144
gene_id_15297	446	81.84	0
gene_id_15298	335	97.01	0
gene_id_15299	273	99.63	7.00E-171
gene_id_15540	230	98.26	8.00E-141
gene_id_15541	629	93.96	0
gene_id_15542	133	100	4.00E-91
gene_id_15543	258	90.7	3.00E-114
gene_id_15544	787	94.92	0
gene_id_15545	677	98.08	0
gene_id_15546	103	77.67	5.00E-52
gene_id_15547	396	98.48	0
gene_id_15548	393	97.2	0
gene_id_15549	127	94.49	8.00E-73
gene_id_15550	238	99.16	3.00E-169
gene_id_15551	255	99.22	0
gene_id_15552	316	97.15	0
gene_id_15553	301	98.34	1.00E-131
gene_id_15554	350	99.14	0
gene_id_15555	198	95.45	1.00E-113
gene_id_15556	426	98.36	0
gene_id_15557	341	99.41	0
gene_id_15558	373	97.86	0
gene_id_15559	449	98.44	0
gene_id_15562	341	99.12	0
gene_id_15563	363	98.9	0
gene_id_15564	232	96.55	3.00E-133
gene_id_15565	472	94.07	0
gene_id_15566	1166	92.2	0
gene_id_15567	251	96.81	1.00E-151

gene_id_15568	201	99	1.00E-130
gene_id_15569	100	100	5.00E-52
gene_id_15570	195	89.74	1.00E-81
gene_id_15570	79	97.47	4.00E-25
gene_id_15759	266	99.25	0
gene_id_15760	364	92.58	0
gene_id_15761	491	98.57	0
gene_id_15762	213	94.84	3.00E-148
gene_id_15763	416	96.63	0
gene_id_15764	1452	94.77	0
gene_id_15765	274	90.88	2.00E-148
gene_id_15766	345	95.65	2.00E-152
gene_id_15767	181	95.58	2.00E-109
gene_id_15768	335	98.81	0
gene_id_15769	536	99.25	0
gene_id_15770	126	100	1.00E-90
gene_id_15771	259	99.61	0
gene_id_15772	387	98.71	0
gene_id_15773	432	83.1	0
gene_id_15774	537	96.09	0
gene_id_15775	130	99.23	9.00E-87
gene_id_15776	55	98.18	2.00E-30
gene_id_15777	814	98.4	0
gene_id_15778	291	99.31	0
gene_id_15779	450	99.33	0
gene_id_15780	299	93.31	0
gene_id_15781	247	100	2.00E-160
gene_id_15782	291	98.28	0
gene_id_15783	632	99.05	0
gene_id_15784	253	94.07	2.00E-159
gene_id_15785	88	100	6.00E-49
gene_id_15786	206	94.17	3.00E-119
gene_id_15787	460	98.26	0
gene_id_15788	401	99.5	0
gene_id_15789	300	99	0
gene_id_15790	342	76.9	6.00E-174
gene_id_16235	68	72.06	1.00E-11
gene_id_16237	60	100	9.00E-38
gene_id_16238	432	99.54	0
gene_id_16239	186	98.92	5.00E-130
gene_id_16240	432	98.38	0
gene_id_16241	294	99.32	8.00E-115
gene_id_16242	113	96.46	6.00E-68
gene_id_16243	704	99.01	0
gene_id_16244	275	85.82	3.00E-156
gene_id_16246	47	100	2.00E-24
gene_id_16247	695	95.11	0

gene_id_16248	403	98.26	0
gene_id_16249	225	97.33	2.00E-77
gene_id_16250	276	92.03	7.00E-156
gene_id_16251	259	96.91	1.00E-160
gene_id_16252	316	99.05	4.00E-168
gene_id_16253	295	97.97	3.00E-127
gene_id_16254	691	95.37	0
gene_id_16255	514	89.69	0
gene_id_16256	569	98.95	0
gene_id_16258	365	91.78	0
gene_id_16259	171	92.4	5.00E-106
gene_id_16260	431	98.84	0
gene_id_16261	263	95.44	3.00E-162
gene_id_16262	233	95.28	4.00E-88
gene_id_16263	369	43.36	3.00E-95
gene_id_16264	528	99.05	0
gene_id_16265	159	99.37	2.00E-89
gene_id_16266	977	88.43	0
gene_id_16267	563	94.14	0
gene_id_16268	38	78.95	1.00E-12
gene_id_16269	450	98	0
gene_id_16270	2514	74.34	0
gene_id_16304	637	86.5	0
gene_id_16305	639	96.87	0
gene_id_16306	182	99.45	8.00E-125
gene_id_16307	120	94.17	6.00E-58
gene_id_16308	529	90.74	0
gene_id_16309	562	98.58	0
gene_id_16310	401	92.27	0
gene_id_16311	137	67.88	3.00E-41
gene_id_16312	170	37.65	2.00E-31
gene_id_16313	104	52.88	2.00E-32
gene_id_16314	108	38.89	3.00E-09
gene_id_16316	238	63.87	3.00E-97
gene_id_16317	404	71.29	0
gene_id_16318	491	42.77	8.00E-126
gene_id_16319	408	61.76	1.00E-166
gene_id_16320	83	62.65	4.00E-27
gene_id_16321	227	45.37	4.00E-67
gene_id_16322	132	55.3	1.00E-36
gene_id_16323	320	66.25	3.00E-154
gene_id_16324	140	47.86	6.00E-30
gene_id_16325	182	44.51	5.00E-46
gene_id_16326	785	41.4	2.00E-113
gene_id_16327	172	31.98	1.00E-16
gene_id_16328	84	52.38	4.00E-19
gene_id_16329	130	66.92	5.00E-58

gene_id_16330	454	50.44	1.00E-146
gene_id_16331	383	62.92	8.00E-171
gene_id_16332	287	49.48	1.00E-95
gene_id_16333	83	62.65	5.00E-29
gene_id_16334	396	54.55	1.00E-111
gene_id_16335	313	40.26	6.00E-53
gene_id_16336	314	47.13	5.00E-90
gene_id_16337	65	93.85	9.00E-36
gene_id_16338	282	98.94	2.00E-176
gene_id_16344	828	94.69	0
gene_id_16379	401	36.91	8.00E-73
gene_id_16380	77	42.86	5.00E-19
gene_id_16381	271	60.52	8.00E-119
gene_id_16383	486	50.82	2.00E-157
gene_id_16384	373	42.09	5.00E-84
gene_id_16385	219	48.86	3.00E-49
gene_id_16404	417	88.97	0
gene_id_16404	189	98.94	5.00E-92
gene_id_16405	604	99.01	0
gene_id_16406	716	98.74	0
gene_id_16407	209	96.17	3.00E-142
gene_id_16408	353	99.43	0
gene_id_16409	403	99.26	0
gene_id_16410	704	99.72	0
gene_id_16411	430	99.07	0
gene_id_16412	461	99.35	0
gene_id_16413	1215	99.18	0
gene_id_16414	504	94.05	0
gene_id_16415	1125	93.33	0
gene_id_16416	219	94.52	2.00E-141
gene_id_16417	125	99.2	1.00E-84
gene_id_16418	377	95.23	0
gene_id_16419	537	96.46	0
gene_id_16420	295	27.46	9.00E-16
gene_id_16421	295	56.95	6.00E-120
gene_id_16422	516	43.22	6.00E-134
gene_id_16432	219	89.5	1.00E-103
gene_id_16433	581	98.97	0
gene_id_16434	283	99.65	0
gene_id_16435	208	99.04	7.00E-148
gene_id_16436	60	100	1.00E-34
gene_id_16437	317	97.79	0
gene_id_16438	592	98.48	0
gene_id_16439	302	93.71	1.00E-167
gene_id_16441	320	98.12	0
gene_id_16442	251	96.81	1.00E-168
gene_id_16443	289	84.78	2.00E-117

gene_id_16444	811	99.01	0
gene_id_16445	61	57.38	4.00E-17
gene_id_16446	383	97.65	0
gene_id_16447	436	91.74	0
gene_id_16448	174	97.13	3.00E-121
gene_id_16449	264	98.48	5.00E-170
gene_id_16450	262	99.24	4.00E-161
gene_id_16451	268	98.88	0
gene_id_16452	328	99.7	0
gene_id_16453	255	98.82	0
gene_id_16454	656	92.99	0
gene_id_16455	77	100	1.00E-46
gene_id_16456	94	96.81	2.00E-59
gene_id_16457	382	100	0
gene_id_16458	277	99.28	0
gene_id_16459	207	98.55	1.00E-134
gene_id_16460	98	98.98	6.00E-64
gene_id_16461	517	58.03	0
gene_id_16462	527	99.62	0
gene_id_16463	205	99.02	5.00E-123
gene_id_16464	625	97.44	0
gene_id_16465	231	97.4	2.00E-125
gene_id_16466	384	98.7	0
gene_id_16467	277	89.17	1.00E-131
gene_id_16468	271	97.42	3.00E-166
gene_id_16572	1018	96.27	0
gene_id_16573	679	96.61	0
gene_id_16574	511	93.93	0
gene_id_16575	175	98.86	1.00E-71
gene_id_16576	121	97.52	1.00E-49
gene_id_16577	92	88.04	6.00E-44
gene_id_16578	208	97.6	5.00E-150
gene_id_16579	123	96.75	1.00E-82
gene_id_16580	344	97.38	0
gene_id_16581	465	93.33	0
gene_id_16582	481	99.17	0
gene_id_16583	443	99.55	0
gene_id_16584	127	99.21	2.00E-84
gene_id_16585	137	99.27	2.00E-89
gene_id_16586	549	99.27	0
gene_id_16588	366	98.63	0
gene_id_16591	534	91.57	0
gene_id_16592	399	96.74	0
gene_id_16593	107	96.26	2.00E-69
gene_id_16594	316	91.46	0
gene_id_16595	314	90.76	0
gene_id_16596	110	97.27	3.00E-69

gene_id_16597	271	81.18	3.00E-136
gene_id_16598	441	97.96	0
gene_id_16600	243	99.59	3.00E-178
gene_id_16601	252	99.21	0
gene_id_16602	596	98.66	0
gene_id_16603	366	94.26	0
gene_id_16604	711	97.19	0
gene_id_16605	215	93.95	5.00E-100
gene_id_16606	201	98.01	5.00E-119
gene_id_16607	273	98.17	0
gene_id_16608	647	96.75	0
gene_id_16609	752	95.21	0
gene_id_16610	313	94.57	0
gene_id_16611	183	85.79	3.00E-74
gene_id_16612	388	98.71	0
gene_id_16613	233	89.7	4.00E-125
gene_id_16614	350	94.57	0
gene_id_16615	719	96.38	0
gene_id_16616	203	99.01	2.00E-114
gene_id_16617	227	96.04	4.00E-136
gene_id_16618	147	97.96	4.00E-97
gene_id_16619	503	98.81	0
gene_id_16620	150	98	3.00E-99
gene_id_16621	270	40.74	6.00E-44
gene_id_16622	109	40.37	4.00E-18
gene_id_16623	883	98.07	0
gene_id_16624	432	92.82	0
gene_id_16937	39	82.05	4.00E-14
gene_id_16938	320	91.25	0
gene_id_16939	231	99.13	8.00E-153
gene_id_16940	100	99	3.00E-61
gene_id_16941	169	99.41	9.00E-93
gene_id_16942	106	97.17	1.00E-66
gene_id_16943	76	98.68	7.00E-33
gene_id_16944	562	99.47	0
gene_id_16945	162	98.77	3.00E-109
gene_id_16946	330	100	0
gene_id_16947	188	98.94	9.00E-132
gene_id_16948	71	100	3.00E-43
gene_id_16949	29	96.55	4.00E-10
gene_id_16950	32	96.88	6.00E-14
gene_id_16951	98	97.96	2.00E-63
gene_id_16952	177	99.44	2.00E-92
gene_id_16953	578	98.96	0
gene_id_16954	418	99.04	0
gene_id_16955	253	89.33	8.00E-79
gene_id_16956	185	98.92	3.00E-131

gene_id_16957	711	99.3	0
gene_id_16958	466	97.85	0
gene_id_16959	156	97.44	9.00E-98
gene_id_16960	175	94.29	3.00E-96
gene_id_16961	218	98.62	4.00E-157
gene_id_16962	536	98.88	0
gene_id_16963	190	97.89	5.00E-129
gene_id_16964	253	94.86	7.00E-142
gene_id_16965	316	96.84	0
gene_id_16966	176	97.73	1.00E-90
gene_id_16967	174	98.85	5.00E-94
gene_id_16993	531	99.25	0
gene_id_16994	105	100	2.00E-59
gene_id_16995	242	97.93	2.00E-163
gene_id_16996	201	93.03	3.00E-93
gene_id_16998	551	97.82	0
gene_id_16999	80	92.5	5.00E-47
gene_id_17000	229	86.9	2.00E-71
gene_id_17001	300	94.67	0
gene_id_17002	164	95.73	3.00E-112
gene_id_17003	317	97.48	0
gene_id_17004	509	94.7	0
gene_id_17005	541	94.82	0
gene_id_17006	419	99.28	0
gene_id_17006	224	99.11	3.00E-120
gene_id_17007	71	97.18	3.00E-17
gene_id_17008	185	97.84	1.00E-88
gene_id_17009	106	96.23	2.00E-43
gene_id_17010	352	98.58	0
gene_id_17011	289	99.31	0
gene_id_17012	426	93.66	0
gene_id_17013	317	79.81	3.00E-128
gene_id_17014	447	100	0
gene_id_17015	466	95.49	0
gene_id_17016	217	98.16	1.00E-157
gene_id_17017	117	91.45	3.00E-47
gene_id_17018	460	98.7	0
gene_id_17019	860	93.84	0
gene_id_17020	57	98.25	6.00E-31
gene_id_17021	479	99.16	0
gene_id_17022	905	94.36	0
gene_id_17023	554	92.42	0
gene_id_17024	202	96.53	6.00E-121
gene_id_17025	57	100	5.00E-31
gene_id_17234	536	94.22	0
gene_id_17234	359	25.91	6.00E-09
gene_id_17235	423	88.42	0

gene_id_17236	449	99.11	0
gene_id_17237	52	100	3.00E-25
gene_id_17238	428	47.66	6.00E-149
gene_id_17239	130	52.31	5.00E-37
gene_id_17240	262	99.62	7.00E-148
gene_id_17241	108	99.07	6.00E-56
gene_id_17242	224	97.77	2.00E-104
gene_id_17243	506	98.02	0
gene_id_17244	499	62.12	0
gene_id_17245	260	46.15	1.00E-59
gene_id_17246	144	81.94	4.00E-75
gene_id_17247	258	100	3.00E-132
gene_id_17247	160	83.75	6.00E-77
gene_id_17247	85	92.94	2.00E-31
gene_id_17248	121	95.04	1.00E-75
gene_id_17250	286	83.22	2.00E-139
gene_id_17251	397	98.74	0
gene_id_17252	203	99.01	2.00E-127
gene_id_17253	731	97.54	0
gene_id_17254	319	72.41	1.00E-142
gene_id_17341	123	95.12	5.00E-60
gene_id_17342	146	67.81	1.00E-43
gene_id_17343	471	94.06	0
gene_id_17344	400	96.75	0
gene_id_17379	322	78.57	4.00E-130
gene_id_17381	331	90.03	4.00E-160
gene_id_17382	206	92.23	3.00E-123
gene_id_17383	355	99.15	0
gene_id_17449	365	99.18	0
gene_id_17450	264	98.48	0
gene_id_17451	344	94.48	0
gene_id_17452	605	98.02	0
gene_id_17453	379	96.31	0
gene_id_17454	308	98.05	0
gene_id_17455	228	96.93	1.00E-138
gene_id_17464	247	98.79	6.00E-169
gene_id_17465	607	99.67	0
gene_id_17466	193	96.37	2.00E-118
gene_id_17467	50	100	5.00E-16
gene_id_17667	242	97.11	3.00E-169
gene_id_17668	223	98.65	2.00E-134
gene_id_17669	248	98.79	6.00E-157
gene_id_17670	653	96.48	0
gene_id_17671	270	96.67	2.00E-145
gene_id_17672	98	96.94	4.00E-56
gene_id_17673	414	93.48	0
gene_id_17674	112	97.32	9.00E-73

gene_id_17676	745	89.93	0
gene_id_17677	210	94.29	2.00E-132
gene_id_17678	265	99.25	9.00E-158
gene_id_17679	107	85.98	1.00E-61
gene_id_17680	166	99.4	2.00E-69
gene_id_17681	425	97.41	0
gene_id_17682	431	99.3	0
gene_id_17683	413	94.92	0
gene_id_17684	402	99	0
gene_id_17685	635	94.17	0
gene_id_17686	350	98.29	0
gene_id_17687	111	96.4	2.00E-63
gene_id_17688	389	98.2	0
gene_id_17689	404	97.77	0
gene_id_17691	82	97.56	1.00E-19
gene_id_17692	726	99.31	0
gene_id_17693	460	96.74	0
gene_id_17694	349	82.81	2.00E-179
gene_id_17695	719	97.22	0
gene_id_17696	795	98.49	0
gene_id_17697	266	96.62	5.00E-174
gene_id_17698	169	97.04	4.00E-59
gene_id_17709	131	99.24	4.00E-76
gene_id_17710	112	98.21	3.00E-54
gene_id_17711	986	96.96	0
gene_id_17712	220	86.82	3.00E-109
gene_id_17713	248	100	2.00E-180
gene_id_17714	263	99.24	0
gene_id_17715	246	99.19	7.00E-164
gene_id_17716	201	98.51	1.00E-130
gene_id_17717	123	87.8	3.00E-49
gene_id_17718	105	99.05	6.00E-68
gene_id_17719	213	98.59	5.00E-151
gene_id_17720	234	93.59	1.00E-134
gene_id_17721	148	100	1.00E-96
gene_id_17722	273	98.17	0
gene_id_17723	267	98.88	2.00E-155
gene_id_17724	255	96.47	1.00E-118
gene_id_17725	551	98.37	0
gene_id_17726	320	98.12	0
gene_id_17745	406	99.26	0
gene_id_17746	386	98.7	0
gene_id_17747	225	98.67	1.00E-133
gene_id_17748	389	99.49	0
gene_id_17749	327	96.64	0
gene_id_17750	142	99.3	2.00E-97
gene_id_17751	152	91.45	4.00E-91

gene_id_17752	285	93.33	0
gene_id_17753	493	98.38	0
gene_id_17754	222	34.23	3.00E-31
gene_id_17755	539	98.33	0
gene_id_17768	820	99.76	0
gene_id_17769	417	99.76	0
gene_id_17770	201	99.5	6.00E-131
gene_id_17771	432	98.15	0
gene_id_17772	320	98.44	0
gene_id_17773	332	98.19	0
gene_id_17774	120	100	2.00E-80
gene_id_17775	347	100	0
gene_id_17776	198	98.99	5.00E-141
gene_id_17777	129	100	2.00E-68
gene_id_17778	122	97.54	1.00E-79
gene_id_17779	264	97.73	4.00E-174
gene_id_17780	437	99.54	0
gene_id_17781	149	99.33	9.00E-81
gene_id_17782	56	100	7.00E-31
gene_id_17783	163	99.39	8.00E-110
gene_id_17784	119	100	5.00E-68
gene_id_17785	178	98.88	1.00E-108
gene_id_17786	126	96.03	3.00E-82
gene_id_17787	54	100	3.00E-30
gene_id_17788	179	100	5.00E-127
gene_id_17789	107	100	5.00E-47
gene_id_17790	122	100	1.00E-80
gene_id_17791	88	100	2.00E-56
gene_id_17792	61	98.36	1.00E-32
gene_id_17793	137	100	8.00E-92
gene_id_17794	213	99.06	4.00E-149
gene_id_17795	112	100	4.00E-74
gene_id_17796	83	100	1.00E-53
gene_id_17797	276	100	0
gene_id_17798	98	100	8.00E-49
gene_id_17799	206	99.03	5.00E-144
gene_id_17800	209	100	6.00E-149
gene_id_17801	105	100	3.00E-69
gene_id_17802	676	98.96	0
gene_id_17803	144	99.31	6.00E-100
gene_id_17804	123	98.37	5.00E-80
gene_id_17805	428	99.77	0
gene_id_17806	297	45.12	7.00E-69
gene_id_17807	1736	83.76	0
gene_id_17808	501	93.61	0
gene_id_17809	65	96.92	4.00E-37
gene_id_17810	282	97.87	1.00E-175

gene_id_17833	216	98.15	7.00E-140
gene_id_17834	624	98.24	0
gene_id_17834	223	99.1	9.00E-141
gene_id_17835	361	88.92	9.00E-165
gene_id_17835	155	96.13	4.00E-79
gene_id_17836	90	96.67	6.00E-56
gene_id_17837	881	97.39	0
gene_id_17838	122	99.18	1.00E-62
gene_id_17839	373	98.66	0
gene_id_17840	354	100	0
gene_id_17841	230	98.7	7.00E-134
gene_id_17842	299	99.33	0
gene_id_17843	131	96.95	4.00E-59
gene_id_17844	539	99.44	0
gene_id_17845	234	86.32	5.00E-134
gene_id_17846	654	91.13	0
gene_id_17847	474	94.3	0
gene_id_17848	596	94.8	0
gene_id_17849	380	97.37	0
gene_id_17850	101	95.05	3.00E-60
gene_id_17851	161	96.27	1.00E-89
gene_id_17852	455	92.53	0
gene_id_17853	184	89.67	2.00E-101
gene_id_17854	368	99.73	0
gene_id_17855	152	98.03	8.00E-100
gene_id_17856	304	99.34	0
gene_id_17857	132	96.97	2.00E-80
gene_id_17858	149	64.43	9.00E-15
gene_id_17859	184	99.46	2.00E-103
gene_id_17860	692	97.11	0
gene_id_17861	205	84.88	8.00E-80
gene_id_17862	170	93.53	2.00E-78
gene_id_17863	775	88.77	0
gene_id_17864	91	89.01	7.00E-49
gene_id_17865	673	96.29	0
gene_id_17866	541	94.64	0
gene_id_17867	560	99.64	0
gene_id_17868	631	97.62	0
gene_id_17869	125	97.6	1.00E-80
gene_id_17870	310	99.35	0
gene_id_17871	188	74.47	5.00E-81
gene_id_17872	193	100	2.00E-136
gene_id_17873	1007	86.59	0
gene_id_17873	557	82.41	2.00E-146
gene_id_17874	215	96.74	1.00E-136
gene_id_17875	210	93.81	3.00E-106
gene_id_17876	594	96.46	0

gene_id_17980	394	98.48	0
gene_id_17981	47	100	1.00E-23
gene_id_17982	629	95.87	0
gene_id_17983	146	99.32	3.00E-102
gene_id_17984	665	99.1	0
gene_id_17985	183	86.34	2.00E-102
gene_id_17986	194	96.39	2.00E-116
gene_id_17987	239	93.72	1.00E-156
gene_id_17988	150	93.33	6.00E-70
gene_id_18026	279	99.64	0
gene_id_18027	174	98.85	6.00E-110
gene_id_18028	409	86.8	0
gene_id_18029	173	73.99	1.00E-46
gene_id_18031	141	88.65	8.00E-44
gene_id_18137	252	87.7	2.00E-117
gene_id_18138	72	90.28	3.00E-31
gene_id_18139	776	96.78	0
gene_id_18140	155	99.35	5.00E-107
gene_id_18141	209	96.17	1.00E-89
gene_id_18142	379	77.84	5.00E-159
gene_id_18143	164	98.78	1.00E-68
gene_id_18144	488	98.77	0
gene_id_18145	643	96.27	0
gene_id_18146	323	97.21	0
gene_id_18221	303	84.16	6.00E-90
gene_id_18222	216	100	1.00E-151
gene_id_18223	387	91.21	0
gene_id_18224	439	91.12	0
gene_id_18225	72	94.44	7.00E-40
gene_id_18227	85	98.82	6.00E-51
gene_id_18228	767	96.35	0
gene_id_18229	140	99.29	1.00E-75
gene_id_18230	400	95.75	0
gene_id_18231	245	100	1.00E-176
gene_id_18232	421	98.81	0
gene_id_18233	237	97.05	1.00E-150
gene_id_18234	387	91.47	2.00E-178
gene_id_18235	159	79.87	1.00E-77
gene_id_18236	396	87.12	1.00E-176
gene_id_18237	140	87.86	3.00E-67
gene_id_18238	268	86.19	3.00E-137
gene_id_18239	210	50.95	7.00E-35
gene_id_18240	450	95.11	0
gene_id_18241	336	94.35	0
gene_id_18242	318	94.65	0
gene_id_18243	473	96.62	0
gene_id_18244	299	96.32	0

gene_id_18245	59	100	4.00E-33
gene_id_18246	464	97.84	0
gene_id_18247	417	98.32	0
gene_id_18285	118	98.31	5.00E-77
gene_id_18287	156	100	3.00E-110
gene_id_18288	561	98.57	0
gene_id_18289	134	73.88	5.00E-32
gene_id_18290	178	97.75	5.00E-120
gene_id_18291	147	97.96	1.00E-97
gene_id_18292	143	99.3	7.00E-97
gene_id_18293	334	98.5	0
gene_id_18294	115	96.52	4.00E-56
gene_id_18295	298	96.98	0
gene_id_18296	436	96.33	0
gene_id_18297	525	96	0
gene_id_18298	42	57.14	7.00E-09
gene_id_18299	486	97.94	0
gene_id_18300	199	98.49	4.00E-101
gene_id_18301	80	100	5.00E-19
gene_id_18302	164	100	8.00E-113
gene_id_18303	45	97.78	7.00E-16
gene_id_18304	139	96.4	3.00E-48
gene_id_18305	192	97.4	5.00E-131
gene_id_18306	103	97.09	3.00E-62
gene_id_18307	149	28.19	4.00E-08
gene_id_18308	148	100	7.00E-104
gene_id_18309	110	97.27	5.00E-69
gene_id_18310	137	97.08	7.00E-92
gene_id_18311	149	100	4.00E-103
gene_id_18312	96	98.96	1.00E-61
gene_id_18313	169	98.22	1.00E-95
gene_id_18314	69	91.3	1.00E-37
gene_id_18315	214	92.99	2.00E-139
gene_id_18316	233	99.14	2.00E-145
gene_id_18317	728	92.17	0
gene_id_18318	91	100	1.00E-57
gene_id_18319	141	100	2.00E-95
gene_id_18320	236	98.73	1.00E-167
gene_id_18323	233	42.49	4.00E-56
gene_id_18324	560	25.54	4.00E-27
gene_id_18325	329	52.58	4.00E-101
gene_id_18326	231	45.89	5.00E-60
gene_id_18327	321	74.77	1.00E-173
gene_id_18328	364	62.64	1.00E-122
gene_id_18329	579	68.91	0
gene_id_18330	278	62.23	6.00E-118
gene_id_18331	435	64.14	8.00E-157

gene_id_18332	373	65.15	4.00E-141
gene_id_18333	541	93.9	0
gene_id_18334	292	97.26	0
gene_id_18335	493	92.09	0
gene_id_18336	427	97.42	0
gene_id_18337	458	96.07	0
gene_id_18338	340	98.82	0
gene_id_18339	303	100	0
gene_id_18340	266	97.37	6.00E-176
gene_id_18341	347	99.42	0
gene_id_18342	450	100	0
gene_id_18343	478	98.33	0
gene_id_18344	363	97.25	0
gene_id_18345	415	91.81	0
gene_id_18376	476	98.95	0
gene_id_18377	163	88.34	1.00E-82
gene_id_18378	846	97.52	0
gene_id_18379	331	99.7	0
gene_id_18380	230	92.17	9.00E-116
gene_id_18381	386	95.34	0
gene_id_18382	341	98.83	0
gene_id_18383	638	82.6	0
gene_id_18384	361	91.97	0
gene_id_18385	316	93.04	4.00E-144
gene_id_18386	89	97.75	1.00E-55
gene_id_18387	862	99.54	0
gene_id_18388	199	96.48	1.00E-125
gene_id_18389	509	93.32	0
gene_id_18390	244	95.49	3.00E-133
gene_id_18391	769	97.4	0
gene_id_18392	292	99.32	0
gene_id_18393	282	99.29	4.00E-173
gene_id_18394	239	95.82	5.00E-121
gene_id_18395	117	51.28	1.00E-14
gene_id_18396	91	100	6.00E-58
gene_id_18397	272	95.59	0
gene_id_18398	325	94.15	2.00E-179
gene_id_18399	373	99.46	0
gene_id_18400	478	98.74	0
gene_id_18401	273	99.27	0
gene_id_18402	474	89.45	0
gene_id_18403	148	93.92	9.00E-87
gene_id_18410	169	100	3.00E-108
gene_id_18411	343	99.42	0
gene_id_18412	276	97.83	0
gene_id_18413	407	97.54	0
gene_id_18414	273	97.07	0

gene_id_18415	559	94.1	0
gene_id_18416	936	95.62	0
gene_id_18417	204	96.08	1.00E-124
gene_id_18418	362	89.23	0
gene_id_18419	483	89.65	0
gene_id_18420	314	94.27	0
gene_id_18421	1622	88.66	0
gene_id_18422	246	90.65	2.00E-157
gene_id_18423	619	89.5	0
gene_id_18424	385	89.61	0
gene_id_18425	359	96.38	0
gene_id_18426	215	99.07	1.00E-151
gene_id_18427	330	97.27	0
gene_id_18428	520	98.85	0
gene_id_18429	325	100	0
gene_id_18430	306	99.02	0
gene_id_18431	333	98.5	0
gene_id_18432	339	97.64	0
gene_id_18453	388	99.23	0
gene_id_18454	262	99.24	0
gene_id_18455	247	95.95	3.00E-146
gene_id_18456	621	95.65	0
gene_id_18457	208	99.52	5.00E-136
gene_id_18458	428	98.36	0
gene_id_18459	221	96.83	3.00E-127
gene_id_18460	383	98.43	0
gene_id_18530	97	97.94	5.00E-62
gene_id_18531	227	95.15	7.00E-94
gene_id_18532	566	95.41	0
gene_id_18533	708	96.47	0
gene_id_18534	215	93.02	2.00E-146
gene_id_18535	439	99.09	0
gene_id_18536	202	97.52	3.00E-138
gene_id_18537	361	97.51	0
gene_id_18538	258	94.19	3.00E-178
gene_id_18539	307	99.35	0
gene_id_18540	332	98.49	0
gene_id_18541	459	98.04	0
gene_id_18542	414	97.1	0
gene_id_18543	651	83.87	0
gene_id_18544	120	99.17	3.00E-79
gene_id_18545	180	92.78	2.00E-93
gene_id_18546	273	89.01	2.00E-159
gene_id_18547	582	98.11	0
gene_id_18548	557	98.38	0
gene_id_18549	184	97.83	9.00E-129
gene_id_18550	498	85.14	0

gene_id_18551	244	98.36	1.00E-177
gene_id_18552	314	100	0
gene_id_18553	187	97.86	5.00E-89
gene_id_18554	89	94.38	1.00E-33
gene_id_18562	67	86.57	4.00E-18
gene_id_18563	148	100	4.00E-100
gene_id_18564	205	98.05	8.00E-139
gene_id_18565	967	91.62	0
gene_id_18566	289	99.31	2.00E-178
gene_id_18567	88	100	9.00E-56
gene_id_18568	209	98.09	8.00E-128
gene_id_18569	255	93.33	2.00E-117
gene_id_18570	281	97.86	0
gene_id_18571	309	96.12	0
gene_id_18572	571	97.9	0
gene_id_18785	1056	83.43	0
gene_id_18786	131	94.66	5.00E-58
gene_id_18787	227	69.16	2.00E-101
gene_id_18789	157	84.08	1.00E-82
gene_id_18790	254	97.24	2.00E-177
gene_id_18791	2925	70.19	0
gene_id_18792	99	75.76	1.00E-45
gene_id_18795	236	90.68	3.00E-136
gene_id_18796	236	52.97	5.00E-74
gene_id_18797	251	67.73	6.00E-111
gene_id_18798	67	71.64	8.00E-27
gene_id_18799	361	98.61	0
gene_id_18800	142	98.59	1.00E-97
gene_id_18801	108	94.44	8.00E-40
gene_id_18802	168	80.36	2.00E-39
gene_id_18805	149	99.33	5.00E-99
gene_id_18806	181	98.9	2.00E-127
gene_id_18807	477	93.92	0
gene_id_18808	238	98.74	1.00E-167
gene_id_18809	215	95.35	3.00E-105
gene_id_18810	264	91.67	7.00E-155
gene_id_18811	175	97.71	4.00E-120
gene_id_18812	272	98.9	9.00E-179
gene_id_18813	536	99.44	0
gene_id_18814	269	99.63	3.00E-170
gene_id_18815	131	96.95	3.00E-88
gene_id_18816	145	97.24	9.00E-83
gene_id_18817	89	100	7.00E-58
gene_id_18818	552	95.65	0
gene_id_18819	193	98.96	4.00E-98
gene_id_18820	217	92.63	1.00E-131
gene_id_18821	434	100	0

gene_id_18822	148	94.59	2.00E-67
gene_id_18823	168	100	3.00E-117
gene_id_18824	363	99.45	0
gene_id_18825	143	99.3	2.00E-97
gene_id_18826	661	95.31	0
gene_id_18840	341	96.19	0
gene_id_18841	771	98.31	0
gene_id_18842	381	98.95	0
gene_id_18843	164	98.78	6.00E-101
gene_id_18844	563	97.69	0
gene_id_18844	162	94.44	6.00E-29
gene_id_18845	242	95.45	7.00E-118
gene_id_18846	545	82.02	0
gene_id_18847	85	100	7.00E-54
gene_id_18848	130	96.92	4.00E-86
gene_id_18849	605	96.86	0
gene_id_18850	198	86.87	4.00E-96
gene_id_18851	342	93.27	0
gene_id_18852	230	52.17	2.00E-84
gene_id_18853	250	97.6	2.00E-153
gene_id_18854	260	96.92	8.00E-157
gene_id_18855	356	91.29	0
gene_id_18856	228	90.79	2.00E-96
gene_id_18857	506	91.9	0
gene_id_18858	338	92.6	0
gene_id_18859	150	88	2.00E-68
gene_id_18860	441	97.28	0
gene_id_18861	256	96.48	8.00E-178
gene_id_18862	307	99.67	0
gene_id_18863	317	99.68	0
gene_id_18965	162	98.15	9.00E-101
gene_id_18966	168	96.43	7.00E-66
gene_id_18967	81	100	1.00E-33
gene_id_18968	499	98.8	0
gene_id_18969	85	98.82	2.00E-24
gene_id_18970	594	98.48	0
gene_id_18971	521	99.42	0
gene_id_18972	475	98.11	0
gene_id_18973	403	91.56	0
gene_id_18974	233	97.42	2.00E-104
gene_id_18975	563	93.96	0
gene_id_18976	233	99.14	1.00E-157
gene_id_18977	157	96.18	6.00E-57
gene_id_18978	185	98.92	1.00E-131
gene_id_18979	789	97.85	0
gene_id_19013	165	87.88	3.00E-64
gene_id_19014	436	98.17	0

gene_id_19015	394	99.75	0
gene_id_19047	428	94.63	0
gene_id_19048	423	93.62	0
gene_id_19049	295	95.59	6.00E-176
gene_id_19050	66	96.97	7.00E-37
gene_id_19051	137	98.54	2.00E-89
gene_id_19052	145	88.97	2.00E-46
gene_id_19053	182	97.8	7.00E-125
gene_id_19054	409	89.98	0
gene_id_19055	80	67.5	6.00E-32
gene_id_19056	143	60.14	2.00E-55
gene_id_19057	120	95	2.00E-73
gene_id_19058	128	93.75	7.00E-78
gene_id_19059	179	96.65	5.00E-119
gene_id_19060	140	96.43	2.00E-92
gene_id_19061	317	97.48	0
gene_id_19062	310	99.03	0
gene_id_19063	400	97.75	0
gene_id_19064	281	98.58	0
gene_id_19065	327	99.39	0
gene_id_19066	338	98.82	0
gene_id_19067	526	98.86	0
gene_id_19068	103	97.09	1.00E-64
gene_id_19069	405	99.26	0
gene_id_19070	380	96.58	0
gene_id_19071	305	96.07	0
gene_id_19072	599	95.16	0
gene_id_19073	90	97.78	2.00E-55
gene_id_19074	412	95.15	0
gene_id_19075	248	79.84	2.00E-72
gene_id_19076	404	91.09	0
gene_id_19077	544	97.98	0
gene_id_19078	75	97.33	2.00E-47
gene_id_19135	72	50	6.00E-08
gene_id_19136	80	72.5	2.00E-21
gene_id_19137	141	48.23	7.00E-27
gene_id_19138	56	62.5	1.00E-17
gene_id_19139	606	70.3	0
gene_id_19140	170	69.41	4.00E-61
gene_id_19141	139	56.83	5.00E-52
gene_id_19143	494	59.92	2.00E-171
gene_id_19144	506	74.9	0
gene_id_19145	332	93.98	0
gene_id_19146	470	98.51	0
gene_id_19147	444	94.14	0
gene_id_19148	380	98.68	0
gene_id_19149	302	94.04	9.00E-170

gene_id_19150	163	98.16	2.00E-89
gene_id_19152	295	98.98	0
gene_id_19153	363	95.59	0
gene_id_19154	497	96.98	0
gene_id_19155	652	99.54	0
gene_id_19156	286	97.9	2.00E-173
gene_id_19157	186	98.92	7.00E-118
gene_id_19158	229	99.56	2.00E-163
gene_id_19159	105	96.19	7.00E-62
gene_id_19160	130	96.92	1.00E-88
gene_id_19161	205	98.54	5.00E-137
gene_id_19162	589	95.08	0
gene_id_19168	301	96.68	0
gene_id_19169	388	90.98	3.00E-130
gene_id_19170	345	93.62	2.00E-178
gene_id_19171	258	100	0
gene_id_19172	380	96.05	9.00E-179
gene_id_19173	185	95.68	8.00E-124
gene_id_19174	314	94.59	0
gene_id_19175	692	94.94	0
gene_id_19176	102	99.02	2.00E-63
gene_id_19177	408	98.77	0
gene_id_19310	183	98.91	2.00E-131
gene_id_19311	721	96.95	0
gene_id_19312	913	96.5	0
gene_id_19313	299	31.44	2.00E-35
gene_id_19314	666	94.59	0
gene_id_19315	148	92.57	9.00E-83
gene_id_19316	138	98.55	3.00E-92
gene_id_19317	233	98.71	2.00E-155
gene_id_19318	235	96.6	2.00E-150
gene_id_19329	294	98.98	1.00E-109
gene_id_19330	342	93.86	6.00E-178
gene_id_19331	243	93.42	2.00E-150
gene_id_19332	488	99.39	0
gene_id_19333	371	98.65	0
gene_id_19334	157	91.08	3.00E-92
gene_id_19335	912	93.86	0
gene_id_19336	566	98.94	0
gene_id_19388	288	98.26	2.00E-148
gene_id_19389	313	82.43	2.00E-132
gene_id_19390	424	94.81	0
gene_id_19391	440	94.32	4.00E-160
gene_id_19392	196	93.88	3.00E-42
gene_id_19393	173	99.42	3.00E-122
gene_id_19394	240	88.75	2.00E-92
gene_id_19395	334	99.1	0

gene_id_19396	312	97.76	0
gene_id_19397	183	86.89	3.00E-61
gene_id_19398	427	98.13	0
gene_id_19399	340	94.41	2.00E-168
gene_id_19401	194	95.88	4.00E-139
gene_id_19402	297	93.6	4.00E-119
gene_id_19403	320	90.94	1.00E-163
gene_id_19404	79	91.14	8.00E-30
gene_id_19405	543	95.21	0
gene_id_19406	358	97.21	0
gene_id_19407	257	99.22	6.00E-148
gene_id_19408	309	97.09	2.00E-163
gene_id_19409	399	99	0
gene_id_19453	150	94	3.00E-72
gene_id_19454	445	83.15	0
gene_id_19455	500	99.2	0
gene_id_19456	79	100	3.00E-50
gene_id_19457	231	97.4	4.00E-152
gene_id_19458	290	93.79	0
gene_id_19459	377	95.23	0
gene_id_19460	239	100	5.00E-175
gene_id_19461	228	94.74	7.00E-131
gene_id_19462	122	100	2.00E-84
gene_id_19463	334	92.81	0
gene_id_19465	193	98.45	4.00E-139
gene_id_19467	116	96.55	3.00E-74
gene_id_19468	330	97.27	0
gene_id_19469	186	98.39	4.00E-128
gene_id_19470	44	95.45	4.00E-21
gene_id_19471	136	100	4.00E-96
gene_id_19472	145	99.31	4.00E-101
gene_id_19473	110	100	1.00E-71
gene_id_19474	538	99.44	0
gene_id_19475	338	99.7	0
gene_id_19476	243	100	1.00E-137
gene_id_19477	453	98.9	0
gene_id_19478	239	86.19	1.00E-78
gene_id_19479	300	98.67	0
gene_id_19480	248	97.98	0
gene_id_19481	75	100	2.00E-45
gene_id_19482	374	99.47	0
gene_id_19483	481	96.26	0
gene_id_19484	315	92.7	0
gene_id_19485	860	97.21	0
gene_id_19486	196	95.92	1.00E-118
gene_id_19489	221	95.93	2.00E-153
gene_id_19490	334	94.61	0

gene_id_19491	259	98.07	0
gene_id_19492	212	98.58	2.00E-152
gene_id_19493	1078	99.44	0
gene_id_19494	467	98.93	0
gene_id_19495	333	98.8	0
gene_id_19496	136	99.26	4.00E-82
gene_id_19497	461	95.01	0
gene_id_19498	537	94.23	0
gene_id_19498	317	94.01	3.00E-121
gene_id_19498	309	89	1.00E-37
gene_id_19499	500	91.6	0
gene_id_19500	471	85.99	0
gene_id_19513	184	95.65	1.00E-86
gene_id_19514	52	100	9.00E-30
gene_id_19515	458	93.67	4.00E-161
gene_id_19516	363	88.98	1.00E-175
gene_id_19517	185	97.3	4.00E-96
gene_id_19518	414	98.07	0
gene_id_19519	180	92.22	2.00E-111
gene_id_19520	367	97.55	0
gene_id_19521	308	99.35	0
gene_id_19522	297	97.98	0
gene_id_19525	316	98.73	0
gene_id_19526	362	99.17	0
gene_id_19527	434	99.08	0
gene_id_19528	298	98.99	0
gene_id_19529	254	96.85	1.00E-167
gene_id_19531	108	97.22	2.00E-70
gene_id_19532	196	90.82	2.00E-99
gene_id_19533	390	82.05	0
gene_id_19534	346	100	0
gene_id_19535	341	88.56	5.00E-149
gene_id_19536	156	97.44	5.00E-97
gene_id_19537	766	94.65	0
gene_id_19538	371	99.73	0
gene_id_19539	113	97.35	3.00E-71
gene_id_19540	138	95.65	3.00E-53
gene_id_19541	189	97.88	9.00E-114
gene_id_19542	183	95.63	9.00E-103
gene_id_19543	481	98.96	0
gene_id_19544	293	99.32	2.00E-179
gene_id_19545	471	99.15	0
gene_id_19546	134	98.51	4.00E-62
gene_id_19547	78	94.87	2.00E-48
gene_id_19548	115	99.13	3.00E-78
gene_id_19549	636	97.33	0
gene_id_19550	652	98.01	0

gene_id_19551	95	98.95	1.00E-60
gene_id_19552	495	98.59	0
gene_id_19553	351	97.72	0
gene_id_19554	167	97.6	2.00E-110
gene_id_19555	98	97.96	2.00E-61
gene_id_19556	511	97.46	0
gene_id_19557	415	84.1	1.00E-159
gene_id_19561	135	94.81	7.00E-86
gene_id_19562	283	93.99	2.00E-155
gene_id_19564	78	96.15	2.00E-46
gene_id_19565	391	95.4	0
gene_id_19566	571	98.6	0
gene_id_19567	376	95.74	0
gene_id_19568	470	96.17	0
gene_id_19569	190	100	1.00E-136
gene_id_19570	251	96.02	9.00E-156
gene_id_19571	226	99.56	2.00E-141
gene_id_19572	261	98.08	6.00E-173
gene_id_19573	212	98.58	4.00E-131
gene_id_19574	472	98.09	0
gene_id_19575	230	95.65	1.00E-157
gene_id_19576	137	59.85	2.00E-34
gene_id_19577	122	74.59	7.00E-38
gene_id_19578	389	80.46	0
gene_id_19579	400	96.25	0
gene_id_19580	656	99.39	0
gene_id_19581	142	97.18	4.00E-93
gene_id_19582	94	98.94	5.00E-60
gene_id_19583	520	99.04	0
gene_id_19584	481	98.96	0
gene_id_19585	480	96.46	0
gene_id_19586	321	99.38	0
gene_id_19587	68	94.12	1.00E-40
gene_id_19588	275	92	2.00E-172
gene_id_19589	417	96.88	0
gene_id_19590	444	90.99	0
gene_id_19591	228	95.18	8.00E-150
gene_id_19592	275	98.91	0
gene_id_19593	442	97.29	0
gene_id_19594	111	89.19	2.00E-63
gene_id_19595	355	91.27	1.00E-176
gene_id_19596	223	99.1	6.00E-159
gene_id_19597	87	98.85	8.00E-26
gene_id_19598	705	96.45	0
gene_id_19599	290	98.97	0
gene_id_19600	505	83.37	0
gene_id_19601	190	87.37	8.00E-59

gene_id_19601	101	99.01	3.00E-54
gene_id_19602	317	98.11	0
gene_id_19603	404	93.56	0
gene_id_19604	1180	98.64	0
gene_id_19605	158	100	2.00E-87
gene_id_19606	74	98.65	6.00E-44
gene_id_19700	445	97.53	0
gene_id_19701	235	93.62	1.00E-156
gene_id_19702	856	99.42	0
gene_id_19703	156	97.44	1.00E-73
gene_id_19704	402	96.52	0
gene_id_19705	111	90.09	8.00E-44
gene_id_19706	139	90.65	6.00E-74
gene_id_19707	641	92.82	0
gene_id_19707	390	95.64	0
gene_id_19708	333	96.7	4.00E-163
gene_id_19709	246	94.31	1.00E-152
gene_id_19710	505	95.05	0
gene_id_19711	40	95	7.00E-19
gene_id_19712	147	97.28	2.00E-97
gene_id_19713	500	97.6	0
gene_id_19714	1077	95.45	0
gene_id_19715	422	95.26	0
gene_id_19716	227	92.95	9.00E-147
gene_id_19717	281	93.59	0
gene_id_19718	150	91.33	4.00E-70
gene_id_19719	174	89.66	5.00E-92
gene_id_19720	383	95.56	0
gene_id_19721	530	92.45	0
gene_id_19722	265	95.47	5.00E-177
gene_id_19723	409	95.6	0
gene_id_19725	406	66.75	0
gene_id_19725	65	53.85	4.00E-11
gene_id_19726	559	61.54	0
gene_id_19763	438	97.03	0
gene_id_19764	1055	90.43	0
gene_id_19765	260	98.85	0
gene_id_19766	360	98.33	0
gene_id_19767	149	97.99	5.00E-103
gene_id_19768	361	98.61	0
gene_id_19822	64	92.19	4.00E-21
gene_id_19823	412	94.42	0
gene_id_19824	182	100	2.00E-129
gene_id_19825	194	94.85	2.00E-121
gene_id_19826	368	99.46	0
gene_id_19827	641	98.13	0
gene_id_19828	292	99.32	0

gene_id_19829	257	99.22	6.00E-168
gene_id_19830	140	90	7.00E-53
gene_id_19833	395	97.22	0
gene_id_19834	66	92.42	3.00E-31
gene_id_19835	312	94.87	0
gene_id_19836	241	96.27	1.00E-168
gene_id_19837	530	98.49	0
gene_id_19838	349	98.28	0
gene_id_19839	302	96.36	0
gene_id_19840	465	99.14	0
gene_id_19841	249	97.99	1.00E-177
gene_id_19842	292	97.26	0
gene_id_19843	265	98.87	1.00E-150
gene_id_19844	354	98.59	0
gene_id_19845	251	99.2	0
gene_id_19846	369	98.64	0
gene_id_19847	493	97.57	0
gene_id_19848	571	99.47	0
gene_id_19849	279	98.21	0
gene_id_19850	262	98.09	0
gene_id_19851	686	78.13	0
gene_id_19852	168	93.45	2.00E-82
gene_id_19853	498	98.8	0
gene_id_19854	613	81.73	0
gene_id_19855	382	95.81	0
gene_id_19856	253	88.14	7.00E-137
gene_id_19858	507	88.36	0
gene_id_19859	83	91.57	3.00E-44
gene_id_19860	389	95.63	0
gene_id_19861	414	99.03	0
gene_id_19862	326	97.55	0
gene_id_19863	833	97.36	0
gene_id_19864	167	98.2	2.00E-88
gene_id_19865	198	97.47	2.00E-125
gene_id_19866	341	95.01	4.00E-173
gene_id_19867	220	88.18	5.00E-134
gene_id_19868	443	97.52	0
gene_id_19869	445	96.4	0
gene_id_19870	219	98.17	5.00E-125
gene_id_19871	445	98.88	0
gene_id_19872	144	97.92	4.00E-69
gene_id_19873	188	96.81	2.00E-110
gene_id_19874	305	98.69	0
gene_id_19875	322	77.02	1.00E-157
gene_id_19876	665	95.79	0
gene_id_19877	394	92.13	0
gene_id_19878	775	98.71	0

gene_id_19879	244	91.39	7.00E-133
gene_id_19880	145	91.72	6.00E-84
gene_id_19881	269	93.68	2.00E-157
gene_id_19882	408	94.85	0
gene_id_19883	390	99.49	0
gene_id_19884	132	98.48	2.00E-88
gene_id_19885	147	98.64	4.00E-99
gene_id_19886	236	94.92	7.00E-162
gene_id_19887	185	90.81	9.00E-115
gene_id_19888	130	100	1.00E-76
gene_id_19889	144	99.31	8.00E-101
gene_id_19890	419	97.85	0
gene_id_19891	165	98.79	2.00E-101
gene_id_19892	342	97.08	0
gene_id_19893	470	95.96	0
gene_id_19894	149	96.64	3.00E-97
gene_id_19895	361	97.23	0
gene_id_19896	95	96.84	4.00E-43
gene_id_19897	715	98.32	0
gene_id_19898	498	95.78	0
gene_id_19899	358	98.32	0
gene_id_19900	441	96.6	0
gene_id_19901	396	99.49	0
gene_id_19902	371	93.8	2.00E-176
gene_id_19903	455	99.78	0
gene_id_19904	306	94.77	0
gene_id_19905	275	97.82	2.00E-161
gene_id_19906	408	99.75	0
gene_id_19907	426	99.77	0
gene_id_19908	270	93.33	5.00E-128
gene_id_19909	239	94.14	2.00E-142
gene_id_19910	141	97.16	6.00E-95
gene_id_19911	285	99.3	0
gene_id_19912	318	96.23	0
gene_id_19913	31	87.1	7.00E-11
gene_id_19914	243	93.83	4.00E-148
gene_id_19915	549	91.62	0
gene_id_19916	274	98.54	0
gene_id_19917	96	98.96	1.00E-58
gene_id_19918	481	98.75	0
gene_id_19919	282	99.65	2.00E-179
gene_id_19920	155	92.9	1.00E-44
gene_id_19921	808	93.07	0
gene_id_19922	274	98.54	0
gene_id_19923	275	92.73	2.00E-124
gene_id_19924	195	96.92	7.00E-137
gene_id_19925	743	96.64	0

gene_id_19926	322	80.75	7.00E-118
gene_id_19927	526	93.16	0
gene_id_19928	130	84.62	5.00E-65
gene_id_19929	925	93.73	0
gene_id_19930	235	97.87	3.00E-133
gene_id_19931	361	95.84	0
gene_id_19932	724	99.59	0
gene_id_19932	263	82.89	4.00E-45
gene_id_19933	509	98.04	0
gene_id_19934	533	97.56	0
gene_id_19935	588	95.07	0
gene_id_19936	273	94.87	5.00E-155
gene_id_19937	310	98.06	0
gene_id_19938	176	96.59	5.00E-120
gene_id_19939	205	95.61	5.00E-143
gene_id_19970	229	82.1	1.00E-134
gene_id_19971	39	92.31	4.00E-15
gene_id_19972	160	30.63	4.00E-11
gene_id_19973	343	22.74	4.00E-26
gene_id_19974	229	39.74	6.00E-33
gene_id_19975	281	93.95	0
gene_id_19976	130	95.38	1.00E-58
gene_id_19977	311	97.11	0
gene_id_19978	426	57.51	3.00E-147
gene_id_19979	544	43.38	5.00E-128
gene_id_19980	624	99.2	0
gene_id_19981	115	99.13	4.00E-75
gene_id_19982	156	28.85	4.00E-10
gene_id_19983	492	41.26	3.00E-116
gene_id_19984	184	28.8	1.00E-11
gene_id_19985	303	24.75	4.00E-15
gene_id_19987	118	43.22	9.00E-19
gene_id_19988	152	98.68	9.00E-102
gene_id_19989	57	96.49	3.00E-29
gene_id_19990	141	97.87	1.00E-94
gene_id_19991	70	98.57	9.00E-42
gene_id_20074	429	93.01	0
gene_id_20075	121	99.17	4.00E-80
gene_id_20076	606	92.41	0
gene_id_20077	879	97.61	0
gene_id_20078	150	98.67	2.00E-101
gene_id_20079	685	95.91	0
gene_id_20080	99	98.99	2.00E-54
gene_id_20081	1191	92.53	0
gene_id_20082	484	95.04	0
gene_id_20083	226	84.96	2.00E-120
gene_id_20084	472	95.55	0

gene_id_20085	1066	98.03	0
gene_id_20086	353	97.17	0
gene_id_20087	219	97.26	2.00E-151
gene_id_20088	178	93.82	1.00E-117
gene_id_20089	244	98.36	4.00E-180
gene_id_20090	803	97.63	0
gene_id_20091	188	97.34	1.00E-119
gene_id_20092	643	88.96	0
gene_id_20093	131	96.18	4.00E-85
gene_id_20143	175	93.14	7.00E-85
gene_id_20144	349	93.12	7.00E-175
gene_id_20145	322	94.41	0
gene_id_20146	391	87.21	5.00E-178
gene_id_20147	113	100	2.00E-74
gene_id_20148	629	95.55	0
gene_id_20149	455	96.92	0
gene_id_20150	356	94.94	0
gene_id_20151	130	60.77	2.00E-26
gene_id_20152	450	97.11	0
gene_id_20153	267	98.5	4.00E-178
gene_id_20154	293	97.61	8.00E-145
gene_id_20155	428	99.53	0
gene_id_20156	565	88.67	0
gene_id_20157	125	90.4	3.00E-74
gene_id_20158	899	95.11	0
gene_id_20159	292	92.47	0
gene_id_20160	247	96.36	1.00E-177
gene_id_20161	311	70.42	1.00E-144
gene_id_20162	440	84.09	2.00E-177
gene_id_20163	921	98.05	0
gene_id_20164	341	97.36	0
gene_id_20165	317	96.85	0
gene_id_20166	83	98.8	6.00E-48
gene_id_20167	122	99.18	5.00E-77
gene_id_20168	622	98.87	0
gene_id_20169	155	87.74	5.00E-78
gene_id_20170	224	100	5.00E-141
gene_id_20171	329	97.57	0
gene_id_20172	273	95.6	0
gene_id_20173	142	95.07	4.00E-90
gene_id_20174	873	96.79	0
gene_id_20175	908	97.91	0
gene_id_20211	327	97.25	3.00E-175
gene_id_20212	302	85.43	5.00E-148
gene_id_20213	381	95.8	0
gene_id_20214	226	96.9	1.00E-155
gene_id_20215	1046	99.43	0

gene_id_20216	371	97.04	0
gene_id_20217	541	92.05	0
gene_id_20218	245	96.73	7.00E-134
gene_id_20219	323	97.21	0
gene_id_20220	269	99.26	7.00E-161
gene_id_20221	283	99.29	0
gene_id_20222	291	98.97	0
gene_id_20223	371	99.73	0
gene_id_20224	277	96.75	0
gene_id_20225	822	98.54	0
gene_id_20226	296	98.99	0
gene_id_20227	467	99.57	0
gene_id_20228	549	91.26	0
gene_id_20229	70	100	1.00E-42
gene_id_20231	52	80.77	1.00E-10
gene_id_20259	184	79.89	2.00E-88
gene_id_20260	160	99.38	5.00E-95
gene_id_20261	297	97.31	0
gene_id_20262	451	85.14	0
gene_id_20263	186	98.92	7.00E-117
gene_id_20264	565	89.38	0
gene_id_20265	135	91.11	3.00E-82
gene_id_20266	779	98.2	0
gene_id_20267	149	96.64	8.00E-96
gene_id_20268	585	95.9	0
gene_id_20269	49	97.96	1.00E-21
gene_id_20295	259	98.46	4.00E-150
gene_id_20296	398	87.19	3.00E-167
gene_id_20297	219	79.45	6.00E-121
gene_id_20298	750	98.13	0
gene_id_20299	238	97.48	2.00E-132
gene_id_20300	436	97.48	0
gene_id_20301	210	61.9	3.00E-38
gene_id_20303	73	100	3.00E-40
gene_id_20304	58	94.83	2.00E-15
gene_id_20305	58	98.28	3.00E-16
gene_id_20306	58	100	1.00E-16
gene_id_20307	196	98.98	1.00E-58
gene_id_20308	251	100	3.00E-165
gene_id_20309	447	98.66	0
gene_id_20310	71	85.92	1.00E-34
gene_id_20311	484	96.9	0
gene_id_20312	191	81.68	2.00E-52
gene_id_20380	359	97.21	0
gene_id_20381	479	97.29	0
gene_id_20382	62	100	2.00E-33
gene_id_20383	221	97.74	3.00E-155

gene_id_20384	130	100	2.00E-91
gene_id_20385	207	99.03	3.00E-143
gene_id_20386	361	95.84	0
gene_id_20387	416	92.55	0
gene_id_20388	286	91.96	1.00E-169
gene_id_20389	462	76.41	0
gene_id_20390	373	91.96	0
gene_id_20391	695	98.56	0
gene_id_20393	417	99.28	0
gene_id_20394	412	93.69	0
gene_id_20395	263	98.86	8.00E-177
gene_id_20396	188	91.49	5.00E-84
gene_id_20397	559	92.67	0
gene_id_20398	452	80.97	0
gene_id_20399	231	92.64	4.00E-103
gene_id_20400	314	95.22	0
gene_id_20530	58	94.83	2.00E-26
gene_id_20531	164	90.85	4.00E-72
gene_id_20532	279	99.28	0
gene_id_20533	361	96.12	0
gene_id_20534	349	95.7	0
gene_id_20593	108	50	8.00E-30
gene_id_20594	197	77.66	8.00E-107
gene_id_20596	179	37.43	2.00E-22
gene_id_20597	156	65.38	3.00E-60
gene_id_20598	108	32.41	7.00E-11
gene_id_20600	330	66.36	3.00E-167
gene_id_20601	124	73.39	7.00E-52
gene_id_20602	471	54.56	3.00E-122
gene_id_20603	116	65.52	1.00E-41
gene_id_20630	260	97.31	3.00E-156
gene_id_20631	609	100	0
gene_id_20632	229	97.82	3.00E-161
gene_id_20633	580	95.69	0
gene_id_20643	334	97.6	0
gene_id_20644	128	98.44	2.00E-71
gene_id_20645	259	100	0
gene_id_20646	139	100	5.00E-94
gene_id_20647	234	95.3	1.00E-145
gene_id_20648	164	98.78	1.00E-84
gene_id_20649	251	93.63	1.00E-121
gene_id_20650	349	94.27	1.00E-154
gene_id_20651	127	97.64	1.00E-80
gene_id_20652	164	93.9	2.00E-51
gene_id_20653	188	97.34	2.00E-133
gene_id_20654	751	97.74	0
gene_id_20655	220	86.36	8.00E-85

gene_id_20656	341	98.53	0
gene_id_20657	429	99.53	0
gene_id_20658	260	94.62	9.00E-150
gene_id_20659	281	89.68	1.00E-133
gene_id_20660	445	91.01	0
gene_id_20661	269	90.71	1.00E-139
gene_id_20662	235	95.74	2.00E-135
gene_id_20663	390	100	0
gene_id_20664	52	98.08	7.00E-28
gene_id_20665	121	99.17	1.00E-82
gene_id_20666	673	99.11	0
gene_id_20667	1030	92.52	0
gene_id_20668	1007	99.01	0
gene_id_20669	836	98.8	0
gene_id_20670	331	98.49	0
gene_id_20671	239	97.49	8.00E-144
gene_id_20672	49	100	3.00E-25
gene_id_20673	77	97.4	6.00E-44
gene_id_20674	438	96.58	0
gene_id_20675	68	100	2.00E-39
gene_id_20676	360	93.89	0
gene_id_20677	68	97.06	1.00E-37
gene_id_20678	196	96.43	2.00E-69
gene_id_20678	128	98.44	5.00E-36
gene_id_20679	130	96.92	6.00E-57
gene_id_20680	273	94.14	1.00E-161
gene_id_20681	419	91.41	8.00E-147
gene_id_20682	425	96.71	0
gene_id_20683	166	98.8	1.00E-87
gene_id_20684	330	99.39	0
gene_id_20685	131	96.18	5.00E-88
gene_id_20686	650	97.54	0
gene_id_20687	72	100	9.00E-28
gene_id_20688	718	97.77	0
gene_id_20689	87	100	4.00E-54
gene_id_20690	308	99.68	0
gene_id_20691	330	97.58	0
gene_id_20716	165	95.15	1.00E-90
gene_id_20717	188	97.87	2.00E-95
gene_id_20718	91	95.6	3.00E-55
gene_id_20719	93	100	5.00E-44
gene_id_20720	233	98.71	1.00E-104
gene_id_20721	109	99.08	4.00E-17
gene_id_20722	215	100	5.00E-155
gene_id_20723	265	96.98	9.00E-179
gene_id_20724	187	95.19	3.00E-80
gene_id_20728	72	95.83	2.00E-43

gene_id_20729	170	99.41	7.00E-109
gene_id_20730	563	97.34	0
gene_id_20731	283	96.82	0
gene_id_20732	115	99.13	8.00E-77
gene_id_20733	163	92.02	4.00E-88
gene_id_20734	327	99.69	0
gene_id_20735	284	97.18	0
gene_id_20736	134	97.76	3.00E-69
gene_id_20737	35	91.43	4.00E-11
gene_id_20738	900	93.67	0
gene_id_20739	208	88.94	6.00E-106
gene_id_20740	219	96.35	4.00E-118
gene_id_20741	65	96.92	1.00E-18
gene_id_20742	63	82.54	2.00E-28
gene_id_20743	237	80.17	2.00E-129
gene_id_20744	366	88.52	0
gene_id_20745	576	97.92	0
gene_id_20746	405	91.36	0
gene_id_20747	152	96.71	4.00E-102
gene_id_20748	302	91.39	8.00E-145
gene_id_20749	88	95.45	5.00E-54
gene_id_20750	461	97.18	0
gene_id_20751	435	86.21	0
gene_id_20752	314	97.45	0
gene_id_20753	121	99.17	2.00E-79
gene_id_20754	612	97.88	0
gene_id_20755	433	97.69	0
gene_id_20756	236	96.19	3.00E-138
gene_id_20757	129	93.02	6.00E-60
gene_id_20758	65	81.54	1.00E-27
gene_id_20759	119	100	4.00E-79
gene_id_20760	54	100	1.00E-28
gene_id_21073	207	100	7.00E-140
gene_id_21074	213	95.77	1.00E-132
gene_id_21075	296	98.65	0
gene_id_21076	303	95.71	0
gene_id_21077	299	92.64	0
gene_id_21078	244	89.75	6.00E-160
gene_id_21079	351	87.75	0
gene_id_21080	162	83.95	5.00E-95
gene_id_21081	334	89.82	0
gene_id_21082	242	97.52	1.00E-152
gene_id_21083	283	99.29	0
gene_id_21084	389	100	0
gene_id_21085	111	97.3	4.00E-71
gene_id_21086	323	97.83	0
gene_id_21087	276	96.74	0

gene_id_21088	255	94.12	3.00E-142
gene_id_21089	106	95.28	2.00E-67
gene_id_21090	307	98.37	0
gene_id_21091	114	99.12	5.00E-78
gene_id_21092	87	96.55	1.00E-55
gene_id_21093	138	96.38	1.00E-68
gene_id_21094	662	99.24	0
gene_id_21095	220	95	1.00E-129
gene_id_21096	265	96.6	9.00E-176
gene_id_21097	375	97.87	0
gene_id_21098	298	99.66	0
gene_id_21099	543	99.26	0
gene_id_21100	260	99.62	9.00E-168
gene_id_21101	235	98.3	7.00E-145
gene_id_21102	200	99	3.00E-130
gene_id_21103	385	98.44	0
gene_id_21104	266	98.5	0
gene_id_21105	238	100	1.00E-172
gene_id_21106	186	98.92	5.00E-127
gene_id_21107	265	89.43	1.00E-167
gene_id_21108	268	96.27	4.00E-147
gene_id_21183	324	95.68	0
gene_id_21184	240	95	6.00E-137
gene_id_21185	557	73.07	0
gene_id_21186	667	99.1	0
gene_id_21188	417	98.56	0
gene_id_21266	466	92.7	0
gene_id_21267	572	90.73	0
gene_id_21268	289	98.96	0
gene_id_21269	75	96	7.00E-44
gene_id_21270	463	99.35	0
gene_id_21271	406	97.78	0
gene_id_21272	592	96.28	0
gene_id_21273	168	100	1.00E-120
gene_id_21274	534	91.95	0
gene_id_21275	421	94.06	0
gene_id_21276	445	99.78	0
gene_id_21277	377	98.67	0
gene_id_21292	259	95.37	4.00E-160
gene_id_21293	810	87.65	0
gene_id_21294	271	94.83	6.00E-142
gene_id_21295	346	100	0
gene_id_21296	680	98.53	0
gene_id_21297	176	93.75	1.00E-99
gene_id_21298	274	96.35	1.00E-153
gene_id_21299	807	98.02	0
gene_id_21300	100	96	1.00E-61

gene_id_21301	216	96.3	4.00E-110
gene_id_21302	97	95.88	6.00E-29
gene_id_21303	125	93.6	5.00E-73
gene_id_21304	225	99.11	2.00E-160
gene_id_21305	358	98.88	0
gene_id_21306	275	98.91	0
gene_id_21307	700	98.29	0
gene_id_21308	120	98.33	3.00E-80
gene_id_21309	591	96.11	0
gene_id_21310	697	96.41	0
gene_id_21311	467	98.5	0
gene_id_21312	320	94.38	0
gene_id_21313	179	99.44	3.00E-123
gene_id_21314	155	99.35	5.00E-107
gene_id_21315	134	98.51	5.00E-91
gene_id_21316	782	93.99	0
gene_id_21317	421	96.44	0
gene_id_21318	545	97.8	0
gene_id_21319	288	96.88	0
gene_id_21320	119	94.96	2.00E-72
gene_id_21321	150	96	4.00E-100
gene_id_21322	485	98.14	0
gene_id_21323	485	98.14	0
gene_id_21324	195	90.26	5.00E-82
gene_id_21325	185	99.46	1.00E-113
gene_id_21326	302	92.38	8.00E-177
gene_id_21327	312	99.04	0
gene_id_21328	191	100	2.00E-126
gene_id_21329	202	98.51	3.00E-143
gene_id_21330	171	98.83	5.00E-118
gene_id_21331	429	99.77	0
gene_id_21332	664	88.7	0
gene_id_21333	335	96.72	0
gene_id_21334	590	100	0
gene_id_21335	599	99.17	0
gene_id_21336	450	98.44	0
gene_id_21404	252	88.1	2.00E-110
gene_id_21405	315	89.84	2.00E-176
gene_id_21406	293	99.32	0
gene_id_21407	133	98.5	4.00E-93
gene_id_21408	386	89.12	0
gene_id_21409	352	95.17	0
gene_id_21410	781	95.52	0
gene_id_21411	524	88.93	0
gene_id_21412	67	98.51	5.00E-29
gene_id_21413	154	90.91	2.00E-89
gene_id_21414	512	81.45	0

gene_id_21415	246	95.12	3.00E-164
gene_id_21423	212	96.23	1.00E-134
gene_id_21424	265	95.85	8.00E-102
gene_id_21425	204	97.55	6.00E-92
gene_id_21426	453	87.64	0
gene_id_21427	187	98.4	1.00E-132
gene_id_21428	414	96.86	0
gene_id_21429	580	88.79	0
gene_id_21430	565	93.27	0
gene_id_21481	174	93.68	2.00E-70
gene_id_21482	238	91.18	7.00E-114
gene_id_21483	128	100	8.00E-86
gene_id_21484	103	96.12	1.00E-62
gene_id_21485	836	94.62	0
gene_id_21486	210	97.62	8.00E-124
gene_id_21487	354	99.15	0
gene_id_21488	325	96.31	0
gene_id_21489	479	98.96	0
gene_id_21490	308	99.03	0
gene_id_21491	107	97.2	5.00E-70
gene_id_21492	496	87.3	0
gene_id_21493	72	100	2.00E-44
gene_id_21494	88	100	1.00E-56
gene_id_21495	96	90.62	1.00E-53
gene_id_21496	101	94.06	1.00E-62
gene_id_21505	201	90.05	2.00E-124
gene_id_21506	594	91.58	0
gene_id_21507	212	94.81	4.00E-139
gene_id_21508	236	96.19	1.00E-134
gene_id_21509	233	95.28	1.00E-137
gene_id_21510	648	94.91	0
gene_id_21554	422	95.97	0
gene_id_21555	433	93.76	0
gene_id_21556	133	96.24	1.00E-62
gene_id_21557	255	96.86	2.00E-91
gene_id_21558	138	100	4.00E-84
gene_id_21559	191	97.38	4.00E-90
gene_id_21560	187	98.4	7.00E-130
gene_id_21561	338	97.93	0
gene_id_21563	258	96.9	1.00E-162
gene_id_21564	82	98.78	2.00E-53
gene_id_21565	359	98.05	0
gene_id_21566	357	99.16	0
gene_id_21710	388	98.2	0
gene_id_21711	118	99.15	3.00E-79
gene_id_21712	191	98.95	2.00E-135
gene_id_21713	75	98.67	2.00E-45

gene_id_21714	268	98.51	3.00E-159
gene_id_21715	376	99.47	0
gene_id_21716	264	96.97	2.00E-162
gene_id_21717	515	99.61	0
gene_id_21727	337	99.7	0
gene_id_21728	321	99.07	0
gene_id_21729	308	92.53	2.00E-160
gene_id_21730	109	100	2.00E-72
gene_id_21731	96	100	7.00E-44
gene_id_21732	195	96.92	2.00E-112
gene_id_21733	298	98.66	0
gene_id_21734	215	98.6	7.00E-139
gene_id_21735	142	100	2.00E-96
gene_id_21736	436	99.31	0
gene_id_21737	96	87.5	1.00E-42
gene_id_21738	1192	99.33	0
gene_id_21739	1234	99.59	0
gene_id_21740	325	84	2.00E-156
gene_id_21741	472	91.53	0
gene_id_21742	306	99.67	0
gene_id_21743	164	99.39	1.00E-96
gene_id_21745	154	100	1.00E-95
gene_id_21746	152	98.68	1.00E-100
gene_id_21747	293	98.29	0
gene_id_21761	119	99.16	9.00E-77
gene_id_21762	914	96.5	0
gene_id_21763	238	98.74	2.00E-152
gene_id_21764	239	97.07	3.00E-144
gene_id_21765	415	99.76	0
gene_id_21766	224	95.98	1.00E-75
gene_id_21767	861	95.7	0
gene_id_21768	177	98.31	5.00E-125
gene_id_21769	334	94.61	1.00E-122
gene_id_21770	355	90.7	0
gene_id_21771	105	96.19	4.00E-54
gene_id_21772	76	93.42	3.00E-42
gene_id_21773	399	46.62	1.00E-105
gene_id_21774	149	81.88	6.00E-46
gene_id_21779	219	98.63	3.00E-140
gene_id_21780	228	97.81	4.00E-119
gene_id_21781	478	99.37	0
gene_id_21782	69	100	1.00E-41
gene_id_21783	335	97.01	0
gene_id_21784	282	98.58	2.00E-154
gene_id_21785	1118	91.14	0
gene_id_21786	349	97.99	0
gene_id_21841	430	97.67	0

gene_id_21842	735	96.73	0
gene_id_21843	228	96.93	5.00E-125
gene_id_21844	451	97.34	0
gene_id_21845	823	97.21	0
gene_id_21846	300	96.33	0
gene_id_21848	267	95.88	2.00E-161
gene_id_21849	349	99.43	0
gene_id_21850	279	98.92	4.00E-138
gene_id_21851	260	99.62	2.00E-156
gene_id_21852	255	99.22	1.00E-174
gene_id_21853	257	100	0
gene_id_21854	286	98.25	3.00E-180
gene_id_21855	484	97.31	0
gene_id_21856	459	99.35	0
gene_id_21857	199	100	9.00E-141
gene_id_21858	606	93.89	0
gene_id_21860	570	98.07	0
gene_id_21932	356	94.38	5.00E-175
gene_id_21933	201	96.52	8.00E-104
gene_id_21934	134	98.51	2.00E-89
gene_id_21935	39	94.87	4.00E-14
gene_id_21970	299	90.3	2.00E-160
gene_id_21971	508	87.99	0
gene_id_21972	155	87.1	6.00E-89
gene_id_21973	210	80.95	2.00E-78
gene_id_21974	902	88.8	0
gene_id_21975	905	97.02	0
gene_id_21976	347	95.68	0
gene_id_21977	193	96.89	3.00E-116
gene_id_21978	802	95.01	0
gene_id_21979	215	94.42	7.00E-152
gene_id_21980	317	84.86	8.00E-124
gene_id_21981	188	92.55	3.00E-116
gene_id_21982	808	98.27	0
gene_id_21983	219	99.54	4.00E-161
gene_id_21984	321	95.33	0
gene_id_21985	133	84.21	5.00E-63
gene_id_22045	690	98.41	0
gene_id_22046	222	95.05	2.00E-107
gene_id_22076	137	95.62	6.00E-61
gene_id_22077	94	96.81	2.00E-30
gene_id_22078	130	100	2.00E-68
gene_id_22079	104	100	8.00E-70
gene_id_22080	38	65.79	2.00E-07
gene_id_22081	253	98.81	6.00E-164
gene_id_22082	222	97.3	1.00E-103
gene_id_22083	968	98.04	0

gene_id_22084	152	100	2.00E-107
gene_id_22085	300	98.33	0
gene_id_22086	426	92.72	0
gene_id_22087	296	91.89	4.00E-180
gene_id_22088	399	98.75	0
gene_id_22089	500	92.6	0
gene_id_22160	492	98.37	0
gene_id_22161	413	96.61	0
gene_id_22162	91	93.41	3.00E-52
gene_id_22163	440	97.27	0
gene_id_22164	247	95.14	5.00E-167
gene_id_22165	507	99.61	0
gene_id_22166	369	98.92	0
gene_id_22167	276	97.83	2.00E-175
gene_id_22168	601	93.84	0
gene_id_22169	102	99.02	2.00E-52
gene_id_22170	508	98.23	0
gene_id_22171	361	93.91	0
gene_id_22172	67	98.51	2.00E-36
gene_id_22173	102	100	2.00E-52
gene_id_22174	239	92.47	1.00E-154
gene_id_22175	541	99.82	0
gene_id_22176	198	97.47	7.00E-127
gene_id_22177	108	87.04	7.00E-41
gene_id_22178	405	96.79	0
gene_id_22179	285	90.53	3.00E-122
gene_id_22180	140	98.57	6.00E-80
gene_id_22181	292	95.21	0
gene_id_22182	270	97.04	5.00E-144
gene_id_22183	271	97.79	6.00E-67
gene_id_22184	999	95.5	0
gene_id_22321	547	98.17	0
gene_id_22322	323	95.36	0
gene_id_22323	137	99.27	2.00E-72
gene_id_22324	78	97.44	4.00E-47
gene_id_22325	200	98	9.00E-132
gene_id_22326	519	99.23	0
gene_id_22327	677	98.52	0
gene_id_22328	491	98.57	0
gene_id_22329	556	93.88	0
gene_id_22330	274	100	0
gene_id_22331	213	97.18	9.00E-138
gene_id_22332	263	98.48	3.00E-154
gene_id_22333	606	90.92	0
gene_id_22334	130	83.08	9.00E-53
gene_id_22335	418	97.85	0
gene_id_22405	179	99.44	1.00E-123

gene_id_22406	670	97.91	0
gene_id_22407	169	96.45	6.00E-117
gene_id_22408	267	88.76	3.00E-133
gene_id_22409	706	84.42	0
gene_id_22410	453	83.89	0
gene_id_22411	519	97.88	0
gene_id_22412	142	85.21	2.00E-72
gene_id_22413	79	83.54	4.00E-42
gene_id_22414	190	98.95	1.00E-109
gene_id_22439	1372	99.27	0
gene_id_22440	127	99.21	1.00E-42
gene_id_22441	173	97.69	9.00E-117
gene_id_22442	235	100	6.00E-147
gene_id_22443	140	100	4.00E-95
gene_id_22444	184	99.46	3.00E-128
gene_id_22445	83	100	3.00E-39
gene_id_22446	49	100	2.00E-26
gene_id_22447	397	99.5	0
gene_id_22448	288	100	0
gene_id_22449	361	82.55	1.00E-164
gene_id_22511	444	97.3	0
gene_id_22512	455	93.85	0
gene_id_22513	292	97.95	0
gene_id_22514	218	98.17	4.00E-155
gene_id_22515	933	89.28	0
gene_id_22516	599	91.49	0
gene_id_22517	155	98.06	2.00E-101
gene_id_22518	50	74	6.00E-14
gene_id_22519	326	99.39	0
gene_id_22520	288	94.79	1.00E-168
gene_id_22521	178	98.31	7.00E-85
gene_id_22548	180	97.78	3.00E-101
gene_id_22549	182	98.9	2.00E-125
gene_id_22550	101	98.02	9.00E-47
gene_id_22551	259	93.05	1.00E-121
gene_id_22552	303	97.03	0
gene_id_22553	254	95.67	9.00E-137
gene_id_22554	257	82.49	2.00E-125
gene_id_22555	350	96.57	0
gene_id_22592	574	96.69	0
gene_id_22593	607	99.34	0
gene_id_22594	449	95.77	0
gene_id_22595	535	98.32	0
gene_id_22596	214	97.2	1.00E-131
gene_id_22597	66	95.45	2.00E-35
gene_id_22598	577	99.65	0
gene_id_22599	297	99.33	0

gene_id_22600	309	90.61	0
gene_id_22601	512	95.7	0
gene_id_22602	402	97.01	0
gene_id_22670	318	95.6	3.00E-158
gene_id_22671	138	79.71	5.00E-69
gene_id_22672	66	96.97	8.00E-37
gene_id_22673	266	99.25	7.00E-167
gene_id_22674	432	91.2	0
gene_id_22675	207	96.62	8.00E-120
gene_id_22676	200	97.5	3.00E-138
gene_id_22677	315	96.19	1.00E-116
gene_id_22678	298	89.26	5.00E-121
gene_id_22679	102	87.25	2.00E-54
gene_id_22680	559	98.39	0
gene_id_22681	175	96.57	3.00E-95
gene_id_22682	1069	99.44	0
gene_id_22683	576	93.92	0
gene_id_22684	722	98.89	0
gene_id_22685	281	100	0
gene_id_22686	125	93.6	4.00E-36
gene_id_22767	388	98.2	0
gene_id_22768	305	94.43	3.00E-174
gene_id_22769	128	100	1.00E-67
gene_id_22770	148	92.57	3.00E-53
gene_id_22771	470	98.72	0
gene_id_22772	75	93.33	3.00E-41
gene_id_22773	138	96.38	2.00E-61
gene_id_22774	281	92.53	0
gene_id_22775	93	98.92	1.00E-58
gene_id_22776	439	95.44	0
gene_id_22777	270	98.52	6.00E-169
gene_id_22778	296	98.65	0
gene_id_22853	1163	87.53	0
gene_id_22854	549	90.53	3.00E-154
gene_id_22856	235	81.28	7.00E-108
gene_id_22857	99	94.95	2.00E-44
gene_id_22858	224	94.64	9.00E-134
gene_id_22859	223	96.86	7.00E-121
gene_id_22897	439	99.32	0
gene_id_22898	659	97.88	0
gene_id_22899	323	91.33	6.00E-169
gene_id_22900	64	81.25	1.00E-22
gene_id_22901	412	97.57	0
gene_id_22902	171	98.25	6.00E-95
gene_id_22903	1028	96.79	0
gene_id_22904	88	100	3.00E-51
gene_id_22905	152	99.34	3.00E-43

gene_id_22906	184	99.46	4.00E-133
gene_id_22907	292	97.6	1.00E-132
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gene_id_22909	397	96.47	0
gene_id_22910	293	97.61	8.00E-175
gene_id_22911	286	97.55	0
gene_id_22912	305	94.75	0
gene_id_22915	177	99.44	4.00E-120
gene_id_22916	171	97.08	5.00E-108
gene_id_22917	229	98.25	2.00E-137
gene_id_22918	251	99.6	9.00E-179
gene_id_22919	284	95.07	0
gene_id_22967	168	98.21	2.00E-115
gene_id_22968	143	96.5	8.00E-69
gene_id_22969	953	95.38	0
gene_id_22970	294	85.03	2.00E-153
gene_id_22971	401	97.01	0
gene_id_22972	519	99.23	0
gene_id_22973	306	93.46	4.00E-141
gene_id_22974	453	92.94	0
gene_id_22975	359	89.97	0
gene_id_22976	1531	93.27	0
gene_id_23001	192	98.44	2.00E-133
gene_id_23002	518	98.07	0
gene_id_23003	263	97.72	0
gene_id_23004	450	98.22	0
gene_id_23012	353	96.03	3.00E-174
gene_id_23013	354	94.07	0
gene_id_23014	562	98.75	0
gene_id_23015	101	97.03	2.00E-50
gene_id_23016	212	93.87	3.00E-123
gene_id_23017	286	95.45	1.00E-138
gene_id_23018	215	96.28	8.00E-108
gene_id_23019	134	98.51	3.00E-86
gene_id_23027	279	92.83	8.00E-176
gene_id_23029	214	97.66	9.00E-150
gene_id_23030	98	96.94	3.00E-53
gene_id_23031	143	94.41	9.00E-81
gene_id_23032	389	99.49	0
gene_id_23033	545	95.23	0
gene_id_23034	290	98.28	3.00E-174
gene_id_23035	598	97.32	0
gene_id_23089	1052	98.95	0
gene_id_23147	200	99.5	2.00E-107
gene_id_23148	243	98.77	2.00E-164
gene_id_23149	307	97.39	0
gene_id_23150	107	100	7.00E-71

gene_id_23151	427	88.99	0
gene_id_23162	291	98.28	0
gene_id_23164	331	91.54	0
gene_id_23165	276	91.3	2.00E-120
gene_id_23166	195	98.97	1.00E-139
gene_id_23167	58	96.55	6.00E-31
gene_id_23168	518	94.98	0
gene_id_23169	306	99.02	1.00E-152
gene_id_23170	357	96.08	0
gene_id_23171	385	92.73	0
gene_id_23172	163	99.39	1.00E-113
gene_id_23173	261	97.32	2.00E-160
gene_id_23174	131	92.37	2.00E-85
gene_id_23175	112	90.18	8.00E-67
gene_id_23176	517	94	0
gene_id_23177	79	96.2	5.00E-41
gene_id_23197	124	98.39	2.00E-76
gene_id_23198	216	98.15	7.00E-143
gene_id_23199	754	99.34	0
gene_id_23200	303	99.01	0
gene_id_23253	461	81.78	0
gene_id_23254	242	98.35	9.00E-171
gene_id_23255	580	88.28	0
gene_id_23256	45	73.33	6.00E-13
gene_id_23257	314	62.1	6.00E-140
gene_id_23258	279	82.8	1.00E-163
gene_id_23259	1035	81.93	0
gene_id_23260	208	95.67	4.00E-110
gene_id_23261	382	100	0
gene_id_23281	117	99.15	9.00E-63
gene_id_23282	453	99.34	0
gene_id_23283	390	99.74	0
gene_id_23284	337	93.18	0
gene_id_23291	758	95.51	0
gene_id_23292	555	99.1	0
gene_id_23293	302	98.68	2.00E-130
gene_id_23294	283	93.99	2.00E-162
gene_id_23295	758	98.15	0
gene_id_23296	241	92.95	6.00E-131
gene_id_23297	95	98.95	9.00E-60
gene_id_23298	233	77.25	7.00E-94
gene_id_23299	372	80.65	0
gene_id_23300	350	93.43	0
gene_id_23308	325	90.77	3.00E-167
gene_id_23309	370	94.59	4.00E-121
gene_id_23310	335	87.46	2.00E-153
gene_id_23311	291	87.29	1.00E-141

gene_id_23312	255	96.08	2.00E-157
gene_id_23313	681	87.96	0
gene_id_23314	192	95.83	1.00E-100
gene_id_23315	27	96.3	6.00E-10
gene_id_23320	872	98.62	0
gene_id_23321	85	89.41	3.00E-46
gene_id_23322	331	96.68	3.00E-171
gene_id_23323	594	98.99	0
gene_id_23324	118	93.22	5.00E-75
gene_id_23325	229	98.25	6.00E-152
gene_id_23326	307	98.7	2.00E-112
gene_id_23345	439	94.53	0
gene_id_23346	150	95.33	1.00E-45
gene_id_23347	159	97.48	3.00E-111
gene_id_23348	414	92.27	0
gene_id_23349	333	98.8	0
gene_id_23350	393	99.49	0
gene_id_23351	244	96.31	5.00E-150
gene_id_23352	111	99.1	3.00E-55
gene_id_23353	399	88.47	0
gene_id_23353	44	100	5.00E-18
gene_id_23361	488	97.75	0
gene_id_23362	294	99.66	0
gene_id_23363	540	99.26	0
gene_id_23364	409	98.78	0
gene_id_23365	194	80.93	1.00E-61
gene_id_23366	150	96.67	3.00E-99
gene_id_23367	581	85.89	0
gene_id_23368	126	97.62	8.00E-49
gene_id_23369	241	96.68	6.00E-145
gene_id_23370	445	99.33	0
gene_id_23371	69	65.22	3.00E-24
gene_id_23372	224	29.91	2.00E-12
gene_id_23373	74	74.32	2.00E-31
gene_id_23374	443	64.11	0
gene_id_23375	311	93.57	0
gene_id_23376	129	97.67	1.00E-85
gene_id_23377	191	98.43	2.00E-137
gene_id_23378	275	95.27	0
gene_id_23379	221	92.76	2.00E-145
gene_id_23380	408	98.77	0
gene_id_23381	239	95.4	8.00E-160
gene_id_23382	362	96.41	0
gene_id_23383	572	99.65	0
gene_id_23384	367	98.91	0
gene_id_23385	340	99.71	0
gene_id_23386	252	95.24	3.00E-172

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gene_id_23388	171	96.49	2.00E-102
gene_id_23389	251	97.21	2.00E-160
gene_id_23390	113	91.15	4.00E-42
gene_id_23391	213	95.77	7.00E-146
gene_id_23392	75	94.67	4.00E-45
gene_id_23393	258	96.9	2.00E-169
gene_id_23394	416	97.6	0
gene_id_23395	153	99.35	1.00E-106
gene_id_23396	947	97.47	0
gene_id_23397	382	98.95	0
gene_id_23398	92	100	4.00E-47
gene_id_23399	165	100	9.00E-119
gene_id_23400	471	92.99	0
gene_id_23404	406	95.07	0
gene_id_23405	274	98.54	0
gene_id_23406	180	97.22	8.00E-111
gene_id_23407	522	93.68	0
gene_id_23408	440	97.73	0
gene_id_23409	185	58.92	8.00E-67
gene_id_23410	556	94.96	0
gene_id_23411	192	98.96	2.00E-134
gene_id_23412	516	98.26	0
gene_id_23413	211	100	9.00E-144
gene_id_23414	691	98.41	0
gene_id_23415	255	97.65	0
gene_id_23416	417	99.04	0
gene_id_23417	222	97.3	2.00E-123
gene_id_23418	291	97.25	7.00E-166
gene_id_23419	359	92.2	3.00E-166
gene_id_23420	848	92.81	0
gene_id_23420	438	29.45	1.00E-07
gene_id_23425	508	99.21	0
gene_id_23426	259	98.46	8.00E-174
gene_id_23427	304	98.68	0
gene_id_23430	313	93.29	5.00E-169
gene_id_23431	273	96.7	2.00E-164
gene_id_23432	128	92.97	8.00E-51
gene_id_23433	257	96.11	1.00E-133
gene_id_23434	400	98.25	0
gene_id_23435	416	97.12	0
gene_id_23436	237	95.36	7.00E-140
gene_id_23437	502	99.2	0
gene_id_23438	144	97.92	1.00E-75
gene_id_23439	322	99.07	0
gene_id_23440	387	99.48	0
gene_id_23441	94	97.87	5.00E-43

gene_id_23442	84	97.62	9.00E-33
gene_id_23443	109	95.41	1.00E-25
gene_id_23444	254	95.67	4.00E-91
gene_id_23445	126	98.41	8.00E-85
gene_id_23446	219	100	5.00E-155
gene_id_23447	271	100	0
gene_id_23448	421	95.01	0
gene_id_23449	704	99.43	0
gene_id_23450	356	95.22	0
gene_id_23451	248	99.19	2.00E-134
gene_id_23578	488	99.18	0
gene_id_23579	749	91.46	0
gene_id_23580	569	96.66	0
gene_id_23581	231	99.57	3.00E-168
gene_id_23582	284	99.3	0
gene_id_23583	378	99.74	0
gene_id_23584	453	96.03	0
gene_id_23585	128	98.44	8.00E-71
gene_id_23586	589	97.79	0
gene_id_23587	173	94.8	5.00E-101
gene_id_23588	154	98.05	6.00E-108
gene_id_23589	217	96.31	2.00E-149
gene_id_23590	323	97.52	2.00E-179
gene_id_23591	71	98.59	1.00E-42
gene_id_23603	457	95.19	0
gene_id_23604	155	99.35	1.00E-80
gene_id_23605	274	91.24	9.00E-149
gene_id_23606	251	86.06	1.00E-116
gene_id_23607	197	91.88	4.00E-121
gene_id_23614	459	99.78	0
gene_id_23615	480	98.75	0
gene_id_23616	453	98.01	0
gene_id_23617	390	98.97	0
gene_id_23618	251	97.61	6.00E-165
gene_id_23619	91	95.6	6.00E-38
gene_id_23620	307	99.35	0
gene_id_23621	225	97.33	2.00E-116
gene_id_23622	252	98.81	2.00E-174
gene_id_23623	306	98.04	3.00E-169
gene_id_23706	440	97.73	0
gene_id_23707	176	87.5	2.00E-105
gene_id_23708	350	99.43	0
gene_id_23709	262	86.64	2.00E-144
gene_id_23710	629	97.62	0
gene_id_23723	38	100	5.00E-15
gene_id_23724	590	96.1	0
gene_id_23725	243	97.53	2.00E-167

gene_id_23726	223	95.52	2.00E-141
gene_id_23727	196	99.49	1.00E-136
gene_id_23728	230	96.96	2.00E-143
gene_id_23729	56	100	4.00E-20
gene_id_23730	515	99.22	0
gene_id_23731	486	99.59	0
gene_id_23732	198	98.99	6.00E-139
gene_id_23733	46	100	2.00E-24
gene_id_23734	202	99.01	2.00E-137
gene_id_23735	225	96.89	3.00E-96
gene_id_23736	219	97.72	8.00E-136
gene_id_23737	614	97.56	0
gene_id_23738	140	99.29	2.00E-73
gene_id_23739	344	97.97	0
gene_id_23740	249	84.34	1.00E-85
gene_id_23741	344	97.09	0
gene_id_23773	470	97.66	0
gene_id_23774	157	91.72	1.00E-70
gene_id_23775	177	97.74	1.00E-105
gene_id_23776	123	91.06	2.00E-70
gene_id_23821	153	98.04	3.00E-103
gene_id_23822	88	97.73	3.00E-42
gene_id_23823	312	94.23	2.00E-173
gene_id_23824	154	91.56	6.00E-65
gene_id_23825	272	97.43	3.00E-160
gene_id_23826	317	95.27	0
gene_id_23827	291	89.35	4.00E-167
gene_id_23828	346	98.84	0
gene_id_23829	575	97.57	0
gene_id_23830	496	95.56	0
gene_id_23831	329	85.11	5.00E-178
gene_id_23832	102	85.29	2.00E-46
gene_id_23833	306	95.1	6.00E-168
gene_id_23834	629	99.36	0
gene_id_23835	161	96.89	4.00E-63
gene_id_23906	478	95.19	0
gene_id_23907	46	95.65	7.00E-24
gene_id_23908	292	97.95	0
gene_id_23909	102	100	1.00E-64
gene_id_23910	89	100	7.00E-57
gene_id_23911	371	97.57	0
gene_id_23912	396	100	0
gene_id_23913	283	96.11	3.00E-180
gene_id_23914	429	95.8	0
gene_id_23915	428	94.86	0
gene_id_23916	83	91.57	1.00E-49
gene_id_23917	690	97.54	0

gene_id_23935	86	98.84	2.00E-35
gene_id_23936	517	95.74	0
gene_id_23937	350	98.57	0
gene_id_23938	138	90.58	6.00E-52
gene_id_23939	368	92.93	0
gene_id_23940	167	97.6	5.00E-100
gene_id_23982	353	97.73	0
gene_id_23983	684	95.61	0
gene_id_23984	194	87.63	2.00E-103
gene_id_23985	163	96.32	9.00E-86
gene_id_24116	221	88.69	2.00E-61
gene_id_24117	274	99.64	0
gene_id_24118	108	99.07	2.00E-68
gene_id_24128	80	90	7.00E-41
gene_id_24129	657	86.91	0
gene_id_24130	360	98.89	0
gene_id_24131	266	94.36	2.00E-137
gene_id_24132	191	93.72	8.00E-117
gene_id_24133	220	77.73	6.00E-60
gene_id_24134	857	42.47	7.00E-156
gene_id_24134	274	56.93	2.00E-53
gene_id_24135	142	38.73	1.00E-12
gene_id_24136	182	55.49	1.00E-42
gene_id_24137	430	94.88	0
gene_id_24141	142	99.3	1.00E-97
gene_id_24142	429	98.6	0
gene_id_24143	725	85.24	0
gene_id_24144	322	98.45	0
gene_id_24145	504	82.34	0
gene_id_24146	1030	99.42	0
gene_id_24147	119	97.48	8.00E-57
gene_id_24154	156	99.36	3.00E-88
gene_id_24155	247	99.6	2.00E-144
gene_id_24156	201	99.5	3.00E-146
gene_id_24157	606	85.31	0
gene_id_24252	162	58.64	1.00E-41
gene_id_24253	44	56.82	1.00E-07
gene_id_24254	487	77.21	0
gene_id_24255	118	75.42	7.00E-56
gene_id_24256	85	58.82	2.00E-27
gene_id_24258	541	49.91	6.00E-142
gene_id_24259	397	61.21	6.00E-96
gene_id_24260	370	72.97	8.00E-157
gene_id_24261	202	66.83	3.00E-80
gene_id_24262	136	66.18	4.00E-42
gene_id_24263	350	66	5.00E-111
gene_id_24264	198	71.21	6.00E-82

gene_id_24265	104	64.42	8.00E-23
gene_id_24266	62	56.45	6.00E-13
gene_id_24267	99	49.49	3.00E-18
gene_id_24268	124	36.29	2.00E-06
gene_id_24270	61	65.57	4.00E-23
gene_id_24271	127	53.54	1.00E-37
gene_id_24273	85	76.47	7.00E-27
gene_id_24275	218	56.88	4.00E-53
gene_id_24276	198	31.31	3.00E-21
gene_id_24277	151	45.03	2.00E-23
gene_id_24278	81	60.49	2.00E-28
gene_id_24279	146	82.19	4.00E-78
gene_id_24280	65	80	1.00E-26
gene_id_24323	330	99.7	0
gene_id_24324	500	91	0
gene_id_24325	479	86.22	0
gene_id_24326	1490	93.22	0
gene_id_24326	422	25.59	2.00E-11
gene_id_24326	537	25.51	2.00E-11
gene_id_24327	575	92.35	0
gene_id_24348	1038	98.84	0
gene_id_24349	421	91.45	0
gene_id_24350	242	91.32	6.00E-103
gene_id_24555	262	97.33	1.00E-161
gene_id_24556	204	99.02	1.00E-130
gene_id_24557	187	80.21	9.00E-74
gene_id_24558	802	98.38	0
gene_id_24585	70	92.86	7.00E-39
gene_id_24586	141	99.29	2.00E-96
gene_id_24587	57	92.98	7.00E-21
gene_id_24588	152	97.37	9.00E-101
gene_id_24589	77	54.55	6.00E-21
gene_id_24590	331	68.28	2.00E-168
gene_id_24591	1036	54.15	0
gene_id_24592	255	52.16	2.00E-77
gene_id_24593	107	69.16	8.00E-42
gene_id_24619	282	96.1	0
gene_id_24620	385	97.92	0
gene_id_24621	391	96.68	0
gene_id_24622	295	94.24	0
gene_id_24623	260	85.38	3.00E-130
gene_id_24624	519	99.81	0
gene_id_24625	87	100	2.00E-53
gene_id_24626	78	100	6.00E-27
gene_id_24627	455	98.24	0
gene_id_24628	156	99.36	3.00E-93
gene_id_24629	206	97.09	2.00E-123

gene_id_24630	497	98.99	0
gene_id_24631	251	98.8	9.00E-156
gene_id_24632	542	98.52	0
gene_id_24633	320	99.06	0
gene_id_24634	178	93.82	5.00E-85
gene_id_24667	66	98.48	8.00E-38
gene_id_24668	262	97.71	2.00E-153
gene_id_24669	394	99.49	0
gene_id_24670	308	100	0
gene_id_24671	313	99.04	0
gene_id_24672	238	98.32	5.00E-171
gene_id_24673	234	98.72	4.00E-149
gene_id_24674	217	98.62	2.00E-152
gene_id_24675	726	99.31	0
gene_id_24676	124	99.19	9.00E-73
gene_id_24677	76	85.53	6.00E-31
gene_id_24678	296	98.99	0
gene_id_24683	263	95.82	2.00E-164
gene_id_24684	567	97	0
gene_id_24685	281	87.54	2.00E-144
gene_id_24686	386	98.19	0
gene_id_24687	597	96.15	0
gene_id_24688	227	88.99	4.00E-102
gene_id_24689	229	98.69	3.00E-160
gene_id_24690	107	98.13	3.00E-69
gene_id_24728	575	98.78	0
gene_id_24729	147	95.24	4.00E-86
gene_id_24730	259	99.61	0
gene_id_24840	439	98.86	0
gene_id_24841	454	97.36	0
gene_id_24842	221	100	3.00E-137
gene_id_24843	373	97.32	0
gene_id_24844	318	94.03	2.00E-180
gene_id_24845	304	97.7	0
gene_id_24846	129	96.12	3.00E-70
gene_id_24849	292	99.32	0
gene_id_24850	172	98.26	2.00E-103
gene_id_24851	726	99.17	0
gene_id_24852	116	100	3.00E-42
gene_id_24853	201	100	5.00E-141
gene_id_24904	115	99.13	3.00E-75
gene_id_24905	646	97.21	0
gene_id_24906	140	99.29	2.00E-83
gene_id_24965	490	86.94	0
gene_id_24966	98	96.94	1.00E-60
gene_id_24967	593	96.29	0
gene_id_24968	638	86.83	0

gene_id_24971	209	98.09	1.00E-147
gene_id_24972	572	90.91	0
gene_id_24973	598	84.28	0
gene_id_24974	520	96.92	0
gene_id_24975	133	96.24	1.00E-58
gene_id_24976	554	97.83	0
gene_id_24977	76	92.11	3.00E-14
gene_id_24978	384	97.92	0
gene_id_24979	140	98.57	4.00E-52
gene_id_25067	397	97.98	0
gene_id_25068	644	93.48	0
gene_id_25069	231	98.27	7.00E-164
gene_id_25137	681	89.43	0
gene_id_25138	212	95.28	2.00E-136
gene_id_25139	301	98.01	0
gene_id_25140	207	96.62	5.00E-119
gene_id_25141	256	99.22	0
gene_id_25179	250	75.2	9.00E-81
gene_id_25181	191	89.53	4.00E-97
gene_id_25182	147	99.32	5.00E-100
gene_id_25183	464	97.63	0
gene_id_25280	291	84.54	9.00E-151
gene_id_25281	844	99.05	0
gene_id_25282	416	98.08	0
gene_id_25283	80	93.75	8.00E-09
gene_id_25284	119	97.48	2.00E-76
gene_id_25285	301	91.36	1.00E-177
gene_id_25286	532	93.61	0
gene_id_25287	704	93.47	0
gene_id_25288	163	93.25	8.00E-105
gene_id_25289	311	95.82	4.00E-144
gene_id_25290	132	100	1.00E-61
gene_id_25291	240	96.67	5.00E-169
gene_id_25292	245	96.73	2.00E-160
gene_id_25293	163	98.16	2.00E-64
gene_id_25294	210	99.05	2.00E-136
gene_id_25295	70	75.71	3.00E-27
gene_id_25296	201	96.52	4.00E-115
gene_id_25297	166	98.19	2.00E-98
gene_id_25324	455	98.24	0
gene_id_25325	245	91.02	3.00E-131
gene_id_25326	382	91.1	0
gene_id_25327	958	96.66	0
gene_id_25328	513	98.44	0
gene_id_25329	95	93.68	4.00E-34
gene_id_25331	359	95.54	0
gene_id_25332	222	93.24	7.00E-135

gene_id_25333	206	91.75	4.00E-61
gene_id_25334	214	98.6	2.00E-152
gene_id_25335	249	99.2	2.00E-166
gene_id_25336	514	96.69	0
gene_id_25337	418	98.56	0
gene_id_25338	163	99.39	2.00E-114
gene_id_25339	358	97.77	0
gene_id_25340	152	90.79	1.00E-85
gene_id_25341	80	98.75	2.00E-28
gene_id_25342	246	96.34	4.00E-100
gene_id_25343	292	97.26	2.00E-132
gene_id_25480	410	97.56	0
gene_id_25481	325	99.69	0
gene_id_25482	201	96.52	8.00E-111
gene_id_25495	459	98.04	0
gene_id_25496	478	96.23	0
gene_id_25497	285	91.58	2.00E-135
gene_id_25498	136	94.85	3.00E-36
gene_id_25499	518	99.03	0
gene_id_25522	462	97.62	0
gene_id_25523	327	98.17	0
gene_id_25524	326	80.98	2.00E-135
gene_id_25567	302	95.36	3.00E-161
gene_id_25568	150	96	2.00E-89
gene_id_25569	492	97.15	0
gene_id_25570	364	97.25	0
gene_id_25571	242	94.63	6.00E-137
gene_id_25609	232	89.22	2.00E-123
gene_id_25610	316	97.47	0
gene_id_25611	281	97.15	0
gene_id_25612	358	93.85	0
gene_id_25666	397	99.75	0
gene_id_25667	318	98.11	3.00E-158
gene_id_25668	274	90.15	6.00E-139
gene_id_25669	318	96.54	0
gene_id_25706	345	99.42	0
gene_id_25707	117	100	1.00E-75
gene_id_25708	65	100	2.00E-37
gene_id_25709	176	100	5.00E-112
gene_id_25710	644	97.98	0
gene_id_25746	109	95.41	2.00E-65
gene_id_25747	89	98.88	1.00E-43
gene_id_25748	277	95.67	4.00E-151
gene_id_25749	203	95.57	3.00E-94
gene_id_25750	132	100	4.00E-75
gene_id_25751	169	98.22	1.00E-81
gene_id_25752	274	91.97	7.00E-126

gene_id_25934	711	96.2	0
gene_id_25935	289	100	0
gene_id_25936	308	99.68	0
gene_id_25937	1020	96.96	0
gene_id_25938	129	97.67	3.00E-61
gene_id_25939	748	81.95	0
gene_id_25954	218	99.54	2.00E-156
gene_id_25955	117	99.15	1.00E-75
gene_id_25956	275	96.36	2.00E-143
gene_id_25957	289	93.43	6.00E-148
gene_id_25958	65	96.92	9.00E-36
gene_id_25959	858	96.85	0
gene_id_25960	140	100	1.00E-97
gene_id_25961	501	96.61	0
gene_id_25962	629	98.09	0
gene_id_25963	91	90.11	6.00E-26
gene_id_26021	775	95.61	0
gene_id_26022	112	48.21	3.00E-29
gene_id_26023	425	98.59	0
gene_id_26024	139	100	9.00E-96
gene_id_26061	107	96.26	7.00E-62
gene_id_26062	448	91.29	0
gene_id_26063	337	98.52	0
gene_id_26064	334	84.13	1.00E-149
gene_id_26065	562	97.15	0
gene_id_26066	177	98.31	1.00E-86
gene_id_26067	379	94.46	0
gene_id_26068	402	92.04	0
gene_id_26172	124	99.19	8.00E-85
gene_id_26173	490	98.16	0
gene_id_26174	478	96.23	0
gene_id_26175	322	95.34	1.00E-172
gene_id_26223	1390	89.42	0
gene_id_26224	450	97.56	0
gene_id_26225	167	98.8	2.00E-109
gene_id_26226	87	100	6.00E-55
gene_id_26227	101	100	2.00E-65
gene_id_26228	370	95.95	0
gene_id_26229	765	89.54	0
gene_id_26230	186	97.85	3.00E-135
gene_id_26231	1018	97.54	0
gene_id_26232	62	96.77	7.00E-35
gene_id_26233	272	99.26	3.00E-180
gene_id_26234	337	98.22	0
gene_id_26235	243	99.59	4.00E-176
gene_id_26236	255	87.06	6.00E-124
gene_id_26237	149	95.97	1.00E-79

gene_id_26238	271	98.89	2.00E-158
gene_id_26239	425	99.06	0
gene_id_26240	275	99.27	3.00E-152
gene_id_26241	155	94.84	6.00E-84
gene_id_26242	179	97.77	2.00E-100
gene_id_26243	403	95.78	0
gene_id_26268	414	97.58	0
gene_id_26269	480	97.5	0
gene_id_26270	461	98.7	0
gene_id_26313	611	91.98	0
gene_id_26314	172	99.42	2.00E-121
gene_id_26315	190	96.32	4.00E-129
gene_id_26316	407	95.09	0
gene_id_26317	140	98.57	1.00E-93
gene_id_26318	159	93.71	1.00E-102
gene_id_26319	158	100	5.00E-103
gene_id_26319	62	98.39	1.00E-30
gene_id_26320	290	98.28	2.00E-154
gene_id_26321	383	98.43	0
gene_id_26332	809	92.21	0
gene_id_26333	644	98.76	0
gene_id_26445	603	99.5	0
gene_id_26446	595	97.98	0
gene_id_26447	117	98.29	7.00E-75
gene_id_26567	403	95.29	0
gene_id_26568	393	98.22	0
gene_id_26569	161	98.76	4.00E-101
gene_id_26594	141	96.45	2.00E-61
gene_id_26595	343	93.88	0
gene_id_26596	291	91.75	7.00E-148
gene_id_26632	89	85.39	2.00E-33
gene_id_26633	728	90.93	0
gene_id_26634	468	81.2	0
gene_id_26635	469	83.8	0
gene_id_26637	223	99.55	4.00E-157
gene_id_26638	288	99.31	0
gene_id_26639	363	92.84	0
gene_id_26640	843	98.34	0
gene_id_26848	188	98.94	1.00E-133
gene_id_26849	550	99.09	0
gene_id_26850	482	95.44	0
gene_id_26851	170	100	4.00E-90
gene_id_26852	446	98.65	0
gene_id_26853	169	98.82	4.00E-88
gene_id_26898	1187	98.9	0
gene_id_26930	198	95.45	2.00E-92
gene_id_26931	308	95.78	4.00E-163

gene_id_26932	490	96.94	0
gene_id_26933	233	95.28	3.00E-132
gene_id_26934	156	76.28	9.00E-46
gene_id_27227	233	98.28	5.00E-144
gene_id_27228	384	97.14	0
gene_id_27229	754	97.08	0
gene_id_27230	412	99.51	0
gene_id_27345	378	96.3	0
gene_id_27346	656	89.33	0
gene_id_27381	653	95.87	0
gene_id_27382	379	96.57	0
gene_id_27434	461	93.28	0
gene_id_27435	263	98.48	0
gene_id_27436	382	98.69	0
gene_id_27437	301	94.35	1.00E-164
gene_id_27438	408	96.08	0
gene_id_27576	562	90.21	0
gene_id_27577	197	82.23	4.00E-93
gene_id_27578	375	99.73	0
gene_id_27579	612	92.97	0
gene_id_27582	223	97.76	1.00E-151
gene_id_27583	560	97.86	0
gene_id_27584	354	98.87	0
gene_id_27679	1324	99.47	0
gene_id_27738	430	98.14	0
gene_id_27739	641	98.28	0
gene_id_27740	568	97.71	0
gene_id_27914	579	98.45	0
gene_id_27915	114	97.37	9.00E-66
gene_id_27916	189	97.35	7.00E-130
gene_id_27917	89	96.63	3.00E-54
gene_id_27918	190	97.37	4.00E-132
gene_id_27919	159	96.23	1.00E-92
gene_id_27920	358	98.88	0
gene_id_28089	93	92.47	4.00E-26
gene_id_28090	536	98.88	0
gene_id_28091	119	91.6	4.00E-69
gene_id_28092	27	96.3	5.00E-08
gene_id_28396	274	96.72	8.00E-168
gene_id_28397	91	98.9	2.00E-57
gene_id_28398	187	93.58	4.00E-115
gene_id_28399	283	97.17	0
gene_id_28605	479	98.54	0
gene_id_28606	123	77.24	5.00E-56
gene_id_28607	218	95.87	4.00E-150
gene_id_28608	475	99.79	0
gene_id_28609	253	99.6	0

gene_id_28610	252	95.24	1.00E-155
gene_id_28656	417	98.56	0
gene_id_28657	790	86.71	0
gene_id_29364	136	99.26	1.00E-88
gene_id_29365	270	97.78	0
gene_id_29366	93	89.25	2.00E-54
gene_id_29367	201	98.01	3.00E-127
gene_id_29368	350	97.43	0
gene_id_29369	97	97.94	1.00E-41
gene_id_29452	666	94.59	0
gene_id_29453	364	85.71	5.00E-98
gene_id_29754	174	99.43	2.00E-94
gene_id_29755	332	88.86	2.00E-149
gene_id_29756	27	100	4.00E-07
gene_id_29757	523	97.71	0
gene_id_29758	143	94.41	5.00E-44
gene_id_30270	205	30.73	2.00E-19
gene_id_30271	201	31.84	3.00E-21
gene_id_30272	70	41.43	1.00E-09
gene_id_30273	152	39.47	1.00E-18
gene_id_30879	79	94.94	5.00E-34
gene_id_30880	176	96.02	8.00E-76
gene_id_30881	239	98.74	5.00E-135
gene_id_30882	389	96.4	0
gene_id_30883	354	96.33	0
gene_id_31988	247	93.93	7.00E-135
gene_id_31989	577	97.57	0
gene_id_31990	391	90.79	0

Annotation
EchA
Ech hydrogenase subunit EchB
MULTISPECIES: NADH ubiquinone oxidoreductase
NADH dehydrogenase
NADH dehydrogenase
4Fe-4S binding domain protein
flavoredoxin
antibiotic biosynthesis monooxygenase
chromate transporter
hypothetical protein
cardiolipin synthase
universal stress protein
diguanylate cyclase
agmatinase
hypothetical protein
hypothetical protein
carboxynorspermidine decarboxylase
hypothetical protein
hypothetical protein
saccharopine dehydrogenase
arginine decarboxylase
diguanylate cyclase
cytosol aminopeptidase
MULTISPECIES: hypothetical protein
tail protein
hypothetical protein
hypothetical protein
baseplate assembly protein
baseplate assembly protein
baseplate assembly protein
hypothetical protein
tail fiber protein
hypothetical protein
hypothetical protein
hypothetical protein
chromosome partitioning ATPase
putative plasmid conjugal transfer protein
IncP-type DNA relaxase TraI
IncP-type DNA relaxase TraI
P pilus assembly/Cpx signaling pathway, periplasmic inhibitor/zinc-resistance associated protein
hypothetical protein
MULTISPECIES: histidine kinase
MULTISPECIES: acetoacetate metabolism regulatory protein AtoC
hypothetical protein, partial
trehalose-binding protein
molybdopterin oxidoreductase

polysulfide reductase, NrfD family protein
(4Fe-4S)-binding protein
HAMP domain protein
phosphonate ABC transporter substrate-binding protein
arsenate reductase
Phosphotyrosine protein phosphatase I superfamily
arsenic resistance protein ArsB
arsenic transporter ATPase
arsenic transporter ATPase
arsenic resistance operon repressor
ArsR family transcriptional regulator
permease
cytochrome C biosynthesis protein
thioredoxin
hypothetical protein, partial
DGC domain protein, partial
thioredoxin
phosphohydrolase
hypothetical protein HMPREF0326_02645
hypothetical protein
hypothetical protein
hypothetical protein
conjugal transfer protein TraG
hypothetical protein
pilus assembly protein PilV
putative PilM protein
hypothetical protein
pilus protein PilS
hypothetical protein
secretion system protein E
hypothetical protein
R64 PilN family type IVB pilus formation outer membrane protein
conserved exported protein of unknown function
conjugal transfer protein TrbG
conjugal transfer protein
hypothetical protein
IncP-type conjugative transfer protein TrbJ
conjugal transfer protein TrbE
single-stranded DNA-binding protein
Conjugative transfer protein TrbD
conjugal transfer protein TrbC
putative conjugal transfer protein trbB
hypothetical protein
IncP-type DNA transfer protein TraL
hypothetical protein
glycosyl transferase
hypothetical protein

hypothetical protein
methionyl-tRNA synthetase
hypothetical protein
HD family phosphohydrolase
glycosyl transferase family 2
diphosphate--fructose-6-phosphate 1-phosphotransferase
ATP-dependent DNA helicase UvrD
hypothetical protein
2-nitropropane dioxygenase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
phosphoglycerate mutase
hypothetical protein
hypothetical protein
ATPase P
ATPase P
hypothetical protein
chemotaxis protein CheY
transglycosylase
thioesterase
amidohydrolase
hypothetical protein
amidohydrolase
cell division protein FtsK
elongation factor P
3-dehydroquinate dehydratase
GTP-binding protein YsxC
permease
permease
hypothetical protein
UDP-diphosphatase
membrane protein
lactate permease
PhoU family transcriptional regulator
transcription elongation factor GreA
hypothetical protein
hypothetical protein
hypothetical protein
phage integrase family protein
DNA methyltransferase
restriction modification system DNA specificity domain-containing protein
DEAD/DEAH box helicase
hypothetical protein
MULTISPECIES: BRO domain-containing protein
rlgA1 gene product

aminoacyl-histidine dipeptidase
hypothetical protein
hypothetical protein
beta-lactamase
hypothetical protein
carbonic anhydrase
histidine kinase
HAMP domain protein
calcium-binding protein
histidine kinase
radical SAM protein
hypothetical protein
hypothetical protein
SlyX
teicoplanin resistance protein VanZ
sulfurtransferase
MULTISPECIES: FMN reductase
MULTISPECIES: hypothetical protein
NADH:flavin oxidoreductase
MULTISPECIES: 4-oxalocrotonate tautomerase
NADH dehydrogenase
transcriptional regulator
hypothetical protein
ABC transporter ATP-binding protein
DNA mismatch repair protein MutT
membrane protein
semialdehyde dehydrogenase
aminotransferase
glycosyl transferase family 1
cytochrome C nitrite reductase
7-cyano-7-deazaguanine reductase
glutamate synthase (NADPH) GltB1 subunit
glutamate synthase
pyridine nucleotide-disulfide oxidoreductase
hypothetical protein
hypothetical protein
glycosyl transferase family 2
hypothetical protein
cheW-like protein
nickel ABC transporter substrate-binding protein
nickel ABC transporter substrate-binding protein
transporter
major Facilitator Superfamily protein
hypothetical protein
putative membrane protein
SPFH domain / Band 7 family protein
hypothetical protein

cyclic peptide transporter family protein
hypothetical protein
hypothetical protein
4'-phosphopantetheinyl transferase superfamily protein
thioesterase domain protein
kamA family protein
amino acid adenylation domain protein
amino acid adenylation domain protein
amino acid adenylation domain protein
amino acid adenylation domain protein
histidine kinase
outer membrane transport family protein
chemotaxis protein
cytochrome C
methyl-accepting chemotaxis protein
arsenate reductase
radical SAM protein
4Fe-4S ferredoxin
hypothetical protein
hypothetical protein
hypothetical protein
elongation factor 4
signal peptidase I
magnesium chelatase
rlgA1 gene product
hypothetical protein, partial
hypothetical protein
putative DNA-damage-inducible protein D
phage antirepressor protein
magnesium chelatase
hypothetical protein
histidine kinase
pilus biosynthesis protein TadE
von Willebrand factor A
pilus biosynthesis protein TadE
hypothetical protein
bacterial type II secretion system F domain protein
bacterial type II secretion system F domain protein
type II secretion system protein E
MerR family transcriptional regulator
histidine kinase
MULTISPECIES: translation initiation factor IF-1
prolipoprotein diacylglyceryl transferase
transcriptional regulator
glycosyl transferase
polymerase
glycosyl transferase

glycosyl transferase family 1
aminotransferase class I/II
HD family phosphohydrolase
Fis family transcriptional regulator
oxidoreductase FAD-binding domain protein
dinitrogenase iron-molybdenum cofactor biosynthesis protein
thiamine-phosphate pyrophosphorylase
hydroxyethylthiazole kinase
GntR family transcriptional regulator
pyridoxamine 5'-phosphate oxidase family protein
aspartate aminotransferase
hypothetical protein
UDP-N-acetylglucosamine acyltransferase
MULTISPECIES: 3-hydroxyacyl-ACP dehydratase
UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase
membrane protein
N-acetylmuramoyl-L-alanine amidase
membrane protein
ABC transporter ATP-binding protein
ABC transporter permease
lysyl-tRNA synthetase
transcriptional regulator
rubrerythrin
DNA topoisomerase III
hypothetical protein
6-phosphogluconolactonase
osmotically inducible protein OsmC
beta-lactamase
chemotaxis protein
hypothetical protein
conjugal transfer protein TraR
inorganic phosphate transporter
phosphate transport regulator
iron-sulfur protein
hydrogenase nickel incorporation protein HypA
carbon monoxide-induced hydrogenase
hydrogenase
hydrogenase
MULTISPECIES: NADH ubiquinone oxidoreductase
hydrogenase
oxidoreductase
membrane protein
hypothetical protein
hypothetical protein
hypothetical protein
membrane protein
cobinamide kinase

hypothetical protein
alkaline phosphatase
membrane protein
2-oxoacid:ferredoxin oxidoreductase subunit gamma
MFS transporter
2-ketoisovalerate ferredoxin reductase
MULTISPECIES: (Fe-S)-binding protein
S-adenosylmethionine tRNA ribosyltransferase
hypothetical protein
phosphopantothenoylcysteine decarboxylase
hypothetical protein
membrane protein
short chain dehydrogenase family protein
chromosome partitioning protein ParA
hypothetical protein
plasmid stablization protein ParB
ADP-heptose synthase
molecular chaperone DnaJ
hypothetical protein
hypothetical protein
methionyl-tRNA formyltransferase
peptide deformylase
aspartyl-tRNA synthetase
histidyl-tRNA synthetase
DEAD/DEAH box helicase
aminoglycoside phosphotransferase
peptide methionine sulfoxide reductase MsrA
radical SAM protein
4Fe-4S ferredoxin
molybdenum ABC transporter substrate-binding protein
hypothetical protein
excinuclease ABC subunit A
excinuclease ABC subunit A
membrane protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
transcriptional activator Ogr/delta
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
holin
lysozyme
ammonia monooxygenase

hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
tail protein
hypothetical protein
hypothetical protein
tail fiber protein
hypothetical protein
hypothetical protein
conjugal transfer protein TraR
hypothetical protein
antibiotic ABC transporter permease
ammonium transporter
nitrogen regulatory protein P-II
alanine dehydrogenase
Fis family transcriptional regulator
glutamate--ammonia ligase
acyl-CoA:6-aminopenicillanic acid acyl-transferase
amidotransferase
transcriptional antiterminator
sugar ABC transporter permease
sugar ABC transporter permease
sugar ABC transporter ATP-binding protein
ABC transporter ATP-binding protein
radical SAM protein
molybdopterin oxidoreductase, partial
hypothetical protein
histidine kinase
catalase
Fur family transcriptional regulator, partial
membrane protein
conjugal transfer protein TraR
putative membrane protein
uracil-DNA glycosylase
radical SAM protein
MULTISPECIES: HIT family hydrolase
MULTISPECIES: DNA-binding protein
sodium:sulfate symporter
MarR family transcriptional regulator
hypothetical protein
cobyrinic acid a,c-diamide synthase
MULTISPECIES: dsvD
sulfite reductase
sulfite reductase
hypothetical protein
hypothetical protein

lysine transporter LysE
histidine kinase
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
cytochrome C
AP endonuclease
beta-lactamase
Fis family transcriptional regulator
histidine kinase
hypothetical protein
hypothetical protein
universal stress protein UspA
large conductance mechanosensitive channel protein MscL
branched-chain amino acid ABC transporter substrate-binding protein
branched-chain amino acid transporter permease subunit LivH
branched-chain amino acid ABC transporter permease
ABC transporter
amino acid ABC transporter ATPase
homocitrate synthase
nitrogenase iron protein
nitrogen fixation nifHD region glnB 1
nitrogen regulatory protein P-II
nitrogenase molybdenum-iron protein alpha chain
nitrogenase molybdenum-iron protein beta chain
dinitrogenase iron-molybdenum cofactor biosynthesis protein
ferredoxin
aminotransferase class IV
chloride transporter
glutamine amidotransferase
multicopper polyphenol oxidase
5-formyltetrahydrofolate cyclo-ligase
Ser/Thr protein phosphatase
hypothetical protein
IncP-type DNA transfer protein TraL
hypothetical protein
putative conjugal transfer protein trbB
Conjugative transfer protein TrbC
conjugal transfer protein TrbD
single-stranded DNA-binding protein
Conjugative transfer protein TrbE
IncP-type conjugative transfer protein TrbJ
Conjugative transfer protein TrbL

conjugal transfer protein
conjugal transfer protein TrbG
hypothetical protein
R64 PilN family type IVB pilus formation outer membrane protein
hypothetical protein
secretion system protein E
hypothetical protein
pilus protein PilS
hypothetical protein
putative type IV pilus protein PilM
pilus assembly protein PilV
hypothetical protein
conjugal transfer protein TraG
hypothetical protein
hypothetical protein
hypothetical protein
lytic transglycosylase
hypothetical protein
integrase
transposase
hypothetical protein
hypothetical protein
MFS transporter permease
membrane protein
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)
hypothetical protein
HD domain protein, partial
glycolate oxidase
glycolate oxidase
MULTISPECIES: single-stranded DNA-binding protein
phosphoenolpyruvate-protein phosphotransferase
phosphocarrier protein HPr
PTS 3-keto-L-gulonate transporter subunit IIA
tetrapyrrole methylase
hypothetical protein
ribonuclease HII
50S ribosomal protein L19
tRNA (guanine-N1)-methyltransferase
ribosome maturation factor RimM
hypothetical protein
30S ribosomal protein S16
signal recognition particle protein
sugar synthetase
nucleoside recognition protein
dTDP-4-dehydrorhamnose reductase
spore coat protein
sirohydrochlorin cobaltochelatase

hypothetical protein
preprotein translocase subunit TatA
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
hypothetical protein
membrane protein
exlusion protein FxsA
hypothetical protein
50S ribosomal protein L28
hypothetical protein
MULTISPECIES: 50S ribosomal protein L32
phosphate acyltransferase
3-oxoacyl-ACP synthase
3-ketoacyl-ACP reductase
acyl carrier protein
3-oxoacyl-ACP synthase
serine hydroxymethyltransferase
cytidine deaminase
riboflavin biosynthesis protein RibD
riboflavin synthase subunit alpha
3,4-dihydroxy-2-butanone 4-phosphate synthase
6,7-dimethyl-8-ribityllumazine synthase
nitrogen utilization protein B
leucyl-tRNA synthetase
hypothetical protein
DNA polymerase III subunit delta
DNA repair protein RadC
acylphosphatase
peptidase
diguanylate cyclase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
nucleoside triphosphate pyrophosphohydrolase
colicin V synthesis protein
phosphohydrolase
histidine kinase
response regulator
thiS family protein
chemotaxis protein
Fis family transcriptional regulator
pilus biosynthesis protein PilZ
hypothetical protein
chorismate mutase
3-dehydroquinate synthase
fructose-bisphosphate aldolase
hypothetical protein

diguanylate phosphodiesterase
DHH family phosphoesterase
xylose isomerase
MULTISPECIES: hypothetical protein
ATP-dependent DNA helicase UvrD
ATP-dependent DNA helicase UvrD
hypothetical protein
chloride channel protein
riboflavin biosynthesis protein RibF
hypothetical protein
hypothetical protein ACD_79C01376G0004, partial
hypothetical protein
hypothetical protein ACD_79C00716G0003
Fe-S oxidoreductase
methyltransferase family protein
hypothetical protein RCCGE510_20859
hypothetical protein
NAD-dependent dehydratase
hypothetical protein
NAD-dependent dehydratase
alcohol dehydrogenase
hypothetical protein ACD_79C00145G0002
ATP-binding cassette, subfamily C, bacterial
n-acetylneuraminate synthase
hypothetical protein ACD_79C00647G0004
related to iron-sulfur flavoprotein of Methanosarcina thermophila
AMP-dependent synthetase and ligase
DegT/DnrJ/EryC1/StrS aminotransferase
hypothetical protein
hypothetical protein
hypothetical protein
imidazole glycerol phosphate synthase
imidazole glycerol phosphate synthase
flagellin modification protein, PseA
CMP-N-acetylneuraminic acid synthetase
N-acetylneuraminate synthase
N-Acetylneuraminate cytidylyltransferase
aminotransferase DegT
flagellin modification protein FlmA
S-adenosylmethionine (SAM)-dependent methyltransferase
glycosyl transferase family 1
hypothetical protein
glycosyl transferase group 1
ATPase AAA
membrane protein
membrane protein
Fis family transcriptional regulator

hypothetical protein
histidine kinase
response regulator
hypothetical protein
hypothetical protein
response regulator
histidine kinase
hypothetical protein
translation initiation factor IF-2
translation initiation factor IF-2
translation initiation factor IF-2
transcription termination factor NusA
hypothetical protein
flagellar basal body rod protein FlgG
flagellar basal body rod protein FlgG
FlgA
flagellar L-ring protein
flagellar P-ring family protein
peptidase M23
peptidase M23
peptidase M23
flgN family protein
flagellar hook-associated protein FlgK
flagellar hook-associated protein FlgL
MULTISPECIES: carbon storage regulator
flagellar assembly protein FliW
Fis family transcriptional regulator
ribonucleoside-triphosphate reductase
radical SAM protein
chemotaxis protein X
hypothetical protein
hypothetical protein
MULTISPECIES: ferredoxin
hypothetical protein
hypothetical protein
pantothenate kinase
enolase
5,10-methylene-tetrahydrofolate dehydrogenase
flagellar basal body rod protein
membrane protein
transcriptional regulator
glyoxalase
alkyl hydroperoxide reductase
alkyl hydroperoxide reductase
hypothetical protein
molybdenum cofactor biosynthesis protein MoeA
transcriptional regulator

ammonium transporter
lipid hydroperoxide peroxidase
hypothetical protein
hypothetical protein
RNA-binding protein
hypothetical protein
hypothetical protein
nuclease
sodium:neurotransmitter symporter
thiamine biosynthesis protein
recombinase RecA
alanyl-tRNA synthetase
hypothetical protein
hypothetical protein
hypothetical protein
PhoU family transcriptional regulator
phosphate ABC transporter ATP-binding protein
ArsR family transcriptional regulator
3'-exoribonuclease
4Fe-4S ferredoxin
nitrite reductase
tRNA modification GTPase TrmE
single-stranded DNA-binding protein
single-stranded DNA-binding protein
chemotaxis protein CheY
hisitidine kinase
histidine kinase
hypothetical protein
alkyl hydroperoxide reductase
transposase
formate dehydrogenase
formate dehydrogenase subunit alpha
formate dehydrogenase subunit beta
molybdopterin-guanine dinucleotide biosynthesis protein MobB
Tat pathway signal protein
methyl-accepting chemotaxis protein
Fis family transcriptional regulator
hypothetical protein
histidine kinase
hypothetical protein
chemotaxis protein
hypothetical protein
histidine kinase
histidine kinase
hypothetical protein
flagellar motor protein MotA
chemotaxis protein MotB

hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
dienelactone hydrolase
competence protein ComEC
formamidopyrimidine-DNA glycosylase
CopG family transcripitonal regulator
peptide-binding protein
peptide-binding protein
peptide-binding protein
MULTISPECIES: phenylacetate-CoA ligase
membrane protein
short-chain dehydrogenase
hypothetical protein
beta-lactamase family protein
methyltransferase domain protein
hypothetical protein
diaminopimelate epimerase
branched-chain amino acid ABC transporter substrate-binding protein
branched-chain amino acid ABC transporter permease
branched-chain amino acid ABC transporter permease
branched-chain amino acid ABC transporter ATP-binding protein
amino acid ABC transporter ATPase
hemolysin-type calcium-binding repeat family protein
F0F1 ATP synthase subunit alpha
3-hydroxyisobutyrate dehydrogenase
hypothetical protein
chromosome partitioning ATPase
rha family phage regulatory protein
putative plasmid conjugal transfer protein
IncP-type DNA relaxase TraI
IncP-type DNA relaxase TraI
hypothetical protein
hypothetical protein
hypothetical protein
multicopper oxidase
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)
hypothetical protein
hypothetical protein
elongation factor P
hypothetical protein
dimethyladenosine transferase

DNA-binding protein
hypothetical protein
30S ribosomal protein S21
aspartyl-tRNA amidotransferase subunit B
DNA mismatch repair protein MutS
hypothetical protein
hypothetical protein
thioredoxin reductase
chemotaxis protein CheY
(Fe-S)-binding protein
tol-pal system protein YbgF
membrane protein
peptidase A8
isoleucyl-tRNA synthetase
GDSL family lipase
hydantoin utilization protein B
hydrogenase
hydrogenase 2 large subunit
oxidoreductase
hydrogenase
chemotaxis protein
chemotaxis protein CheW
ArsR family transcriptional regulator
hypothetical protein
GntR family transcriptional regulator
FMN-dependent dehydrogenase family protein
membrane protein
hypothetical protein
membrane protein
C4-dicarboxylate ABC transporter substrate-binding protein
ABC transporter substrate-binding protein
hypothetical protein
hypothetical protein
MULTISPECIES: sulfite reductase
heptosyltransferase
histidine kinase
diguanylate phosphodiesterase
chemotaxis protein CheA
chemotaxis protein CheW
methyl-accepting chemotaxis protein
Rrf2 family transcriptional regulator
Rrf2 family transcriptional regulator
oxidoreductase
hypothetical protein
histidine kinase
hypothetical protein
multidrug ABC transporter permease

ABC transporter ATP-binding protein
ABC transporter ATP-binding protein
hemolysin secretion protein D
hypothetical protein
hypothetical protein
metal dependent phosphohydrolase
hypothetical protein
amino acid ABC transporter ATPase
amino acid ABC transporter substrate-binding protein
ABC transporter permease
amino acid ABC transporter permease
50S ribosomal protein L11 methyltransferase
endonuclease
peptidase M24
peptidase S41
sugar deacetylase
MULTISPECIES: nucleoside diphosphate kinase
pyrroline-5-carboxylate reductase
DNA mismatch repair protein MutS
signal peptidase
ATPase
mgtC family protein
diguanylate cyclase
hypothetical protein
hypothetical protein
hypothetical protein
diguanylate cyclase
hypothetical protein, partial
queuine tRNA-ribosyltransferase
phosphoribosylglycinamide formyltransferase
histidine kinase
amino acid ABC transporter ATPase
ABC transporter
branched-chain amino acid ABC transporter permease
ABC transporter permease
amino acid ABC transporter substrate-binding protein
hypothetical protein
Fis family transcriptional regulator
NAD dependent epimerase/dehydratase family protein
glycosyl transferase
exopolysaccharide biosynthesis protein
hydrogenase
hydrogenase formation protein HypD
phosphohydrolase
3-deoxy-D-manno-octulosonic acid transferase
histidine kinase
PBS lyase

recombinase RecR
hypothetical protein
DNA polymerase III subunit gamma/tau
DNA polymerase III subunit gamma/tau
tRNA (adenine-N1)-methyltransferase
radical SAM protein
ribonuclease
hypothetical protein
coproporphyrinogen III oxidase
histidine kinase
hypothetical protein
membrane protein
hypothetical protein
menaquinol oxidoreductase
Hdr menaquinol oxidoreductase iron-sulfur subunit
cytochrome C
4Fe-4S ferredoxin
Hdr menaquinol oxidoreductase integral membrane subunit
membrane protein
histidine kinase
chemotaxis protein CheY
hypothetical protein
primosomal protein N'
UTP--glucose-1-phosphate uridylyltransferase
phosphoglucosamine mutase
hypothetical protein
membrane protein
dihydropteroate synthase
ATP-dependent metalloprotease
ABC transporter substrate-binding protein
RNA-binding protein
hypothetical protein
argininosuccinate lyase
argininosuccinate synthase
ornithine carbamoyltransferase
endonuclease/exonuclease/phosphatase
hypothetical protein
FmdB family transcriptional regulator
adenylosuccinate lyase
orotate phosphoribosyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
ribonucleoside triphosphate reductase
flagellin
membrane protein
diguanylate cyclase

ABC transporter substrate-binding protein
GntR family transcriptional regulator
amino acid ABC transporter ATPase
ABC transporter ATP-binding protein
ABC transporter permease
ABC transporter permease
dehydrogenase
divergent AAA domain protein
glutaminyl-tRNA synthetase
GTP-binding protein
acetyltransferase
hypothetical protein
4Fe-4S binding domain protein
lysine transporter LysE
hypothetical protein
cytochrome C nitrite reductase
7-cyano-7-deazaguanine reductase
histidine kinase
Fis family transcriptional regulator
hypothetical protein
channel protein TolC
von Willebrand factor A
LuxR family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
bacterial type II and III secretion system family protein
general secretion pathway protein E
general secretion pathway protein F
prepilin-type N-terminal cleavage/methylation domain protein
hypothetical protein
hypothetical protein OR1_02613
hypothetical protein OR1_02614
3-ketoacyl-ACP reductase
beta-ketoacyl synthase
All-trans-retinol 13,14-reductase
3-oxoacyl-ACP synthase
acyl carrier protein
hypothetical protein
putative lipoprotein
radical SAM protein
hypothetical protein
outer membrane lipoprotein carrier protein LolA
putative exporter
hypothetical protein
hypothetical protein, partial
putative thioesterase

lipid biosynthesis B12-binding/radical SAM protein
glycosyl transferase family 2
lipid A biosynthesis acyltransferase, partial
acyl carrier protein
beta-ketoacyl synthase
hypothetical protein, partial
4-coumarate--CoA ligase
DNA binding , excisionase family domain protein
terminase
mechanosensitive ion channel protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein EV102420_11_00480
hypothetical protein
hypothetical protein
chemotaxis protein
(Fe-S)-binding protein
hypothetical protein
hypothetical protein
acetate kinase
phosphate acetyltransferase
(Fe-S)-binding protein
FAD-binding protein
pyruvate:ferredoxin (flavodoxin) oxidoreductase
Fis family transcriptional regulator
histidine kinase
hypothetical protein
hypothetical protein
aminotransferase DegT
oxidoreductase
hypothetical protein
methyltransferase
putative membrane protein
hypothetical protein
hypothetical protein
inorganic polyphosphate/ATP-NAD kinase
phosphoheptose isomerase
FmdB family transcriptional regulator
porphobilinogen deaminase
methyl-accepting chemotaxis protein
helix-turn-helix family protein
hypothetical protein
hypothetical protein
glycosyl transferase

ATP-dependent protease
hypothetical protein
MFS transporter
4Fe-4S ferredoxin
glutamine amidotransferase
phosphonate ABC transporter permease
phosphonate ABC transporter permease
phosphonate ABC transporter ATP-binding protein
phosphonate ABC transporter substrate-binding protein
HAD family hydrolase
dihydroxyacetone kinase
hypothetical protein
pyruvate ferredoxin oxidoreductase
2-oxoglutarate ferredoxin oxidoreductase subunit alpha
2-oxoacid ferredoxin oxidoreductase subunit beta
pyruvate ferredoxin/flavodoxin oxidoreductase family protein
hypothetical protein
hypothetical protein, partial
regulatory protein
indolepyruvate ferredoxin oxidoreductase
indolepyruvate ferredoxin oxidoreductase
hypothetical protein
gamma-glutamyl phosphate reductase
nicotinic acid mononucleotide adenylyltransferase
hypothetical protein
cell envelope biogenesis protein AsmA
histidine kinase
Fis family transcriptional regulator
hypothetical protein
histidine kinase
hypothetical protein
peroxiredoxin
hypothetical protein
membrane protein
2-oxoglutarate dehydrogenase E3
glycine dehydrogenase subunit 2
glycine dehydrogenase subunit 1
glycine cleavage system protein H
chemotaxis protein CheY
phosphoglucomutase
GTP-binding protein YchF
hypothetical protein
peptidase M29
hypothetical protein
pirin
hypothetical protein
pilus biosynthesis protein PilZ

hypothetical protein
histidine kinase
amino acid ABC transporter ATPase
amino acid ABC transporter substrate-binding protein
amino acid ABC transporter permease
transcriptional regulator
3-hydroxypropionyl-CoA synthetase
ABC transporter ATP-binding protein
ABC transporter permease
tungsten ABC transporter substrate-binding protein
Fis family transcriptional regulator
histidine kinase
universal stress protein UspA
hypothetical protein
membrane protein
hypothetical protein
ABC transporter substrate-binding protein
histidine kinase
lysine transporter LysE
phosphoribosylglycinamide formyltransferase
molybdenum cofactor sulfurase
uroporphyrin-III C-methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
valyl-tRNA synthetase
biotin--protein ligase
hypothetical protein
hypothetical protein
HAD family hydrolase
hypothetical protein
arabinan synthesis protein
hypothetical protein
MULTISPECIES: hypothetical protein
acetolactate synthase
acetolactate synthase
ketol-acid reductoisomerase
ACP phosphodiesterase
hypothetical protein
hesB-like domain-containing protein
adhesin
adhesin
phosphoribosyl transferase
membrane protein
aminopeptidase
hypothetical protein
4Fe-4S ferredoxin

formate dehydrogenase
RNA polymerase subunit sigma-24
hypothetical protein
cytidine deaminase
decarboxylase
metallo-beta-lactamase
methyltransferase
phosphopantetheine adenylyltransferase
tRNA delta(2)-isopentenylpyrophosphate transferase
hypothetical protein
hypothetical protein
RNA helicase
hypothetical protein
hydrolase
phenolic acid decarboxylase subunit B
lactate permease
hypothetical protein
rRNA methyltransferase
ADP-ribosylglycohydrolase
hypothetical protein
peptide ABC transporter ATP-binding protein
Fis family transcriptional regulator
histidine kinase
ATP-dependent protease
ATP-dependent protease
hypothetical protein
hypothetical protein
hypothetical protein
membrane protein
universal stress protein UspA
MFS transporter
hypothetical protein
glutamine synthetase
MFS transporter
flavodoxin
hypothetical protein
Fis family transcriptional regulator
histidine kinase
hypothetical protein
membrane protein
glucosidase
hypothetical protein
rubrerythrin family protein
MULTISPECIES: transcriptional regulator
histidine kinase
histidine kinase
lytic transglycosylase

ribonuclease BN
MULTISPECIES: membrane protein
hypothetical protein
hypothetical protein
DSBA oxidoreductase
branched-chain amino acid transport family protein
AzlC family protein
GntR family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
hydantoinase
hydantoinase
hydantoinase
tRNA-binding protein
type 11 methyltransferase
metallo-beta-lactamase
heat shock protein Hsp20
malate synthase
hypothetical protein
membrane protein
hypothetical protein
putative membrane protein
LysR family transcriptional regulator
hypothetical protein
hypothetical protein
co-chaperone GrpE
HrcA family transcriptional regulator
radical SAM superfamily protein
methyltransferase domain protein
hypothetical protein
asparagine synthase
aminotransferase DegT
radical SAM superfamily protein
UDP-N-acetylglucosamine 2-epimerase
fumarate reductase
fumarate reductase
fumarate reductase
hypothetical protein
peptide ABC transporter ATP-binding protein
glutamine ABC transporter permease
amino acid ABC transporter substrate-binding protein
ATPase P
dihydroorotate dehydrogenase
membrane protein
hypothetical protein
membrane protein

DNA mismatch repair protein MutL
ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein
N5-carboxyaminoimidazole ribonucleotide mutase
phosphoribosylamine--glycine ligase
phenylacetate--CoA ligase
diguanylate phosphodiesterase
HD family phosphohydrolase
methyl-accepting chemotaxis protein
N-acetyl-gamma-glutamyl-phosphate reductase
hypothetical protein
aminotransferase
SAM-dependent methyltransferase
hemolysin-type calcium-binding repeat family protein
ABC transporter
hemolysin secretion protein D
transglutaminase
HD family phosphohydrolase
chemotaxis protein
rRNA methyltransferase
hypothetical protein
ammonium transporter
nitrogen regulatory protein P-II
protein-P-II uridylyltransferase
hypothetical protein
amino acid ABC transporter ATPase
amino acid ABC transporter permease
amino acid ABC transporter substrate-binding protein
membrane protein
hypothetical protein
cupin
ABC transporter
toluene tolerance, Ttg2 family protein
ABC transporter substrate-binding protein
ABC transporter ATP-binding protein
ABC transporter permease
sporulation protein
arginyl-tRNA synthetase
malonyl CoA-ACP transacylase
ABC transporter permease
multidrug ABC transporter substrate-binding protein
peptide transporter
RND transporter
hypothetical protein
molecular chaperone Hsp20
molecular chaperone Hsp20

magnesium transporter CorA
GCN5 family acetyltransferase
conserved hypothetical protein
aldehyde dehydrogenase
peptidase
ATPase AAA
ATP-dependent Clp protease proteolytic subunit
trigger factor
LysR family transcriptional regulator
segregation protein A
50S ribosomal protein L17
DNA-directed RNA polymerase subunit alpha
30S ribosomal protein S4
MULTISPECIES: 30S ribosomal protein S11
30S ribosomal protein S13
methionine aminopeptidase
preprotein translocase subunit SecY
MULTISPECIES: 50S ribosomal protein L15
MULTISPECIES: 50S ribosomal protein L30
30S ribosomal protein S5
MULTISPECIES: 50S ribosomal protein L18
50S ribosomal protein L6
MULTISPECIES: 30S ribosomal protein S8
MULTISPECIES: 30S ribosomal protein S14
MULTISPECIES: 50S ribosomal protein L5
50S ribosomal protein L24
MULTISPECIES: 50S ribosomal protein L14
MULTISPECIES: 30S ribosomal protein S17
MULTISPECIES: 50S ribosomal protein L29
MULTISPECIES: 50S ribosomal protein L16
MULTISPECIES: 30S ribosomal protein S3
50S ribosomal protein L22
MULTISPECIES: 30S ribosomal protein S19
50S ribosomal protein L2
50S ribosomal protein L23
50S ribosomal protein L4
50S ribosomal protein L3
MULTISPECIES: 30S ribosomal protein S10
elongation factor P
30S ribosomal protein S7
MULTISPECIES: 30S ribosomal protein S12
sulfate adenylyltransferase
ankyrin
hypothetical protein, partial
peptide transporter, partial
DNA binding , excisionase family domain protein
terminase

lysine transporter LysE
peptidase M16
peptidase M16
chemotaxis protein CheA
chemotaxis protein CheA
hypothetical protein
radical SAM protein
hypothetical protein
MFS transporter
hypothetical protein
ribonuclease III
flagellin
hypothetical protein
flagellar hook protein FlgE
basal-body rod modification protein FlgD
flagellar hook-length control protein
glycosyl transferase
CgeB
hypothetical protein
anti-anti-sigma factor
histidine kinase
serine phosphatase
D-tyrosyl-tRNA(Tyr) deacylase
long-chain fatty acid--CoA ligase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
phage Tail Collar domain protein
hypothetical protein
methyl-accepting chemotaxis protein
histidine kinase
heme ABC transporter ATP-binding protein
methyl-accepting chemotaxis protein
hypothetical protein
magnesium transporter CorA
hypothetical protein
TetR family transcriptional regulator
histidine kinase
histidine kinase
hypothetical protein
RNA 2'-O ribose methyltransferase substrate binding family protein
lytic transglycosylase

aspartate aminotransferase
hypothetical protein
5-enolpyruvylshikimate-3-phosphate synthase
adenylylsulfate reductase subunit beta
adenylylsulfate reductase subunit alpha
nuclease
hydrolase GDSL
ABC transporter
permease
fumarate hydratase
fumarate hydratase
hypothetical protein
hypothetical protein
hypothetical protein
16S rRNA methyltransferase
hypothetical protein
membrane protein
50S rRNA methyltransferase
translation factor Sua5
glycosyl transferase
NUDIX hydrolase
glycogen synthase
glycogen branching protein
asparaginase
hpt domain protein
LuxR family transcriptional regulator
peptide ABC transporter ATP-binding protein
peptidase M20
iron transporter
iron transporter FeoA
iron transporter FeoB
peptidylprolyl isomerase
peptidase M20
sugar-specific transcriptional regulator TrmB family protein
diaminopimelate decarboxylase
dethiobiotin synthase
aminotransferase class I/II
hypothetical protein
beta-ketoacyl synthase
acyl carrier protein
short-chain dehydrogenase
hypothetical protein
adenosylmethionine-8-amino-7-oxononanoate aminotransferase, partial
biotin synthase
ArsR family transcriptional regulator
multidrug transporter MatE
hypothetical protein

nitrogen-fixing protein NifU
glutaminyl-tRNA synthetase
phosphohydrolase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
phage virion morphogenesis protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
phage head morphogenesis protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
lysozyme
holin
hypothetical protein DesteDRAFT_0032
DNA-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
host-nuclease inhibitor protein Gam
MULTISPECIES: hypothetical protein
hypothetical protein
DNA transposition protein
transposase
hypothetical protein
hypothetical protein
MULTISPECIES: Cro/Cl family transcriptional regulator
cytochrome C
hypothetical protein
phosphonate metabolism protein PhnM
GntR family transcriptional regulator
phosphonate ABC transporter substrate-binding protein
Sulfate and thiosulfate import ATP-binding protein CysA
Ferric iron ABC transporter, permease protein
phosphonoacetaldehyde hydrolase
4-aminobutyrate aminotransferase

2-aminoethylphosphonate--pyruvate aminotransferase
amidohydrolase
carbon-nitrogen family hydrolase
sensory box protein
4-aminobutyrate aminotransferase
succinate-semialdehyde dehdyrogenase
spermidine/putrescine ABC transporter ATPase
spermidine/putrescine ABC transporter permease
ABC transporter permease
polyamine ABC transporter substrate-binding protein
putrescine--2-oxoglutarate aminotransferase
gamma-aminobutyraldehyde dehydrogenase
agmatine deiminase
hypothetical protein
aspartyl/glutamyl-tRNA amidotransferase subunit B
16S rRNA maturation RNase YbeY
HD family phosphohydrolase
phosphate starvation protein PhoH
hypothetical protein
glycosyl transferase
threonine aldolase
transporter
polysaccharide deacetylase
molecular chaperone DnaJ
hypothetical protein
ATP-dependent Clp protease ATP-binding protein
peptidylprolyl isomerase
aspartate ammonia-lyase
cyclase
chemotaxis protein
dihydrodipicolinate synthase
diaminopimelate epimerase
hypothetical protein
hypothetical protein
DNA-binding protein
flagellar synthesis regulator FleN
diguanylate cyclase
peptide chain release factor 2
apolipoprotein N-acyltransferase, partial
magnesium transporter
hypothetical protein
tRNA uridine 5-carboxymethylaminomethyl modification protein
UDP-N-acetylglucosamine 2-epimerase
polysaccharide biosynthesis protein
dTDP-4-dehydrorhamnose reductase
glycosyl transferases group 1 family protein
glycosyl transferase 2 family protein

glycosyl transferases group 1 family protein
glycosyl transferase 2 family protein
adenylylsulfate kinase
type 11 methyltransferase
radical SAM protein
glycosyl transferase family 2
FkbM family methyltransferase
methyltransferase
acylneuraminate cytidylyltransferase
glycosyltransferase
N-acylneuraminate-9-phosphate synthase
MarR family transcriptional regulator
hypothetical protein
cytochrome C
ABC transporter permease
ABC transporter permease
peptide ABC transporter substrate-binding protein
peptide ABC transporter ATP-binding protein
hypothetical protein
ABC transporter ATP-binding protein
peptidase S54
ribosomal large subunit pseudouridine synthase D
uracil phosphoribosyltransferase
uracil transporter
cytidylate kinase
histidinol-phosphate aminotransferase
hypothetical protein
hypothetical protein
indole-3-pyruvate decarboxylase
succinyl-CoA synthetase subunit beta
lactate utilization protein B/C
histone deacetylase
thymidylate kinase
DNA-binding protein
stationary phase survival protein SurE
fructose-bisphosphate aldolase
glyceraldehyde-3-phosphate dehydrogenase
serine dehydratase
diguanylate phosphodiesterase
fibronectin-binding protein
conjugal transfer protein TraR
hypothetical protein
methyltransferase
hypothetical protein
acetyl-CoA synthetase
DNA-binding protein
chromosomal replication initiator protein DnaA

FAD-dependent thymidylate synthase
Holliday junction DNA helicase RuvB
Holliday junction DNA helicase RuvA
diguanylate cyclase
hypothetical protein
flavodoxin
membrane protein
histidine kinase
hypothetical protein
MULTISPECIES: hypothetical protein
guanylate kinase
orotidine 5'-phosphate decarboxylase
hypothetical protein
HD family phosphohydrolase
single-stranded DNA exonuclease
histidine kinase
transcriptional regulator
hypothetical protein
hypothetical protein
cell filamentation protein Fic
Protein of unknown function DUF2329
transporter
transcriptional regulator, Crp/Fnr family
Crp/Fnr family transcriptional regulator
transporter
general stress protein CsbD
integrase
hypothetical protein
hypothetical protein
hypothetical protein
PTS fructose transporter subunit IIA
ribose ABC transporter permease
RNA polymerase sigma54 factor
ABC transporter
organic solvent tolerance protein OstA
hypothetical protein
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
2-dehydro-3-deoxyphosphooctonate aldolase
CTP synthase
phosphoribosylformylglycinamidine synthase
hypothetical protein
hypothetical protein
hypothetical protein
phosphoglyceromutase
ribosome-associated protein IOJAP
nitroreductase
phenylacetate-CoA ligase

hypothetical protein
(Fe-S)-binding protein
glutamate synthase
amino acid-binding protein
molybdopterin oxidoreductase
cell division protein FtsY
histidine kinase
hypothetical protein
hypothetical protein
DEAD/DEAH box helicase
DEAD/DEAH box helicase
Precorrin-8X methylmutase
cobyrinic acid a,c-diamide synthase
hypothetical protein
transcriptional regulator
chemotaxis protein
hypothetical protein
radical SAM protein
hypothetical protein
ABC transporter
hypothetical protein
hypothetical protein
hypothetical protein
ribosome-associated GTPase EngA
DNA-binding protein
MarR family transcriptional regulator
hypothetical protein
twin-arginine translocation pathway signal protein
branched-chain amino acid aminotransferase
DNA polymerase III subunit gamma/tau
4Fe-4S ferredoxin
NADH-quinone oxidoreductase subunit J
NADH-ubiquinone oxidoreductase subunit 4L
cation:proton antiporter
MULTISPECIES: hypothetical protein
cation:proton antiporter
NADH dehydrogenase subunit 4
NADH-quinone oxidoreductase subunit N
hypothetical protein
LuxR family transcriptional regulator
histidine kinase
molecular chaperone TorD
dimethyl sulfoxide reductase subunit C
dimethyl sulfoxide reductase subunit B
dimethyl sulfoxide reductase subunit A
phosphoglycerate mutase
homoserine dehydrogenase

glutamate-pyruvate aminotransferase
ATPase AAA
peptidase U32
phosphotransferase
hypothetical protein
molecular chaperone Hsp20
heat shock protein Hsp20
phosphodiesterase
dihydrouridine synthase
hypothetical protein
hypothetical protein
MerR family transcriptional regulator
4-carboxymuconolactone decarboxylase
hypothetical protein
glyoxalase
serine O-acetyltransferase
cysteine synthase
cysteine desulfurase
nitrogen fixation protein NifU
HD family phosphohydrolase
HD family phosphohydrolase
chemotaxis protein
hypothetical protein
hypothetical protein
HPr kinase
glutathione synthase
PhoU family transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
signal protein PDZ
glutamate synthase
hypothetical protein
portal protein
hypothetical protein
hypothetical protein
DNA-binding protein
terminase
hypothetical protein
hypothetical protein
primase
primase
ADP-ribosylglycohydrolase
chemotaxis protein CheY
histidine kinase
alcohol dehydrogenase
hypothetical protein

rubrerythrin
hydrogenase
hydrogenase
hydrogenase
disulfide reductase
heterodisulfide reductase subunit B
heterodisulfide reductase subunit C
alcohol dehydrogenase
DNA polymerase III subunit alpha
6-pyruvoyl tetrahydrobiopterin synthase
membrane protein
methyl-accepting chemotaxis protein
4Fe-4S ferredoxin
hypothetical protein
permease
hypothetical protein
hypothetical protein
hypothetical protein
phosphonate ABC transporter substrate-binding protein
histidine kinase
response regulator
pyruvate phosphate dikinase
hypothetical protein
potassium transporter KefB
methyl-accepting chemotaxis protein
hypothetical protein
molecular chaperone Hsp90
alanyl-tRNA synthetase
thioesterase
hypothetical protein
hypothetical protein
methyl-accepting chemotaxis protein
sulfolactate dehydrogenase
GntR family transcriptional regulator
Fis family transcriptional regulator
histidine kinase
chemotaxis protein CheY
phosphoenolpyruvate synthase
histidine kinase
cobalt-precorrin-4 C(11)-methyltransferase
extracellular solute-binding protein family 3
precorrin-6y C5,15-methyltransferase subunit CbiE
cobalamin biosynthesis protein CbiD
hypothetical protein
sulfurtransferase
hypothetical protein
quinone oxidoreductase

C4-dicarboxylate ABC transporter
C4-dicarboxylate ABC transporter permease
C4-dicarboxylate ABC transporter permease
LysR family transcriptional regulator
flavodoxin
multidrug transporter
AraC family transcriptional regulator
hypothetical protein
glycosyl transferase family 2
spermidine/putrescine ABC transporter substrate-binding protein
spermidine/putrescine ABC transporter permease
spermidine/putrescine ABC transporter permease
spermidine/putrescine ABC transporter ATP-binding protein
hypothetical protein
pseudouridine synthase
histidine kinase
hypothetical protein
LuxR family transcriptional regulator
(2Fe-2S)-binding protein
FAD-dependent oxidoreductase
7-cyano-7-deazaguanine synthase
7-cyano-7-deazaguanine reductase
6-carboxy-5,6,7,8-tetrahydropterin synthase
peptidase S11
hypothetical protein
ArsR family transcriptional regulator
membrane protein
hypothetical protein
hypothetical protein
flagellar basal body rod protein FlgB
flagellar basal body rod protein FlgC
flagellar basal body protein FliE
flagellar M-ring protein FliF
flagellar motor switch protein FliG
flagellar assembly protein FliH
ATP synthase
PA-phosphatase
peptidase M24
arginosuccinate synthase
DNA-directed RNA polymerase subunit omega
molecular chaperone DnaJ
transporter
hypothetical protein
diguanylate cyclase
molybdenum cofactor biosynthesis protein MoaC
demethylmenaquinone methyltransferase family protein
esterase

imidazole glycerol phosphate synthase
imidazole glycerol phosphate synthase
carbamoyl phosphate synthase large subunit
amidophosphoribosyltransferase
sugar isomerase, KpsF/GutQ family protein
thioesterase
GTPase
hypothetical protein
hypothetical protein
hypothetical protein
metallophosphoesterase
DNA polymerase IV
transporter
rubredoxin
chromate transporter
ChrB protein
hypothetical protein
MFS transporter
phosphohydrolase
aminotransferase
glutamate racemase
pyridoxamine kinase
membrane protein
integrase
histidinol dehydrogenase
phosphoribosylaminoimidazole-succinocarboxamide synthase
enoyl-ACP reductase
hypothetical protein
methylated-DNA-protein-cysteine methyltransferase
radical SAM protein
MULTISPECIES: rod shape-determining protein Mbl
rod shape-determining protein MreC
membrane protein
penicillin-binding protein 2
rod shape-determining protein RodA
membrane protein
MULTISPECIES: ATP synthase F0 subunit B'
ATP synthase subunit B
ATP synthase F0F1 subunit delta
F0F1 ATP synthase subunit alpha
F0F1 ATP synthase subunit gamma
F0F1 ATP synthase subunit beta
F0F1 ATP synthase subunit epsilon
hypothetical protein
hypothetical protein
chaperone protein DnaK
hypothetical protein

glutamyl-tRNA amidotransferase
glutamyl-tRNA(Gln) amidotransferase
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
chemotaxis protein CheY
amino acid-binding protein
Fis family transcriptional regulator
histidine kinase
transcriptional regulator
quinone oxidoreductase
hypothetical protein
AraC family transcriptional regulator
sulfate permease
glycosyl transferase
UDP-phosphate galactose phosphotransferase
flavoredoxin
amino acid ABC transporter substrate-binding protein
amino acid ABC transporter permease
ABC transporter
amino acid ABC transporter permease
glycolate oxidase
hypothetical protein
pilus biosynthesis protein TadE
pilus biosynthesis protein TadE
hypothetical protein
aminotransferase
ATP-dependent protease
molecular chaperone Hsp20
peptidyl-prolyl cis-trans isomerase
30S ribosomal protein S1
peptidase
ATP-dependent protease
acetylglutamate kinase
hypothetical protein
ABC transporter substrate-binding protein
CgeB
heptosyltransferase
siroheme synthase
cytochrome C assembly protein
glutamyl-tRNA reductase
hypothetical protein
tRNA(Ile)-lysidine synthetase
adenylate kinase
30S ribosomal protein S20
glycyl-tRNA synthetase subunit beta
glycyl-tRNA synthetase subunit alpha
recombinase RecO
XRE family transcriptional regulator

XRE family transcriptional regulator
peptidylprolyl isomerase
surA N-terminal domain protein
transcription-repair coupling factor
MULTISPECIES: chemotaxis protein CheW
MULTISPECIES: hypothetical protein
tRNA (uracil-5-)-methyltransferase
extracellular solute-binding protein family 3
alpha-glucan phosphorylase
deoxyuridine 5'-triphosphate nucleotidohydrolase
acetylornithine aminotransferase
hypothetical protein
antibiotic ABC transporter permease
ABC transporter ATP-binding protein
ABC transporter ATP-binding protein
hlyD secretion family protein
TetR family transcriptional regulator
RND transporter
membrane protein
MarR family transcriptional regulator
RND transporter
transporter
hemolysin D
TetR family transcriptional regulator
hypothetical protein
MarR family transcriptional regulator
cupin
diguanylate cyclase
Mur ligase
alpha/beta hydrolase
D-alanine--D-alanine ligase
RNA polymerase subunit sigma-54
RNA polymerase subunit sigma-54
response regulator receiver protein
aminotransferase
diguanylate cyclase
glucose-1-phosphate cytidylyltransferase
CDP-glucose 4,6-dehydratase
dTDP-4-dehydrorhamnose 3,5-epimerase
aminotransferase
hypothetical protein
glucose dehydrogenase
hypothetical protein
hypothetical protein
chemotaxis protein CheY
hypothetical protein
chemotaxis protein

chromosome partitioning protein ParA
chemotaxis protein CheW
aldo/keto reductase
hypothetical protein
hypothetical protein
1-(5-phosphoribosyl)-5-amino-4-imidazole-carboxylate carboxylase
aspartate oxidase
quinolinate synthetase
nicotinate-nucleotide pyrophosphorylase
magnesium transporter
ABC transporter
ABC transporter permease
ABC transporter permease
nitrate ABC transporter substrate-binding protein
ABC transporter
alanine dehydrogenase
taurine--pyruvate aminotransferase
sulfoacetaldehyde acetyltransferase
phosphonoacetaldehyde hydrolase
GntR family transcriptional regulator
bacterial regulatory helix-turn-helix , lysR family protein
hypothetical protein
diguanylate cyclase
group 1 glycosyl transferase
glycosyl transferase family 1
hypothetical protein
Fis family transcriptional regulator
hypothetical protein
phosphate ABC transporter permease
phosphate ABC transporter permease
phosphate ABC transporter substrate-binding protein
methyl-accepting chemotaxis protein
hypothetical protein
thiazole biosynthesis protein ThiJ
AraC family transcriptional regulator
hypothetical protein
porin
hypothetical protein
tmcC1
ferredoxin
cytochrome C
hypothetical protein
universal stress protein
response regulator receiver protein
histidine kinase
histidine kinase
histidine kinase

Rrf2 family transcriptional regulator
Rrf2 family transcriptional regulator
phosphohydrolase
transketolase
phosphoglycerate kinase
transcriptional regulator
hypothetical protein
hypothetical protein
shikimate kinase
MULTISPECIES: 30S ribosomal protein S9
50S ribosomal protein L13
phosphohydrolase
CBS domain pair family protein
HD family phosphohydrolase
pyruvate kinase
cell division protein MraZ
16S rRNA methyltransferase
hypothetical protein
penicillin-binding protein
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
phospho-N-acetylmuramoyl-pentapeptide-transferase
UDP-N-acetylmuramoylalanine--D-glutamate ligase
cell division protein FtsW
UDP-diphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase
UDP-N-acetylmuramate--alanine ligase
UDP-N-acetylenolpyruvoylglucosamine reductase
cell division protein FtsQ
cell division protein FtsA
cell division protein FtsZ
hypothetical protein
hypothetical protein
thioesterase
protease
4Fe-4S ferredoxin
hypothetical protein
N-(5'-phosphoribosyl)anthranilate isomerase
ABC transporter
histidinol phosphatase
competence protein ComFB
dihydropyrimidine dehydrogenase subunit A
ferredoxin-NADP(+) reductase subunit alpha
hypothetical protein
glycoside hydrolase
hypothetical protein
putative membrane protein
DMSO reductase subunit B
DMSO reductase subunit A

molecular chaperone TorD
LuxR family transcriptional regulator
hypothetical protein
sensory box protein
membrane protein
tetraacyldisaccharide 4'-kinase
ribonuclease R
ribonuclease R
hypothetical protein
DNA repair protein RecN
hypothetical protein
peptide ABC transporter permease
peptide ABC transporter permease
hypothetical protein
hypothetical protein
hypothetical protein
nuclease
hypothetical protein
hypothetical protein
putative D-alanyl-d-alanine dipeptidase
nuclease
transcriptional regulator
HIT family hydrolase
hypothetical protein, partial
hypothetical protein
putative ATP/GTP binding protein
nucleotide pyrophosphohydrolase
hypothetical protein
conserved hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
histidine kinase
chemotaxis protein CheY
methyl-accepting chemotaxis protein
histidine kinase
chemotaxis protein CheY
histidine kinase
hypothetical protein
histidine kinase
Fis family transcriptional regulator
methyltransferase type 11
multidrug transporter

multidrug transporter
hemolysin D
bacterial regulatory s, tetR family protein
TetR family transcriptional regulator
formate dehydrogenase
formate dehydrogenase subunit alpha
formate dehydrogenase
cytochrome C
cytochrome C
membrane protein
glycosyl transferase family 2
ABC transporter
aminoglycoside phosphotransferase
prokaryotic dksA/traR C4-type zinc finger family protein
glycosyl transferase family 2
amine oxidase
peptidase M24
hypothetical protein
deoxyribodipyrimidine photo-lyase
chemotaxis protein CheY
DNA polymerase III subunit delta'
adenylosuccinate synthetase
lytic transglycosylase
hypothetical protein
histidine kinase
ABC transporter substrate-binding protein
hypothetical protein
hypothetical protein
pyridine nucleotide-disulfide oxidoreductase
glycosyl transferase
glycosyl transferase family 2
PP-loop family protein
hypothetical protein
chemotaxis protein CheY
histidine kinase
chemotaxis protein CheY
peptidase M50
tryptophanyl-tRNA synthase
hypothetical protein
cytidyltransferase
phosphoenolpyruvate synthase
Fis family transcriptional regulator
mammalian cell entry protein
polyamine ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein
transporter

RND transporter
RND transporter
hypothetical protein
ABC transporter
nitrate ABC transporter permease
ABC transporter
ABC transporter permease
nitrate ABC transporter substrate-binding protein
amidohydrolase
formate acetyltransferase
pyruvate formate lyase-activating protein
sensory box protein
diguanylate cyclase
hypothetical protein
hypothetical protein
sulfurtransferase
acetolactate synthase
phosphohydrolase MutT
butyrate kinase
TetR family transcriptional regulator
hypothetical protein
hypothetical protein
penicillin-binding protein 1A
hypothetical protein
dolichyl-phosphate-mannose-protein mannosyltransferase
aldehyde dehydrogenase
glycosyl transferase family 2
hypothetical protein
hypothetical protein
DNA topoisomerase I
hypothetical protein
hypothetical protein
ATPase P
Fis family transcriptional regulator
pilin
MULTISPECIES: pilin
MULTISPECIES: pilin
peptidase A24
pilus assembly protein CpaB
pilus assembly protein CpaC
hypothetical protein
histidine kinase
type II/IV secretion system family protein
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
peptidase
MULTISPECIES: ferredoxin
hypothetical protein

MULTISPECIES: hypothetical protein
hypothetical protein
glycosyl transferase family 1
polysaccharide biosynthesis family protein
glycosyl transferase 2 family protein
putative membrane protein
glycosyl transferase family 1
HAMP domain protein
PhoH
peptidoglycan transglycosylase
4Fe-4S ferredoxin
sulfurtransferase
hypothetical protein
MFS transporter
inositol-phosphate phosphatase
endonuclease
DNA processing protein DprA
hypothetical protein
HD family phosphohydrolase
diguanylate cyclase
integrase
hypothetical protein
hypothetical protein
hypothetical protein
lysozyme
hypothetical protein
head protein
hypothetical protein
capsid protein
portal protein
hypothetical protein
histone-lysine N-methyltransferase
rare lipoA family protein
glycosyl transferase
transporter
flagellar basal body rod protein FlgG
GTP cyclohydrolase
NAD+ synthetase
methyltransferase
biotin biosynthesis protein BioY
ABC transporter
hypothetical protein
AraC family transcriptional regulator
membrane protein
DMSO reductase subunit B
DMSO reductase subunit A
molecular chaperone TorD

cytochrome C oxidase assembly protein
cytochrome D ubiquinol oxidase subunit I
molybdate ABC transporter substrate-binding protein
hypothetical protein
integrase
molybdenum ABC transporter ATPase
molybdate ABC transporter permease
lactamase
MULTISPECIES: rubredoxin
desulfoferrodoxin
chemotaxis protein
sensory box protein, partial
phosphoribosylformylglycinamidine synthase
diguanylate cyclase
octaprenyl-diphosphate synthase
futalosine nucleosidase
hypothetical protein
hypothetical protein
GDP-mannose dehydrogenase
hypothetical protein
ubiquinone biosynthesis protein
hypothetical protein
hypothetical protein
hypothetical protein
cytochrome C
precorrin-3B C17-methyltransferase
cobalamin biosynthesis protein CbiG
glutamate-1-semialdehyde aminotransferase
transcriptional regulator
glycerol-3-phosphate dehydrogenase
hypothetical protein
translation elongation factor
hypothetical protein
polynucleotide phosphorylase/polyadenylase
MULTISPECIES: 30S ribosomal protein S15
tRNA pseudouridine synthase B
DHH family phosphoesterase
cytochrome C
pyridoxamine 5'-phosphate oxidase
ATP synthase I
putative membrane protein
ATP synthase F0F1 subunit A
ATP synthase subunit C
REX family transcriptional regulator
hypothetical protein
cobalamin synthase
hypothetical protein

ferritin
pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-binding domain protein
2-oxoacid ferredoxin oxidoreductase subunit beta
hypothetical protein
hypothetical protein
MULTISPECIES: fructose 1,6-bisphosphatase
formyltetrahydrofolate deformylase
hypothetical protein
hypothetical protein
ATP-dependent helicase
hypothetical protein
hypothetical protein
hypothetical protein
ogr/Delta-like zinc finger family protein
hypothetical protein
4-hydroxythreonine-4-phosphate dehydrogenase
hydantoinase
glycosyl hydrolase family 3
tRNA methyltransferase
cobalamin biosynthesis protein CobD
hypothetical protein
hemolysin
oxidoreductase
alpha/beta hydrolase
hypothetical protein
GTP-binding protein
permease
cytochrome C biosynthesis protein
thioredoxin
hypothetical protein, partial
DGC domain protein, partial
thioredoxin
phosphohydrolase
membrane protein
flagellin
3-methyl-2-oxobutanoate hydroxymethyltransferase
AraC family transcriptional regulator
carboxymuconolactone decarboxylase
hypothetical protein
cupin
alpha/beta hydrolase
hypothetical protein
pantoate--beta-alanine ligase
S-adenosylmethionine synthetase
pilus biosynthesis protein PilZ
chemotaxis protein CheV
exonuclease

endonuclease III
dihydroorotate dehydrogenase
carbohydrate kinase
ferredoxin thioredoxin reductase
glutaredoxin
hypothetical protein
elongation factor G
GntR family transcriptional regulator
hydroxypyruvate isomerase
peptidoglycan bridge formation protein FemAB
tartronate semialdehyde reductase
ribonuclease J
2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
30S ribosomal protein S2
elongation factor Ts
spore coat protein
glycosyl transferase family 2
uridylate kinase
ribosome recycling factor
UDP pyrophosphate synthase
phosphatidate cytidylyltransferase
histidine kinase
hypothetical protein
hypothetical protein
acetyl-CoA synthetase
GCN5 family N-acetyltransferase
chemotaxis protein CheY
hypothetical protein
membrane protein
hypothetical protein
pyridine nucleotide-disulfide oxidoreductase family protein
aldehyde dehydrogenase
thioredoxin reductase
peptidyl-prolyl cis-trans isomerase
epimerase
peptidase M24
chromosomal replication initiator protein DnaA
DNA polymerase III subunit beta
dihydrodipicolinate reductase
NAD-dependent DNA ligase LigA
hypothetical protein
potassium transporter TrkA
excinuclease ABC subunit B
hypothetical protein
leucyl-tRNA--protein transferase
ATP-dependent Clp protease ATP-binding protein
Clp protease ClpS

adenylate cyclase
chromosome condensation protein CrcB
hypothetical protein
sulfite reductase
chemotaxis protein
chemotaxis protein CheR
chemotaxis protein CheA
MULTISPECIES: Fis family transcriptional regulator
methyl-accepting chemotaxis protein
methyl-accepting chemotaxis protein
DNA repair protein RadA
hypothetical protein
hypoxanthine phosphoribosyltransferase
acetyltransferase
thioredoxin
homocysteine S-methyltransferase
RNA polymerase subunit sigma-70
hypothetical protein
hypothetical protein
hypothetical protein
ribose 5-phosphate isomerase B
cysteinyl-tRNA synthetase
peptidase M48 family protein
Appr-1-p processing protein
ATP-dependent protease
4-diphosphocytidyl-2C-methyl-D-erythritol kinase
ribose-phosphate pyrophosphokinase
50S ribosomal protein L25
peptidyl-tRNA hydrolase
CarD family transcriptional regulator
transcription termination factor Rho
multicopper oxidase
diguanylate cyclase
RNA polymerase sigma-70 factor
DNA primase
DNA mismatch repair protein MutS
polysaccharide deacetylase
shikimate dehydrogenase
ATP phosphoribosyltransferase
phosphoribosyl-AMP cyclohydrolase
aldolase
thiamine-monophosphate kinase
ATP-dependent DNA helicase UvrD
phosphodiesterase
tautomerase
hypothetical protein
primase

primase
cobalt ABC transporter ATP-binding protein
cobalt ABC transporter permease
cobalt transporter CbiM
sodium:proton antiporter
tRNA methyltransferase
glycosyl transferase family 2
glycosyl transferase family 2
glycosyl transferase family 2
phosphatidylglycerophosphatase
septum formation inhibitor Maf
hypothetical protein
flagellar biosynthesis anti-sigma factor FlgM
phosphoenolpyruvate-protein phosphotransferase
dihydroxyacetone kinase subunit DhaL
dihydroxyacetone kinase
cation transporter
S-adenosyl-L-homocysteine hydrolase
ArsR family transcriptional regulator
hypothetical protein
4Fe-4S ferredoxin
translation initiation factor IF-1
MULTISPECIES: RNA-binding protein
transcriptional regulator
addiction module protein
hypothetical protein
ABC transporter ATP-binding protein
hypothetical protein
ribosomal large subunit pseudouridine synthase B
cell envelope biogenesis protein LolA
cell division protein FtsK
alcohol dehydrogenase
SOS mutagenesis and repair protein UmuC
SOS mutagenesis error-prone repair processed to UmuD' forms complex with UmuC domain protein
cobalt transporter
MarR family transcriptional regulator
membrane protein
cyclic diguanylate phosphodiesterase
glyceraldehyde-3-phosphate dehydrogenase
hemolysin
50S ribosomal protein L31
hypothetical protein
peptide chain release factor 1
transporter
Fur family transcriptional regulator
rubrerythrin
rubredoxin

hypothetical protein
carbamoyl phosphate synthase small subunit
3-deoxy-manno-octulosonate cytidylyltransferase
peptide chain release factor 3
fructose-1,6-bisphosphatase
hypothetical protein
hypothetical protein
septum formation initiator
hypothetical protein
CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
MULTISPECIES: ATPase
protein-L-isoaspartate O-methyltransferase
membrane protein
peptidase M24
hypothetical protein
phosphoenolpyruvate synthase
pyruvate carboxylase
biotin-(acetyl-CoA carboxylase) ligase
phosphohydrolase
inorganic pyrophosphatase
hypothetical protein
PTS sugar transporter subunit IIBC
PTS sugar transporter subunit IIA
nucleotide-binding protein
response regulator
phosphoenolpyruvate synthase
superoxide dismutase
hypothetical protein
membrane protein
phosphoglycolate phosphatase
histidine kinase
bacterioferritin
membrane protein
bacterial regulatory helix-turn-helix s, AraC family protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
hypothetical protein
(dimethylallyl)adenosine tRNA methylthiotransferase
heavy metal-binding domain-containing protein
hypothetical protein
hypothetical protein
hypothetical protein
Fis family transcriptional regulator
AICARFT/IMPCHase bienzyme family protein

ribonuclease II
hypothetical protein
threonine synthase
formate acetyltransferase
pyruvate formate lyase-activating protein
gluconate 5-dehydrogenase
aliphatic sulfonate ABC transporter
ABC transporter permease
nitrate ABC transporter permease
ABC transporter
ABC transporter
6-phosphogluconate dehydrogenase
succinate-semialdehyde dehdyrogenase
Fis family transcriptional regulator
IMP cyclohydrolase
GTP-binding protein HflX
pyridine nucleotide-disulfide oxidoreductase
glycosyl transferase family 2
lysine transporter LysE
esterase
Fis family transcriptional regulator
coenzyme F390 synthetase-like protein
hypothetical protein, partial
hypothetical protein
methyltransferase type 11
hypothetical protein
aldehyde oxidoreductase
molybdopterin-binding protein
formate dehydrogenase subunit alpha
formate dehydrogenase subunit alpha
formate dehydrogenase subunit beta
formate dehydrogenase accessory protein
formate dehydrogenase
formate dehydrogenase subunit alpha
formate dehydrogenase subunit beta
formate dehydrogenase accessory protein FdhE
cytochrome C
histidine kinase
hypothetical protein
chemotaxis protein
DNA-binding protein
hypothetical protein
glycoside hydrolase
hypothetical protein
hypothetical protein
diguanylate cyclase
peptidase M16

Fur family transcriptional regulator
permease
molybdopterin biosynthesis protein MoeA
metallophosphoesterase
tyrosyl-tRNA synthetase
hcalcium-binding protein
tRNA uridine 5-carboxymethylaminomethyl modification protein
diaminopimelate aminotransferase
hypothetical protein
S-adenosylhomocysteine deaminase
thermostable monoacylglycerol lipase
glutamate synthase
hypothetical protein
hypothetical protein
sodium/hydrogen exchanger
preprotein translocase subunit YajC
preprotein translocase subunit SecD
preprotein translocase subunit SecF
cytochrome C553
cytochrome C553
hypothetical protein
cytochrome C oxidase subunit I
cytochrome C oxidase subunit III
cytochrome C oxidase
cytochrome C oxidase subunit II
ubiquinone biosynthesis protein UbiA
membrane protein
AraC family transcriptional regulator
ABC transporter permease
ABC transporter
diguanylate cyclase
trehalose-binding protein
AraC family transcriptional regulator
hypothetical protein
hypothetical protein
flagellar hook capping protein
hypothetical protein
flagellar hook protein FlgK
flagellar hook protein
flagellar hook protein
flagellin
RNA polymerase subunit sigma-24
transcriptional regulator
histidine kinase
calcium-binding EF-hand-containing protein
RND transporter
alcohol dehydrogenase

thiosulfate reductase
4Fe-4S ferredoxin
DNA polymerase III
signal transduction protein
signal transduction protein with CBS domains
actetate permease
hypothetical protein
hypothetical protein
ATP-dependent protease
DNA-directed RNA polymerase subunit beta
50S ribosomal protein L7/L12
50S ribosomal protein L10
50S ribosomal protein L1
MULTISPECIES: 50S ribosomal protein L11
transcription termination/antitermination factor NusG
preprotein translocase subunit SecE
MULTISPECIES: 50S ribosomal protein L33
elongation factor Tu
UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase
protein-(glutamine-N5) methyltransferase
hydrolase Nlp/P60
radical SAM protein
radical SAM protein
octanoyltransferase
small ribosomal subunit Rsm22 family protein
FeS-binding protein
hypothetical protein
hypothetical protein
flagellar motor switch protein FliM
tRNA pseudouridine synthase A
hypothetical protein
creA family protein
hypothetical protein
hypothetical protein
methionine sulfoxide reductase
formate dehydrogenase accessory protein FdhE
formate dehydrogenase accessory protein FdhD
molybdopterin-guanine dinucleotide biosynthesis protein MobA
molybdenum cofactor biosynthesis protein MoeA
chemotaxis protein
glutamine amidotransferase
ribosomal protein S12 methylthiotransferase RimO
histidine kinase
deoxyribonucleotide triphosphate pyrophosphatase
hypothetical protein
30S ribosomal protein S1
signal peptide peptidase SppA

GCN5 family acetyltransferase
4-alpha-glucanotransferase
6-phosphofructokinase
hypothetical protein
universal stress protein UspA
MULTISPECIES: thiamine biosynthesis protein ThiS
thiazole synthase
thiamine biosynthesis protein ThiH
thiamine biosynthesis protein ThiF
thiamine-phosphate pyrophosphorylase
calcium-binding protein
calcium-binding protein
XRE family transcriptional regulator
chemotaxis protein
chemotaxis protein CheW
helicase
peptide-binding protein
GTP pyrophosphokinase
flagellin
hypothetical protein
diguanylate cyclase
phosphohydrolase
endoribonuclease L-PSP
hypothetical protein
Fis family transcriptional regulator
hypothetical protein
hypothetical protein
aromatic ring-cleaving dioxygenase
hypothetical protein
sulfate transporter
iron ABC transporter ATP-binding protein
mammalian cell entry protein
histidine kinase
membrane protein
hypothetical protein
hpt domain protein
hypothetical protein
hypothetical protein
sodium:proton antiporter
heme ABC transporter ATPase
methyl-accepting chemotaxis protein
magnesium transporter CorA
response regulator
hypothetical protein
diguanylate cyclase
RNA-binding protein
hypothetical protein

hypothetical protein
chloramphenical resistance permease RarD
spermidine/putrescine ABC transporter substrate-binding protein
spermidine/putrescine ABC transporter ATP-binding protein
spermidine/putrescine ABC transporter permease
ABC transporter permease
glycerophosphoryl diester phosphodiesterase
acetyl-CoA carboxylase
pilus biosynthesis protein PilZ
motB protein, putative
flagellar motor protein MotP
purine nucleoside phosphorylase
hypothetical protein
hypothetical protein
histidine kinase
ABC transporter substrate-binding protein
secretion protein HlyD
DSBA oxidoreductase
thiF family protein
glycosyl transferase family 1
chemotaxis protein CheY
histidine kinase
anthranilate synthase
anthranilate synthase
prephenate dehydrogenase
3-phosphoshikimate 1-carboxyvinyltransferase
membrane protein
histidine kinase
AMP-binding protein
stress responsive protein
type 11 methyltransferase
LysR family transcriptional regulator
hemolysin
cell division protein FtsY
acyltransferase
transaldolase
TRASH domain protein
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
diaminopimelate aminotransferase
methyl-accepting chemotaxis protein
tyrosine recombinase XerD
polya polymerase
DNA polymerase III subunit alpha
membrane protein
membrane protein
thioredoxin reductase
MULTISPECIES: thioredoxin

tRNA threonylcarbamoyladenosine modification protein TsaD
5,10-methylenetetrahydrofolate reductase
hypothetical protein
dienelactone hydrolase
glutamine amidotransferase
FmdB family transcriptional regulator
branched-chain amino acid ABC transporter ATP-binding protein
ABC transporter permease
branched-chain amino acid ABC transporter permease
membrane protein
xanthine phosphoribosyltransferase
cupin domain protein
hypothetical protein
nitrogen regulatory protein P-II
ammonium transporter
peptidyl-prolyl cis-trans isomerase
hypothetical protein
biotin attachment protein
acetyl-CoA carboxylase
acetyl-CoA carboxylase
serine/threonine protein kinase
serine/threonine protein phosphatase
restriction endonuclease subunit M
hypothetical protein
hypothetical protein
methionine sulfoxide reductase
hypothetical protein
hypothetical protein
isocitrate dehydrogenase
phosphoglyceromutase
histidine kinase
hypothetical protein
hypothetical protein
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
dihydroxy-acid dehydratase
permease
cell division protein FtsE
ribonucleotide-diphosphate reductase subunit alpha
MerR family transcriptional regulator
DNA-binding protein
glycoside hydrolase
inositol monophosphatase
hypothetical protein
sirohydrochlorin cobaltochelatase
iron ABC transporter permease
iron ABC transporter ATP-binding protein
ABC transporter substrate-binding protein

precorrin-2 C20-methyltransferase
chemotaxis protein
ABC transporter
mammalian cell entry protein
DNA polymerase I
hypothetical protein
hypothetical protein
adenylylsulfate reductase subunit alpha
4Fe-4S ferredoxin
Crp/Fnr family transcriptional regulator
hypothetical protein
hypothetical protein
membrane protein
transcriptional regulator
radical SAM protein
delta-aminolevulinic acid dehydratase
Fe-S oxidoreductase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
HysB
iron hydrogenase
leuA allosteric domain protein
aspartokinase
hypothetical protein
membrane protein
carbohydrate kinase
4'-phosphopantetheinyl transferase
pyridoxine 5'-phosphate synthase
UDP-glucose 6-dehydrogenase
cytosine-specific methyltransferase
hypothetical protein C814_01160
hypothetical protein
integrase
glutamyl-Q tRNA(Asp) ligase
hypothetical protein
TetR family transcriptional regulator
glycerol acyltransferase
glycosyl transferase family 2
recombinase RarA
16S rRNA methyltransferase
glycine cleavage system protein T
hypothetical protein
cyclic diguanylate phosphodiesterase
rod shape-determining protein Mbl
Myo-inositol-monophosphatase

NUDIX hydrolase
alanine acetyltransferase
triosephosphate isomerase
preprotein translocase subunit SecG
ABC transporter substrate-binding protein
hypothetical protein
repressor
diaminopimelate decarboxylase
hypothetical protein
DNA mismatch repair protein MutS
hypothetical protein
membrane protein
HIT family hydrolase
polya polymerase
hypothetical protein
nitroreductase
hypothetical protein
gamma-glutamyltransferase
histidine kinase
hypothetical protein
histidine kinase
dTDP-4-dehydrorhamnose 3,5-epimerase
mannose-1-phosphate guanylyltransferase
cytochrome C
molybdopterin oxidoreductase
molybdopterin oxidoreductase
molybdopterin oxidoreductase
polar amino acid ABC transporter permease
amino acid ABC transporter substrate-binding protein
ABC transporter permease
histidine kinase
histidine kinase
membrane protein
2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase
NAD-dependent epimerase
hypothetical protein
TatD family hydrolase
hypothetical protein
carbon monoxide dehydrogenase
methyl-accepting chemotaxis protein
transcriptional regulator
tellurium resistance protein TerC
hypothetical protein
putative membrane protein
bug family protein
D-galactarate dehydratase
flagellar protein FlgA

hypothetical protein
hypothetical protein
flagellar basal body protein FliL
histidine kinase
RNA polymerase sigma factor
flagellar synthesis regulator FleN
flagellar biosynthesis protein FlhF
flagellar biosynthesis protein FlhA
flagellar biosynthesis protein FlhB
flagellar biosynthesis protein FliR
chemotaxis protein CheY
histidine kinase
histidine kinase
DNA-binding protein
membrane protein
membrane protein
phosphomannomutase
(Fe-S)-binding protein
aldehyde ferredoxin oxidoreductase
hypothetical protein
ribonuclease H
pilus biosynthesis protein PilZ
membrane protein
hypothetical protein
lytic transglycosylase
hypothetical protein
hypothetical protein
hypothetical protein
phosphoadenosine phosphosulfate reductase
acetoacetate metabolism regulatory protein AtoC
histidine kinase
glucose-6-phosphate isomerase
aspartate aminotransferase
sugar fermentation stimulation protein
hypothetical protein
GTP-binding protein Era
hypothetical protein
flagellar motor protein MotP
flagellar motor protein MotB
tryptophan synthase subunit alpha
isochorismatase
methylthioribose-1-phosphate isomerase
transcriptional regulator
carbon monoxide dehydrogenase
gamma-glutamyltransferase
hypothetical protein
1-(5-phosphoribosyl)-5- imidazole-4-carboxamide isomerase

hypothetical protein
imidazoleglycerol-phosphate dehydratase
preprotein translocase subunit TatC
preprotein translocase subunit TatA
GMP synthase
inosine 5'-monophosphate dehydrogenase
hypothetical protein
hypothetical protein
cytochrome C biogenesis protein CcmC
cytochrome C biogenesis protein CcmB
ABC transporter ATP-binding protein
cytochrome C biogenesis protein CcmF
cytochrome C biogenesis protein CcmE
hypothetical protein
HAD family hydrolase
heptosyltransferase
methyl-accepting chemotaxis protein
hemerythrin
phosphohydrolase
membrane protein
hypothetical protein
hypothetical protein
hypothetical protein
Fur family transcriptional regulator
membrane protein
cation ABC transporter ATP-binding protein
cation ABC transporter substrate-binding protein
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
prolyl-tRNA synthetase
exodeoxyribonuclease VII large subunit
peptidase M23
exodeoxyribonuclease VII small subunit
farnesyl-diphosphate synthase
1-deoxy-D-xylulose-5-phosphate synthase
methyl-accepting chemotaxis protein
RNA methyltransferase
hypothetical protein
glucose-1-phosphate thymidylyltransferase
50S ribosomal protein L21
50S ribosomal protein L27
GTPase CgtA
gamma-glutamyl kinase
phosphomethylpyrimidine kinase
histidine kinase
histidine kinase
hypothetical protein
chemotaxis protein

hypothetical protein
radical SAM protein
phosphoribosylaminoimidazole synthetase
hypothetical protein
hypothetical protein
cob(I)alamin adenosyltransferase
chorismate synthase
phosphohydrolase
flagellar motor protein MotB
hypothetical protein
hypothetical protein
AraC family transcriptional regulator
hypothetical protein
PhoH
type II secretory pathway component ExeA (Predicted ATPase)-like protein
twitching motility protein PilT
peptidase
lytic transglycosylase
hypothetical protein
N-terminal cleavage protein
N-terminal cleavage protein
hypothetical protein
N-terminal cleavage protein
twitching motility protein PilT
hypothetical protein
phosphomethylpyrimidine synthase
signal peptide protein
glycerate dehydrogenase
ABC transporter substrate-binding protein
histidine kinase
cell envelope biogenesis protein AsmA
Holliday junction resolvase
MULTISPECIES: transcriptional regulator
50S rRNA methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
tail protein
tail protein
hypothetical protein
hypothetical protein
tail protein
tail protein
baseplate assembly protein
tail protein
tail protein
tail protein

tail protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
CopG family transcripitonal regulator
hypothetical protein, partial
hypothetical protein
helix-turn-helix family protein
hypothetical protein
transcriptional regulator
transcriptional regulator
hypothetical protein
NAD-dependent dehydratase
selenocysteine synthase
folylpolyglutamate synthase
amino acid adenylation domain protein
amino acid adenylation domain protein
amino acid adenylation domain protein
methyltransferase domain protein
multidrug transporter
RND transporter
TetR family transcriptional regulator
transketolase
ribulose-phosphate 3-epimerase
MerR family transcriptional regulator
phenylalanyl-tRNA synthetase subunit beta
hypothetical protein
hypothetical protein
hypothetical protein
transcriptional regulator
hypothetical protein
ATPase AAA
hypothetical protein, partial
hypothetical protein
CRISPR-associated protein Cas2
hypothetical protein
hypothetical protein
hypothetical protein
1,4-dihydroxy-6-naphthoate synthase
ABC transporter substrate-binding protein
ribonuclease
hypothetical protein
hypothetical protein
N-acetylglucosamine-1-phosphate uridyltransferase
ahpF
AraC family transcriptional regulator

glycerol kinase
aquaporin-3
glycerol-3-phosphate dehydrogenase
transcriptional regulator
single-stranded DNA-binding protein
hypothetical protein
polysaccharide deacetylase
ABC transporter substrate-binding protein
branched-chain amino acid ABC transporter permease
ABC transporter permease
ABC transporter
amino acid ABC transporter ATPase
hypothetical protein
glutamine synthetase
hypothetical protein
hypothetical protein
hypothetical protein
2-hydroxyglutaryl-CoA dehydratase
hydroxylamine reductase
(Fe-S)-binding protein
alcohol dehydrogenase
histidine kinase
membrane protein
transcriptional regulator
hypothetical protein
histidine kinase
hemerythrin
exodeoxyribonuclease III
malate dehydrogenase
potassium transporter TrkH
potassium transporter TrkA
response regulator
hypothetical protein
sulfurtransferase
hypothetical protein
membrane protein
rare lipoA family protein
diguanylate phosphodiesterase
hypothetical protein
hypothetical protein
conjugal transfer protein TraR
acyltransferase
hypothetical protein
multidrug transporter MatE
hypothetical protein
hypothetical protein
hypothetical protein

cytochrome B561
cytochrome C
(4Fe-4S)-binding protein
Fis family transcriptional regulator
hypothetical protein
capreomycidine hydroxylase
hypothetical protein
hypothetical protein
chemotaxis protein
aminotransferase
cytidine 5'-phosphate N-acetylneuraminic acid synthetase
glycosyl transferase family 2
hypothetical protein
HAD family hydrolase
2-hydroxyacid dehydrogenase
acetyltransferase
3-deoxy-manno-octulosonate cytidylyltransferase
2'-5' RNA ligase
hypothetical protein
universal stress protein
pyridine nucleotide-disulfide oxidoreductase
glycolate oxidase
preprotein translocase subunit SecA
ornithine acetyltransferase
transglycosylase
hypothetical protein
hypothetical protein
cobyric acid synthase
cell envelope biogenesis protein AsmA
bacterioferritin comigratory protein
preprotein translocase subunit Tim44
chemotaxis protein CheY
ATP-dependent DNA ligase
3-ketoacyl-ACP reductase
phosphoribosyltransferase
flavodoxin
hypothetical protein
beta-lactamase
nitroreductase
sodium:proton antiporter
isoprenylcysteine carboxyl methyltransferase
radical SAM protein
ATPase
membrane protein
hydrolase
hypothetical protein
HAD family hydrolase

hypothetical protein
phosphatidylserine decarboxylase
CDP-diacylglycerol--serine O-phosphatidyltransferase
2-isopropylmalate synthase
3-isopropylmalate dehydratase
3-isopropylmalate dehydratase small subunit
3-isopropylmalate dehydrogenase
phage shock protein C
phage-shock protein
phage-shock protein
transcriptional regulator
dihydroorotase
aspartate carbamoyltransferase
amidohydrolase
ethanolamin permease
ethanolamine ammonia lyase large subunit
ethanolamine ammonia-lyase small subunit
hypothetical protein, partial
lactate permease
histidine kinase
ADP-L-glycero-D-manno-heptose-6-epimerase
hypothetical protein
acyl-ACP thioesterase
MarR family transcriptional regulator
MFS transporter
50S rRNA methyltransferase
hypothetical protein
pseudouridine synthase
chemotaxis protein CheV
4-hydroxy-3-methylbut-2-enyl diphosphate reductase
dihydrouridine synthase
chemotaxis protein CheA
membrane protein
tol-pal system protein YbgF
DNA processing protein DprA
phenylalanyl-tRNA synthetase subunit alpha
MULTISPECIES: 50S ribosomal protein L20
MULTISPECIES: 50S ribosomal protein L35
MULTISPECIES: translation initiation factor IF-3
threonyl-tRNA synthetase
RNA 2'-O ribose methyltransferase substrate binding family protein
flagellar biosynthesis protein FliQ
flagellar biosynthesis protein FliP
flagellar biosynthesis protein FliO
flagellar motor switch protein FliN
flagellar basal body protein FliL
flagellar motor protein MotB

peptidase U32
MULTISPECIES: dihydroorotate dehydrogenase
diguanylate cyclase
1-pyrroline-5-carboxylate dehydrogenase
zinc resistance protein
histidine kinase
hydantoin utilization protein A
hydrogenase nickel incorporation protein HypA
hypothetical protein
hypothetical protein
mercury transporter
copper-translocating P-type ATPase
hypothetical protein
UTP-glucose-1-phosphate uridylyltransferase
3-octaprenyl-4-hydroxybenzoate carboxy-lyase
transcriptional regulator
permease
hypothetical protein
seryl-tRNA synthetase
hypothetical protein
amino acid decarboxylase
1-deoxy-D-xylulose 5-phosphate reductoisomerase
zinc metalloprotease
peptidase M22
flagellar hook protein FliD
flagellar biosynthesis protein FliS
glycosyl transferase
hypothetical protein
phosphoglyceromutase
Fis family transcriptional regulator
hisitdine kinase
epimerase family protein
hypothetical protein
DNA helicase
50S ribosomal protein L9
MULTISPECIES: 30S ribosomal protein S18
30S ribosomal protein S6
alanine racemase
organic solvent tolerance protein
7-cyano-7-deazaguanine reductase
amino acid dehydrogenase
hypothetical protein
amino acid ABC transporter substrate-binding protein
ABC transporter permease
amino acid ABC transporter ATPase
lysine transporter LysE
hypothetical protein

molybdenum cofactor biosynthesis protein
HD family phosphohydrolase
prenyltransferase
hypothetical protein
hypothetical protein
histidine kinase
nitrogen fixation protein NifB
nitrogenase
nitrogenase iron-molybdenum cofactor biosynthesis protein NifE
thio:disulfide interchange protein
hypothetical protein
TetR family transcriptional regulator
peptidase M24
CoA-binding protein
hypothetical protein
molecular chaperone DnaJ
molecular chaperone DnaJ
hypothetical protein
hypothetical protein
DEAD/DEAH box helicase
4Fe-4S ferredoxin
carbon starvation protein CstA
transcriptional regulator
chemotaxis protein CheY
aminopeptidase 1
alcohol dehydrogenase
AraC family transcriptional regulator
hypothetical protein
diguanylate cyclase
hypothetical protein
histidine kinase
excinuclease ABC subunit C
porin
porin
membrane protein
membrane protein
hypothetical protein
diguanylate cyclase domain protein
DNA-binding protein
AMP-binding protein
fumarate reductase
peptidoglycan-binding protein
translocation protein TolB
cell envelope biogenesis protein TonB
oxidoreductase
hypothetical protein
endonuclease IV

mercuric reductase
hypothetical protein
glucokinase
hypothetical protein
heterodisulfide reductase subunit E
heterodisulfide reductase subunit A
heterodisulfide reductase subunit A
adenine glycosylase
membrane protein
potassium transporter Kup
hypothetical protein
histidine kinase
transcriptional regulator
ABC transporter permease
ABC transporter
RND transporter
potassium-transporting ATPase subunit B
ATPase
kinase
histidine kinase
hexapeptide transferase
hypothetical protein
acetylneuraminic acid synthetase
DNA-directed RNA polymerase subunit beta'
transcriptional regulator
aconitate hydratase
peptidyl-prolyl cis-trans isomerase
acetolactate synthase
pilus biosynthesis protein PilZ
LOG family protein
heme biosynthesis protein HemY
DNA-3-methyladenine glycosylase
hypothetical protein
alcohol dehydrogenase
single-stranded DNA-binding protein
membrane protein
ribonuclease P
MULTISPECIES: 50S ribosomal protein L34
hydrolase
DNA-binding protein
chemotaxis protein CheD
glycosyl transferase
cation transporter
hypothetical protein
lactate utilization protein B/C
(Fe-S)-binding protein
Fe-S oxidoreductase

malonic semialdehyde reductase
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
competence protein ComEC
chemotaxis protein CheY
hypothetical protein
membrane protein
hypothetical protein
membrane protein
membrane protein
sulfate permease
hypothetical protein
dienelactone hydrolase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
helix-turn-helix family protein
transcriptional regulator, partial
hypothetical protein HMPREF0178_03453
methyltransferase type 11
hypothetical protein
HAD family hydrolase
hypothetical protein
UDP-glucose 4-epimerase
extracellular solute-binding protein family 3
multicopper oxidase
4Fe-4S binding domain protein

Gene ID	Length (aa)	Identity	e-value	Annotation
gene_id_1329	328	42.38	3.00E-73	hypothetical protein
gene_id_1330	201	31.34	5.00E-12	hypothetical protein
gene_id_1331	252	52.38	1.00E-75	hypothetical protein
gene_id_1333	368	33.97	1.00E-40	type III restriction enzyme res subunit family
gene_id_1334	253	62.85	3.00E-114	hypothetical protein CBDKU1_27920
gene_id_1335	510	74.9	0	GMP synthase
gene_id_1337	485	98.97	0	hypothetical protein
gene_id_1338	444	95.5	0	hypothetical protein
gene_id_1339	124	99.19	5.00E-81	hypothetical protein
gene_id_1340	350	97.43	0	hypothetical protein
gene_id_1341	161	98.14	4.00E-109	hypothetical protein
gene_id_1343	237	95.78	1.00E-164	hypothetical protein
gene_id_1344	249	97.19	2.00E-140	hypothetical protein
gene_id_1345	30	93.33	7.00E-09	hypothetical protein
gene_id_1346	343	95.92	0	hypothetical protein
gene_id_1347	659	99.24	0	hypothetical protein
gene_id_1349	103	96.12	3.00E-63	hypothetical protein
gene_id_1350	454	98.24	0	hypothetical protein
gene_id_1351	121	99.17	1.00E-81	hypothetical protein
gene_id_1352	171	98.83	3.00E-116	hypothetical protein
gene_id_1353	598	63.88	0	ABC transporter ATP-binding protein
gene_id_1354	602	97.51	0	hypothetical protein
gene_id_1355	349	97.71	0	hypothetical protein
gene_id_1356	188	98.4	1.00E-133	hypothetical protein
gene_id_1357	295	100	0	hypothetical protein
gene_id_1358	227	100	7.00E-151	hypothetical protein
gene_id_1359	375	99.2	0	hypothetical protein
gene_id_1360	338	96.75	0	hypothetical protein
gene_id_1361	80	100	4.00E-48	hypothetical protein
gene_id_1362	74	98.65	1.00E-43	hypothetical protein
gene_id_1363	212	92.45	9.00E-142	hypothetical protein
gene_id_1364	119	99.16	9.00E-81	dinitrogenase iron-molybdenum cofactor biosynthesi
gene_id_1365	94	87.23	1.00E-18	hypothetical protein
gene_id_1366	186	99.46	1.00E-132	GTP cyclohydrolase
gene_id_1367	270	98.52	0	dihydropteroate synthase
gene_id_1368	119	63.03	1.00E-47	dienelactone hydrolase
gene_id_1369	157	94.27	4.00E-103	hypothetical protein
gene_id_1370	158	97.47	1.00E-107	hypothetical protein
gene_id_1371	283	97.88	0	hypothetical protein
gene_id_1372	397	96.73	0	hypothetical protein
gene_id_1373	354	96.89	0	hypothetical protein
gene_id_1374	78	98.72	2.00E-48	hypothetical protein
gene_id_1375	77	97.4	4.00E-46	hypothetical protein, partial
gene_id_1376	172	93.6	9.00E-113	hypothetical protein, partial
gene_id_1377	165	94.55	3.00E-103	hypothetical protein, partial
gene_id_1378	157	95.54	1.00E-94	hypothetical protein

gene_id_1379	105	97.14	4.00E-62	hypothetical protein
gene_id_1380	198	97.47	2.00E-126	hypothetical protein
gene_id_1381	280	97.14	0	hypothetical protein
gene_id_1382	116	100	5.00E-65	hypothetical protein
gene_id_1383	635	96.85	0	chemotaxis protein
gene_id_1384	213	63.85	4.00E-98	hypothetical protein, partial
gene_id_1385	212	96.7	2.00E-150	peroxiredoxin, partial
gene_id_1386	118	79.66	1.00E-59	dinitrogenase iron-molybdenum cofactor biosynthesi
gene_id_1387	283	74.91	1.00E-148	ATPase
gene_id_1388	285	76.49	1.00E-156	ATPase
gene_id_1389	119	93.28	2.00E-58	hypothetical protein
gene_id_1390	516	96.51	0	hypothetical protein
gene_id_1391	294	96.6	0	hypothetical protein
gene_id_1392	141	49.65	4.00E-39	hypothetical protein
gene_id_1393	78	97.44	5.00E-46	hypothetical protein
gene_id_1394	250	99.6	0	hypothetical protein
gene_id_1395	177	97.18	4.00E-118	hypothetical protein
gene_id_1396	221	93.21	6.00E-145	hypothetical protein
gene_id_1397	139	94.24	6.00E-79	hypothetical protein
gene_id_1398	320	93.12	0	hypothetical protein
gene_id_1399	168	95.24	3.00E-94	hypothetical protein
gene_id_1400	87	98.85	1.00E-38	hypothetical protein
gene_id_1401	294	56.12	1.00E-92	exported hypothetical protein
gene_id_1402	150	95.33	2.00E-95	hypothetical protein
gene_id_1403	318	95.6	0	hypothetical protein
gene_id_1404	296	98.99	0	hypothetical protein
gene_id_1405	286	94.76	0	hypothetical protein
gene_id_1406	276	96.74	3.00E-161	hypothetical protein
gene_id_1407	249	95.58	9.00E-172	hypothetical protein
gene_id_1408	140	93.57	2.00E-87	hypothetical protein
gene_id_1409	235	97.87	2.00E-156	tRNA synthetase subunit beta
gene_id_1411	170	97.06	4.00E-96	hypothetical protein
gene_id_1412	170	98.24	2.00E-121	hypothetical protein
gene_id_1413	125	99.2	1.00E-80	hypothetical protein, partial
gene_id_1414	155	96.13	1.00E-100	hypothetical protein
gene_id_1415	178	98.88	3.00E-123	amidase
gene_id_1416	150	98	9.00E-91	peptide deformylase
gene_id_1417	202	98.51	9.00E-142	hypothetical protein
gene_id_1418	185	82.7	6.00E-111	NADPH-dependent FMN reductase
gene_id_1419	349	99.43	0	hypothetical protein
gene_id_1420	192	96.88	6.00E-129	hypothetical protein
gene_id_1421	126	92.86	4.00E-78	hypothetical protein
gene_id_1422	172	97.67	7.00E-104	phospholipid methyltransferase
gene_id_1423	159	98.11	1.00E-108	hypothetical protein, partial
gene_id_1424	187	97.33	6.00E-116	hypothetical protein
gene_id_1425	128	96.88	8.00E-88	glyoxalase
gene_id_1426	83	100	3.00E-54	hypothetical protein

gene_id_1427	60	98.33	2.00E-30	hypothetical protein
gene_id_1428	198	55.05	6.00E-61	hypothetical protein
gene_id_1429	229	100	3.00E-146	phosphohydrolase
gene_id_1431	128	95.31	3.00E-80	hypothetical protein
gene_id_1432	73	95.89	2.00E-25	hypothetical protein
gene_id_1433	128	96.09	6.00E-86	hypothetical protein
gene_id_1434	151	94.04	3.00E-87	hypothetical protein, partial
gene_id_1435	180	96.67	3.00E-123	GCN5 family acetyltransferase
gene_id_1436	303	96.37	2.00E-179	hypothetical protein
gene_id_1437	349	97.13	0	hypothetical protein
gene_id_1439	52	94.23	1.00E-24	hypothetical protein
gene_id_1440	153	92.81	2.00E-99	hypothetical protein
gene_id_1441	190	97.37	5.00E-131	hypothetical protein
gene_id_1442	165	87.88	6.00E-102	hypothetical protein
gene_id_1444	252	96.43	4.00E-169	methyltransferase
gene_id_1445	451	37.92	9.00E-104	hypothetical protein
gene_id_1446	89	59.55	4.00E-25	hypothetical protein
gene_id_1447	79	93.67	2.00E-27	hypothetical protein
gene_id_1448	276	96.38	0	hypothetical protein
gene_id_1449	185	98.38	3.00E-128	hypothetical protein
gene_id_1450	61	95.08	4.00E-19	hypothetical protein
gene_id_1451	189	96.83	6.00E-129	hypothetical protein
gene_id_1452	217	98.16	3.00E-151	hypothetical protein
gene_id_1453	151	98.01	2.00E-77	hypothetical protein
gene_id_1454	295	55.93	2.00E-109	hypothetical protein
gene_id_1455	73	98.63	1.00E-40	hypothetical protein
gene_id_1456	276	96.74	0	hypothetical protein
gene_id_1457	67	43.28	3.00E-12	hypothetical protein
gene_id_1458	168	48.21	5.00E-49	hypothetical protein
gene_id_1459	116	96.55	8.00E-73	tRNA-binding protein
gene_id_1460	70	75.71	3.00E-28	GNAT family acetyltransferase
gene_id_1461	213	38.97	1.00E-48	methyltransferase
gene_id_1462	174	56.9	3.00E-69	hypothetical protein
gene_id_1463	40	85	9.00E-14	hypothetical protein
gene_id_1464	175	94.29	5.00E-119	GCN5 family acetyltransferase
gene_id_1465	211	29.86	2.00E-21	Xre family transcriptional regulator
gene_id_1466	172	41.28	6.00E-34	hypothetical protein
gene_id_1467	165	96.36	5.00E-82	hypothetical protein
gene_id_1468	288	96.18	0	hypothetical protein
gene_id_1469	389	46.53	2.00E-85	hypothetical protein
gene_id_1470	111	100	5.00E-72	hypothetical protein
gene_id_1471	140	99.29	1.00E-99	hypothetical protein
gene_id_1472	202	97.03	1.00E-141	N-acetyltransferase GCN5
gene_id_1473	133	99.25	7.00E-89	hypothetical protein
gene_id_1474	59	89.83	3.00E-27	hypothetical protein
gene_id_1475	250	94.4	6.00E-167	hypothetical protein
gene_id_1476	150	94.67	6.00E-101	GNAT family acetyltransferase

gene_id_1477	156	69.87	2.00E-80	acetyltransferase
gene_id_1478	205	77.07	9.00E-96	hypothetical protein
gene_id_1479	210	56.67	8.00E-85	hypothetical protein
gene_id_1480	165	98.18	9.00E-116	hypothetical protein
gene_id_1481	50	100	4.00E-26	hypothetical protein
gene_id_1482	120	58.33	3.00E-26	hypothetical protein
gene_id_1483	315	92.7	0	hypothetical protein, partial
gene_id_1484	422	95.26	0	hypothetical protein, partial
gene_id_1485	662	98.64	0	chemotaxis protein
gene_id_1486	304	98.68	0	hypothetical protein
gene_id_1487	216	68.98	7.00E-111	hypothetical protein
gene_id_1490	92	34.78	7.00E-08	hypothetical protein
gene_id_1491	156	31.41	4.00E-08	MULTISPECIES: hypothetical protein
gene_id_2735	307	100	0	hypothetical protein
gene_id_2736	217	99.54	1.00E-150	branched-chain amino acid dehydrogenase
gene_id_2737	217	99.08	3.00E-152	hypothetical protein
gene_id_2738	224	98.66	1.00E-147	hypothetical protein
gene_id_2739	464	98.92	0	hypothetical protein
gene_id_2740	348	97.99	0	hypothetical protein
gene_id_2741	205	96.59	2.00E-144	hypothetical protein
gene_id_2742	252	99.21	1.00E-179	imidazole glycerol phosphate synthase
gene_id_2743	238	97.48	9.00E-156	hypothetical protein
gene_id_2744	201	98.51	5.00E-123	imidazole glycerol phosphate synthase
gene_id_2745	192	96.35	1.00E-130	hypothetical protein
gene_id_2746	344	95.93	0	hypothetical protein
gene_id_2747	427	98.13	0	hypothetical protein
gene_id_2748	213	99.06	4.00E-129	hypothetical protein
gene_id_2749	315	99.05	0	hypothetical protein
gene_id_2750	269	98.14	8.00E-157	hypothetical protein
gene_id_2751	301	97.34	0	hypothetical protein
gene_id_2752	239	98.33	5.00E-122	cytochrome C biogenesis protein, partial
gene_id_2753	151	99.34	4.00E-106	hypothetical protein
gene_id_2754	283	99.29	0	hypothetical protein
gene_id_2755	109	98.17	6.00E-72	hypothetical protein
gene_id_2756	176	95.45	6.00E-116	hypothetical protein
gene_id_2757	225	98.22	8.00E-122	hypothetical protein
gene_id_2758	127	97.64	5.00E-79	hypothetical protein
gene_id_2759	440	98.41	0	hypothetical protein
gene_id_2760	122	99.18	8.00E-83	lactoylglutathione lyase
gene_id_2761	903	99.56	0	hypothetical protein, partial
gene_id_2762	253	99.6	0	hypothetical protein
gene_id_2763	75	96	2.00E-41	hypothetical protein, partial
gene_id_2764	104	100	5.00E-64	hypothetical protein
gene_id_2765	611	99.35	0	DNA gyrase subunit A
gene_id_2766	633	70.46	0	DNA gyrase subunit B
gene_id_2767	368	46.74	9.00E-92	DNA recombination and repair protein RecF
gene_id_2768	72	100	7.00E-41	hypothetical protein

gene_id_2769	366	99.45	0	DNA polymerase III subunit beta
gene_id_2770	445	99.33	0	chromosomal replication initiator protein DnaA
gene_id_2771	44	100	6.00E-13	50S ribosomal protein L34
gene_id_2772	113	100	2.00E-55	hypothetical protein
gene_id_2773	260	99.62	0	hypothetical protein
gene_id_2774	208	100	2.00E-112	hypothetical protein
gene_id_2775	459	97.17	0	hypothetical protein
gene_id_2776	638	98.59	0	hypothetical protein
gene_id_2777	233	98.71	6.00E-149	16S rRNA methyltransferase
gene_id_2778	262	99.24	1.00E-141	hypothetical protein
gene_id_2779	253	99.6	2.00E-179	hypothetical protein
gene_id_2780	281	98.93	0	hypothetical protein
gene_id_2781	161	99.38	1.00E-112	NADH dehydrogenase
gene_id_2782	107	99.07	5.00E-70	hypothetical protein
gene_id_2783	596	99.83	0	NADH dehydrogenase
gene_id_2784	584	65.41	0	periplasmic
gene_id_2785	217	50.69	5.00E-71	hypothetical protein
gene_id_2786	414	94.93	0	dihydroorotase
gene_id_2787	379	97.89	0	hypothetical protein
gene_id_2788	356	96.91	0	hypothetical protein
gene_id_2789	221	100	2.00E-138	hypothetical protein
gene_id_2790	202	97.03	3.00E-135	hypothetical protein
gene_id_2791	73	98.63	2.00E-45	hypothetical protein
gene_id_2792	308	99.68	0	aspartate carbamoyltransferase
gene_id_2793	141	99.29	9.00E-74	hypothetical protein
gene_id_2794	287	97.21	0	hypothetical protein
gene_id_2795	227	96.04	1.00E-157	hypothetical protein
gene_id_2796	300	98	0	hypothetical protein
gene_id_2797	187	97.86	1.00E-119	hypothetical protein
gene_id_2798	25	100	5.00E-09	hypothetical protein
gene_id_2799	765	93.99	0	hypothetical protein
gene_id_5622	408	97.55	0	arginine deiminase
gene_id_5623	331	98.49	0	ornithine carbamoyltransferase
gene_id_5624	312	97.44	0	carbamate kinase
gene_id_5626	389	97.43	0	ornithine-oxoacid aminotransferase
gene_id_5627	1410	99.08	0	2-hydroxyglutaryl-CoA dehydratase, partial
gene_id_5628	367	99.46	0	hypothetical protein
gene_id_5629	293	98.98	0	ABC transporter permease
gene_id_5630	294	99.66	6.00E-167	hypothetical protein
gene_id_5631	241	97.93	2.00E-150	hypothetical protein
gene_id_5632	239	99.58	1.00E-167	amino acid ABC transporter ATPase
gene_id_5633	229	96.51	4.00E-133	hypothetical protein
gene_id_5634	116	100	2.00E-76	hypothetical protein
gene_id_5753	73	97.26	4.00E-39	hypothetical protein
gene_id_5754	196	92.35	1.00E-127	hypothetical protein
gene_id_5755	234	97.01	2.00E-137	hypothetical protein
gene_id_5756	187	97.33	3.00E-128	hypothetical protein

gene_id_5757	353	95.75	0	hypothetical protein
gene_id_5758	164	98.17	1.00E-112	hypothetical protein
gene_id_5759	421	98.57	0	3-isopropylmalate dehydratase large subunit
gene_id_5760	507	98.62	0	hypothetical protein
gene_id_5761	457	98.25	0	hypothetical protein
gene_id_5762	389	97.43	0	hypothetical protein
gene_id_5763	391	96.16	0	hypothetical protein
gene_id_5764	428	98.13	0	hypothetical protein
gene_id_5765	406	99.01	0	hypothetical protein, partial
gene_id_5766	577	97.92	0	hypothetical protein
gene_id_5767	317	99.37	0	hypothetical protein
gene_id_5768	665	99.4	0	hypothetical protein
gene_id_5769	76	98.68	1.00E-42	50S ribosomal protein L9
gene_id_5770	440	99.77	0	DNA helicase
gene_id_5771	515	99.03	0	hypothetical protein
gene_id_5772	531	74.2	0	CTP synthase
gene_id_5773	386	95.85	0	hypothetical protein
gene_id_5774	215	42.33	7.00E-54	hypothetical protein
gene_id_5776	466	98.93	0	hypothetical protein
gene_id_5777	296	98.99	0	hypothetical protein
gene_id_5778	230	99.57	2.00E-161	hypothetical protein
gene_id_5779	80	98.75	6.00E-51	hypothetical protein
gene_id_5780	274	100	0	hypothetical protein
gene_id_5781	287	97.91	0	hypothetical protein
gene_id_5782	255	96.86	2.00E-166	hypothetical protein, partial
gene_id_5783	340	98.24	0	hypothetical protein
gene_id_5784	637	96.39	0	sulfatase, partial
gene_id_5785	289	97.92	0	hypothetical protein
gene_id_5786	74	100	3.00E-32	hypothetical protein
gene_id_5787	350	98.29	0	hypothetical protein
gene_id_5788	61	100	2.00E-34	hypothetical protein
gene_id_5789	297	97.64	0	hypothetical protein
gene_id_5790	742	98.25	0	hypothetical protein
gene_id_5791	221	97.29	1.00E-155	hypothetical protein
gene_id_5792	453	99.56	0	hypothetical protein
gene_id_5793	157	98.73	2.00E-109	EBSC protein
gene_id_5794	250	98	2.00E-176	thiamine biosynthesis protein ThiF
gene_id_5795	338	97.93	0	hypothetical protein
gene_id_5796	220	99.55	7.00E-125	hypothetical protein
gene_id_5797	243	97.12	1.00E-160	metal ABC transporter substrate-binding protein
gene_id_5798	461	99.35	0	hypothetical protein
gene_id_5799	327	97.25	0	hypothetical protein
gene_id_5800	264	97.35	0	hypothetical protein
gene_id_5801	232	99.57	2.00E-155	hypothetical protein
gene_id_5802	449	95.77	0	hypothetical protein
gene_id_5803	386	87.05	0	hypothetical protein
gene_id_5804	453	99.56	0	hypothetical protein

gene_id_5805	386	98.7	0	hypothetical protein
gene_id_5806	430	97.21	0	hypothetical protein, partial
gene_id_5807	428	96.26	0	metal-dependent phosphohydrolase, partial
gene_id_5808	185	98.38	1.00E-132	NADPH-dependent FMN reductase
gene_id_5809	290	99.31	0	hypothetical protein
gene_id_5810	157	95.54	1.00E-71	hypothetical protein
gene_id_5811	267	93.26	1.00E-157	hypothetical protein
gene_id_5812	637	98.27	0	carbon monoxide dehydrogenase
gene_id_5813	176	98.86	5.00E-113	hypothetical protein
gene_id_5814	346	92.2	0	hypothetical protein
gene_id_5815	455	96.92	0	radical SAM protein
gene_id_5816	404	96.53	0	hypothetical protein
gene_id_5818	340	98.53	0	hypothetical protein
gene_id_5819	311	97.75	0	hypothetical protein
gene_id_5820	296	97.3	0	hypothetical protein
gene_id_5821	263	98.1	0	hypothetical protein
gene_id_5822	72	97.22	3.00E-42	hypothetical protein
gene_id_5823	319	95.92	0	hypothetical protein
gene_id_5824	242	95.45	3.00E-172	hypothetical protein
gene_id_5825	572	97.2	0	hypothetical protein
gene_id_5826	123	93.5	2.00E-77	hypothetical protein
gene_id_5828	503	97.22	0	hypothetical protein
gene_id_5829	318	99.37	0	hypothetical protein
gene_id_5830	273	100	0	hypothetical protein
gene_id_5831	319	97.18	0	hypothetical protein
gene_id_5832	268	98.88	5.00E-171	hypothetical protein
gene_id_5833	249	97.99	4.00E-178	hypothetical protein
gene_id_5834	509	99.02	0	hypothetical protein
gene_id_5835	1042	99.81	0	isoleucyl-tRNA synthetase
gene_id_5836	250	95.6	4.00E-174	hypothetical protein
gene_id_5837	565	98.58	0	phosphoenolpyruvate-protein phosphotransferase, p
gene_id_5838	193	97.41	2.00E-137	hypothetical protein
gene_id_5839	167	99.4	4.00E-118	hypothetical protein
gene_id_5840	448	96.88	0	hypothetical protein
gene_id_5841	230	54.78	5.00E-80	hypothetical protein
gene_id_5842	358	36.03	8.00E-73	Antirestriction protein (ArdA)
gene_id_5843	95	70.53	7.00E-39	hypothetical protein
gene_id_5844	116	62.07	6.00E-44	hypothetical protein
gene_id_5845	271	83.39	2.00E-166	DNA methyltransferase
gene_id_5846	165	65.45	4.00E-72	hypothetical protein
gene_id_5847	185	61.08	5.00E-81	hypothetical protein
gene_id_5848	74	75.68	4.00E-18	hypothetical protein
gene_id_5849	102	76.47	3.00E-52	SpoVG family protein
gene_id_5850	1136	56.95	0	S-layer protein
gene_id_5850	376	72.34	1.00E-148	S-layer protein
gene_id_5851	133	54.14	2.00E-30	hypothetical protein
gene_id_5852	261	73.18	7.00E-138	pilus assembly protein CpaB

gene_id_5853	270	81.11	2.00E-150	ATPase AAA
gene_id_5854	515	80.78	0	type II secretion system protein E
gene_id_5855	309	78.64	6.00E-160	membrane protein
gene_id_5856	290	72.76	1.00E-134	secretion protein F
gene_id_5857	127	82.68	3.00E-73	hypothetical protein
gene_id_5858	52	75	3.00E-21	hypothetical protein
gene_id_5859	117	68.38	6.00E-54	hypothetical protein
gene_id_5860	189	46.56	6.00E-42	hypothetical protein
gene_id_5861	563	73.18	0	hypothetical protein
gene_id_5862	111	84.68	1.00E-60	MULTISPECIES: hypothetical protein
gene_id_5863	300	85.33	5.00E-179	hypothetical protein
gene_id_5864	101	64.36	5.00E-45	hypothetical protein
gene_id_5865	83	83.13	7.00E-43	C-5 cytosine-specific DNA methylase
gene_id_8266	65	100	1.00E-38	hypothetical protein
gene_id_8267	718	99.58	0	hypothetical protein
gene_id_8268	125	100	4.00E-82	aldehyde:ferredoxin oxidoreductase, partial
gene_id_8269	292	98.29	0	hypothetical protein
gene_id_8270	224	97.77	3.00E-159	hypothetical protein, partial
gene_id_8271	51	72.55	3.00E-16	hypothetical protein
gene_id_8272	147	97.28	4.00E-99	hypothetical protein
gene_id_8273	649	99.54	0	C4-dicarboxylate ABC transporter permease
gene_id_8274	164	98.17	1.00E-110	hypothetical protein
gene_id_8275	329	97.87	0	C4-dicarboxylate ABC transporter substrate-binding p
gene_id_8276	254	98.43	5.00E-147	hypothetical protein
gene_id_8277	186	90.86	1.00E-111	hypothetical protein
gene_id_8278	262	98.47	1.00E-170	hypothetical protein
gene_id_8279	233	96.57	3.00E-141	hypothetical protein
gene_id_8280	98	95.92	2.00E-49	hypothetical protein
gene_id_8281	241	98.76	1.00E-157	hypothetical protein
gene_id_8282	241	94.61	2.00E-162	hypothetical protein, partial
gene_id_8283	426	98.59	0	glutamate-1-semialdehyde 2,1-aminomutase
gene_id_8284	321	98.75	0	hypothetical protein
gene_id_8285	498	97.39	0	hypothetical protein
gene_id_8286	306	99.67	0	hypothetical protein
gene_id_8287	209	95.22	2.00E-121	hypothetical protein
gene_id_8288	412	97.09	0	hypothetical protein
gene_id_8289	247	99.19	2.00E-175	hypothetical protein
gene_id_8290	88	100	2.00E-53	hypothetical protein
gene_id_8291	331	99.4	0	hypothetical protein
gene_id_8292	141	100	2.00E-98	hypothetical protein
gene_id_8293	383	99.48	0	hypothetical protein
gene_id_8294	473	98.73	0	hypothetical protein
gene_id_8295	389	96.92	0	hypothetical protein
gene_id_8296	543	98.71	0	hypothetical protein
gene_id_8297	248	97.58	4.00E-161	hypothetical protein
gene_id_8298	337	98.81	0	hypothetical protein
gene_id_8299	369	97.02	0	hypothetical protein

gene_id_8300	123	98.37	6.00E-82	molybdopterin biosynthesis protein
gene_id_8301	712	96.49	0	hypothetical protein
gene_id_8302	137	96.35	6.00E-91	hypothetical protein
gene_id_8303	273	98.53	0	hypothetical protein
gene_id_8304	124	97.58	1.00E-80	hypothetical protein
gene_id_8305	341	97.65	0	hypothetical protein
gene_id_8306	321	96.88	0	hypothetical protein
gene_id_8307	322	99.69	0	hypothetical protein
gene_id_8308	410	96.34	0	hypothetical protein
gene_id_8309	148	99.32	4.00E-101	hypothetical protein
gene_id_8310	89	100	1.00E-44	hypothetical protein
gene_id_8311	501	100	0	hypothetical protein
gene_id_8312	672	99.11	0	hypothetical protein
gene_id_8313	457	99.56	0	hypothetical protein, partial
gene_id_8314	284	99.65	0	hypothetical protein
gene_id_8315	282	99.65	0	hypothetical protein
gene_id_8316	326	99.69	0	hypothetical protein
gene_id_8317	326	99.69	0	ABC transporter
gene_id_8318	539	100	0	hypothetical protein
gene_id_8319	340	98.24	0	hypothetical protein
gene_id_8321	469	98.51	0	hypothetical protein
gene_id_8322	379	99.74	0	hypothetical protein
gene_id_8323	372	99.46	0	hypothetical protein
gene_id_8324	284	100	0	hypothetical protein
gene_id_8325	162	100	4.00E-112	hypothetical protein
gene_id_8326	784	99.87	0	hypothetical protein
gene_id_8327	134	100	1.00E-90	hypothetical protein
gene_id_8328	219	96.8	1.00E-149	hypothetical protein
gene_id_8329	177	98.87	1.00E-100	hypothetical protein
gene_id_8330	268	92.91	0	hypothetical protein
gene_id_8331	361	93.63	0	hypothetical protein
gene_id_8332	344	98.26	0	hypothetical protein
gene_id_8333	963	96.16	0	hypothetical protein, partial
gene_id_8334	378	98.15	0	hypothetical protein
gene_id_8335	108	97.22	4.00E-33	hypothetical protein
gene_id_8336	139	100	8.00E-82	hypothetical protein
gene_id_8337	324	99.07	0	hypothetical protein
gene_id_8338	245	97.55	6.00E-173	hypothetical protein
gene_id_8339	412	98.54	0	sodium:dicarboxylate symporter
gene_id_8340	416	97.84	0	hypothetical protein
gene_id_8341	379	94.72	0	hypothetical protein
gene_id_8342	352	99.72	0	hypothetical protein
gene_id_8343	193	97.41	6.00E-110	co-chaperone GrpE
gene_id_8344	616	99.51	0	chaperone protein DnaK
gene_id_8345	382	99.48	0	hypothetical protein
gene_id_8346	125	99.2	4.00E-85	3-aminobutyryl-CoA ammonia lyase
gene_id_8347	546	65.2	0	type II secretion system protein E

gene_id_8348	349	68.77	4.00E-176	twitching motility protein PilT
gene_id_8349	398	55.53	9.00E-140	Type II secretion system protein
gene_id_8351	142	35.92	4.00E-10	exported protein of unknown function
gene_id_8352	489	29.45	2.00E-35	exported protein of unknown function
gene_id_8354	196	52.55	1.00E-52	peptidase A24
gene_id_8355	351	37.04	4.00E-70	hypothetical protein
gene_id_8356	192	39.58	2.00E-35	hypothetical protein
gene_id_8357	446	39.24	7.00E-103	putative Peptidoglycan-binding LysM
gene_id_8358	489	33.95	5.00E-91	hypothetical protein
gene_id_8358	158	35.44	3.00E-19	hypothetical protein
gene_id_8359	558	85.66	0	hypothetical protein
gene_id_8360	403	81.39	0	hypothetical protein
gene_id_8361	501	67.66	0	hypothetical protein
gene_id_8362	191	69.11	8.00E-82	hypothetical protein
gene_id_8363	131	67.18	1.00E-55	hypothetical protein
gene_id_8364	182	76.37	1.00E-92	hypothetical protein
gene_id_8365	182	80.77	2.00E-101	hypothetical protein
gene_id_8366	143	91.61	3.00E-67	hypothetical protein
gene_id_8367	185	98.38	2.00E-130	hypothetical protein
gene_id_8368	116	92.24	4.00E-45	hypothetical protein
gene_id_8369	257	92.22	6.00E-177	hypothetical protein
gene_id_8370	140	95.71	2.00E-84	hypothetical protein
gene_id_8371	625	95.2	0	hypothetical protein
gene_id_8372	48	100	4.00E-25	hypothetical protein
gene_id_8373	480	58.13	0	MULTISPECIES: arginine utilization regulatory protein
gene_id_8374	387	99.74	0	alanine dehydrogenase
gene_id_8375	469	99.57	0	transporter
gene_id_8376	199	95.98	3.00E-132	hypothetical protein
gene_id_8377	532	97.74	0	hypothetical protein
gene_id_8378	407	99.02	0	hypothetical protein
gene_id_8379	195	99.49	1.00E-101	hypothetical protein
gene_id_8380	102	99.02	2.00E-65	hypothetical protein
gene_id_8381	97	97.94	8.00E-62	hypothetical protein
gene_id_8382	75	96	7.00E-29	hypothetical protein
gene_id_8382	26	84.62	1.00E-06	hypothetical protein
gene_id_8383	119	98.32	2.00E-77	ArsR family transcriptional regulator
gene_id_8384	73	94.52	2.00E-40	hypothetical protein
gene_id_8385	613	98.37	0	zinc ABC transporter ATPase
gene_id_8386	301	99	0	phosphate acetyl/butyryl transferase
gene_id_8387	652	98.62	0	hypothetical protein
gene_id_8388	594	98.15	0	indole pyruvate ferredoxin/flavodoxin oxidoreductas
gene_id_8389	189	95.77	1.00E-125	indolepyruvate oxidoreductase
gene_id_8390	354	97.74	0	hypothetical protein
gene_id_8391	295	97.63	0	hypothetical protein
gene_id_8392	198	97.98	3.00E-139	hypothetical protein
gene_id_8393	184	93.48	4.00E-124	hypothetical protein
gene_id_8394	229	99.56	1.00E-161	hypothetical protein

gene_id_8395	420	98.57	0	hypothetical protein
gene_id_8396	245	90.2	1.00E-156	hypothetical protein
gene_id_8397	194	93.3	4.00E-120	hypothetical protein
gene_id_8398	268	97.01	0	hypothetical protein
gene_id_8399	283	99.65	0	hypothetical protein
gene_id_8400	461	98.92	0	hypothetical protein
gene_id_8401	289	98.62	0	hypothetical protein
gene_id_8402	277	99.64	0	hypothetical protein
gene_id_8403	347	98.27	0	hypothetical protein
gene_id_8404	313	96.49	0	hypothetical protein
gene_id_8405	365	96.71	0	hypothetical protein
gene_id_8406	312	97.76	0	hypothetical protein
gene_id_8407	252	96.83	2.00E-174	hypothetical protein
gene_id_8408	385	94.29	0	hypothetical protein
gene_id_8409	763	98.03	0	hypothetical protein
gene_id_8410	157	98.09	6.00E-107	(2Fe-2S)-binding protein
gene_id_8411	263	95.06	0	hypothetical protein
gene_id_8412	164	99.39	2.00E-101	rubrerythrin
gene_id_8413	121	99.17	6.00E-82	hypothetical protein
gene_id_8414	284	99.3	0	hypothetical protein
gene_id_8415	329	97.26	0	hypothetical protein
gene_id_8416	229	95.2	4.00E-151	hypothetical protein
gene_id_8417	353	75.64	0	oxidoreductase
gene_id_8418	158	68.99	1.00E-72	hypothetical protein
gene_id_8419	490	97.76	0	hypothetical protein
gene_id_8420	68	100	3.00E-40	XRE family transcriptional regulator
gene_id_8421	99	98.99	2.00E-60	hypothetical protein, partial
gene_id_8422	259	92.28	2.00E-164	hypothetical protein
gene_id_8423	294	92.52	1.00E-165	hypothetical protein
gene_id_8424	305	94.75	0	hypothetical protein
gene_id_8425	311	95.5	0	hypothetical protein
gene_id_8426	295	96.95	0	hypothetical protein
gene_id_8427	339	61.06	4.00E-88	MULTISPECIES: cobalamin biosynthesis protein CbiM
gene_id_8428	268	94.4	2.00E-173	hypothetical protein
gene_id_8429	249	98.39	1.00E-176	hypothetical protein
gene_id_8430	270	97.41	0	hypothetical protein
gene_id_8431	247	97.57	1.00E-175	1-(5-phosphoribosyl)-5-amino-4-imidazole-carboxyla
gene_id_8432	301	94.02	2.00E-174	hypothetical protein, partial
gene_id_8432	61	96.72	4.00E-29	hypothetical protein, partial
gene_id_8434	325	96.62	0	hypothetical protein
gene_id_8435	153	70.59	2.00E-64	hypothetical protein
gene_id_8436	223	95.52	8.00E-150	hypothetical protein
gene_id_8437	45	97.78	1.00E-16	hypothetical protein
gene_id_8438	565	96.64	0	hypothetical protein
gene_id_8439	109	96.33	3.00E-68	tRNA-binding protein
gene_id_8440	193	98.45	2.00E-134	hypothetical protein, partial
gene_id_8441	395	97.22	0	hypothetical protein

gene_id_8442	494	99.6	0	hypothetical protein
gene_id_8443	88	97.73	4.00E-54	hypothetical protein, partial
gene_id_8444	175	99.43	3.00E-124	hypothetical protein, partial
gene_id_8445	173	97.11	1.00E-120	hypothetical protein
gene_id_8446	155	98.06	3.00E-87	hypothetical protein
gene_id_8447	343	63.56	6.00E-137	Appr-1-p processing protein
gene_id_8448	216	57.87	5.00E-84	hypothetical protein EAL2_808p00320
gene_id_8449	498	95.58	0	hypothetical protein, partial
gene_id_8450	163	87.12	2.00E-101	hypothetical protein
gene_id_8451	639	97.18	0	hypothetical protein
gene_id_8452	100	100	7.00E-64	hypothetical protein
gene_id_8453	111	95.5	2.00E-69	hypothetical protein
gene_id_8454	333	99.7	0	acetoin:2,6-dichlorophenolindophenol oxidoreducta
gene_id_8455	323	99.38	0	hypothetical protein
gene_id_8456	329	69.3	5.00E-148	hypothetical protein
gene_id_8457	430	96.05	0	hypothetical protein
gene_id_8458	462	97.84	0	hypothetical protein
gene_id_8459	333	98.8	0	hypothetical protein
gene_id_8460	229	97.38	4.00E-146	hypothetical protein
gene_id_8461	207	96.62	4.00E-143	hypothetical protein
gene_id_8462	68	98.53	1.00E-40	4Fe-4S ferredoxin
gene_id_8463	137	98.54	7.00E-91	hypothetical protein
gene_id_8464	132	94.7	4.00E-71	hypothetical protein
gene_id_8465	316	96.52	0	hypothetical protein
gene_id_8466	422	99.76	0	O-acetylhomoserine aminocarboxypropyltransferase
gene_id_8467	162	96.91	2.00E-107	hypothetical protein
gene_id_8468	115	100	1.00E-73	hypothetical protein
gene_id_8470	630	58.57	0	hypothetical protein
gene_id_8471	284	97.89	0	hypothetical protein
gene_id_8472	43	65.12	2.00E-09	peroxiredoxin
gene_id_8473	67	70.15	1.00E-25	peroxiredoxin
gene_id_8474	478	64.23	0	amidohydrolase
gene_id_8475	240	77.92	3.00E-130	peptide ABC transporter ATP-binding protein
gene_id_8476	205	100	3.00E-120	hypothetical protein
gene_id_8477	252	63.49	9.00E-111	MULTISPECIES: hypothetical protein
gene_id_8479	151	96.03	5.00E-98	hypothetical protein, partial
gene_id_8480	474	96.62	0	hypothetical protein, partial
gene_id_8481	174	96.55	3.00E-120	hypothetical protein
gene_id_8482	236	96.61	1.00E-148	hypothetical protein
gene_id_8483	205	94.63	2.00E-95	hypothetical protein
gene_id_8484	369	97.83	0	RNA helicase
gene_id_8485	279	95.34	2.00E-156	hypothetical protein
gene_id_8486	260	95.77	2.00E-175	spermidine/putrescine ABC transporter ATP-binding
gene_id_8487	344	90.99	0	hypothetical protein
gene_id_8488	336	97.32	0	hypothetical protein
gene_id_8489	570	93.51	0	hypothetical protein
gene_id_8490	437	92.68	0	hypothetical protein

gene_id_8491	162	98.77	1.00E-109	hypothetical protein, partial
gene_id_8492	135	96.3	1.00E-88	hypothetical protein
gene_id_8493	261	98.85	2.00E-171	membrane protein
gene_id_8494	212	98.58	1.00E-143	hypothetical protein
gene_id_8495	172	96.51	3.00E-120	hypothetical protein
gene_id_8496	297	95.29	0	hypothetical protein
gene_id_8497	447	98.88	0	hypothetical protein
gene_id_8498	132	100	2.00E-89	hypothetical protein
gene_id_8499	69	95.65	2.00E-38	hypothetical protein
gene_id_8500	179	99.44	5.00E-116	hypothetical protein
gene_id_8501	326	97.24	0	hypothetical protein
gene_id_8502	441	95.69	0	hypothetical protein
gene_id_8503	332	99.7	0	hypothetical protein
gene_id_8504	376	81.91	0	putative chlorophyll synthesis pathway protein BchC
gene_id_8505	412	94.17	0	hypothetical protein
gene_id_8506	553	86.8	0	hypothetical protein
gene_id_8507	434	93.32	0	hypothetical protein
gene_id_8508	196	96.43	8.00E-133	hypothetical protein
gene_id_8509	155	99.35	1.00E-108	hypothetical protein
gene_id_8671	406	97.78	0	hypothetical protein
gene_id_8672	516	98.64	0	hypothetical protein
gene_id_8673	478	97.91	0	hypothetical protein, partial
gene_id_8674	75	98.67	2.00E-44	hypothetical protein
gene_id_8675	59	100	5.00E-33	hypothetical protein
gene_id_8676	435	62.99	0	D-serine ammonia-lyase
gene_id_8677	419	98.09	0	histidyl-tRNA synthetase
gene_id_8678	134	99.25	3.00E-87	hypothetical protein
gene_id_8679	140	99.29	8.00E-89	hypothetical protein
gene_id_8680	462	97.62	0	hypothetical protein, partial
gene_id_8681	88	93.18	1.00E-48	hypothetical protein
gene_id_8682	171	94.74	2.00E-114	hypothetical protein
gene_id_8683	230	100	2.00E-151	hypothetical protein
gene_id_8684	683	97.8	0	hypothetical protein
gene_id_8685	417	99.28	0	hypothetical protein
gene_id_8686	201	98.51	3.00E-136	hypothetical protein
gene_id_8687	241	98.34	7.00E-144	hypothetical protein
gene_id_8688	260	97.69	0	hypothetical protein
gene_id_8689	126	65.08	2.00E-51	S-layer homology domain ribonuclease (modular pro
gene_id_8690	83	46.99	2.00E-12	barstar
gene_id_8691	389	97.69	0	hypothetical protein
gene_id_8692	194	98.45	1.00E-128	hypothetical protein
gene_id_8887	259	92.66	5.00E-163	MULTISPECIES: hypothetical protein
gene_id_8888	632	97.94	0	MULTISPECIES: hypothetical protein
gene_id_8889	287	96.52	0	MULTISPECIES: AraC family transcriptional regulator
gene_id_8890	326	100	0	MULTISPECIES: hypothetical protein, partial
gene_id_8891	195	98.46	5.00E-140	MULTISPECIES: cupin
gene_id_8892	408	98.53	0	MULTISPECIES: hypothetical protein

gene_id_8893	203	99.01	1.00E-126	MULTISPECIES: hypothetical protein
gene_id_8894	314	99.36	0	MULTISPECIES: hypothetical protein
gene_id_8895	117	100	5.00E-78	MULTISPECIES: hypothetical protein
gene_id_8896	65	100	2.00E-35	MULTISPECIES: stage III sporulation protein AC
gene_id_8897	129	100	2.00E-80	MULTISPECIES: hypothetical protein
gene_id_8898	358	99.16	0	MULTISPECIES: hypothetical protein
gene_id_8899	97	100	2.00E-61	MULTISPECIES: hypothetical protein
gene_id_8900	187	98.93	6.00E-112	MULTISPECIES: hypothetical protein
gene_id_8901	245	100	4.00E-140	MULTISPECIES: hypothetical protein
gene_id_8902	132	100	7.00E-76	MULTISPECIES: alkaline-shock protein
gene_id_8903	133	99.25	2.00E-76	MULTISPECIES: hypothetical protein
gene_id_8904	322	95.96	0	MULTISPECIES: hypothetical protein
gene_id_8905	397	97.48	0	MULTISPECIES: hypothetical protein
gene_id_8906	66	98.48	8.00E-37	MULTISPECIES: hypothetical protein
gene_id_8907	263	97.72	0	MULTISPECIES: RNA methyltransferase
gene_id_8908	150	100	8.00E-102	MULTISPECIES: arginine repressor ArgR
gene_id_8909	555	98.38	0	MULTISPECIES: hypothetical protein
gene_id_8910	360	100	0	MULTISPECIES: stage IV sporulation protein FB
gene_id_8911	264	99.62	1.00E-178	MULTISPECIES: chemotaxis protein CheY
gene_id_8912	175	98.86	2.00E-120	MULTISPECIES: ADP-ribose pyrophosphatase
gene_id_8913	175	100	2.00E-69	MULTISPECIES: hypothetical protein
gene_id_8914	291	98.97	0	MULTISPECIES: hypothetical protein
gene_id_8915	390	98.21	0	MULTISPECIES: phosphopentomutase
gene_id_8916	385	98.7	0	MULTISPECIES: D-Ala-D-Ala carboxypeptidase
gene_id_8917	239	100	8.00E-167	MULTISPECIES: hypothetical protein
gene_id_8918	167	100	2.00E-117	MULTISPECIES: Segregation and condensation protei
gene_id_8919	131	96.95	8.00E-85	hypothetical protein
gene_id_8920	126	100	1.00E-81	MULTISPECIES: hypothetical protein
gene_id_8921	340	97.65	0	MULTISPECIES: hypothetical protein
gene_id_8922	240	95	2.00E-151	MULTISPECIES: RNA pseudouridine synthase
gene_id_8923	191	100	8.00E-136	MULTISPECIES: hypothetical protein
gene_id_8924	67	100	1.00E-40	MULTISPECIES: hypothetical protein
gene_id_8925	378	98.94	0	MULTISPECIES: hypothetical protein
gene_id_8926	274	99.64	0	MULTISPECIES: hypothetical protein
gene_id_8927	179	99.44	2.00E-112	MULTISPECIES: hypothetical protein
gene_id_8928	290	100	0	MULTISPECIES: hypothetical protein
gene_id_8929	216	96.76	4.00E-145	cytidylate kinase
gene_id_8930	201	98.51	1.00E-128	MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltr
gene_id_8931	644	99.07	0	MULTISPECIES: hypothetical protein, partial
gene_id_8931	318	25.16	2.00E-21	MULTISPECIES: hypothetical protein, partial
gene_id_8932	346	98.55	0	MULTISPECIES: peptidase M42
gene_id_8933	337	95.25	0	MULTISPECIES: aminopeptidase
gene_id_8934	329	98.48	0	MULTISPECIES: aminopeptidase
gene_id_8935	159	89.94	7.00E-101	MULTISPECIES: hypothetical protein
gene_id_8936	66	95.45	7.00E-37	MULTISPECIES: hypothetical protein
gene_id_8937	245	92.65	1.00E-158	MULTISPECIES: hypothetical protein
gene_id_8938	477	44.65	5.00E-128	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-

gene_id_8940	226	92.48	4.00E-122	MULTISPECIES: hypothetical protein
gene_id_8941	236	96.19	4.00E-170	MULTISPECIES: hypothetical protein
gene_id_8942	662	97.89	0	hypothetical protein
gene_id_8943	450	98	0	MULTISPECIES: hypothetical protein
gene_id_8944	475	98.74	0	MULTISPECIES: hypothetical protein
gene_id_8945	210	97.62	1.00E-149	MULTISPECIES: carbonic anhydrase
gene_id_8946	232	96.98	3.00E-145	MULTISPECIES: hypothetical protein
gene_id_8947	306	98.04	0	MULTISPECIES: hypothetical protein
gene_id_8948	364	97.8	0	MULTISPECIES: hypothetical protein
gene_id_8949	325	98.46	0	MULTISPECIES: hypothetical protein
gene_id_8950	289	96.89	0	MULTISPECIES: hypothetical protein
gene_id_8952	162	98.77	2.00E-115	MULTISPECIES: redox family protein
gene_id_8953	309	94.5	0	MULTISPECIES: hypothetical protein
gene_id_8954	527	99.05	0	MULTISPECIES: peptide chain release factor 3
gene_id_8955	261	95.4	7.00E-157	MULTISPECIES: hypothetical protein
gene_id_8956	79	87.34	2.00E-29	MULTISPECIES: hypothetical protein
gene_id_8957	92	95.65	4.00E-45	MULTISPECIES: hypothetical protein
gene_id_8958	471	95.97	0	MULTISPECIES: (dimethylallyl)adenosine tRNA methy
gene_id_8959	873	97.82	0	MULTISPECIES: DNA mismatch repair protein MutS
gene_id_8960	651	96.47	0	MULTISPECIES: hypothetical protein
gene_id_8961	310	99.03	0	MULTISPECIES: tRNA dimethylallyltransferase
gene_id_8962	78	100	6.00E-48	MULTISPECIES: RNA-binding protein Hfq
gene_id_8963	428	98.6	0	MULTISPECIES: hypothetical protein
gene_id_8964	824	37.5	4.00E-169	LuxR family transcriptional regulator
gene_id_8966	567	25.93	9.00E-18	hypothetical protein
gene_id_8966	400	26	4.00E-09	hypothetical protein
gene_id_8967	495	32.53	3.00E-55	hypothetical protein
gene_id_8967	602	24.75	2.00E-33	hypothetical protein
gene_id_8968	233	35.62	7.00E-32	hypothetical protein dsmv_0897
gene_id_8968	226	34.96	5.00E-31	hypothetical protein dsmv_0897
gene_id_8968	233	34.33	2.00E-30	hypothetical protein dsmv_0897
gene_id_8968	251	31.47	5.00E-30	hypothetical protein dsmv_0897
gene_id_8968	241	32.37	3.00E-28	hypothetical protein dsmv_0897
gene_id_8968	258	31.4	1.00E-27	hypothetical protein dsmv_0897
gene_id_8968	168	36.9	5.00E-24	hypothetical protein dsmv_0897
gene_id_8969	207	100	1.00E-145	MULTISPECIES: XRE family transcriptional regulator
gene_id_8970	104	96.15	1.00E-65	MULTISPECIES: hypothetical protein
gene_id_8971	617	97.89	0	MULTISPECIES: hypothetical protein
gene_id_8972	324	99.38	0	MULTISPECIES: tyrosine recombinase XerC
gene_id_8974	278	92.09	1.00E-163	MULTISPECIES: hypothetical protein
gene_id_8975	187	91.98	2.00E-121	MULTISPECIES: hypothetical protein
gene_id_8976	141	56.74	4.00E-32	hypothetical protein
gene_id_8977	145	70.34	8.00E-65	histidine kinase
gene_id_8978	363	56.75	2.00E-149	hypothetical protein
gene_id_8979	363	95.04	0	MULTISPECIES: hypothetical protein
gene_id_8980	210	96.67	1.00E-148	MULTISPECIES: hypothetical protein
gene_id_8981	159	96.86	7.00E-110	MULTISPECIES: peptide methionine sulfoxide reducta

gene_id_8982	317	95.27	0	MULTISPECIES: hypothetical protein
gene_id_8984	208	98.56	1.00E-136	MULTISPECIES: peptidylprolyl isomerase
gene_id_8985	173	93.64	3.00E-106	MULTISPECIES: hypothetical protein
gene_id_8986	456	97.37	0	MULTISPECIES: hypothetical protein
gene_id_8987	152	49.34	1.00E-41	flavodoxin
gene_id_8988	534	98.13	0	MULTISPECIES: hypothetical protein
gene_id_8989	232	97.41	9.00E-147	MULTISPECIES: hypothetical protein
gene_id_8990	239	58.58	2.00E-90	2-keto-4-pentenoate hydratase
gene_id_8991	477	98.53	0	MULTISPECIES: hypothetical protein
gene_id_8992	517	99.61	0	MULTISPECIES: ribonuclease
gene_id_8993	343	100	0	MULTISPECIES: recombinase RecA
gene_id_8994	177	98.87	4.00E-109	MULTISPECIES: CDP-diacylglycerol--glycerol-3-phosph
gene_id_8995	445	98.65	0	MULTISPECIES: ribosomal protein S12 methylthiotran
gene_id_8996	809	98.52	0	MULTISPECIES: cell division protein FtsK
gene_id_8997	304	98.03	0	MULTISPECIES: hypothetical protein
gene_id_8998	77	98.7	2.00E-44	MULTISPECIES: hypothetical protein
gene_id_8999	143	98.6	3.00E-96	MULTISPECIES: deoxyuridine 5'-triphosphate nucleot
gene_id_9000	412	99.03	0	MULTISPECIES: zinc protease
gene_id_9002	697	99.28	0	MULTISPECIES: polyribonucleotide nucleotidyltransfe
gene_id_9003	87	98.85	5.00E-55	MULTISPECIES: 30S ribosomal protein S15
gene_id_9004	249	97.99	2.00E-174	MULTISPECIES: hypothetical protein
gene_id_9005	290	98.28	0	MULTISPECIES: tRNA pseudouridine synthase B
gene_id_9006	320	97.19	0	MULTISPECIES: hypothetical protein
gene_id_9007	125	99.2	1.00E-80	MULTISPECIES: ribosome-binding factor A
gene_id_9008	755	96.95	0	MULTISPECIES: translation initiation factor IF-2
gene_id_9009	98	96.94	1.00E-57	MULTISPECIES: 50S ribosomal protein L7ae
gene_id_9010	89	100	2.00E-54	MULTISPECIES: hypothetical protein
gene_id_9011	353	100	0	MULTISPECIES: transcription termination factor NusA
gene_id_9012	154	100	5.00E-102	MULTISPECIES: ribosome maturation factor RimP
gene_id_9013	368	97.28	0	MULTISPECIES: lysine 2,3-aminomutase
gene_id_9014	223	99.1	3.00E-157	MULTISPECIES: magnesium transporter
gene_id_9326	89	85.39	2.00E-47	resolvase
gene_id_9328	155	37.42	1.00E-22	conserved domain protein
gene_id_9329	531	29.94	1.00E-54	hypothetical protein
gene_id_9330	66	96.97	1.00E-38	hypothetical protein
gene_id_9331	430	97.67	0	hypothetical protein
gene_id_9332	280	99.29	0	hypothetical protein
gene_id_9333	457	98.91	0	alanine glycine permease, partial
gene_id_9334	288	59.38	9.00E-126	hypothetical protein
gene_id_9335	740	66.62	0	helicase
gene_id_9336	176	83.52	2.00E-100	MULTISPECIES: hypothetical protein
gene_id_9337	110	72.73	2.00E-53	hypothetical protein
gene_id_9338	136	90.44	2.00E-85	DNA-binding protein, excisionase family
gene_id_9339	261	74.33	2.00E-125	putative Zn peptidase
gene_id_9340	132	33.33	3.00E-14	hypothetical protein
gene_id_9341	321	98.13	0	Fic family protein
gene_id_9342	140	65	8.00E-53	hypothetical protein

gene_id_9343	87	52.87	3.00E-16	hypothetical protein
gene_id_9344	91	59.34	4.00E-35	hypothetical protein
gene_id_9345	153	97.39	4.00E-103	spermidine acetyltransferase
gene_id_9346	507	94.87	0	DNA methylase
gene_id_9347	139	94.24	9.00E-91	UV-damage repair protein
gene_id_9348	105	99.05	8.00E-67	PadR family transcriptional regulator
gene_id_9349	168	92.86	1.00E-104	hypothetical protein
gene_id_9350	124	99.19	3.00E-76	MmcQ
gene_id_9351	255	97.25	0	hypothetical protein
gene_id_9352	457	94.53	0	hypothetical protein
gene_id_9354	183	31.69	1.00E-14	hypothetical protein
gene_id_9355	240	95.42	5.00E-126	hypothetical protein
gene_id_9356	469	96.59	0	hypothetical protein
gene_id_9357	179	98.88	2.00E-101	hypothetical protein
gene_id_9358	355	99.15	0	hypothetical protein
gene_id_9360	270	67.04	3.00E-121	hypothetical protein
gene_id_9361	287	96.86	0	hypothetical protein
gene_id_9362	192	99.48	2.00E-136	hypothetical protein
gene_id_9363	282	97.16	0	aspartate kinase, partial
gene_id_9364	290	96.21	0	dihydrodipicolinate synthase
gene_id_9365	409	98.04	0	hypothetical protein
gene_id_9366	304	95.72	0	hypothetical protein
gene_id_9367	622	53.22	0	hypothetical protein
gene_id_9368	328	96.04	0	hypothetical protein
gene_id_9369	394	96.19	0	hypothetical protein
gene_id_9370	167	53.29	2.00E-59	hypothetical protein CLOSTASPAR_01400
gene_id_9371	68	55.88	1.00E-16	sigma-70 family RNA polymerase sigma factor
gene_id_9372	355	34.08	1.00E-56	hypothetical protein
gene_id_9373	218	99.08	4.00E-114	hypothetical protein
gene_id_9374	591	98.31	0	hypothetical protein
gene_id_9375	193	100	2.00E-128	TetR family transcriptional regulator
gene_id_9376	94	97.87	1.00E-56	hypothetical protein
gene_id_9377	311	96.78	0	hypothetical protein, partial
gene_id_9378	381	97.64	0	hypothetical protein
gene_id_9379	438	99.32	0	aminotransferase class I/II
gene_id_9380	375	54.67	4.00E-135	hypothetical protein
gene_id_9381	105	98.1	7.00E-66	hypothetical protein
gene_id_9382	256	97.66	0	hypothetical protein
gene_id_9383	611	99.02	0	hypothetical protein
gene_id_9384	95	100	3.00E-62	hypothetical protein
gene_id_9385	388	99.48	0	carbohydrate hydrolase
gene_id_9386	318	99.06	2.00E-166	hypothetical protein
gene_id_9387	392	95.15	0	hypothetical protein
gene_id_9388	325	98.77	0	hypothetical protein
gene_id_9389	425	99.29	0	hypothetical protein
gene_id_9390	380	98.42	0	hypothetical protein
gene_id_9391	392	97.96	0	hypothetical protein

gene_id_9392	92	57.61	2.00E-32	glutaredoxin
gene_id_9393	337	100	0	hypothetical protein
gene_id_9394	305	99.67	0	hypothetical protein
gene_id_9395	337	99.41	0	hypothetical protein
gene_id_9396	288	96.18	0	hypothetical protein
gene_id_9397	353	96.88	0	hypothetical protein
gene_id_9398	417	93.05	0	hypothetical protein
gene_id_9399	368	93.75	0	hypothetical protein
gene_id_9400	163	87.73	8.00E-86	hypothetical protein
gene_id_9401	139	94.24	2.00E-90	hypothetical protein
gene_id_9402	459	95.64	0	hypothetical protein
gene_id_9403	236	92.8	7.00E-158	hypothetical protein, partial
gene_id_9404	782	92.71	0	hypothetical protein
gene_id_9405	179	98.32	5.00E-123	hypothetical protein
gene_id_9406	330	96.97	0	lipoate-protein ligase A
gene_id_9408	456	97.37	0	hypothetical protein, partial
gene_id_9409	321	99.38	0	acetoin:2,6-dichlorophenolindophenol oxidoreductas
gene_id_9410	325	99.69	0	TPP-dependent acetoin dehydrogenase complex, E1
gene_id_9411	298	99.33	0	hypothetical protein
gene_id_9412	465	91.83	0	hypothetical protein
gene_id_9413	283	97.17	0	hypothetical protein
gene_id_9414	646	42.41	2.00E-162	hypothetical protein, partial
gene_id_9415	342	98.83	0	hypothetical protein
gene_id_9416	158	97.47	2.00E-89	hypothetical protein
gene_id_9417	427	100	0	hypothetical protein
gene_id_9418	157	100	1.00E-107	hypothetical protein
gene_id_9419	343	98.83	0	hypothetical protein
gene_id_9420	348	97.99	0	hypothetical protein
gene_id_9421	150	97.33	4.00E-84	hypothetical protein
gene_id_9422	146	97.95	2.00E-82	hypothetical protein
gene_id_9423	753	99.47	0	hypothetical protein
gene_id_9424	658	99.54	0	NAD-dependent DNA ligase LigA
gene_id_9425	321	99.69	0	hypothetical protein
gene_id_9426	342	97.66	0	hypothetical protein
gene_id_9427	311	98.39	0	hypothetical protein
gene_id_9428	277	100	0	peptide ABC transporter permease
gene_id_9429	354	96.33	0	hypothetical protein
gene_id_9430	555	97.12	0	hypothetical protein
gene_id_9431	281	100	2.00E-173	hypothetical protein
gene_id_9432	183	100	8.00E-116	hypothetical protein
gene_id_9433	457	99.34	0	hypothetical protein
gene_id_9434	428	97.43	0	hypothetical protein
gene_id_9435	102	99.02	5.00E-64	hypothetical protein
gene_id_9436	161	98.76	1.00E-94	hypothetical protein
gene_id_9437	209	98.56	4.00E-147	hypothetical protein
gene_id_9438	1142	99.39	0	hypothetical protein
gene_id_9440	275	97.82	0	hypothetical protein

gene_id_9441	569	76.63	0	C4-dicarboxylate anaerobic carrier
gene_id_9442	395	93.16	0	hypothetical protein
gene_id_9443	678	48.97	0	Fis family transcriptional regulator
gene_id_9444	150	99.33	3.00E-92	hypothetical protein
gene_id_9445	254	99.61	1.00E-170	hypothetical protein
gene_id_9446	291	98.97	0	hypothetical protein
gene_id_9447	335	99.1	0	hypothetical protein, partial
gene_id_9448	402	99.25	0	hypothetical protein
gene_id_9449	334	99.1	0	hypothetical protein
gene_id_9450	1010	41.88	0	hypothetical protein
gene_id_9451	395	97.47	0	hypothetical protein
gene_id_9452	364	99.45	0	hypothetical protein
gene_id_9453	181	97.79	4.00E-103	hypothetical protein
gene_id_9454	204	51.47	3.00E-64	NUDIX hydrolase
gene_id_9455	479	58.04	0	hypothetical protein
gene_id_9456	427	76.58	0	beta-aspartyl peptidase
gene_id_9457	346	76.3	0	sarcosine reductase
gene_id_9458	359	62.4	2.00E-164	hypothetical protein U27_01772
gene_id_9459	354	58.47	8.00E-150	hypothetical protein, partial
gene_id_9460	422	53.55	5.00E-158	transporter
gene_id_9461	352	57.1	1.00E-139	Alanine racemase, N-terminal domain-containing pro
gene_id_9462	403	52.11	3.00E-148	hypothetical protein, partial
gene_id_9463	297	98.65	0	cysteine synthase
gene_id_9464	184	99.46	9.00E-129	hypothetical protein
gene_id_9465	79	96.2	1.00E-44	hypothetical protein
gene_id_9468	64	95.31	3.00E-36	hypothetical protein
gene_id_9469	383	97.65	0	hypothetical protein
gene_id_9470	135	97.04	4.00E-88	hypothetical protein
gene_id_9471	153	88.24	5.00E-92	hypothetical protein
gene_id_9472	342	98.83	0	hypothetical protein
gene_id_9510	343	98.83	0	hypothetical protein
gene_id_9511	245	96.33	6.00E-174	hypothetical protein
gene_id_9512	378	98.15	0	competence protein
gene_id_9513	399	99	0	hypothetical protein
gene_id_9514	500	97.2	0	hypothetical protein
gene_id_9515	395	94.94	0	hypothetical protein
gene_id_9516	414	96.62	0	hypothetical protein
gene_id_9517	268	98.51	4.00E-170	hypothetical protein
gene_id_9518	311	99.04	0	membrane protein, partial
gene_id_9519	274	98.54	0	membrane protein
gene_id_9520	646	98.92	0	hypothetical protein
gene_id_9521	173	95.95	1.00E-119	hypothetical protein
gene_id_9522	234	46.15	7.00E-66	hypothetical protein
gene_id_9523	481	94.39	0	hypothetical protein
gene_id_9524	661	98.03	0	hypothetical protein
gene_id_9525	461	98.05	0	hypothetical protein
gene_id_9526	544	97.24	0	hypothetical protein

gene_id_9527	383	94.78	0	hypothetical protein, partial
gene_id_9528	195	78.97	2.00E-111	hypothetical protein
gene_id_9529	207	33.33	1.00E-11	hypothetical protein
gene_id_9531	154	97.4	6.00E-93	hypothetical protein
gene_id_9532	125	99.2	1.00E-62	hypothetical protein
gene_id_9533	106	100	3.00E-67	hypothetical protein
gene_id_9534	126	95.24	6.00E-63	hypothetical protein
gene_id_9535	362	95.03	0	hypothetical protein
gene_id_9536	396	97.98	0	hypothetical protein
gene_id_9537	416	98.56	0	hypothetical protein
gene_id_9538	559	94.45	0	hypothetical protein
gene_id_9539	93	87.1	2.00E-52	hypothetical protein
gene_id_9540	557	97.85	0	hypothetical protein
gene_id_9541	226	98.23	2.00E-148	hypothetical protein
gene_id_9542	263	92.78	3.00E-147	hypothetical protein
gene_id_9543	180	45.56	2.00E-39	hypothetical protein HMPREF1526_01454
gene_id_9544	122	61.48	2.00E-51	diadenosine polyphosphate hydrolase
gene_id_9545	746	63.94	0	DEAD/DEAH box helicase
gene_id_9548	226	40.71	2.00E-38	hypothetical protein
gene_id_9549	243	32.1	2.00E-22	hypothetical protein
gene_id_9551	523	57.74	0	putative ATPase
gene_id_9552	291	51.89	6.00E-89	NurA domain-containing protein
gene_id_9553	883	52.89	0	hypothetical protein
gene_id_9554	515	34.17	2.00E-75	helicase conserved C-terminal domain protein
gene_id_9555	345	97.97	0	hypothetical protein
gene_id_9557	263	93.92	1.00E-126	hypothetical protein
gene_id_9558	154	75.32	7.00E-85	methylated DNA-protein cysteine methyltransferase
gene_id_9559	508	67.13	0	hypothetical protein, partial
gene_id_9561	398	99.25	0	metallo-beta-lactamase
gene_id_9562	201	99	8.00E-126	hypothetical protein, partial
gene_id_9563	139	93.53	3.00E-76	hypothetical protein
gene_id_9564	110	99.09	8.00E-72	hypothetical protein
gene_id_9565	63	96.83	2.00E-35	hypothetical protein
gene_id_9566	123	95.12	2.00E-81	hypothetical protein
gene_id_9567	476	98.11	0	hypothetical protein
gene_id_9568	396	98.48	0	hypothetical protein
gene_id_9569	512	98.83	0	regulatory protein AepA
gene_id_9570	395	94.43	0	hypothetical protein
gene_id_9571	74	98.65	2.00E-44	hypothetical protein
gene_id_9572	315	99.05	0	hypothetical protein
gene_id_9573	74	97.3	2.00E-39	hypothetical protein, partial
gene_id_9574	691	41.1	4.00E-162	hypothetical protein
gene_id_9575	651	99.23	0	hypothetical protein
gene_id_9576	168	100	6.00E-101	hypothetical protein
gene_id_9577	399	99.25	0	hypothetical protein
gene_id_9578	586	98.81	0	hypothetical protein
gene_id_9579	417	98.56	0	hypothetical protein

gene_id_9580	310	99.35	0	hypothetical protein
gene_id_9581	628	37.26	6.00E-124	hypothetical protein
gene_id_9582	437	47.14	2.00E-124	sugar phosphate permease
gene_id_9583	496	69.56	0	hypothetical protein
gene_id_9584	196	45.92	3.00E-49	4Fe-4S ferredoxin
gene_id_9585	681	50.95	0	hypothetical protein, partial
gene_id_9586	371	35.58	3.00E-57	MFS transporter
gene_id_9587	367	56.95	2.00E-134	acetyl-CoA acetyltransferase
gene_id_9589	416	45.67	5.00E-98	Sugar phosphate permease
gene_id_9590	300	31.67	9.00E-50	hypothetical protein
gene_id_9591	296	61.49	3.00E-126	hypothetical protein, partial
gene_id_9592	276	67.03	3.00E-143	3-keto-5-aminohexanoate cleavage protein
gene_id_9593	348	64.94	2.00E-163	hypothetical protein, partial
gene_id_9594	254	45.28	4.00E-77	enoyl-CoA hydratase
gene_id_9595	653	37.21	2.00E-133	hypothetical protein
gene_id_9597	253	57.71	2.00E-100	Dehydrogenases with different specificities (related t
gene_id_9598	390	97.95	0	glycine/betaine ABC transporter ATP-binding protein
gene_id_9599	288	96.88	3.00E-170	hypothetical protein
gene_id_9600	335	95.52	0	hypothetical protein
gene_id_9601	231	95.67	2.00E-137	hypothetical protein
gene_id_9602	524	97.14	0	hypothetical protein, partial
gene_id_9603	459	99.35	0	hypothetical protein
gene_id_9604	306	99.02	0	hypothetical protein
gene_id_9605	274	97.81	0	hypothetical protein
gene_id_9606	432	99.77	0	hypothetical protein
gene_id_9607	304	98.68	0	hypothetical protein
gene_id_9608	177	98.87	3.00E-118	hypothetical protein
gene_id_9609	210	100	3.00E-124	hypothetical protein
gene_id_9610	621	96.94	0	hypothetical protein
gene_id_9611	450	98	0	hypothetical protein
gene_id_9612	93	97.85	1.00E-58	hypothetical protein, partial
gene_id_9613	424	100	0	hypothetical protein
gene_id_9614	287	95.47	0	hypothetical protein
gene_id_9615	461	98.7	0	hypothetical protein
gene_id_9616	575	99.65	0	hypothetical protein
gene_id_9617	227	100	1.00E-137	hypothetical protein
gene_id_9618	298	100	0	hypothetical protein, partial
gene_id_9619	226	34.07	2.00E-31	uncharacterized protein
gene_id_9620	296	95.95	0	hypothetical protein
gene_id_9621	217	96.77	2.00E-144	hypothetical protein
gene_id_10044	886	99.77	0	transglycosylase, partial
gene_id_10045	195	100	2.00E-137	hypothetical protein
gene_id_10046	426	99.53	0	hypothetical protein
gene_id_10047	214	99.07	1.00E-133	hypothetical protein
gene_id_10048	240	98.33	4.00E-163	hypothetical protein
gene_id_10049	296	46.62	1.00E-79	recombinase
gene_id_10050	918	32.68	2.00E-119	hypothetical protein GCA01S_093_00090

gene_id_10051	386	78.5	0	hypothetical protein
gene_id_10054	157	39.49	3.00E-37	hypothetical protein
gene_id_10055	195	82.56	3.00E-96	resolvase
gene_id_10056	941	31.88	4.00E-110	hypothetical protein
gene_id_10057	133	31.58	6.00E-16	hypothetical protein
gene_id_10059	143	52.45	3.00E-30	hypothetical protein
gene_id_10060	250	67.6	8.00E-104	hypothetical protein
gene_id_10061	486	39.3	4.00E-110	hypothetical protein
gene_id_10062	298	83.56	0	hypothetical protein
gene_id_10063	319	28.21	9.00E-14	hypothetical protein
gene_id_10065	356	96.63	0	hypothetical protein
gene_id_10066	164	94.51	9.00E-99	hypothetical protein
gene_id_10067	451	92.46	0	hypothetical protein
gene_id_10068	146	95.21	2.00E-93	hypothetical protein
gene_id_10069	59	71.19	1.00E-21	hypothetical protein
gene_id_10070	219	98.17	2.00E-155	hypothetical protein
gene_id_10071	700	98.14	0	hypothetical protein
gene_id_10072	188	98.4	1.00E-112	hypothetical protein
gene_id_10073	245	98.78	1.00E-176	hypothetical protein
gene_id_10074	30	96.67	7.00E-11	hypothetical protein
gene_id_10075	176	99.43	9.00E-107	hypothetical protein
gene_id_10076	255	98.82	3.00E-167	ATP-binding protein
gene_id_10077	118	100	9.00E-80	hypothetical protein
gene_id_10078	803	99.63	0	leucyl-tRNA synthetase
gene_id_10079	167	93.41	1.00E-96	hypothetical protein
gene_id_10080	240	95.42	2.00E-163	hypothetical protein
gene_id_10081	231	97.84	6.00E-164	hypothetical protein
gene_id_10082	296	99.66	9.00E-172	hypothetical protein
gene_id_10083	273	100	0	hypothetical protein
gene_id_10084	97	98.97	1.00E-61	hypothetical protein
gene_id_10085	456	99.78	0	hypothetical protein
gene_id_10086	188	98.94	2.00E-119	hypothetical protein
gene_id_10087	1182	99.49	0	hypothetical protein
gene_id_10088	318	99.69	0	hypothetical protein
gene_id_10089	183	100	9.00E-127	AbrB family transcriptional regulator
gene_id_10090	555	99.64	0	hypothetical protein
gene_id_10091	592	99.32	0	hypothetical protein
gene_id_10092	191	100	1.00E-133	hypothetical protein
gene_id_10093	355	99.72	0	butyrate kinase
gene_id_10094	1257	64.52	0	Phosphoribosylformylglycinamidine synthase
gene_id_10095	161	96.89	9.00E-108	hypothetical protein
gene_id_10096	236	98.73	4.00E-148	hypothetical protein
gene_id_10097	421	100	0	amidophosphoribosyltransferase, partial
gene_id_10098	346	100	0	phosphoribosylaminoimidazole synthetase
gene_id_10099	207	99.52	1.00E-144	hypothetical protein
gene_id_10100	516	70.16	0	bifunctional purine biosynthesis protein purH
gene_id_10101	417	99.76	0	hypothetical protein

gene_id_10102	423	99.76	0	hypothetical protein
gene_id_10103	443	99.1	0	hypothetical protein
gene_id_10104	597	99.33	0	hypothetical protein
gene_id_10105	232	100	5.00E-166	hypothetical protein
gene_id_10106	457	99.34	0	hypothetical protein
gene_id_10107	450	99.56	0	hypothetical protein, partial
gene_id_10108	385	100	0	methionine gamma-lyase
gene_id_10109	298	92.28	3.00E-177	tungsten ABC transporter substrate-binding protein
gene_id_10110	218	91.28	9.00E-139	ABC transporter permease
gene_id_10111	228	89.47	2.00E-147	hypothetical protein
gene_id_10112	162	96.3	5.00E-109	hypothetical protein
gene_id_10113	408	98.53	0	hypothetical protein
gene_id_10114	636	98.27	0	LysR family transcriptional regulator
gene_id_10115	318	98.74	0	hypothetical protein
gene_id_10116	156	99.36	9.00E-109	molybdenum cofactor biosynthesis protein C
gene_id_10117	143	100	1.00E-98	molybdenum cofactor sulfurase
gene_id_10118	61	100	7.00E-35	hypothetical protein
gene_id_10119	62	100	3.00E-34	hypothetical protein
gene_id_10120	308	98.7	0	hypothetical protein
gene_id_10121	327	97.55	0	hypothetical protein
gene_id_10122	269	100	1.00E-161	hypothetical protein
gene_id_10123	282	97.52	0	hypothetical protein
gene_id_10124	101	50.5	3.00E-27	hypothetical protein, partial
gene_id_10125	281	98.93	0	ferredoxin
gene_id_10126	160	95	2.00E-93	hypothetical protein, partial
gene_id_10127	250	94	9.00E-137	hypothetical protein
gene_id_10128	104	100	9.00E-61	hypothetical protein
gene_id_10129	469	99.57	0	hypothetical protein
gene_id_10130	66	100	1.00E-17	hypothetical protein
gene_id_10131	490	98.37	0	spore gernimation protein
gene_id_10132	365	96.99	0	hypothetical protein
gene_id_10133	358	97.21	0	hypothetical protein
gene_id_10134	209	97.13	9.00E-106	hypothetical protein, partial
gene_id_10135	467	99.79	0	hypothetical protein
gene_id_10136	139	98.56	9.00E-94	hypothetical protein
gene_id_10137	346	99.71	0	L-erythro-3,5-diaminohexanoate dehydrogenase
gene_id_10138	417	99.52	0	hypothetical protein
gene_id_10139	342	99.42	0	hypothetical protein
gene_id_10140	526	97.91	0	hypothetical protein
gene_id_10141	518	99.23	0	dioxygenase
gene_id_10142	252	100	0	dioxygenase
gene_id_10143	386	96.89	0	hypothetical protein
gene_id_10144	215	99.53	3.00E-152	hypothetical protein
gene_id_10145	329	94.22	0	hypothetical protein
gene_id_10146	309	97.73	0	hypothetical protein
gene_id_10147	457	94.53	0	hypothetical protein
gene_id_10148	372	97.85	0	hypothetical protein

gene_id_10149	821	98.9	0	ATP-dependent protease
gene_id_10150	419	96.66	0	hypothetical protein
gene_id_10151	386	85.49	0	hypothetical protein
gene_id_10152	181	92.82	4.00E-95	hypothetical protein
gene_id_10153	859	54.83	0	hypothetical protein, partial
gene_id_10156	105	98.1	7.00E-67	hypothetical protein
gene_id_10157	144	89.58	2.00E-88	hypothetical protein
gene_id_10158	144	99.31	3.00E-39	hypothetical protein
gene_id_10159	113	96.46	2.00E-72	hypothetical protein, partial
gene_id_10160	136	97.06	1.00E-76	hypothetical protein
gene_id_10161	356	97.75	0	hypothetical protein, partial
gene_id_10162	176	100	2.00E-114	hypothetical protein
gene_id_10163	153	100	9.00E-108	hypothetical protein, partial
gene_id_10164	304	98.03	0	hypothetical protein, partial
gene_id_10165	341	97.36	0	hypothetical protein, partial
gene_id_10166	327	97.55	0	hypothetical protein
gene_id_10167	542	98.34	0	hypothetical protein
gene_id_10168	185	95.68	1.00E-126	hypothetical protein
gene_id_10169	411	99.76	0	hypothetical protein
gene_id_10170	79	98.73	3.00E-49	hypothetical protein
gene_id_10171	336	100	0	hypothetical protein
gene_id_10172	550	99.27	0	hypothetical protein
gene_id_10173	127	98.43	1.00E-83	hypothetical protein, partial
gene_id_10174	509	97.84	0	hypothetical protein
gene_id_10175	182	97.8	4.00E-109	hypothetical protein
gene_id_10176	789	98.73	0	dehydrogenase
gene_id_10177	298	96.98	0	radical SAM protein
gene_id_10178	374	96.26	0	hypothetical protein
gene_id_10179	87	100	1.00E-53	hypothetical protein
gene_id_10180	869	98.27	0	hypothetical protein
gene_id_10181	357	96.36	0	hypothetical protein
gene_id_10182	102	99.02	4.00E-66	hypothetical protein
gene_id_10183	523	95.6	0	hypothetical protein, partial
gene_id_10184	320	94.38	0	hypothetical protein, partial
gene_id_10185	368	97.55	0	hypothetical protein
gene_id_10186	194	97.42	9.00E-135	hypothetical protein
gene_id_10187	74	100	2.00E-45	hypothetical protein
gene_id_10188	245	98.37	9.00E-144	hypothetical protein
gene_id_10189	352	97.44	0	hypothetical protein
gene_id_10190	145	89.66	7.00E-90	hypothetical protein
gene_id_10191	145	100	3.00E-100	hypothetical protein
gene_id_10192	342	99.42	0	hypothetical protein
gene_id_10193	373	99.46	0	hypothetical protein
gene_id_10194	75	100	4.00E-21	hypothetical protein
gene_id_10195	319	98.12	0	hypothetical protein
gene_id_10196	313	99.68	0	hypothetical protein
gene_id_10197	243	98.77	1.00E-174	hypothetical protein

gene_id_10198	412	100	0	hypothetical protein
gene_id_10199	141	97.16	4.00E-92	3-hydroxyacyl-ACP dehydratase
gene_id_10200	129	100	1.00E-89	HxlR family transcriptional regulator
gene_id_10201	122	100	4.00E-59	hypothetical protein
gene_id_10202	649	98.77	0	hypothetical protein
gene_id_10203	160	99.38	3.00E-74	V-type ATP synthase subunit K
gene_id_10204	193	97.41	5.00E-104	hypothetical protein
gene_id_10205	337	99.11	0	hypothetical protein
gene_id_10206	106	100	3.00E-69	hypothetical protein
gene_id_10207	590	100	0	V-type ATP synthase subunit A
gene_id_10208	458	100	0	V-type ATP synthase subunit B
gene_id_10209	231	99.13	3.00E-153	hypothetical protein
gene_id_10210	347	97.98	0	hypothetical protein
gene_id_10211	520	97.69	0	proline:sodium symporter
gene_id_10212	82	93.9	7.00E-47	hypothetical protein
gene_id_10213	337	95.85	0	hypothetical protein
gene_id_10214	614	94.79	0	hypothetical protein
gene_id_10215	330	92.73	0	hypothetical protein
gene_id_10216	405	94.81	0	hypothetical protein
gene_id_10217	273	98.9	2.00E-174	3-methyl-2-oxobutanoate hydroxymethyltransferase
gene_id_10218	560	99.11	0	formate--tetrahydrofolate ligase
gene_id_10219	246	97.56	3.00E-168	hypothetical protein
gene_id_10220	288	94.44	5.00E-176	hypothetical protein
gene_id_10221	152	94.08	4.00E-90	hypothetical protein
gene_id_10222	139	99.28	1.00E-91	hypothetical protein
gene_id_10223	875	96.57	0	hypothetical protein
gene_id_10224	392	99.23	0	S-adenosylmethionine synthetase
gene_id_10225	110	40.91	3.00E-24	hypothetical protein
gene_id_10226	182	46.15	8.00E-36	hypothetical protein, partial
gene_id_10227	1251	53.16	0	peptidase M28
gene_id_10228	453	99.78	0	hypothetical protein
gene_id_10229	486	93.83	0	4-alpha-glucanotransferase, partial
gene_id_10230	605	97.85	0	hypothetical protein
gene_id_10231	237	98.31	2.00E-156	transcriptional regulator
gene_id_10233	702	98.58	0	succinate dehydrogenase
gene_id_10234	427	95.08	0	hypothetical protein, partial
gene_id_10235	620	97.42	0	hypothetical protein, partial
gene_id_10236	477	98.74	0	hypothetical protein
gene_id_10237	373	99.2	0	hypothetical protein
gene_id_10238	381	99.74	0	hypothetical protein
gene_id_10239	637	98.12	0	hypothetical protein
gene_id_10240	283	98.59	0	hypothetical protein
gene_id_10241	107	100	9.00E-49	hypothetical protein, partial
gene_id_10242	235	96.17	2.00E-160	hypothetical protein
gene_id_10243	116	98.28	4.00E-76	hypothetical protein
gene_id_10244	394	97.72	0	hypothetical protein
gene_id_10245	316	98.73	0	hypothetical protein

gene_id_10246	308	97.73	0	hypothetical protein
gene_id_10247	556	94.96	0	hypothetical protein
gene_id_10248	351	98.86	0	hypothetical protein
gene_id_10249	319	98.43	0	hypothetical protein
gene_id_10250	357	97.76	0	hypothetical protein
gene_id_10251	270	98.89	6.00E-180	hypothetical protein
gene_id_10252	324	98.46	0	TIM barrel oxidoreductase NifR3
gene_id_10253	156	100	3.00E-87	transcription elongation factor GreA
gene_id_10254	489	73.01	0	lysyl-tRNA synthetase
gene_id_10579	453	98.23	0	multidrug transporter MatE
gene_id_10580	712	96.91	0	hypothetical protein
gene_id_10581	289	98.62	0	hypothetical protein
gene_id_10582	185	98.38	4.00E-120	hypothetical protein
gene_id_10583	435	100	0	sodium:proton antiporter, partial
gene_id_10584	303	96.7	0	hypothetical protein
gene_id_10585	575	70.61	0	phosphoenolpyruvate carboxykinase (GTP)
gene_id_10586	345	97.68	0	hypothetical protein
gene_id_10587	288	98.26	1.00E-162	hypothetical protein
gene_id_10588	258	98.84	2.00E-173	hypothetical protein
gene_id_10589	245	96.73	2.00E-145	hypothetical protein
gene_id_10590	241	62.66	3.00E-101	(Fe-S)-binding protein
gene_id_10591	229	97.82	5.00E-159	hypothetical protein
gene_id_10592	264	97.35	4.00E-178	hypothetical protein
gene_id_10593	362	98.34	0	hypothetical protein
gene_id_10594	897	96.54	0	hypothetical protein
gene_id_10595	229	99.13	2.00E-164	hypothetical protein
gene_id_10596	344	100	0	L-threonine 3-dehydrogenase
gene_id_10597	396	99.49	0	hypothetical protein
gene_id_10598	340	99.41	0	branched-chain amino acid aminotransferase
gene_id_10599	880	51.14	0	hypothetical protein
gene_id_10600	158	98.1	7.00E-105	hypothetical protein
gene_id_10601	314	99.36	0	hypothetical protein
gene_id_10602	286	95.8	0	hypothetical protein
gene_id_10603	354	74.86	0	peptide chain release factor 1
gene_id_10604	81	98.77	1.00E-49	hypothetical protein
gene_id_10605	178	98.31	4.00E-128	hypothetical protein
gene_id_10606	463	98.06	0	hypothetical protein
gene_id_10607	388	99.23	0	hypothetical protein
gene_id_10608	455	98.68	0	hypothetical protein
gene_id_10609	466	98.93	0	hypothetical protein
gene_id_10611	253	97.63	3.00E-172	MerR family transcriptional regulator
gene_id_10612	242	92.98	1.00E-162	ABC transporter
gene_id_10613	247	93.93	8.00E-146	ABC transporter
gene_id_10614	388	97.94	0	hypothetical protein
gene_id_10615	310	98.39	0	hypothetical protein
gene_id_10616	245	97.14	6.00E-174	hypothetical protein
gene_id_10617	284	100	0	hypothetical protein

gene_id_10618	321	98.13	0	hypothetical protein, partial
gene_id_10619	352	48.3	2.00E-105	phosphatase
gene_id_10620	427	97.66	0	hypothetical protein
gene_id_10621	278	98.92	0	RNA-binding protein, partial
gene_id_10622	233	99.57	7.00E-172	hypothetical protein
gene_id_10623	466	97.85	0	hypothetical protein
gene_id_10624	381	99.21	0	hypothetical protein
gene_id_10625	517	99.42	0	hypothetical protein
gene_id_10626	356	98.88	0	hypothetical protein
gene_id_10627	306	99.67	0	hypothetical protein
gene_id_10628	314	97.77	0	hypothetical protein
gene_id_10629	295	98.64	0	ribokinase
gene_id_10630	67	97.01	1.00E-38	cold-shock protein
gene_id_10631	66	100	3.00E-38	cold-shock protein
gene_id_10632	244	98.36	1.00E-159	hypothetical protein, partial
gene_id_10633	246	98.78	1.00E-172	hypothetical protein, partial
gene_id_10634	318	95.28	0	hypothetical protein
gene_id_10635	384	97.14	0	hypothetical protein
gene_id_10636	393	97.46	0	hypothetical protein
gene_id_10637	264	98.11	0	hypothetical protein
gene_id_10638	448	90.62	0	hypothetical protein
gene_id_10639	137	91.24	1.00E-69	hypothetical protein, partial
gene_id_10640	291	96.56	0	hypothetical protein
gene_id_10641	447	97.76	0	hypothetical protein
gene_id_10642	81	53.09	1.00E-19	hypothetical protein, partial
gene_id_10643	248	58.06	7.00E-82	hypothetical protein, partial
gene_id_10644	136	97.79	1.00E-96	hypothetical protein
gene_id_10645	223	94.62	1.00E-154	hypothetical protein
gene_id_10646	166	95.78	5.00E-103	hypothetical protein, partial
gene_id_10647	208	96.15	2.00E-136	hypothetical protein
gene_id_10648	204	98.04	3.00E-145	hypothetical protein
gene_id_10649	213	95.77	1.00E-127	membrane protein
gene_id_10650	178	94.38	2.00E-115	hypothetical protein
gene_id_10651	140	96.43	1.00E-93	hypothetical protein
gene_id_10652	221	76.02	1.00E-118	heme response regulator HssR
gene_id_10653	280	68.21	2.00E-113	histidine kinase
gene_id_10654	451	30.16	3.00E-55	RND family efflux transporter, MFP subunit
gene_id_10655	216	66.67	8.00E-104	macrolide ABC transporter ATP-binding protein
gene_id_10656	389	49.61	5.00E-118	ABC transporter permease
gene_id_10657	108	97.22	1.00E-68	hypothetical protein
gene_id_10658	155	97.42	1.00E-104	hypothetical protein, partial
gene_id_10660	610	96.39	0	hypothetical protein, partial
gene_id_10660	364	47.53	3.00E-53	hypothetical protein, partial
gene_id_10661	371	77.63	0	hypothetical protein
gene_id_10662	253	67.98	3.00E-123	hypothetical protein
gene_id_10663	302	99.67	0	hypothetical protein
gene_id_10665	347	98.27	0	methionine ABC transporter ATP-binding protein

gene_id_10666	198	98.99	2.00E-102	ABC transporter permease
gene_id_10667	319	97.49	0	L-lactate dehydrogenase
gene_id_10668	275	100	1.00E-172	hypothetical protein
gene_id_10669	388	97.42	0	aminotransferase
gene_id_10670	256	72.66	1.00E-137	glutamate racemase
gene_id_10671	137	58.39	5.00E-17	hypothetical protein
gene_id_10672	98	94.9	6.00E-60	hypothetical protein
gene_id_10673	134	94.78	1.00E-86	hypothetical protein
gene_id_10674	1516	99.41	0	glutamate synthase, partial
gene_id_10675	493	98.58	0	glutamate synthase
gene_id_10676	402	99.75	0	hypothetical protein
gene_id_10677	585	95.73	0	hypothetical protein
gene_id_10678	338	93.79	0	hypothetical protein
gene_id_10679	191	100	1.00E-122	hypothetical protein
gene_id_10680	154	96.1	4.00E-105	hypothetical protein
gene_id_10681	770	99.48	0	hypothetical protein, partial
gene_id_10682	250	96	5.00E-157	hypothetical protein
gene_id_10683	414	98.07	0	hypothetical protein
gene_id_10684	461	94.79	0	hypothetical protein
gene_id_10685	275	93.82	0	hypothetical protein
gene_id_10686	475	97.26	0	hypothetical protein
gene_id_10687	269	97.77	1.00E-152	hypothetical protein
gene_id_10688	495	98.99	0	CstA-like carbon starvation protein
gene_id_11006	230	98.7	3.00E-164	hypothetical protein
gene_id_11007	160	91.88	9.00E-102	hypothetical protein
gene_id_11008	454	97.14	0	cell division protein FtsH, partial
gene_id_11009	332	100	0	hypothetical protein
gene_id_11010	150	98	3.00E-84	hypothetical protein
gene_id_11011	216	84.26	2.00E-130	hypothetical protein
gene_id_11012	441	99.55	0	Betaine reductase complex component B subunit alp
gene_id_11013	347	99.71	0	hypothetical protein
gene_id_11014	79	100	9.00E-50	glycine reductase complex protein B subunit gamma
gene_id_11015	494	99.8	0	hypothetical protein
gene_id_11016	310	98.06	0	hypothetical protein
gene_id_11017	105	95.24	6.00E-66	thioredoxin
gene_id_11018	43	93.02	5.00E-20	hypothetical protein
gene_id_11019	108	100	1.00E-59	glycine/sarcosine/betaine reductase complex protein
gene_id_11020	511	100	0	hypothetical protein
gene_id_11021	390	98.21	0	hypothetical protein
gene_id_11022	466	99.79	0	hypothetical protein
gene_id_11023	146	98.63	4.00E-101	hypothetical protein
gene_id_11024	627	99.68	0	hypothetical protein
gene_id_11025	1102	97.55	0	hypothetical protein, partial
gene_id_11549	139	62.59	5.00E-56	molecular chaperone Tir
gene_id_11550	144	81.25	4.00E-79	hypothetical protein
gene_id_11551	78	70.51	9.00E-28	hypothetical protein, partial
gene_id_11552	708	55.93	0	hypothetical protein

gene_id_11553	115	74.78	2.00E-57	phage integrase family protein
gene_id_11554	143	61.54	2.00E-49	integrase
gene_id_11555	496	55.85	0	hypothetical protein
gene_id_11556	113	45.13	7.00E-28	hypothetical protein
gene_id_11557	96	48.96	5.00E-21	hypothetical protein
gene_id_11557	93	48.39	6.00E-21	hypothetical protein
gene_id_11558	323	38.39	2.00E-67	hypothetical protein
gene_id_11559	395	96.71	0	hypothetical protein
gene_id_11560	131	96.18	1.00E-84	hypothetical protein
gene_id_11561	218	96.33	2.00E-154	hypothetical protein, partial
gene_id_11562	37	72.97	5.00E-09	split soret cytochrome C precursor
gene_id_11563	88	52.27	8.00E-15	hypothetical protein
gene_id_11564	134	89.55	2.00E-67	hypothetical protein
gene_id_11565	391	95.65	0	hypothetical protein
gene_id_11566	496	97.38	0	hypothetical protein
gene_id_11567	94	97.87	2.00E-61	hypothetical protein
gene_id_11568	79	97.47	3.00E-45	redox-active disulfide protein
gene_id_11569	321	98.75	0	permease
gene_id_11570	151	94.7	4.00E-100	ferredoxin
gene_id_11571	542	98.89	0	aspartate aminotransferase
gene_id_11602	159	99.37	5.00E-113	hypothetical protein
gene_id_11603	110	100	3.00E-73	hypothetical protein
gene_id_11604	240	99.58	1.00E-173	hypothetical protein
gene_id_11606	446	97.98	0	hypothetical protein
gene_id_11607	644	98.14	0	hypothetical protein
gene_id_11608	332	99.7	0	hypothetical protein
gene_id_11609	211	91.94	6.00E-125	hypothetical protein
gene_id_11610	582	95.19	0	hypothetical protein
gene_id_11611	784	99.36	0	recombinase
gene_id_11612	616	99.51	0	excinuclease ABC subunit C
gene_id_11613	303	99.67	0	hypothetical protein
gene_id_11614	1182	72.59	0	pyruvate-flavodoxin oxidoreductase NifJ
gene_id_11615	219	73.52	2.00E-103	hypothetical protein
gene_id_11616	112	33.93	1.00E-06	hypothetical protein
gene_id_11620	155	59.35	4.00E-33	hypothetical protein
gene_id_11621	177	97.18	6.00E-108	hypothetical protein
gene_id_11622	484	82.02	0	hypothetical protein
gene_id_11623	177	98.31	6.00E-122	hypothetical protein
gene_id_11627	471	95.97	0	hypothetical protein
gene_id_11651	866	97.11	0	MULTISPECIES: protein disaggregation chaperone
gene_id_11652	282	97.87	2.00E-173	MULTISPECIES: hypothetical protein
gene_id_11653	94	97.87	3.00E-54	hypothetical protein
gene_id_11654	339	99.41	0	MULTISPECIES: hypothetical protein
gene_id_11655	661	87.9	0	MULTISPECIES: hypothetical protein
gene_id_11656	132	88.64	1.00E-41	MULTISPECIES: hypothetical protein
gene_id_11657	102	99.02	9.00E-64	MULTISPECIES: hypothetical protein
gene_id_11658	212	98.58	8.00E-121	MULTISPECIES: hypothetical protein

gene_id_11659	589	100	0	MULTISPECIES: ATP synthase subunit A
gene_id_11660	461	99.78	0	MULTISPECIES: V-type ATP synthase subunit B
gene_id_11661	192	98.96	4.00E-134	MULTISPECIES: hypothetical protein
gene_id_11662	303	95.05	0	MULTISPECIES: hypothetical protein
gene_id_11663	322	99.07	0	MULTISPECIES: hypothetical protein
gene_id_11664	404	95.54	0	MULTISPECIES: hypothetical protein
gene_id_11665	197	95.43	1.00E-136	MULTISPECIES: hypothetical protein
gene_id_11666	241	96.68	2.00E-163	MULTISPECIES: hypothetical protein
gene_id_11667	201	99	1.00E-142	MULTISPECIES: hypothetical protein
gene_id_11668	398	100	0	MULTISPECIES: acetate kinase
gene_id_11669	167	99.4	8.00E-101	MULTISPECIES: hypothetical protein
gene_id_11670	59	100	8.00E-21	MULTISPECIES: 50S ribosomal protein L32
gene_id_11671	332	100	0	MULTISPECIES: phosphate acyltransferase
gene_id_11672	78	98.72	2.00E-28	MULTISPECIES: acyl carrier protein
gene_id_11673	237	99.16	4.00E-144	MULTISPECIES: ribonuclease III
gene_id_11674	358	97.77	0	MULTISPECIES: hypothetical protein
gene_id_11675	1186	99.07	0	MULTISPECIES: hypothetical protein
gene_id_11676	309	99.35	0	MULTISPECIES: cell division protein FtsY
gene_id_11677	115	99.13	3.00E-73	MULTISPECIES: signal peptide protein
gene_id_11678	431	99.77	0	MULTISPECIES: signal recognition particle protein
gene_id_11679	87	100	5.00E-55	MULTISPECIES: 30S ribosomal protein S16
gene_id_11680	76	100	5.00E-44	MULTISPECIES: hypothetical protein
gene_id_11681	166	97.59	3.00E-99	MULTISPECIES: hypothetical protein
gene_id_11682	238	100	6.00E-170	MULTISPECIES: tRNA (guanine-N1)-methyltransferase
gene_id_11683	115	100	9.00E-75	MULTISPECIES: 50S ribosomal protein L19
gene_id_11684	286	95.45	3.00E-180	MULTISPECIES: GTPase YlqF
gene_id_11685	210	95.71	4.00E-145	MULTISPECIES: ribonuclease HII
gene_id_11686	136	94.12	7.00E-90	MULTISPECIES: hypothetical protein
gene_id_11687	221	96.83	1.00E-134	MULTISPECIES: deoxyribose-phosphate aldolase
gene_id_11688	368	99.46	0	MULTISPECIES: hypothetical protein
gene_id_11689	514	98.44	0	MULTISPECIES: heme ABC transporter ATP-binding p
gene_id_11690	348	98.28	0	MULTISPECIES: hypothetical protein
gene_id_11691	306	98.69	3.00E-168	MULTISPECIES: branched-chain amino acid ABC trans
gene_id_11692	512	62.7	0	ATP-binding protein
gene_id_11693	142	99.3	2.00E-95	MULTISPECIES: AsnC family transcriptional regulator
gene_id_11694	118	90.68	1.00E-71	MULTISPECIES: hypothetical protein
gene_id_11695	443	96.84	0	MULTISPECIES: 30S ribosomal protein S12 methylthi
gene_id_11696	113	96.46	6.00E-74	MULTISPECIES: HIT family hydrolase
gene_id_11697	43	100	3.00E-22	MULTISPECIES: 30S ribosomal protein S21
gene_id_11698	147	98.64	2.00E-70	MULTISPECIES: hypothetical protein
gene_id_11699	92	98.91	2.00E-45	MULTISPECIES: hypothetical protein
gene_id_11700	400	99.25	0	MULTISPECIES: hypothetical protein
gene_id_11701	319	99.69	0	MULTISPECIES: phosphate starvation protein PhoH
gene_id_11702	150	100	2.00E-102	MULTISPECIES: 16S rRNA maturation RNase YbeY
gene_id_11703	365	96.16	0	MULTISPECIES: hypothetical protein
gene_id_11704	130	100	5.00E-89	MULTISPECIES: cytidine deaminase
gene_id_11705	296	99.66	0	MULTISPECIES: GTPase Era

gene_id_11706	237	99.58	4.00E-168	MULTISPECIES: hypothetical protein
gene_id_11707	169	99.41	2.00E-114	MULTISPECIES: hypothetical protein
gene_id_11708	464	99.14	0	MULTISPECIES: glycyl-tRNA synthetase subunit beta
gene_id_11709	161	99.38	4.00E-107	MULTISPECIES: transcriptional regulator
gene_id_11710	269	100	1.00E-178	MULTISPECIES: phosphotransferase
gene_id_11711	337	97.63	0	MULTISPECIES: deoxyguanosinetriphosphate triphos
gene_id_11712	585	99.32	0	MULTISPECIES: DNA primase
gene_id_11713	388	99.74	0	MULTISPECIES: RNA polymerase sigma factor RpoD
gene_id_11714	216	95.83	2.00E-148	MULTISPECIES: hypothetical protein
gene_id_12018	445	66.52	0	MULTISPECIES: amino acid permease
gene_id_12019	233	72.96	8.00E-114	MULTISPECIES: isochorismatase family protein
gene_id_12020	786	32.19	1.00E-118	hypothetical protein
gene_id_12021	452	48.89	1.00E-144	hypothetical protein
gene_id_12022	259	87.26	2.00E-167	alpha/beta hydrolase
gene_id_12023	100	99	5.00E-68	hypothetical protein
gene_id_12024	131	99.24	1.00E-86	hypothetical protein
gene_id_12025	193	95.85	2.00E-134	hypothetical protein
gene_id_12026	178	82.02	5.00E-103	methylase involved in ubiquinone/menaquinone bios
gene_id_12027	219	51.6	6.00E-74	hAD-superfamily hydrolase subfamily IA variant 3
gene_id_12028	109	67.89	2.00E-46	hypothetical protein
gene_id_12029	235	80	2.00E-126	hypothetical protein
gene_id_12030	144	95.83	3.00E-96	hypothetical protein, partial
gene_id_12031	279	93.55	6.00E-172	hypothetical protein
gene_id_12032	247	38.87	3.00E-57	hypothetical protein
gene_id_12033	422	24.88	1.00E-17	hypothetical protein
gene_id_12035	573	93.89	0	hypothetical protein
gene_id_12036	227	96.04	1.00E-155	hypothetical protein
gene_id_12037	712	94.24	0	hypothetical protein
gene_id_12038	372	97.31	0	hypothetical protein
gene_id_12039	666	41.89	1.00E-125	repeat, TIGR02543 family, partial
gene_id_12039	402	40.05	1.00E-63	repeat, TIGR02543 family, partial
gene_id_12039	349	42.41	2.00E-60	repeat, TIGR02543 family, partial
gene_id_12039	229	45.41	2.00E-46	repeat, TIGR02543 family, partial
gene_id_12040	339	58.11	4.00E-131	FMN-dependent alpha-hydroxy acid dehydrogenase
gene_id_12041	182	54.4	2.00E-60	XRE family transcriptional regulator
gene_id_12042	98	98.98	2.00E-63	hypothetical protein
gene_id_12043	246	98.78	1.00E-153	nitrate ABC transporter permease
gene_id_12044	337	97.92	0	nitrate ABC transporter substrate-binding protein
gene_id_12045	245	97.55	2.00E-165	hypothetical protein
gene_id_12046	225	92.89	2.00E-147	hypothetical protein
gene_id_12047	87	94.25	2.00E-52	hypothetical protein
gene_id_12048	623	70.14	0	fumarate reductase/succinate dehydrogenase flavop
gene_id_12049	195	56.92	1.00E-77	TetR family transcriptional regulator
gene_id_12050	526	58.75	0	hypothetical protein
gene_id_12051	107	45.79	4.00E-18	hypothetical protein
gene_id_12052	279	34.05	5.00E-38	esterase
gene_id_12053	263	35.36	2.00E-42	esterase

gene_id_12054	464	43.1	1.00E-112	hypothetical protein, partial
gene_id_12055	86	72.09	5.00E-25	hypothetical protein
gene_id_12056	394	96.95	0	aminotransferase
gene_id_12057	66	100	2.00E-24	hypothetical protein, partial
gene_id_12058	155	97.42	1.00E-105	glyoxalase
gene_id_12059	182	48.9	4.00E-55	acetyltransferase, GNAT family
gene_id_12060	96	98.96	6.00E-47	hypothetical protein
gene_id_12061	549	97.09	0	hypothetical protein
gene_id_12675	479	96.87	0	hypothetical protein
gene_id_12676	351	54.99	6.00E-122	flagellar biosynthesis protein FlhB
gene_id_12677	256	93.36	1.00E-137	hypothetical protein
gene_id_12678	88	94.32	6.00E-29	hypothetical protein
gene_id_12679	217	99.54	1.00E-116	flagellar biosynthesis protein flip
gene_id_12680	91	92.31	1.00E-52	hypothetical protein
gene_id_12681	120	97.5	1.00E-76	chemotaxis protein CheY
gene_id_12682	365	94.25	0	hypothetical protein
gene_id_12683	314	96.5	0	hypothetical protein
gene_id_12684	233	97.42	1.00E-146	hypothetical protein, partial
gene_id_12685	266	97.37	1.00E-180	hypothetical protein
gene_id_12686	65	100	4.00E-35	hypothetical protein
gene_id_12687	297	65.66	4.00E-109	hypothetical protein
gene_id_12688	127	97.64	2.00E-80	hypothetical protein
gene_id_12689	133	92.48	3.00E-83	hypothetical protein, partial
gene_id_12690	275	91.27	2.00E-157	hypothetical protein
gene_id_12691	150	97.33	2.00E-67	hypothetical protein
gene_id_12692	436	97.94	0	hypothetical protein
gene_id_12693	258	92.64	1.00E-149	hypothetical protein
gene_id_12694	335	99.7	0	flagellar motor switch protein FliG
gene_id_12695	529	92.06	0	hypothetical protein
gene_id_12696	101	95.05	4.00E-61	hypothetical protein
gene_id_12697	143	97.9	3.00E-98	hypothetical protein
gene_id_12698	111	96.4	3.00E-69	hypothetical protein
gene_id_12700	79	98.73	4.00E-27	hypothetical protein
gene_id_12701	145	95.86	4.00E-95	hypothetical protein
gene_id_12702	201	98.51	4.00E-142	hypothetical protein
gene_id_12703	340	95.88	0	hypothetical protein
gene_id_12704	510	93.92	0	hypothetical protein
gene_id_12705	152	94.74	2.00E-94	hypothetical protein
gene_id_12706	91	93.41	6.00E-48	hypothetical protein
gene_id_12707	275	98.18	0	hypothetical protein
gene_id_12708	166	99.4	5.00E-101	hypothetical protein
gene_id_12709	79	98.73	2.00E-47	hypothetical protein
gene_id_12710	253	99.21	6.00E-163	hypothetical protein
gene_id_12711	151	37.75	8.00E-28	hypothetical protein
gene_id_12713	221	92.76	4.00E-133	hypothetical protein
gene_id_12714	177	36.16	1.00E-19	hypothetical protein CM240_0570
gene_id_12715	93	30.11	3.00E-06	hypothetical protein PDUR_15340

gene_id_12719	113	84.07	6.00E-56	hypothetical protein
gene_id_12721	50	70	5.00E-13	hypothetical protein
gene_id_12724	207	79.71	3.00E-108	hypothetical protein
gene_id_12725	123	69.92	2.00E-54	resolvase
gene_id_12726	98	77.55	2.00E-46	hypothetical protein
gene_id_12729	797	91.84	0	hypothetical protein
gene_id_12729	651	29.49	2.00E-53	hypothetical protein
gene_id_12729	626	30.83	3.00E-52	hypothetical protein
gene_id_12729	588	30.1	2.00E-50	hypothetical protein
gene_id_12729	600	31.33	1.00E-48	hypothetical protein
gene_id_12729	633	29.38	6.00E-45	hypothetical protein
gene_id_12729	542	31.92	9.00E-41	hypothetical protein
gene_id_12730	160	40.62	3.00E-31	hypothetical protein, partial
gene_id_12731	388	47.68	5.00E-109	cell division protein FtsK
gene_id_12733	122	37.7	1.00E-11	hypothetical protein
gene_id_12734	77	59.74	1.00E-14	hypothetical protein
gene_id_12735	91	45.05	1.00E-18	putative phage holin LL-H family
gene_id_12736	181	60.77	1.00E-72	hypothetical protein, partial
gene_id_12737	167	37.72	2.00E-24	hypothetical protein
gene_id_12738	657	61.19	0	hypothetical protein EAL2_808p01880
gene_id_12739	293	49.49	3.00E-83	hypothetical protein
gene_id_12740	74	50	2.00E-12	hypothetical protein EAL2_c05990
gene_id_12741	258	54.26	2.00E-102	hypothetical protein EAL2_c05980
gene_id_12742	358	54.47	8.00E-99	hypothetical protein
gene_id_12744	123	59.35	2.00E-46	hypothetical protein
gene_id_12745	179	53.63	1.00E-52	maj_tail_phi13: phage major tail protein, phi13 famil
gene_id_12746	96	54.17	1.00E-30	Hypothetical protein DPCES_5355
gene_id_12747	111	52.25	2.00E-31	hypothetical protein
gene_id_12748	104	39.42	3.00E-12	phage head-tail adaptor, putative, SPP1 family
gene_id_12749	78	56.41	2.00E-25	hypothetical protein
gene_id_12751	398	76.38	0	hypothetical protein
gene_id_12752	230	72.61	2.00E-121	peptidase S14
gene_id_12753	390	60.51	5.00E-166	portal protein
gene_id_12754	511	75.93	0	terminase
gene_id_12755	113	57.52	5.00E-35	putative uncharacterized protein
gene_id_12756	100	60	6.00E-31	HNH endonuclease
gene_id_12758	195	53.33	4.00E-37	hypothetical protein
gene_id_12759	320	50.94	1.00E-100	hypothetical protein
gene_id_12761	173	38.73	4.00E-23	hypothetical protein
gene_id_12762	183	35.52	9.00E-35	hypothetical protein
gene_id_12763	177	32.77	1.00E-26	hypothetical protein
gene_id_12766	163	54.6	5.00E-53	recombinase
gene_id_12768	106	58.49	3.00E-27	hypothetical protein
gene_id_12769	126	42.86	2.00E-24	hypothetical protein
gene_id_12770	130	36.92	3.00E-10	hypothetical protein
gene_id_12771	70	71.43	1.00E-18	hypothetical protein
gene_id_12772	122	34.43	3.00E-11	hypothetical protein

gene_id_12776	636	48.74	0	hypothetical protein
gene_id_12777	118	49.15	4.00E-30	hypothetical protein
gene_id_12779	246	51.22	2.00E-72	hypothetical protein
gene_id_12781	93	44.09	3.00E-13	hypothetical protein
gene_id_12785	108	48.15	6.00E-21	putative pikk family atypical protein kinase
gene_id_12786	55	52.73	8.00E-11	hypothetical protein
gene_id_12787	63	34.92	2.00E-08	hypothetical protein
gene_id_12788	64	50	3.00E-14	hypothetical protein
gene_id_12790	62	43.55	1.00E-10	hypothetical protein
gene_id_12791	89	44.94	2.00E-17	transcriptional regulator XRE family
gene_id_12792	151	58.28	4.00E-55	membrane protein
gene_id_12793	403	50.62	3.00E-141	integrase
gene_id_12794	528	100	0	molecular chaperone GroEL
gene_id_12795	93	100	4.00E-53	co-chaperonin GroES
gene_id_12796	309	99.35	0	fructose-bisphosphate aldolase
gene_id_12797	398	98.99	0	hypothetical protein
gene_id_12798	620	99.03	0	hypothetical protein
gene_id_12800	325	90.77	5.00E-141	hypothetical protein
gene_id_12801	248	99.19	8.00E-178	hypothetical protein
gene_id_12802	79	100	3.00E-47	hypothetical protein
gene_id_12803	407	99.26	0	DNA polymerase IV
gene_id_12804	257	98.44	8.00E-169	hypothetical protein
gene_id_12805	193	99.48	9.00E-119	hypothetical protein
gene_id_12806	176	98.86	5.00E-120	adenylate cyclase
gene_id_12807	236	99.58	2.00E-133	hypothetical protein
gene_id_12808	97	100	2.00E-60	hypothetical protein, partial
gene_id_12809	128	99.22	6.00E-87	hypothetical protein
gene_id_12810	661	96.67	0	hypothetical protein
gene_id_12812	275	98.55	0	hypothetical protein
gene_id_12813	460	96.3	0	hypothetical protein
gene_id_12814	396	97.73	0	hypothetical protein
gene_id_12815	493	99.59	0	hypothetical protein
gene_id_12816	399	99.75	0	hypothetical protein
gene_id_12817	73	97.26	2.00E-43	hypothetical protein
gene_id_12818	417	90.41	0	hypothetical protein
gene_id_12819	240	96.67	7.00E-156	hypothetical protein
gene_id_12820	211	98.58	2.00E-151	hypothetical protein
gene_id_12821	333	99.7	0	hypothetical protein
gene_id_12822	517	65.76	0	hypothetical protein
gene_id_12823	497	99.8	0	hypothetical protein
gene_id_12824	152	100	4.00E-86	hypothetical protein
gene_id_12825	201	99	1.00E-139	hypothetical protein
gene_id_12826	393	96.44	0	hypothetical protein
gene_id_12827	166	96.99	1.00E-100	hypothetical protein, partial
gene_id_12828	226	96.46	4.00E-154	hypothetical protein, partial
gene_id_12829	126	99.21	3.00E-69	hypothetical protein
gene_id_12830	257	97.67	0	hypothetical protein

gene_id_12831	646	97.06	0	hypothetical protein
gene_id_12832	410	98.54	0	hypothetical protein
gene_id_12833	232	78.45	3.00E-131	hypothetical protein
gene_id_12834	387	97.67	0	hypothetical protein
gene_id_12835	456	99.34	0	C4-dicarboxylate ABC transporter
gene_id_12836	257	98.83	1.00E-164	hypothetical protein, partial
gene_id_12837	68	92.65	1.00E-35	DNA-binding protein
gene_id_12838	135	96.3	1.00E-80	hypothetical protein
gene_id_12839	330	30.91	2.00E-21	hypothetical protein
gene_id_12840	442	43.89	5.00E-110	hypothetical protein
gene_id_12944	296	94.93	0	hypothetical protein, partial
gene_id_12945	60	95	1.00E-30	hypothetical protein
gene_id_12946	330	39.7	9.00E-47	hypothetical protein
gene_id_12947	668	94.46	0	hypothetical protein
gene_id_12948	423	99.05	0	hypothetical protein
gene_id_12950	209	97.61	1.00E-146	polysaccharide deacetylase, partial
gene_id_12951	158	94.94	6.00E-102	hypothetical protein
gene_id_12952	237	93.67	1.00E-158	hypothetical protein
gene_id_12953	151	98.68	1.00E-104	hypothetical protein
gene_id_12954	327	98.47	0	hypothetical protein
gene_id_12955	366	97.81	0	hypothetical protein
gene_id_12956	442	97.29	0	C4-dicarboxylate ABC transporter
gene_id_12957	155	98.06	5.00E-104	hypothetical protein, partial
gene_id_12958	517	99.03	0	peptidase C69, partial
gene_id_12959	351	96.87	0	hypothetical protein
gene_id_12960	123	95.12	6.00E-46	hypothetical protein
gene_id_12961	362	91.99	0	hypothetical protein
gene_id_12962	433	99.31	0	hypothetical protein, partial
gene_id_12963	164	95.12	1.00E-97	hypothetical protein
gene_id_12964	185	97.84	1.00E-120	hypothetical protein
gene_id_12965	192	96.88	3.00E-135	hypothetical protein
gene_id_12966	279	97.85	0	hypothetical protein
gene_id_12967	242	97.11	2.00E-152	hypothetical protein
gene_id_12968	136	94.85	1.00E-87	hypothetical protein
gene_id_12969	192	94.79	1.00E-131	hypothetical protein
gene_id_12970	138	96.38	3.00E-90	hypothetical protein
gene_id_12971	286	97.2	0	hydratase
gene_id_12972	727	96.97	0	hypothetical protein, partial
gene_id_12973	411	96.35	0	hypothetical protein, partial
gene_id_12974	147	97.96	4.00E-101	hypothetical protein
gene_id_12975	326	74.23	9.00E-170	beta-lactamase
gene_id_12976	309	81.88	0	AraC family transcriptional regulator
gene_id_12977	178	93.26	5.00E-116	nitroreductase
gene_id_12978	155	94.19	2.00E-104	mannose-6-phosphate isomerase
gene_id_12979	153	56.21	1.00E-58	N-acetyltransferase GCN5
gene_id_12980	180	72.78	6.00E-95	hypothetical protein
gene_id_12981	275	96.73	0	hypothetical protein

gene_id_12982	370	97.3	0	hypothetical protein
gene_id_12983	287	95.47	0	CAAX protease, partial
gene_id_12984	226	94.69	2.00E-124	hypothetical protein
gene_id_12985	336	98.81	0	hypothetical protein
gene_id_12986	620	71.77	0	hypothetical protein
gene_id_12987	135	45.93	4.00E-32	transcriptional regulator, MarR family
gene_id_12988	598	77.76	0	putative peptidase S15
gene_id_12989	404	44.8	4.00E-91	hypothetical protein
gene_id_12990	614	80.78	0	dipeptidyl aminopeptidase
gene_id_12991	225	43.56	3.00E-54	hypothetical protein
gene_id_12992	455	67.25	0	amino acid permease superfamily
gene_id_12993	179	93.3	3.00E-121	hypothetical protein
gene_id_12994	527	43.83	3.00E-136	putative exporter of polyketide antibiotics
gene_id_12995	256	75.39	1.00E-124	ABC transporter ATP-binding protein, partial
gene_id_12996	208	71.15	4.00E-96	TetR family transcriptional regulator
gene_id_12997	249	36.14	1.00E-36	hypothetical protein
gene_id_12998	261	35.25	6.00E-44	hypothetical protein
gene_id_12999	290	62.07	5.00E-121	ABC transporter
gene_id_13000	203	68.97	9.00E-77	TetR family transcriptional regulator
gene_id_13001	787	68.49	0	phosphoenolpyruvate synthase
gene_id_13002	204	65.2	9.00E-81	TetR family transcriptional regulator
gene_id_13003	319	98.43	0	hypothetical protein
gene_id_13004	114	92.98	1.00E-68	hypothetical protein
gene_id_13005	349	97.42	0	hypothetical protein
gene_id_13006	398	97.49	0	hypothetical protein
gene_id_13007	1618	96.35	0	hypothetical protein
gene_id_13008	297	98.32	0	hypothetical protein
gene_id_13009	110	89.09	8.00E-64	hypothetical protein
gene_id_13010	212	97.17	1.00E-147	hypothetical protein
gene_id_13011	363	99.45	0	hypothetical protein
gene_id_13012	164	100	9.00E-113	hypothetical protein
gene_id_13013	310	98.39	0	hypothetical protein
gene_id_13014	264	68.18	3.00E-126	transketolase
gene_id_13015	215	99.53	3.00E-134	transaldolase
gene_id_13016	255	98.43	3.00E-180	hypothetical protein
gene_id_13017	350	98	0	hypothetical protein
gene_id_13018	716	97.77	0	hypothetical protein
gene_id_13019	273	98.9	0	hypothetical protein
gene_id_13020	137	99.27	7.00E-82	hypothetical protein, partial
gene_id_13021	255	97.65	7.00E-179	hypothetical protein, partial
gene_id_13022	206	99.03	4.00E-103	hypothetical protein
gene_id_13023	181	97.79	8.00E-100	dephospho-CoA kinase
gene_id_13024	913	97.37	0	hypothetical protein
gene_id_13025	204	94.61	3.00E-140	hypothetical protein
gene_id_13026	300	100	0	hypothetical protein
gene_id_13027	145	100	1.00E-100	hypothetical protein
gene_id_13028	204	98.04	1.00E-114	hypothetical protein

gene_id_13029	419	95.7	0	hypothetical protein
gene_id_13030	297	78.45	4.00E-179	glutamate formiminotransferase
gene_id_13031	673	98.37	0	urocanate hydratase
gene_id_13032	553	95.66	0	hypothetical protein
gene_id_13033	89	96.63	6.00E-55	hypothetical protein
gene_id_13034	137	97.08	7.00E-90	iron-sulfur protein, partial
gene_id_13035	187	96.79	5.00E-130	hypothetical protein
gene_id_13036	254	95.28	2.00E-174	hypothetical protein
gene_id_13037	162	96.91	3.00E-86	hypothetical protein, partial
gene_id_13038	166	96.99	2.00E-110	hypothetical protein
gene_id_13039	449	99.78	0	hypothetical protein
gene_id_13040	312	98.72	0	hypothetical protein
gene_id_13041	174	95.4	1.00E-116	hypothetical protein
gene_id_13042	102	98.04	1.00E-61	hypothetical protein, partial
gene_id_13043	638	97.81	0	hypothetical protein
gene_id_13044	340	99.41	0	tRNA threonylcarbamoyladenosine modification prot
gene_id_13045	424	98.35	0	hypothetical protein
gene_id_13046	352	98.01	0	ABC transporter
gene_id_13047	532	99.25	0	sugar ABC transporter ATP-binding protein
gene_id_13048	403	98.26	0	hypothetical protein
gene_id_13049	307	96.09	0	ATPase AAA
gene_id_13050	381	96.06	0	hypothetical protein
gene_id_13051	801	92.13	0	hypothetical protein
gene_id_13052	105	100	1.00E-63	hypothetical protein
gene_id_13053	279	98.21	0	hypothetical protein
gene_id_13054	1206	97.18	0	hypothetical protein
gene_id_13055	1133	96.82	0	hypothetical protein
gene_id_13056	321	98.13	0	CMP-binding protein
gene_id_13057	52	92.31	9.00E-23	DNA-binding protein, partial
gene_id_13058	424	95.28	0	hypothetical protein
gene_id_13059	193	98.96	1.00E-132	hypothetical protein
gene_id_13060	339	98.53	0	hypothetical protein, partial
gene_id_13061	509	99.02	0	hypothetical protein
gene_id_13062	157	93.63	7.00E-101	hypothetical protein
gene_id_13064	144	100	3.00E-82	hypothetical protein
gene_id_13065	81	96.3	5.00E-27	hypothetical protein, partial
gene_id_13066	574	58.71	0	FMN-binding domain-containing protein
gene_id_13067	163	92.64	3.00E-104	hypothetical protein
gene_id_13068	447	97.54	0	hypothetical protein
gene_id_13069	216	99.07	1.00E-151	hypothetical protein
gene_id_13070	228	98.68	2.00E-162	hypothetical protein
gene_id_13071	448	98.88	0	hypothetical protein
gene_id_13072	210	99.52	3.00E-126	FMN reductase
gene_id_13073	203	95.57	4.00E-139	hypothetical protein
gene_id_13074	342	98.83	0	hypothetical protein
gene_id_13075	139	99.28	4.00E-92	hypothetical protein
gene_id_13076	490	96.94	0	hypothetical protein

gene_id_13077	303	99.34	4.00E-180	ribose ABC transporter permease
gene_id_13078	312	96.15	0	hypothetical protein
gene_id_13079	243	98.77	1.00E-160	ABC transporter
gene_id_13080	232	97.84	3.00E-160	hypothetical protein
gene_id_13081	270	98.52	0	hypothetical protein
gene_id_13082	140	93.57	2.00E-67	hypothetical protein
gene_id_13083	241	97.93	2.00E-173	hypothetical protein
gene_id_13084	360	97.78	0	hypothetical protein
gene_id_13085	237	98.31	2.00E-166	hypothetical protein
gene_id_13086	414	98.07	0	hypothetical protein
gene_id_13087	257	93	2.00E-167	hypothetical protein
gene_id_13088	770	95.84	0	hypothetical protein
gene_id_13089	89	98.88	1.00E-55	hypothetical protein
gene_id_13090	122	94.26	2.00E-79	hypothetical protein
gene_id_13091	432	99.07	0	hypothetical protein
gene_id_13092	242	99.17	4.00E-162	hypothetical protein
gene_id_13093	361	96.95	0	membrane protein
gene_id_13094	67	100	2.00E-39	hypothetical protein
gene_id_13095	81	95.06	4.00E-49	hypothetical protein
gene_id_13096	124	96.77	2.00E-81	hypothetical protein
gene_id_13097	536	98.13	0	D-aminoacylase
gene_id_13098	477	97.27	0	sodium:solute symporter
gene_id_13099	394	97.21	0	peptidase M20
gene_id_13100	408	94.61	0	hypothetical protein
gene_id_13101	584	98.97	0	hypothetical protein
gene_id_13102	235	97.45	4.00E-153	EcsC protein family
gene_id_13103	417	97.84	0	MFS transporter
gene_id_13104	122	97.54	1.00E-80	hypothetical protein
gene_id_13105	193	97.41	8.00E-133	hypothetical protein
gene_id_13106	538	94.05	0	hypothetical protein
gene_id_13107	256	98.05	6.00E-176	hypothetical protein
gene_id_13108	134	97.76	1.00E-82	hypothetical protein, partial
gene_id_13197	292	95.55	4.00E-167	hypothetical protein
gene_id_13198	389	98.46	0	hypothetical protein
gene_id_13199	337	97.33	0	hypothetical protein
gene_id_13200	313	99.04	0	hypothetical protein, partial
gene_id_13201	425	98.35	0	hypothetical protein
gene_id_13202	167	97.6	2.00E-92	hypothetical protein
gene_id_13203	200	99.5	7.00E-112	hypothetical protein
gene_id_13204	273	97.8	0	hypothetical protein
gene_id_13205	397	97.98	0	hypothetical protein
gene_id_13206	69	97.1	6.00E-39	hypothetical protein
gene_id_13207	545	97.25	0	hypothetical protein
gene_id_13208	571	96.5	0	hypothetical protein
gene_id_13209	231	99.57	3.00E-164	hypothetical protein
gene_id_13210	215	97.21	1.00E-146	hypothetical protein
gene_id_13211	252	98.02	2.00E-172	phosphate ABC transporter ATP-binding protein

gene_id_13212	292	99.32	0	hypothetical protein
gene_id_13213	293	98.98	1.00E-175	hypothetical protein
gene_id_13214	292	96.58	0	hypothetical protein
gene_id_13215	698	95.56	0	hypothetical protein
gene_id_13216	464	93.1	0	sodium:proton antiporter, partial
gene_id_13217	632	99.53	0	hypothetical protein
gene_id_13218	210	98.1	1.00E-146	hypothetical protein
gene_id_13219	190	99.47	2.00E-132	hypothetical protein
gene_id_13220	371	93.26	0	hypothetical protein
gene_id_13221	427	94.85	0	hypothetical protein
gene_id_13222	696	98.99	0	hypothetical protein
gene_id_13223	439	98.41	0	hypothetical protein
gene_id_13224	189	99.47	2.00E-131	hypothetical protein
gene_id_13225	127	96.06	7.00E-79	hypothetical protein
gene_id_13226	301	99.34	0	hypothetical protein
gene_id_13227	472	97.88	0	hypothetical protein
gene_id_13228	486	97.12	0	glutamyl-tRNA amidotransferase
gene_id_13229	96	98.96	3.00E-60	hypothetical protein
gene_id_13230	581	98.28	0	aspartyl-tRNA synthetase
gene_id_13231	814	99.26	0	hypothetical protein
gene_id_13232	334	98.2	0	hypothetical protein
gene_id_13233	167	98.8	1.00E-118	hypothetical protein
gene_id_13234	156	97.44	8.00E-103	hypothetical protein
gene_id_13235	444	70.05	0	NADP-specific glutamate dehydrogenase
gene_id_13236	624	98.4	0	ATPase AAA
gene_id_13237	604	95.36	0	hypothetical protein
gene_id_13238	74	94.59	6.00E-42	hypothetical protein
gene_id_13239	387	71.06	0	amidohydrolase
gene_id_13241	76	98.68	8.00E-46	hypothetical protein
gene_id_13242	95	98.95	4.00E-61	hypothetical protein
gene_id_13243	186	95.7	3.00E-120	hypothetical protein
gene_id_13244	226	71.24	2.00E-121	hypothetical protein
gene_id_13245	349	97.42	0	arsenic transporter
gene_id_13246	111	82.88	3.00E-61	hypothetical protein
gene_id_13247	113	67.26	2.00E-49	arsenical resistance operon trans-acting repressor Ar
gene_id_13248	115	93.91	1.00E-61	hypothetical protein
gene_id_13249	297	95.96	0	hypothetical protein
gene_id_13250	183	96.72	4.00E-117	hypothetical protein
gene_id_13251	80	100	1.00E-50	iron-binding protein
gene_id_13252	665	98.8	0	fructose-1,6-bisphosphatase
gene_id_13253	233	99.57	1.00E-161	hypothetical protein
gene_id_13254	230	83.04	4.00E-74	hypothetical protein
gene_id_13255	265	95.85	0	hypothetical protein
gene_id_13256	97	100	1.00E-62	hypothetical protein, partial
gene_id_13257	154	93.51	1.00E-97	hypothetical protein
gene_id_13258	481	95.63	0	hypothetical protein
gene_id_13259	199	96.98	3.00E-139	hypothetical protein

gene_id_13260	167	97.01	7.00E-112	hypothetical protein
gene_id_13261	122	99.18	2.00E-81	hypothetical protein
gene_id_13262	128	99.22	3.00E-88	hypothetical protein
gene_id_13263	413	48.18	3.00E-122	D-alanyl-D-alanine carboxypeptidase
gene_id_13264	197	93.91	1.00E-122	hypothetical protein
gene_id_13265	314	98.09	0	hypothetical protein
gene_id_13266	466	98.28	0	hypothetical protein
gene_id_13267	629	56.76	0	hypothetical protein
gene_id_13268	228	99.12	1.00E-147	hypothetical protein
gene_id_13269	357	99.72	0	hypothetical protein
gene_id_13270	1068	99.63	0	hypothetical protein
gene_id_13271	122	98.36	3.00E-80	hypothetical protein
gene_id_13272	100	100	3.00E-62	hypothetical protein
gene_id_13273	497	96.38	0	hypothetical protein
gene_id_13274	233	99.57	3.00E-166	ABC transporter
gene_id_13275	599	95.66	0	hypothetical protein
gene_id_13276	448	98.66	0	hypothetical protein
gene_id_13277	302	98.68	5.00E-165	hypothetical protein, partial
gene_id_13278	256	87.5	3.00E-168	hypothetical protein
gene_id_13279	127	95.28	2.00E-82	hypothetical protein
gene_id_13280	153	98.04	4.00E-103	hypothetical protein
gene_id_13281	210	94.29	2.00E-126	hypothetical protein
gene_id_13282	296	91.22	0	hypothetical protein
gene_id_13283	63	100	4.00E-38	membrane protein, partial
gene_id_13284	159	100	1.00E-94	hypothetical protein
gene_id_13285	80	96.25	1.00E-33	hypothetical protein
gene_id_13286	192	96.88	1.00E-131	septum formation inhibitor Maf
gene_id_13287	229	98.69	3.00E-162	hypothetical protein
gene_id_13288	352	98.58	0	hypothetical protein, partial
gene_id_13289	279	98.57	9.00E-179	hypothetical protein
gene_id_13290	163	96.32	7.00E-67	hypothetical protein
gene_id_13291	847	96.93	0	hypothetical protein, partial
gene_id_13292	232	96.98	9.00E-158	hypothetical protein
gene_id_13293	190	95.79	2.00E-126	hypothetical protein
gene_id_13294	171	99.42	3.00E-106	hypothetical protein
gene_id_13295	124	95.97	2.00E-80	hypothetical protein, partial
gene_id_13296	245	98.37	1.00E-161	hypothetical protein
gene_id_13298	232	96.98	3.00E-160	hypothetical protein, partial
gene_id_13299	117	96.58	9.00E-74	hypothetical protein
gene_id_13300	141	99.29	4.00E-96	hypothetical protein
gene_id_13301	410	99.51	0	hypothetical protein
gene_id_13302	110	95.45	2.00E-58	hypothetical protein
gene_id_13303	209	96.65	3.00E-142	hypothetical protein
gene_id_13304	181	98.34	1.00E-124	hypothetical protein
gene_id_13305	443	99.77	0	hypothetical protein
gene_id_13306	316	99.05	5.00E-172	hypothetical protein
gene_id_13307	188	100	1.00E-130	hypothetical protein

gene_id_13308	198	100	2.00E-117	hypothetical protein
gene_id_13309	191	99.48	1.00E-127	hypothetical protein
gene_id_13310	291	98.97	4.00E-177	hypothetical protein
gene_id_13311	212	95.28	6.00E-146	hypothetical protein
gene_id_13312	483	70.39	0	nicotinate phosphoribosyltransferase
gene_id_13313	396	97.98	0	F420-0:Gamma-glutamyl ligase
gene_id_13314	153	98.69	1.00E-51	hypothetical protein, partial
gene_id_13315	80	100	9.00E-44	hypothetical protein
gene_id_13317	467	99.14	0	hypothetical protein
gene_id_13318	203	100	2.00E-144	hypothetical protein
gene_id_13319	110	99.09	8.00E-48	hypothetical protein
gene_id_13320	326	97.24	0	hypothetical protein
gene_id_13321	293	99.66	0	hypothetical protein
gene_id_13322	56	100	8.00E-30	ferredoxin
gene_id_13323	431	97.45	0	hypothetical protein
gene_id_13324	441	99.32	0	ribosome-associated GTPase EngA
gene_id_13325	192	95.31	2.00E-124	hypothetical protein
gene_id_13326	332	97.89	0	hypothetical protein
gene_id_13327	492	99.8	0	stage IV sporulation protein A
gene_id_13328	25	100	4.00E-08	hypothetical protein
gene_id_13329	385	96.88	0	hypothetical protein
gene_id_13330	234	97.01	2.00E-148	hypothetical protein
gene_id_13331	145	100	1.00E-89	hypothetical protein
gene_id_13332	69	100	3.00E-40	hypothetical protein
gene_id_13333	261	95.4	3.00E-180	hypothetical protein
gene_id_13334	156	97.44	1.00E-101	hypothetical protein
gene_id_13335	296	98.65	0	pseudouridine synthase
gene_id_13336	176	99.43	4.00E-114	hypothetical protein
gene_id_13337	99	97.98	7.00E-61	hypothetical protein
gene_id_13338	583	91.77	0	fibronectin-binding protein
gene_id_13339	295	99.66	0	hypothetical protein
gene_id_13340	85	100	8.00E-54	hypothetical protein
gene_id_13341	201	99.5	2.00E-129	guanylate kinase
gene_id_13342	52	100	2.00E-26	DNA-directed RNA polymerase subunit omega, partia
gene_id_13343	806	97.64	0	hypothetical protein
gene_id_13344	147	98.64	2.00E-100	hypothetical protein
gene_id_13345	309	96.12	0	methionyl-tRNA formyltransferase
gene_id_13346	442	97.06	0	hypothetical protein
gene_id_13347	342	99.71	0	hypothetical protein
gene_id_13348	250	99.2	2.00E-160	hypothetical protein
gene_id_13349	682	98.24	0	hypothetical protein
gene_id_13350	292	97.6	0	GTPase RsgA
gene_id_13351	219	97.72	1.00E-152	hypothetical protein
gene_id_13352	211	94.31	8.00E-124	hypothetical protein
gene_id_13353	462	99.13	0	asparaginyl-tRNA synthetase
gene_id_13354	65	95.38	3.00E-08	hypothetical protein
gene_id_13355	63	100	3.00E-36	50S ribosomal protein L28

gene_id_13356	114	100	3.00E-73	hypothetical protein
gene_id_13357	538	99.07	0	hypothetical protein
gene_id_13358	684	96.2	0	hypothetical protein
gene_id_13359	186	97.85	6.00E-127	hypothetical protein
gene_id_13360	158	98.73	2.00E-84	hypothetical protein
gene_id_13361	148	98.65	1.00E-94	hypothetical protein
gene_id_13362	230	99.57	2.00E-151	hydrolase
gene_id_13363	166	98.8	4.00E-116	hypothetical protein, partial
gene_id_13364	446	98.43	0	trigger factor
gene_id_13365	194	100	4.00E-137	ATP-dependent Clp protease proteolytic subunit
gene_id_13366	418	100	0	ATP-dependent protease
gene_id_13367	775	98.97	0	hypothetical protein
gene_id_13368	198	98.99	8.00E-142	hypothetical protein
gene_id_13369	129	100	9.00E-84	hypothetical protein
gene_id_13370	778	98.97	0	hypothetical protein
gene_id_13371	236	98.31	8.00E-167	hypothetical protein, partial
gene_id_13372	382	96.86	0	hypothetical protein
gene_id_13373	386	98.96	0	hypothetical protein
gene_id_13375	398	99.75	0	hypothetical protein
gene_id_13376	146	99.32	8.00E-103	RNaseH ribonuclease
gene_id_13377	158	97.47	5.00E-104	hypothetical protein, partial
gene_id_13378	262	99.62	5.00E-174	hypothetical protein
gene_id_13379	170	100	1.00E-119	hypothetical protein
gene_id_13380	296	99.66	0	hypothetical protein
gene_id_13381	176	99.43	2.00E-123	hypothetical protein
gene_id_13382	370	95.95	0	hypothetical protein
gene_id_13383	303	94.06	0	GCN5 family acetyltransferase
gene_id_13384	71	90.14	2.00E-27	hypothetical protein
gene_id_13385	233	98.71	6.00E-166	hypothetical protein
gene_id_13386	365	100	0	hypothetical protein
gene_id_13387	453	98.9	0	hypothetical protein
gene_id_13388	477	71.7	0	Na+/H+ antiporter family protein
gene_id_13389	101	98.02	2.00E-65	2-amino-4-ketopentanoate thiolase subunit alpha
gene_id_13439	489	94.48	0	MULTISPECIES: hypothetical protein
gene_id_13440	65	95.38	5.00E-37	MULTISPECIES: hypothetical protein
gene_id_13441	193	99.48	4.00E-107	MULTISPECIES: hypothetical protein
gene_id_13442	186	100	9.00E-95	MULTISPECIES: hypothetical protein
gene_id_13443	226	95.58	5.00E-155	MULTISPECIES: hypothetical protein
gene_id_13444	373	58.45	2.00E-132	hypothetical protein
gene_id_13445	701	96.15	0	MULTISPECIES: hypothetical protein
gene_id_13446	299	99.67	1.00E-112	MULTISPECIES: hypothetical protein
gene_id_13446	183	68.85	3.00E-32	MULTISPECIES: hypothetical protein
gene_id_13446	78	70.51	1.00E-14	MULTISPECIES: hypothetical protein
gene_id_13447	213	99.06	1.00E-135	MULTISPECIES: hypothetical protein
gene_id_13448	277	96.75	9.00E-156	hypothetical protein
gene_id_13449	66	100	1.00E-37	MULTISPECIES: cold-shock protein
gene_id_13450	162	99.38	1.00E-115	MULTISPECIES: CMP deaminase

gene_id_13451	1448	98.76	0	MULTISPECIES: DNA polymerase III subunit alpha
gene_id_13452	555	93.87	0	MULTISPECIES: hypothetical protein
gene_id_13453	91	95.6	2.00E-55	MULTISPECIES: hypothetical protein
gene_id_13454	283	96.82	0	MULTISPECIES: hypothetical protein
gene_id_13455	983	94.51	0	MULTISPECIES: hypothetical protein
gene_id_13456	130	96.15	2.00E-80	MULTISPECIES: hypothetical protein
gene_id_13457	636	97.64	0	MULTISPECIES: peptide transporter
gene_id_13458	485	96.7	0	MULTISPECIES: aminoacyl-histidine dipeptidase
gene_id_13459	263	50.95	9.00E-88	hypothetical protein
gene_id_13460	380	68.68	2.00E-180	alcohol dehydrogenase
gene_id_13461	485	94.85	0	MULTISPECIES: hypothetical protein
gene_id_13462	46	84.78	8.00E-17	MULTISPECIES: hypothetical protein
gene_id_13463	374	96.52	0	MULTISPECIES: hypothetical protein
gene_id_13464	426	59.15	3.00E-171	hypothetical protein
gene_id_13465	149	99.33	3.00E-89	MULTISPECIES: single-stranded DNA-binding protein
gene_id_13466	66	53.03	2.00E-19	hypothetical protein
gene_id_13467	207	89.86	4.00E-130	MULTISPECIES: hypothetical protein
gene_id_13468	351	93.73	0	MULTISPECIES: hypothetical protein
gene_id_13469	287	96.86	7.00E-164	cell wall hydrolase
gene_id_13472	557	97.49	0	MULTISPECIES: hypothetical protein
gene_id_13473	489	95.71	0	MULTISPECIES: hypothetical protein
gene_id_13474	299	97.99	0	MULTISPECIES: arginase
gene_id_13475	102	64.71	2.00E-33	MULTISPECIES: alkaline-shock protein
gene_id_13476	176	98.3	2.00E-121	hypothetical protein
gene_id_13477	146	96.58	5.00E-94	MULTISPECIES: hypothetical protein
gene_id_13478	386	97.15	0	MULTISPECIES: isocitrate dehydrogenase
gene_id_13479	644	98.14	0	MULTISPECIES: aconitate hydratase
gene_id_13480	347	93.08	0	MULTISPECIES: hypothetical protein
gene_id_13481	207	95.17	1.00E-139	MULTISPECIES: hypothetical protein
gene_id_13482	336	94.64	3.00E-176	MULTISPECIES: hypothetical protein
gene_id_13483	292	99.66	0	MULTISPECIES: hypothetical protein
gene_id_13484	71	98.59	1.00E-39	MULTISPECIES: hypothetical protein
gene_id_13485	356	96.63	0	MULTISPECIES: hypothetical protein
gene_id_13486	224	99.55	5.00E-157	MULTISPECIES: ABC transporter ATP-binding protein
gene_id_13487	841	98.45	0	hypothetical protein
gene_id_13488	99	98.99	5.00E-64	beta-lactamase
gene_id_13489	447	69.57	0	ABC transporter substrate-binding protein
gene_id_13490	438	98.63	0	hypothetical protein
gene_id_13491	445	99.1	0	hypothetical protein
gene_id_13492	168	97.02	5.00E-115	hypothetical protein
gene_id_13493	423	98.58	0	3-isopropylmalate dehydratase large subunit
gene_id_13494	631	93.34	0	hypothetical protein
gene_id_13495	613	33.44	1.00E-76	hypothetical protein
gene_id_13496	133	55.64	5.00E-45	protein export chaperone secb
gene_id_13498	125	34.4	1.00E-08	hypothetical protein
gene_id_13500	706	99.15	0	hypothetical protein
gene_id_13501	372	98.92	0	hypothetical protein

gene_id_13502	237	99.58	5.00E-148	hypothetical protein
gene_id_13524	180	98.89	5.00E-105	hypothetical protein
gene_id_13525	454	99.12	0	hypothetical protein
gene_id_13526	468	98.93	0	hypothetical protein, partial
gene_id_13527	178	98.88	8.00E-127	hypothetical protein
gene_id_13528	626	99.2	0	heat shock protein 90
gene_id_13529	286	98.25	1.00E-175	hypothetical protein
gene_id_13530	148	100	4.00E-91	hypothetical protein
gene_id_13531	229	100	4.00E-149	hypothetical protein
gene_id_13532	156	99.36	1.00E-90	hypothetical protein
gene_id_13533	450	98.44	0	hypothetical protein
gene_id_13534	296	98.65	0	hypothetical protein
gene_id_13535	793	98.99	0	hypothetical protein
gene_id_13536	293	99.66	0	hypothetical protein
gene_id_13537	565	98.41	0	hypothetical protein
gene_id_13538	321	100	0	hypothetical protein
gene_id_13539	297	99.66	0	hypothetical protein
gene_id_13540	330	100	0	hypothetical protein
gene_id_13541	322	63.35	3.00E-150	peptide ABC transporter substrate-binding protein
gene_id_13542	75	98.67	8.00E-44	hypothetical protein
gene_id_13543	66	100	1.00E-38	cold-shock protein
gene_id_13544	88	98.86	7.00E-55	hypothetical protein
gene_id_13545	534	100	0	heme ABC transporter ATP-binding protein
gene_id_13546	358	99.44	0	hypothetical protein
gene_id_13547	95	97.89	1.00E-57	hypothetical protein
gene_id_13548	231	100	4.00E-163	hypothetical protein
gene_id_13549	145	100	8.00E-96	hypothetical protein, partial
gene_id_13550	208	99.52	1.00E-142	hypothetical protein
gene_id_13551	418	99.52	0	hypothetical protein
gene_id_13552	375	99.47	0	hypothetical protein
gene_id_13553	373	99.46	0	hypothetical protein
gene_id_13554	458	98.25	0	hypothetical protein
gene_id_13555	324	100	0	hypothetical protein
gene_id_13556	494	99.6	0	hypothetical protein
gene_id_13557	567	99.65	0	stage V sporulation protein D, partial
gene_id_13558	156	100	2.00E-95	hypothetical protein
gene_id_13559	309	100	0	16S rRNA methyltransferase
gene_id_13560	145	100	1.00E-100	hypothetical protein
gene_id_13561	92	70.65	6.00E-37	excinuclease ABC subunit C
gene_id_13562	242	100	4.00E-142	hypothetical protein
gene_id_13563	797	99.5	0	phenylalanyl-tRNA synthetase subunit beta
gene_id_13564	340	100	0	phenylalanyl-tRNA synthetase subunit alpha
gene_id_13565	263	97.72	0	hypothetical protein
gene_id_13566	213	99.53	4.00E-149	hypothetical protein
gene_id_13567	451	99.33	0	hypothetical protein
gene_id_13568	116	100	1.00E-75	50S ribosomal protein L20
gene_id_13569	64	100	5.00E-36	50S ribosomal protein L35

gene_id_13570	135	100	2.00E-76	translation initiation factor IF-3
gene_id_13571	460	99.57	0	cell division protein FtsH
gene_id_13572	374	100	0	hypothetical protein
gene_id_13573	301	100	6.00E-144	hypothetical protein
gene_id_13574	231	99.57	1.00E-164	hypothetical protein
gene_id_13575	114	99.12	6.00E-74	hypothetical protein
gene_id_13576	130	100	1.00E-88	hypothetical protein
gene_id_13577	72	98.61	3.00E-39	hypothetical protein, partial
gene_id_13579	80	76.25	1.00E-31	methylmalonyl-CoA carboxyltransferase
gene_id_13581	349	53.58	8.00E-132	butyrate kinase
gene_id_13582	263	56.27	1.00E-79	phosphate butyryltransferase
gene_id_13583	209	66.03	1.00E-100	hypothetical protein
gene_id_13584	230	61.74	1.00E-102	hypothetical protein
gene_id_13585	322	45.96	3.00E-82	membrane protein
gene_id_13586	292	67.12	2.00E-128	pyruvate ferredoxin oxidoreductase beta subunit
gene_id_13587	397	65.99	0	MULTISPECIES: hypothetical protein
gene_id_13588	85	65.88	8.00E-33	pyruvate/2-ketoisovalerate family 2-oxoacid:accepto
gene_id_13589	181	64.64	1.00E-79	pyruvate/2-ketoisovalerate family 2-oxoacid:accepto
gene_id_13590	254	48.82	2.00E-85	hypothetical protein
gene_id_13592	195	81.03	2.00E-109	resolvase
gene_id_13593	166	97.59	1.00E-115	hypothetical protein
gene_id_13594	68	76.47	4.00E-28	hypothetical protein
gene_id_13595	189	24.87	6.00E-06	hypothetical protein
gene_id_13596	212	72.64	7.00E-104	transcriptional regulator
gene_id_13597	329	96.05	0	tryptophanyl-tRNA synthase
gene_id_13598	448	99.33	0	hypothetical protein
gene_id_13599	353	100	0	hypothetical protein
gene_id_13600	532	99.44	0	hypothetical protein
gene_id_13601	230	98.7	2.00E-165	hypothetical protein
gene_id_13602	492	98.17	0	hypothetical protein
gene_id_13603	755	96.16	0	hypothetical protein
gene_id_13604	359	98.61	0	hypothetical protein
gene_id_13605	187	98.93	7.00E-101	hypothetical protein
gene_id_13606	441	99.77	0	hypothetical protein
gene_id_13607	307	99.02	0	hypothetical protein
gene_id_13608	277	99.64	0	hypothetical protein
gene_id_13609	366	99.45	0	hypothetical protein
gene_id_13610	224	97.77	2.00E-155	hypothetical protein
gene_id_13611	284	97.54	0	hypothetical protein
gene_id_13612	79	94.94	1.00E-43	hypothetical protein
gene_id_13613	322	96.27	0	hypothetical protein
gene_id_13614	84	92.86	2.00E-11	hypothetical protein
gene_id_13615	270	96.67	0	alpha/beta hydrolase
gene_id_13616	77	98.7	4.00E-45	cysteine synthase
gene_id_13617	573	95.29	0	hypothetical protein
gene_id_13618	167	34.73	5.00E-20	hypothetical protein
gene_id_13619	474	73.84	0	amidohydrolase

gene_id_13620	506	69.17	0	sodium:proton antiporter
gene_id_13621	455	49.89	1.00E-162	arginine utilization regulatory protein RocR
gene_id_13622	465	75.48	0	dihydropyrimidinase
gene_id_13623	238	70.17	1.00E-121	Asp/Glu/hydantoin racemase
gene_id_13624	383	52.22	3.00E-127	hypothetical protein
gene_id_13625	387	56.85	3.00E-162	aspartate aminotransferase
gene_id_13626	220	54.09	1.00E-74	hypothetical protein HMPREF0866_02937
gene_id_13627	340	72.65	5.00E-180	2-dehydro-3-deoxygluconokinase
gene_id_13628	204	50.98	3.00E-68	putative KHG/KDPG aldolase
gene_id_13629	266	51.5	1.00E-95	hypothetical protein
gene_id_13630	162	97.53	3.00E-109	hypothetical protein
gene_id_13631	298	95.97	4.00E-169	hypothetical protein
gene_id_13632	739	52.77	0	diguanylate cyclase YdaM
gene_id_13633	368	95.92	0	hypothetical protein
gene_id_13634	128	47.66	1.00E-33	hypothetical protein
gene_id_13635	177	51.98	5.00E-52	hypothetical protein
gene_id_13636	721	26.77	6.00E-64	hypothetical protein
gene_id_13637	188	59.57	7.00E-71	hypothetical protein
gene_id_13638	445	51.69	3.00E-152	LuxR family transcriptional regulator
gene_id_13639	486	98.77	0	hypothetical protein
gene_id_13640	361	57.06	7.00E-141	diguanylate cyclase
gene_id_13641	333	94.89	0	hypothetical protein
gene_id_13642	568	97.01	0	hypothetical protein
gene_id_13643	117	98.29	4.00E-77	hypothetical protein
gene_id_13644	142	97.89	1.00E-94	hypothetical protein
gene_id_13645	393	98.22	0	hypothetical protein
gene_id_13646	454	99.78	0	sodium:alanine symporter
gene_id_13647	252	99.21	7.00E-174	hypothetical protein
gene_id_13648	155	99.35	2.00E-82	hypothetical protein
gene_id_13649	637	97.49	0	hypothetical protein
gene_id_13651	265	95.85	0	hypothetical protein
gene_id_13652	347	96.25	0	hypothetical protein
gene_id_13653	249	68.27	1.00E-120	allophanate hydrolase
gene_id_13654	257	98.83	0	hypothetical protein
gene_id_13655	245	94.29	3.00E-167	hypothetical protein
gene_id_13656	287	97.56	0	hypothetical protein
gene_id_13657	762	98.03	0	hypothetical protein
gene_id_13658	108	98.15	2.00E-68	PadR family transcriptional regulator
gene_id_13659	324	97.84	0	hypothetical protein
gene_id_13660	403	99.75	0	hypothetical protein
gene_id_13661	48	77.08	2.00E-17	competence protein TfoX
gene_id_13662	170	96.47	3.00E-36	hypothetical protein
gene_id_13663	405	98.02	0	hypothetical protein
gene_id_13664	403	66.5	7.00E-171	MFS transporter
gene_id_13665	875	73.26	0	phosphoenolpyruvate synthase
gene_id_13666	186	63.98	1.00E-75	hypothetical protein
gene_id_13667	450	97.78	0	multidrug transporter MatE, partial

gene_id_13668	185	94.05	3.00E-126	hypothetical protein
gene_id_13669	114	97.37	3.00E-63	hypothetical protein, partial
gene_id_13670	108	98.15	2.00E-72	hypothetical protein
gene_id_13671	355	97.46	0	hypothetical protein, partial
gene_id_13672	281	94.66	0	hypothetical protein
gene_id_13673	182	96.7	1.00E-105	hypothetical protein
gene_id_13674	281	99.29	0	hypothetical protein
gene_id_13675	286	98.6	1.00E-179	hypothetical protein
gene_id_13676	447	100	0	glutamate dehydrogenase
gene_id_13677	217	99.08	7.00E-147	hypothetical protein
gene_id_13678	207	98.07	1.00E-144	hypothetical protein
gene_id_13679	279	100	3.00E-176	inorganic phosphate transporter PiT
gene_id_13680	65	100	6.00E-35	inorganic phosphate transporter PiT
gene_id_13681	332	99.7	0	hypothetical protein
gene_id_13682	343	99.13	0	hypothetical protein
gene_id_13683	267	96.63	0	hypothetical protein
gene_id_13684	456	97.59	0	hypothetical protein
gene_id_13685	896	98.55	0	hypothetical protein
gene_id_13686	459	99.13	0	FAD-dependent oxidoreductase
gene_id_13687	377	98.41	0	hypothetical protein
gene_id_13688	781	98.72	0	hypothetical protein
gene_id_13689	235	99.15	2.00E-168	hypothetical protein
gene_id_13690	203	98.03	4.00E-141	hypothetical protein
gene_id_13691	594	97.47	0	hypothetical protein
gene_id_13692	238	96.64	4.00E-170	hypothetical protein
gene_id_13693	149	97.99	5.00E-101	cysteinyl-tRNA(Pro) deacylase
gene_id_13694	89	94.38	3.00E-52	hypothetical protein
gene_id_13695	212	98.11	4.00E-153	hypothetical protein
gene_id_13696	177	97.18	3.00E-109	hypothetical protein
gene_id_13697	441	59.64	0	aspartate kinase
gene_id_13698	233	97.85	4.00E-132	hypothetical protein
gene_id_13699	234	96.58	2.00E-162	dihydrodipicolinate reductase
gene_id_13700	293	97.27	0	hypothetical protein
gene_id_13701	168	94.64	2.00E-114	hypothetical protein
gene_id_13702	165	99.39	1.00E-113	hypothetical protein
gene_id_13703	367	96.19	0	hypothetical protein
gene_id_13704	107	94.39	2.00E-68	hypothetical protein
gene_id_13705	287	96.52	0	hypothetical protein
gene_id_13706	88	98.86	1.00E-54	hypothetical protein
gene_id_13707	228	90.35	1.00E-143	hypothetical protein
gene_id_13708	474	97.26	0	hypothetical protein
gene_id_13709	386	97.93	0	hypothetical protein
gene_id_13710	561	49.91	0	aldehyde ferredoxin oxidoreductase
gene_id_13712	396	97.47	0	aspartate aminotransferase
gene_id_13713	769	68.27	0	ATP-dependent Clp protease ATP-binding subunit Clp
gene_id_13714	280	99.64	3.00E-169	hypothetical protein
gene_id_13715	147	98.64	6.00E-87	hypothetical protein

gene_id_13716	196	97.45	3.00E-136	hypothetical protein
gene_id_13717	257	97.67	0	hypothetical protein
gene_id_13718	171	98.83	1.00E-93	hypothetical protein
gene_id_13719	324	99.38	0	hypothetical protein
gene_id_13720	401	99.5	0	hypothetical protein
gene_id_13721	179	100	2.00E-126	hypothetical protein
gene_id_13722	274	98.91	0	hypothetical protein
gene_id_13723	251	100	0	hypothetical protein
gene_id_13725	148	94.59	6.00E-93	hypothetical protein
gene_id_13726	73	100	4.00E-42	hypothetical protein
gene_id_13727	688	96.95	0	hypothetical protein
gene_id_13728	280	96.79	0	hypothetical protein
gene_id_13729	168	98.81	4.00E-116	hypothetical protein
gene_id_13730	411	99.27	0	N-glycosyltransferase
gene_id_13731	331	98.79	0	N-acetyl-gamma-glutamyl-phosphate reductase
gene_id_13732	406	98.28	0	hypothetical protein
gene_id_13733	289	97.23	0	hypothetical protein
gene_id_13734	399	96.74	0	hypothetical protein
gene_id_13735	548	97.63	0	glutamyl-tRNA synthetase
gene_id_13736	145	97.93	6.00E-99	hypothetical protein
gene_id_13737	246	70.73	3.00E-122	3-oxoacyl-ACP reductase
gene_id_13738	61	100	4.00E-35	hypothetical protein, partial
gene_id_13739	81	98.77	1.00E-45	CopG family transcripitonal regulator
gene_id_13740	325	96.62	0	hypothetical protein
gene_id_13741	241	49.79	1.00E-78	ABC transporter permease
gene_id_13742	199	96.48	2.00E-136	hypothetical protein, partial
gene_id_13746	92	96.74	3.00E-56	hypothetical protein
gene_id_13747	120	86.67	8.00E-70	hypothetical protein
gene_id_13748	491	44.4	2.00E-135	adenylyltransferase
gene_id_13749	271	80.07	1.00E-154	amino acid ABC transporter substrate-binding proteir
gene_id_13750	256	77.73	1.00E-141	glutamine ABC transporter ATP-binding protein
gene_id_13751	224	79.46	4.00E-116	amino acid ABC transporter permease
gene_id_13752	219	73.06	5.00E-95	polar amino acid ABC transporter permease
gene_id_13753	397	68.26	0	amidohydrolase
gene_id_13754	344	60.17	2.00E-143	methionine ABC transporter ATP-binding protein
gene_id_13755	226	65.93	3.00E-87	ABC transporter permease
gene_id_13756	238	56.3	1.00E-91	metal ABC transporter substrate-binding protein
gene_id_13757	82	100	3.00E-22	hypothetical protein
gene_id_13758	60	95	3.00E-29	membrane protein, partial
gene_id_13759	436	97.48	0	peptidase U62
gene_id_13760	463	99.35	0	hypothetical protein
gene_id_13761	410	99.27	0	tyrosyl-tRNA synthetase
gene_id_13762	133	99.25	2.00E-88	hypothetical protein
gene_id_13762	82	96.34	3.00E-26	hypothetical protein
gene_id_13763	621	98.23	0	hypothetical protein
gene_id_13764	255	98.82	0	ABC transporter ATP-binding protein
gene_id_13765	334	97.6	0	hypothetical protein

gene_id_13766	223	99.55	3.00E-163	PhoB family transcriptional regulator
gene_id_13767	557	100	0	dihydroxy-acid dehydratase
gene_id_13768	486	98.35	0	guanine permease
gene_id_13771	532	56.95	0	sulfate permease
gene_id_13772	423	98.58	0	hypothetical protein
gene_id_13773	185	55.14	7.00E-57	hypothetical protein
gene_id_14481	402	99.25	0	N-acetylglucosaminyltransferase
gene_id_14482	420	98.33	0	hypothetical protein
gene_id_14483	605	60.99	0	cell division protein FtsH
gene_id_14484	195	96.92	1.00E-132	hypothetical protein
gene_id_14485	172	98.84	2.00E-113	hypothetical protein
gene_id_14486	101	98.02	1.00E-63	hypothetical protein, partial
gene_id_14487	437	89.02	0	hypothetical protein
gene_id_14488	207	99.52	6.00E-144	hypothetical protein
gene_id_14489	238	97.48	1.00E-158	hypothetical protein
gene_id_14490	360	96.94	0	cobalt-precorrin-6A synthase, partial
gene_id_14491	251	97.61	2.00E-168	hypothetical protein
gene_id_14492	252	96.03	1.00E-177	hypothetical protein
gene_id_14493	403	43.42	1.00E-110	hypothetical protein
gene_id_14494	447	97.99	0	cobyrinic acid a,c-diamide synthase
gene_id_14495	316	96.2	0	hypothetical protein
gene_id_14496	354	95.2	0	hypothetical protein
gene_id_14497	337	94.96	0	hypothetical protein, partial
gene_id_14498	494	97.17	0	hypothetical protein
gene_id_14499	347	96.83	0	hypothetical protein
gene_id_14500	210	98.1	3.00E-132	hypothetical protein
gene_id_14501	231	95.24	3.00E-157	hypothetical protein
gene_id_14502	237	98.31	8.00E-139	hypothetical protein
gene_id_14503	330	96.67	0	hypothetical protein
gene_id_14504	310	97.74	8.00E-180	hypothetical protein
gene_id_14505	260	98.46	8.00E-177	hypothetical protein
gene_id_14507	165	94.55	1.00E-112	hypothetical protein
gene_id_14508	734	98.91	0	hypothetical protein
gene_id_14509	481	98.75	0	hypothetical protein
gene_id_14510	452	99.34	0	hypothetical protein
gene_id_14511	101	97.03	1.00E-55	hypothetical protein
gene_id_14512	366	97.81	0	hypothetical protein
gene_id_14513	163	96.93	2.00E-110	hypothetical protein
gene_id_14514	90	98.89	7.00E-57	hypothetical protein
gene_id_14515	382	65.97	0	FAD-dependent oxidoreductase
gene_id_14516	350	97.71	0	hypothetical protein
gene_id_14517	688	98.4	0	hypothetical protein
gene_id_14518	342	97.37	0	hypothetical protein
gene_id_14519	169	97.63	5.00E-103	hypothetical protein
gene_id_14520	478	98.74	0	hypothetical protein
gene_id_14521	305	99.67	0	hypothetical protein
gene_id_14522	419	98.33	0	hypothetical protein

gene_id_14523	343	98.83	0	hypothetical protein
gene_id_14524	329	99.39	0	peptide ABC transporter ATP-binding protein
gene_id_14525	563	98.4	0	hypothetical protein
gene_id_14526	278	96.76	0	hypothetical protein
gene_id_14527	47	97.87	5.00E-21	hypothetical protein
gene_id_14528	54	100	7.00E-28	asparagine synthase, partial
gene_id_14529	307	96.09	0	radical SAM protein
gene_id_14530	137	97.08	1.00E-93	hypothetical protein
gene_id_14531	184	98.37	2.00E-125	hypothetical protein
gene_id_14532	166	93.98	2.00E-93	hypothetical protein
gene_id_14533	304	98.68	0	hypothetical protein
gene_id_14534	532	58.83	0	hypothetical protein
gene_id_14535	383	99.48	0	hypothetical protein
gene_id_14536	163	96.32	2.00E-101	hypothetical protein
gene_id_14537	198	95.45	1.00E-126	hypothetical protein
gene_id_14538	345	99.71	0	ATP-dependent DNA helicase RuvB
gene_id_14539	562	90.39	0	hypothetical protein
gene_id_14540	348	98.28	0	hypothetical protein
gene_id_14541	369	99.19	0	queuine tRNA-ribosyltransferase
gene_id_14542	91	97.8	5.00E-57	preprotein translocase subunit YajC, partial
gene_id_14543	883	97.51	0	hypothetical protein
gene_id_14545	78	100	1.00E-47	hypothetical protein
gene_id_14546	445	96.4	0	hypothetical protein
gene_id_14547	77	100	2.00E-23	hypothetical protein, partial
gene_id_14548	585	97.95	0	hypothetical protein, partial
gene_id_14549	171	98.25	1.00E-115	hypothetical protein
gene_id_14550	728	99.86	0	hypothetical protein
gene_id_14551	149	95.3	1.00E-88	hypothetical protein
gene_id_14552	206	100	1.00E-144	hypothetical protein
gene_id_14553	403	97.27	0	hypothetical protein, partial
gene_id_14554	86	94.19	1.00E-52	hypothetical protein
gene_id_14555	126	100	8.00E-80	hypothetical protein
gene_id_14556	268	95.9	8.00E-178	hypothetical protein
gene_id_14557	591	99.83	0	aspartyl-tRNA synthetase
gene_id_14558	138	96.38	5.00E-67	hypothetical protein
gene_id_14559	436	99.54	0	ATPase AAA
gene_id_14560	167	97.6	1.00E-108	hypothetical protein
gene_id_14561	97	98.97	8.00E-63	hypothetical protein
gene_id_14562	86	100	5.00E-55	hypothetical protein
gene_id_14563	545	92.11	0	hypothetical protein
gene_id_14564	140	99.29	1.00E-93	hypothetical protein
gene_id_14565	397	98.99	0	hypothetical protein
gene_id_14566	136	100	4.00E-94	nitrogen fixation protein NifU
gene_id_14567	877	98.75	0	alanyl-tRNA synthetase
gene_id_14568	87	98.85	3.00E-53	hypothetical protein
gene_id_14569	315	98.1	0	hypothetical protein
gene_id_14570	137	97.81	7.00E-89	hypothetical protein

gene_id_14571	63	100	3.00E-19	hypothetical protein
gene_id_14572	144	100	5.00E-99	hypothetical protein
gene_id_14573	555	99.64	0	hypothetical protein, partial
gene_id_14574	212	95.75	3.00E-149	peroxiredoxin, partial
gene_id_14575	82	97.56	5.00E-49	hypothetical protein
gene_id_14576	348	98.28	0	hypothetical protein
gene_id_14577	214	97.2	5.00E-149	hypothetical protein
gene_id_14578	407	99.26	0	hypothetical protein
gene_id_14579	137	94.89	1.00E-80	hypothetical protein
gene_id_14580	158	94.3	2.00E-101	hypothetical protein
gene_id_14581	405	70.37	1.00E-152	sodium:dicarboxylate symporter
gene_id_14582	267	98.13	0	hypothetical protein
gene_id_15195	176	92.05	2.00E-83	hypothetical protein
gene_id_15196	177	97.18	6.00E-122	hypothetical protein
gene_id_15197	132	95.45	4.00E-66	hypothetical protein
gene_id_15198	61	100	3.00E-35	hypothetical protein
gene_id_15199	229	99.13	1.00E-155	hypothetical protein
gene_id_15200	227	98.24	4.00E-157	hypothetical protein
gene_id_15201	281	97.51	0	ABC transporter ATP-binding protein
gene_id_15202	197	83.76	7.00E-118	hypothetical protein
gene_id_15203	245	95.92	1.00E-156	hypothetical protein
gene_id_15204	283	96.47	0	hypothetical protein, partial
gene_id_15205	594	97.14	0	hypothetical protein
gene_id_15206	79	94.94	5.00E-30	hypothetical protein
gene_id_15207	99	96.97	4.00E-61	hypothetical protein
gene_id_15208	276	87.32	7.00E-178	hypothetical protein
gene_id_15209	76	96.05	2.00E-44	hypothetical protein
gene_id_15210	95	100	9.00E-60	hypothetical protein, partial
gene_id_15211	610	96.56	0	hypothetical protein, partial
gene_id_15212	123	92.68	2.00E-73	hypothetical protein
gene_id_15213	201	96.52	4.00E-116	hypothetical protein
gene_id_15214	187	94.65	4.00E-129	hypothetical protein
gene_id_15215	158	97.47	1.00E-108	hypothetical protein
gene_id_15216	98	98.98	4.00E-63	hypothetical protein
gene_id_15217	837	98.21	0	hypothetical protein
gene_id_15218	191	96.86	6.00E-113	hypothetical protein
gene_id_15220	672	97.17	0	hypothetical protein
gene_id_15221	77	100	2.00E-46	hypothetical protein
gene_id_15432	646	98.92	0	hypothetical protein
gene_id_15433	1363	95.23	0	hypothetical protein
gene_id_15434	439	98.86	0	hypothetical protein
gene_id_15435	398	93.47	0	hypothetical protein
gene_id_15436	192	98.44	4.00E-131	hypothetical protein
gene_id_15437	1025	99.32	0	hypothetical protein
gene_id_15438	355	98.87	0	hypothetical protein
gene_id_15439	181	97.24	8.00E-93	hypothetical protein
gene_id_15440	159	97.48	7.00E-91	permease

gene_id_15441	359	94.99	0	hypothetical protein
gene_id_15442	267	95.13	8.00E-165	hypothetical protein
gene_id_15443	314	85.99	0	hypothetical protein
gene_id_15444	408	83.09	0	hypothetical protein
gene_id_15445	221	85.97	8.00E-121	hypothetical protein
gene_id_15446	453	47.02	5.00E-141	hypothetical protein
gene_id_15447	211	64.45	1.00E-85	hypothetical protein
gene_id_15448	449	62.36	0	hypothetical protein
gene_id_15449	557	94.25	0	hypothetical protein
gene_id_15450	140	98.57	4.00E-96	hypothetical protein
gene_id_15451	218	98.62	2.00E-151	hypothetical protein
gene_id_15452	227	98.24	8.00E-133	hypothetical protein
gene_id_15453	316	99.05	0	MFS transporter
gene_id_15454	86	100	3.00E-55	hypothetical protein
gene_id_15455	898	99.44	0	MFS transporter
gene_id_15456	782	96.16	0	Clp protease ClpX
gene_id_15457	138	100	7.00E-95	hypothetical protein
gene_id_15458	462	99.13	0	F0F1 ATP synthase subunit beta
gene_id_15459	295	98.31	0	hypothetical protein
gene_id_15460	493	98.17	0	ATP F0F1 synthase subunit alpha
gene_id_15461	146	96.58	1.00E-92	hypothetical protein
gene_id_15462	74	100	1.00E-24	F0F1 ATP synthase subunit C
gene_id_15463	228	97.37	1.00E-121	hypothetical protein
gene_id_15464	481	99.58	0	prolyl-tRNA synthetase
gene_id_15465	582	98.45	0	hypothetical protein
gene_id_15466	265	96.23	0	hypothetical protein
gene_id_15467	83	100	7.00E-39	hypothetical protein
gene_id_15468	311	96.78	0	hypothetical protein
gene_id_15469	288	96.18	0	hypothetical protein
gene_id_15470	178	97.75	1.00E-102	hypothetical protein
gene_id_15471	380	98.16	0	hypothetical protein
gene_id_15472	260	96.92	0	hypothetical protein
gene_id_15473	536	96.08	0	hypothetical protein
gene_id_15474	237	99.16	6.00E-143	hypothetical protein
gene_id_15475	341	69.21	7.00E-163	threonine aldolase
gene_id_15476	286	99.3	0	hypothetical protein
gene_id_15477	210	97.62	1.00E-95	hypothetical protein
gene_id_15478	183	98.36	7.00E-129	hypothetical protein
gene_id_15479	401	98.25	0	hypothetical protein
gene_id_15480	323	100	0	hypothetical protein, partial
gene_id_15481	219	99.09	8.00E-140	hypothetical protein
gene_id_15482	423	98.58	0	hypothetical protein
gene_id_15483	309	99.03	0	hypothetical protein
gene_id_15484	52	86.54	1.00E-23	MULTISPECIES: rubredoxin
gene_id_15485	278	97.84	0	hypothetical protein
gene_id_15486	346	98.55	0	tRNA (5-methylaminomethyl-2-thiouridylate)-methyl
gene_id_15487	238	95.38	4.00E-142	hypothetical protein

gene_id_15488	302	95.7	0	hypothetical protein
gene_id_15489	283	98.59	0	hypothetical protein
gene_id_15490	277	99.28	0	S-adenosylmethionine decarboxylase
gene_id_15491	391	96.93	0	metallo-beta-lactamase
gene_id_15492	114	93.86	5.00E-70	hypothetical protein
gene_id_15493	185	99.46	2.00E-127	hypothetical protein
gene_id_15494	201	97.01	4.00E-138	hypothetical protein
gene_id_15495	68	100	1.00E-41	hypothetical protein
gene_id_15496	545	99.08	0	hydroxylamine reductase
gene_id_15497	90	67.78	6.00E-37	GNAT family acetyltransferase
gene_id_15498	176	99.43	5.00E-123	glutathione peroxidase, partial
gene_id_15499	533	95.87	0	hypothetical protein
gene_id_15500	540	97.41	0	hypothetical protein, partial
gene_id_15501	579	64.25	0	antibiotic ABC transporter ATPase
gene_id_15502	59	100	8.00E-32	ACGS family amino acid carrier protein, partial
gene_id_15574	299	99.33	0	hypothetical protein
gene_id_15575	298	98.99	0	hypothetical protein, partial
gene_id_15576	460	96.3	0	hypothetical protein, partial
gene_id_15577	649	97.23	0	hypothetical protein
gene_id_15578	414	97.34	0	hypothetical protein
gene_id_15579	379	95.78	0	hypothetical protein
gene_id_15580	244	96.72	2.00E-170	hypothetical protein
gene_id_15581	415	99.52	0	hypothetical protein
gene_id_15582	203	86.21	1.00E-117	hypothetical protein, partial
gene_id_15583	243	90.53	4.00E-149	hypothetical protein, partial
gene_id_15584	158	99.37	2.00E-107	hypothetical protein
gene_id_15585	396	98.48	0	hypothetical protein
gene_id_15586	490	98.57	0	hypothetical protein
gene_id_15587	231	98.27	4.00E-151	PhoP family transcriptional regulator
gene_id_15588	114	94.74	9.00E-52	hypothetical protein
gene_id_15589	217	97.24	6.00E-142	hypothetical protein
gene_id_15590	409	97.56	0	transporter
gene_id_15591	230	62.61	7.00E-98	molecular chaperone
gene_id_15592	224	98.21	2.00E-145	hypothetical protein
gene_id_15593	538	94.98	0	dockerin type 1, partial
gene_id_15594	344	95.64	0	hypothetical protein
gene_id_15595	467	99.57	0	hypothetical protein
gene_id_15596	288	98.96	0	hypothetical protein
gene_id_15597	89	97.75	5.00E-54	hypothetical protein
gene_id_15598	429	99.3	0	hypothetical protein
gene_id_15599	390	98.46	0	malate dehydrogenase
gene_id_15600	228	95.61	2.00E-154	hypothetical protein
gene_id_15601	527	97.53	0	histidine kinase
gene_id_15602	73	97.26	2.00E-31	hypothetical protein
gene_id_15603	296	94.26	0	hypothetical protein
gene_id_15604	160	96.25	2.00E-78	hypothetical protein
gene_id_15605	111	100	4.00E-43	hypothetical protein

gene_id_15606	430	96.74	0	hypothetical protein
gene_id_15608	189	97.88	2.00E-135	GNAT family acetyltransferase
gene_id_15609	148	93.92	3.00E-97	hypothetical protein
gene_id_15610	446	91.48	0	hypothetical protein
gene_id_15611	352	98.3	0	hypothetical protein
gene_id_15612	283	99.65	2.00E-180	spermidine/putrescine ABC transporter permease
gene_id_15613	598	98.16	0	spermidine/putrescine ABC transporter permease
gene_id_15614	177	96.61	5.00E-117	hypothetical protein
gene_id_15615	252	95.63	5.00E-163	hypothetical protein
gene_id_15616	102	92.16	2.00E-43	hypothetical protein
gene_id_15617	42	57.14	2.00E-08	hypothetical protein CBO05C_1230
gene_id_15618	356	91.29	0	hypothetical protein, partial
gene_id_15619	229	93.01	9.00E-153	hypothetical protein
gene_id_15620	117	88.89	2.00E-58	hypothetical protein, partial
gene_id_15621	113	72.57	5.00E-53	hypothetical protein
gene_id_15622	70	74.29	2.00E-26	hypothetical protein
gene_id_15623	407	94.35	0	hypothetical protein
gene_id_15624	195	93.33	7.00E-130	hypothetical protein
gene_id_15625	684	97.22	0	hypothetical protein
gene_id_15626	736	82.34	0	hypothetical protein
gene_id_15627	202	93.56	3.00E-113	hypothetical protein
gene_id_15628	159	94.34	3.00E-106	hypothetical protein
gene_id_15629	277	93.14	1.00E-176	hypothetical protein
gene_id_15630	778	94.47	0	hypothetical protein
gene_id_15631	62	95.16	2.00E-33	hypothetical protein
gene_id_15632	302	99.01	0	hypothetical protein
gene_id_15633	89	78.65	1.00E-24	hypothetical protein
gene_id_15634	596	98.66	0	hypothetical protein
gene_id_15635	57	100	4.00E-32	hypothetical protein
gene_id_15636	789	31.31	3.00E-91	hypothetical protein
gene_id_15636	280	43.21	7.00E-55	hypothetical protein
gene_id_15637	31	96.77	3.00E-09	hypothetical protein
gene_id_15993	177	50.28	6.00E-54	hypothetical protein, partial
gene_id_15994	425	98.35	0	hypothetical protein
gene_id_15995	382	98.95	0	hypothetical protein, partial
gene_id_15996	119	68.91	2.00E-52	hypothetical protein
gene_id_15996	53	58.49	1.00E-06	hypothetical protein
gene_id_15997	182	98.9	3.00E-130	5-nitroimidazole antibiotic resistance protein
gene_id_15998	550	95.45	0	hypothetical protein
gene_id_15999	92	94.57	7.00E-44	hypothetical protein
gene_id_16000	510	62.75	0	hypothetical protein
gene_id_16001	449	57.46	2.00E-169	exopolysaccharide biosynthesis polyprenyl glycosylph
gene_id_16002	242	46.69	3.00E-70	hypothetical protein
gene_id_16003	322	53.11	1.00E-120	mannose-6-phosphate isomerase class I
gene_id_16004	422	52.84	5.00E-154	hypothetical protein C814_01731
gene_id_16005	359	65.46	0	mannose-1-phosphate guanylyltransferase/mannose
gene_id_16006	343	86.88	0	gDP-mannose 4 6-dehydratase

gene_id_16007	313	66.45	4.00E-156	hypothetical protein
gene_id_16008	258	70.93	3.00E-128	ABC transporter
gene_id_16009	418	56.7	3.00E-157	hypothetical protein
gene_id_16010	576	38.37	3.00E-120	hypothetical protein C814_02340
gene_id_16011	338	65.98	6.00E-163	hypothetical protein
gene_id_16012	752	61.57	0	hypothetical protein C814_02338
gene_id_16013	458	28.6	2.00E-33	hypothetical protein CLOSTHATH_03448
gene_id_16014	375	73.33	0	TDP-4-oxo-6-deoxy-D-glucose aminotransferase
gene_id_16015	250	36.4	3.00E-33	hypothetical protein
gene_id_16016	35	74.29	1.00E-07	acyl carrier protein
gene_id_16017	415	48.67	7.00E-131	hypothetical protein
gene_id_16018	241	70.12	7.00E-119	3-oxoacyl-ACP reductase
gene_id_16019	312	60.58	9.00E-128	hypothetical protein
gene_id_16020	94	54.26	5.00E-28	transporter
gene_id_16021	82	56.1	2.00E-24	multidrug ABC transporter
gene_id_16022	293	73.04	4.00E-161	glucose-1-phosphate thymidylyltransferase
gene_id_16023	337	78.34	0	spore coat protein
gene_id_16024	329	62.01	1.00E-152	uDP-galactose 4-epimerase
gene_id_16025	718	41.36	1.00E-151	hypothetical protein
gene_id_16026	597	66.16	0	hypothetical protein
gene_id_16027	226	83.63	3.00E-139	hypothetical protein
gene_id_16028	204	60.29	4.00E-73	UDP-galactose phosphate transferase
gene_id_16029	296	42.57	2.00E-68	UDP-3-O-
gene_id_16031	364	67.86	3.00E-173	glycosyltransferase
gene_id_16032	379	44.85	5.00E-106	Glycosyltransferase
gene_id_16033	219	54.79	3.00E-81	Exopolysaccharide biosynthesis protein
gene_id_16034	310	52.9	1.00E-100	Predicted glycosyltransferases
gene_id_16035	428	53.04	8.00E-132	hypothetical protein
gene_id_16036	467	60.17	1.00E-169	Membrane protein involved in the export of O-antige
gene_id_16037	315	42.54	1.00E-62	hypothetical protein
gene_id_16038	292	83.56	9.00E-149	UTP--glucose-1-phosphate uridylyltransferase
gene_id_16039	453	85.87	0	UDP-glucose 6-dehydrogenase
gene_id_16040	348	81.03	0	NAD-dependent epimerase
gene_id_16042	236	43.64	9.00E-54	chain length determinant family protein
gene_id_16043	160	47.5	3.00E-38	capsular biosynthesis protein
gene_id_16044	242	39.26	1.00E-50	tyrosine protein phosphatase
gene_id_16045	405	38.27	1.00E-67	uncharacterized protein
gene_id_16046	199	38.19	3.00E-34	hypothetical protein
gene_id_16047	221	27.15	5.00E-07	uncharacterized protein
gene_id_16048	194	46.91	1.00E-52	capsular biosynthesis protein
gene_id_16049	299	97.32	2.00E-173	hypothetical protein
gene_id_16050	186	46.24	2.00E-40	hypothetical protein
gene_id_16051	74	93.24	1.00E-39	hypothetical protein
gene_id_16052	103	99.03	4.00E-65	hypothetical protein
gene_id_16053	104	54.81	4.00E-31	hypothetical protein
gene_id_16054	245	93.06	1.00E-166	hypothetical protein
gene_id_16055	358	96.37	0	spermidine/putrescine ABC transporter ATP-binding

gene_id_16056	290	96.55	0	ABC transporter permease
gene_id_16057	273	98.53	1.00E-179	ABC transporter permease
gene_id_16058	354	98.02	0	hypothetical protein
gene_id_16059	331	96.68	0	glucosamine-fructose-6-phosphate aminotransferase
gene_id_16060	272	62.13	5.00E-126	fructoselysine 3-epimerase
gene_id_16061	265	90.94	2.00E-176	hypothetical protein
gene_id_16062	343	62.97	2.00E-137	membrane protein
gene_id_16063	650	96.62	0	C4-dicarboxylate ABC transporter permease
gene_id_16064	324	99.07	0	hypothetical protein
gene_id_16065	383	97.39	0	hypothetical protein
gene_id_16066	342	97.08	0	hypothetical protein
gene_id_16067	639	98.12	0	fumarate reductase
gene_id_16068	147	96.6	1.00E-74	hypothetical protein
gene_id_16069	121	98.35	9.00E-83	hypothetical protein
gene_id_16071	816	39.22	3.00E-175	lysyl transferase
gene_id_16072	447	97.32	0	multidrug transporter MatE, partial
gene_id_16073	511	99.02	0	hypothetical protein
gene_id_16074	272	99.26	0	3-keto-5-aminohexanoate cleavage enzyme
gene_id_16075	314	99.68	0	3-hydroxyacyl-CoA dehydrogenase
gene_id_16076	457	99.56	0	hypothetical protein
gene_id_16077	139	99.28	4.00E-97	hypothetical protein
gene_id_16078	150	99.33	6.00E-102	hypothetical protein
gene_id_16079	397	97.73	0	hypothetical protein
gene_id_16080	416	93.03	0	hypothetical protein
gene_id_16081	256	98.83	0	cytochrome C biogenesis protein ResC
gene_id_16082	417	96.64	0	hypothetical protein
gene_id_16083	238	98.32	4.00E-170	hypothetical protein
gene_id_16084	64	93.75	2.00E-34	hypothetical protein
gene_id_16085	45	95.56	7.00E-22	hypothetical protein
gene_id_16086	322	96.27	0	hypothetical protein
gene_id_16087	186	96.77	3.00E-118	hypothetical protein
gene_id_16088	242	99.17	3.00E-177	hypothetical protein
gene_id_16089	491	96.95	0	hypothetical protein
gene_id_16090	384	99.48	0	hypothetical protein
gene_id_16091	567	98.06	0	hypothetical protein
gene_id_16092	66	90.91	1.00E-34	hypothetical protein
gene_id_16093	136	94.85	2.00E-75	hypothetical protein
gene_id_16094	255	99.22	5.00E-164	hypothetical protein
gene_id_16095	398	98.74	0	argininosuccinate synthase, partial
gene_id_16096	144	98.61	7.00E-98	hypothetical protein
gene_id_16097	569	98.24	0	hypothetical protein
gene_id_16098	603	97.35	0	hypothetical protein
gene_id_16099	94	93.62	1.00E-55	hypothetical protein
gene_id_16100	209	100	3.00E-145	hypothetical protein
gene_id_16104	82	91.46	4.00E-48	hypothetical protein
gene_id_16105	66	96.97	9.00E-39	hypothetical protein, partial
gene_id_16106	188	39.89	3.00E-33	hypothetical protein

gene_id_16107	429	41.49	1.00E-90	hypothetical protein
gene_id_16108	119	43.7	3.00E-23	hypothetical protein, partial
gene_id_16109	147	31.97	4.00E-11	hypothetical protein
gene_id_16110	316	25.63	5.00E-14	alkaline serine proteinase
gene_id_16113	131	57.25	1.00E-27	hypothetical protein
gene_id_16113	122	54.92	3.00E-20	hypothetical protein
gene_id_16114	396	27.78	2.00E-31	hypothetical protein
gene_id_16115	102	39.22	7.00E-15	hypothetical protein THYS13_07330
gene_id_16116	324	53.4	7.00E-88	tail tape measure protein TP901 core region
gene_id_16116	271	29.52	7.00E-27	tail tape measure protein TP901 core region
gene_id_16117	64	42.19	7.00E-06	hypothetical protein
gene_id_16118	101	36.63	3.00E-09	hypothetical protein
gene_id_16119	196	53.57	4.00E-62	hypothetical protein
gene_id_16121	145	50.34	2.00E-39	hypothetical protein
gene_id_16122	96	51.04	1.00E-24	prophage pi2 protein
gene_id_16123	84	63.1	2.00E-23	hypothetical protein
gene_id_16124	433	65.59	0	capsid protein
gene_id_16125	185	76.76	3.00E-101	primosome assembly protein PriA
gene_id_16126	393	74.81	0	portal protein
gene_id_16127	565	72.74	0	phage terminase
gene_id_16128	119	63.87	2.00E-46	hypothetical protein
gene_id_16129	242	55.79	2.00E-90	HNH endonuclease
gene_id_16130	210	64.29	6.00E-84	YqaS
gene_id_16131	189	55.03	7.00E-63	integrase
gene_id_16135	154	57.14	2.00E-54	single-stranded DNA-binding protein
gene_id_16136	262	64.5	5.00E-125	hypothetical protein
gene_id_16137	87	49.43	2.00E-18	hypothetical protein
gene_id_16138	278	36.69	1.00E-41	hypothetical protein
gene_id_16139	229	39.3	2.00E-56	hypothetical protein
gene_id_16140	110	41.82	6.00E-16	hypothetical protein
gene_id_16142	138	38.41	2.00E-18	putative prophage lambdaCh01, transcriptional regul
gene_id_16146	49	67.35	4.00E-15	hypothetical protein
gene_id_16147	84	72.62	6.00E-36	hypothetical protein
gene_id_16148	49	61.22	2.00E-13	hypothetical protein
gene_id_16149	67	64.18	1.00E-22	DNA-binding protein
gene_id_16150	117	48.72	1.00E-21	transcriptional regulator
gene_id_16151	124	64.52	5.00E-52	hypothetical protein
gene_id_16153	123	36.59	2.00E-09	hypothetical protein
gene_id_16154	205	40.49	5.00E-37	hypothetical protein
gene_id_16155	324	33.33	1.00E-54	hypothetical protein
gene_id_16156	145	42.76	2.00E-32	hypothetical protein
gene_id_16157	532	58.65	0	resolvase
gene_id_16158	92	94.57	3.00E-58	hypothetical protein, partial
gene_id_16159	159	94.97	3.00E-93	hypothetical protein
gene_id_16160	88	100	5.00E-52	hypothetical protein
gene_id_16161	228	100	2.00E-157	hypothetical protein
gene_id_16162	276	97.1	0	hypothetical protein

gene_id_16163	140	99.29	2.00E-96	hypothetical protein
gene_id_16164	565	98.94	0	hypothetical protein
gene_id_16165	147	99.32	1.00E-73	hypothetical protein
gene_id_16166	142	100	1.00E-95	hypothetical protein
gene_id_16167	142	98.59	1.00E-94	hypothetical protein
gene_id_16168	289	78.89	5.00E-141	serine dehydratase
gene_id_16169	226	100	5.00E-146	hypothetical protein
gene_id_16170	387	99.74	0	hypothetical protein
gene_id_16171	339	97.94	0	hypothetical protein
gene_id_16172	306	95.1	0	hypothetical protein
gene_id_16173	776	99.1	0	hypothetical protein
gene_id_16174	518	99.61	0	heme ABC transporter ATP-binding protein
gene_id_16175	375	98.93	0	hypothetical protein
gene_id_16176	407	98.28	0	serine hydroxymethyltransferase
gene_id_16177	379	98.42	0	hypothetical protein
gene_id_16178	297	99.66	4.00E-166	hypothetical protein
gene_id_16179	346	98.84	1.00E-180	hypothetical protein
gene_id_16180	258	98.84	1.00E-162	hypothetical protein
gene_id_16181	236	99.15	5.00E-163	amino acid ABC transporter ATPase
gene_id_16182	286	51.75	4.00E-92	hypothetical protein
gene_id_16183	91	100	5.00E-57	transcriptional regulator
gene_id_16184	477	98.95	0	hypothetical protein
gene_id_16185	531	99.81	0	hypothetical protein
gene_id_16186	748	99.6	0	hypothetical protein
gene_id_16187	239	97.07	1.00E-169	hypothetical protein
gene_id_16188	190	94.74	3.00E-126	hypothetical protein
gene_id_16189	205	100	5.00E-132	hypothetical protein
gene_id_16190	321	100	0	hypothetical protein
gene_id_16191	111	99.1	6.00E-66	hypothetical protein
gene_id_16192	192	98.44	1.00E-110	hypothetical protein
gene_id_16193	307	99.67	0	peptidase
gene_id_16194	143	100	6.00E-71	hypothetical protein
gene_id_16195	185	97.84	2.00E-125	hypothetical protein, partial
gene_id_16196	269	95.91	0	hypothetical protein
gene_id_16197	255	99.61	0	hypothetical protein
gene_id_16198	318	98.74	0	ABC transporter permease
gene_id_16199	364	99.45	0	hypothetical protein
gene_id_16200	511	99.41	0	ABC transporter ATP-binding protein
gene_id_16201	394	98.48	0	hypothetical protein
gene_id_16202	250	99.6	0	exodeoxyribonuclease III
gene_id_16203	411	98.54	0	membrane protein
gene_id_16204	114	98.25	6.00E-75	hypothetical protein
gene_id_16205	62	100	1.00E-35	hypothetical protein
gene_id_16206	362	98.9	0	hypothetical protein
gene_id_16207	306	97.06	0	hypothetical protein, partial
gene_id_16208	150	98	5.00E-102	hypothetical protein
gene_id_16209	355	97.75	0	hypothetical protein

gene_id_16210	256	99.22	0	ABC transporter permease
gene_id_16211	252	96.43	2.00E-163	glycosyl transferase family 8
gene_id_16212	116	100	1.00E-76	hypothetical protein
gene_id_16213	115	99.13	3.00E-78	hypothetical protein
gene_id_16214	107	98.13	2.00E-68	PadR family transcriptional regulator
gene_id_16215	578	98.27	0	hypothetical protein
gene_id_16216	298	97.99	0	hypothetical protein
gene_id_16217	123	95.93	2.00E-77	hypothetical protein
gene_id_16218	307	98.37	0	hypothetical protein
gene_id_16219	311	98.71	0	hypothetical protein
gene_id_16220	348	99.71	0	peptide ABC transporter ATP-binding protein
gene_id_16221	322	99.69	0	ABC transporter permease
gene_id_16222	313	99.36	0	hypothetical protein
gene_id_16223	605	99.5	0	hypothetical protein
gene_id_16224	386	98.19	0	hypothetical protein
gene_id_16225	312	94.23	0	hypothetical protein
gene_id_16226	343	97.67	0	hypothetical protein
gene_id_16227	277	97.83	0	hypothetical protein
gene_id_16228	138	97.83	4.00E-95	hypothetical protein
gene_id_16229	182	98.9	9.00E-127	carbonic anhydrase
gene_id_16230	195	96.41	6.00E-118	hypothetical protein
gene_id_16231	183	94.54	4.00E-122	hypothetical protein
gene_id_16232	422	97.16	0	seryl-tRNA synthetase
gene_id_16233	184	96.74	3.00E-124	hypothetical protein
gene_id_16234	744	98.39	0	hypothetical protein
gene_id_16469	792	98.74	0	hypothetical protein
gene_id_16470	726	98.21	0	hypothetical protein
gene_id_16471	359	97.49	0	hypothetical protein
gene_id_16473	304	96.38	3.00E-174	hypothetical protein
gene_id_16474	202	96.04	5.00E-136	hypothetical protein
gene_id_16475	198	100	7.00E-116	hypothetical protein
gene_id_16476	196	100	3.00E-134	electron transport complex RsxE subunit
gene_id_16477	338	96.45	0	hypothetical protein
gene_id_16478	243	97.53	2.00E-175	hypothetical protein
gene_id_16479	619	97.9	0	hypothetical protein
gene_id_16480	874	99.2	0	hypothetical protein
gene_id_16481	169	97.04	6.00E-108	hypothetical protein
gene_id_16482	276	99.64	0	thymidylate synthase
gene_id_16483	64	100	1.00E-37	hypothetical protein
gene_id_16484	238	99.16	2.00E-172	hypothetical protein, partial
gene_id_16485	212	99.06	4.00E-153	hypothetical protein
gene_id_16486	96	100	9.00E-61	hypothetical protein
gene_id_16487	423	99.76	0	GTPase CgtA
gene_id_16488	97	100	1.00E-62	50S ribosomal protein L27
gene_id_16489	96	98.96	3.00E-60	hypothetical protein
gene_id_16490	103	100	9.00E-47	50S ribosomal protein L21
gene_id_16491	499	99.2	0	hypothetical protein

gene_id_16492	226	99.56	7.00E-156	hypothetical protein
gene_id_16493	617	99.35	0	Fe-S oxidoreductase
gene_id_16494	437	96.8	0	hypothetical protein
gene_id_16495	116	99.14	1.00E-75	growth inhibitor PemK
gene_id_16496	91	98.9	4.00E-55	hypothetical protein
gene_id_16497	147	97.28	7.00E-98	hypothetical protein
gene_id_16498	121	99.17	2.00E-82	hypothetical protein
gene_id_16499	209	100	3.00E-148	uracil phosphoribosyltransferase
gene_id_16500	455	99.78	0	hypothetical protein
gene_id_16501	313	98.4	0	hypothetical protein
gene_id_16502	169	96.45	8.00E-75	hypothetical protein
gene_id_16503	209	47.85	3.00E-46	restriction endonuclease subunit R, partial
gene_id_16504	485	65.57	0	transposase
gene_id_16505	149	44.3	6.00E-33	hypothetical protein
gene_id_16506	129	100	1.00E-85	30S ribosomal protein S9
gene_id_16507	142	100	2.00E-98	50S ribosomal protein L13
gene_id_16508	249	99.2	0	hypothetical protein
gene_id_16509	265	98.87	4.00E-169	hypothetical protein
gene_id_16510	286	99.3	0	hypothetical protein
gene_id_16511	275	100	0	hypothetical protein
gene_id_16512	352	83.81	0	hypothetical protein
gene_id_16513	443	91.87	0	hypothetical protein
gene_id_16514	447	98.43	0	hypothetical protein
gene_id_16515	434	99.08	0	hypothetical protein
gene_id_16516	447	99.55	0	hypothetical protein
gene_id_16517	379	97.89	0	hypothetical protein
gene_id_16518	113	100	3.00E-74	50S ribosomal protein L17
gene_id_16519	315	100	0	DNA-directed RNA polymerase subunit alpha
gene_id_16520	207	100	1.00E-151	30S ribosomal protein S4
gene_id_16521	132	99.24	3.00E-90	30S ribosomal protein S11
gene_id_16522	122	100	4.00E-80	30S ribosomal protein S13
gene_id_16523	72	100	9.00E-45	translation initiation factor IF-1
gene_id_16524	100	99	6.00E-65	hypothetical protein
gene_id_16525	248	100	0	hypothetical protein
gene_id_16526	215	98.6	5.00E-152	hypothetical protein
gene_id_16527	422	99.76	0	preprotein translocase subunit SecY
gene_id_16528	146	100	4.00E-97	50S ribosomal protein L15
gene_id_16529	58	100	7.00E-31	hypothetical protein
gene_id_16530	169	100	2.00E-112	30S ribosomal protein S5
gene_id_16531	122	99.18	3.00E-81	50S ribosomal protein L18
gene_id_16532	179	100	2.00E-124	50S ribosomal protein L6
gene_id_16533	132	100	4.00E-88	30S ribosomal protein S8
gene_id_16534	179	100	9.00E-127	50S ribosomal protein L5
gene_id_16535	101	100	8.00E-64	50S ribosomal protein L24
gene_id_16536	122	100	8.00E-66	50S ribosomal protein L14
gene_id_16537	84	98.81	2.00E-42	30S ribosomal protein S17
gene_id_16538	67	100	9.00E-38	50S ribosomal protein L29

gene_id_16539	147	100	2.00E-102	50S ribosomal protein L16
gene_id_16540	226	100	8.00E-161	30S ribosomal protein S3
gene_id_16541	111	100	3.00E-74	50S ribosomal protein L22
gene_id_16542	93	100	5.00E-62	30S ribosomal protein S19
gene_id_16543	277	99.64	0	50S ribosomal protein L2
gene_id_16544	96	100	8.00E-61	50S ribosomal protein L23
gene_id_16545	207	100	7.00E-148	50S ribosomal protein L4
gene_id_16546	210	100	6.00E-131	50S ribosomal protein L3
gene_id_16547	103	100	4.00E-67	30S ribosomal protein S10
gene_id_16548	494	99.6	0	hypothetical protein
gene_id_16549	153	83.01	1.00E-88	elongation factor Tu, partial
gene_id_16816	304	94.74	0	hypothetical protein
gene_id_16817	256	95.7	7.00E-167	hypothetical protein
gene_id_16818	675	99.56	0	potassium transporter
gene_id_16819	76	98.68	2.00E-30	preprotein translocase subunit SecG
gene_id_16820	430	99.53	0	enolase
gene_id_16821	509	98.23	0	hypothetical protein
gene_id_16822	252	96.83	1.00E-168	hypothetical protein
gene_id_16823	397	97.73	0	phosphoglycerate kinase
gene_id_16824	335	99.7	0	hypothetical protein
gene_id_16825	341	100	0	hypothetical protein
gene_id_16827	472	99.79	0	hypothetical protein
gene_id_16828	89	100	2.00E-55	hypothetical protein
gene_id_16829	452	98.45	0	hypothetical protein
gene_id_16830	389	99.49	0	hypothetical protein
gene_id_16831	510	98.24	0	hypothetical protein
gene_id_16832	108	100	2.00E-55	glycine/sarcosine/betaine reductase complex protein
gene_id_16833	43	100	2.00E-08	hypothetical protein
gene_id_16834	105	100	2.00E-69	thioredoxin
gene_id_16835	311	98.07	9.00E-174	hypothetical protein
gene_id_16836	77	100	1.00E-45	glycine reductase complex protein B subunit gamma
gene_id_16837	347	99.71	0	beta-aspartate methyltransferase
gene_id_16838	426	99.77	0	beta-aspartyl peptidase
gene_id_16839	119	98.32	6.00E-77	hypothetical protein
gene_id_16840	540	98.33	0	hypothetical protein
gene_id_16841	156	96.79	1.00E-106	hypothetical protein
gene_id_16842	215	96.28	1.00E-144	hypothetical protein
gene_id_16843	93	98.92	4.00E-56	hypothetical protein
gene_id_16844	349	93.98	0	hypothetical protein
gene_id_16845	182	100	1.00E-125	hypothetical protein
gene_id_16846	248	99.6	1.00E-172	MFS transporter
gene_id_16847	353	98.3	0	hypothetical protein
gene_id_16848	71	100	1.00E-42	hypothetical protein
gene_id_16849	224	100	8.00E-162	ATP-binding protein
gene_id_16850	355	99.15	0	hypothetical protein
gene_id_16851	297	98.65	0	hypothetical protein
gene_id_16852	463	58.53	3.00E-175	ATPase AAA

gene_id_16853	370	97.3	0	hypothetical protein
gene_id_16854	275	99.27	0	hypothetical protein
gene_id_16855	356	98.6	0	hypothetical protein, partial
gene_id_16856	597	99.5	0	hypothetical protein
gene_id_16857	191	99.48	6.00E-133	hypothetical protein
gene_id_16858	298	94.63	0	hypothetical protein
gene_id_16859	41	65.85	1.00E-11	hypothetical protein
gene_id_16860	182	97.8	2.00E-126	hypothetical protein
gene_id_16861	41	82.93	2.00E-14	hypothetical protein
gene_id_16862	86	100	2.00E-52	hypothetical protein, partial
gene_id_16863	188	98.4	1.00E-101	hypothetical protein
gene_id_16864	171	99.42	2.00E-108	hypothetical protein
gene_id_16865	290	98.97	0	hypothetical protein
gene_id_16866	211	97.16	3.00E-145	hypothetical protein
gene_id_16867	215	97.67	8.00E-147	hypothetical protein
gene_id_16868	714	65.69	0	DNA topoisomerase III
gene_id_16869	226	100	6.00E-164	hypothetical protein
gene_id_16870	363	98.9	0	GTP-binding protein YchF
gene_id_16871	50	98	1.00E-23	hypothetical protein
gene_id_16872	317	99.37	0	hypothetical protein
gene_id_16873	428	99.3	0	hypothetical protein
gene_id_16874	253	99.6	0	hypothetical protein
gene_id_16875	216	98.15	6.00E-135	succinyl-CoA:3-ketoacid-CoA transferase
gene_id_16876	217	99.08	3.00E-117	hypothetical protein
gene_id_16877	389	100	0	hypothetical protein
gene_id_16878	567	98.77	0	hypothetical protein
gene_id_16879	286	72.38	1.00E-150	3-demethylubiquinone-9 3-methyltransferase
gene_id_16880	240	97.5	2.00E-160	histidine kinase, partial
gene_id_16881	232	98.71	4.00E-144	hypothetical protein
gene_id_16978	153	83.66	4.00E-89	elongation factor Tu, partial
gene_id_16979	562	99.82	0	adenylate cyclase, partial
gene_id_16980	49	100	8.00E-26	50S ribosomal protein L33
gene_id_16981	70	100	2.00E-41	preprotein translocase subunit SecE
gene_id_16982	175	100	9.00E-111	transcription termination/antitermination factor Nus
gene_id_16983	141	100	1.00E-94	50S ribosomal protein L11
gene_id_16984	232	100	4.00E-146	50S ribosomal protein L1
gene_id_16985	167	99.4	4.00E-115	50S ribosomal protein L10
gene_id_16986	126	99.21	4.00E-57	50S ribosomal protein L7/L12
gene_id_16987	1197	100	0	DNA-directed RNA polymerase subunit beta
gene_id_16988	1160	99.83	0	DNA-directed RNA polymerase subunit beta'
gene_id_16989	77	100	3.00E-39	hypothetical protein
gene_id_16990	139	100	8.00E-94	30S ribosomal protein S12
gene_id_16991	156	99.36	7.00E-109	30S ribosomal protein S7
gene_id_16992	690	99.86	0	hypothetical protein
gene_id_17027	240	99.17	1.00E-156	hypothetical protein, partial
gene_id_17028	73	100	2.00E-43	hypothetical protein
gene_id_17029	94	90.43	9.00E-46	hypothetical protein

gene_id_17030	614	98.05	0	hypothetical protein
gene_id_17031	252	99.21	2.00E-180	hypothetical protein
gene_id_17032	603	98.18	0	hypothetical protein
gene_id_17033	158	100	5.00E-111	hypothetical protein
gene_id_17034	611	99.02	0	aldehyde:ferredoxin oxidoreductase
gene_id_17035	159	99.37	9.00E-111	hypothetical protein
gene_id_17036	74	97.3	3.00E-43	hypothetical protein
gene_id_17037	400	94.5	0	hypothetical protein
gene_id_17038	764	98.04	0	hypothetical protein
gene_id_17039	311	99.36	0	hypothetical protein
gene_id_17040	381	97.38	0	hypothetical protein
gene_id_17041	442	98.19	0	MmgE/PrpD family protein, partial
gene_id_17042	424	97.17	0	hypothetical protein
gene_id_17043	331	95.77	0	hypothetical protein
gene_id_17044	165	98.18	6.00E-92	hypothetical protein
gene_id_17045	499	99.4	0	hypothetical protein
gene_id_17046	347	94.52	0	hypothetical protein
gene_id_17047	329	96.35	0	hypothetical protein
gene_id_17048	96	100	7.00E-60	citrate lyase subunit gamma
gene_id_17049	298	99.33	0	hypothetical protein
gene_id_17050	513	99.03	0	hypothetical protein
gene_id_17051	196	98.98	5.00E-135	hypothetical protein, partial
gene_id_17052	459	96.3	0	hypothetical protein
gene_id_17053	389	80.98	0	butanol dehydrogenase
gene_id_17054	159	96.23	5.00E-105	hypothetical protein
gene_id_17055	435	96.55	0	hypothetical protein
gene_id_17056	221	97.74	1.00E-125	hypothetical protein
gene_id_17057	333	97.9	0	hypothetical protein
gene_id_17058	394	97.97	0	hypothetical protein
gene_id_17059	595	99.5	0	hypothetical protein
gene_id_17060	161	93.79	2.00E-99	hypothetical protein
gene_id_17061	464	98.06	0	hypothetical protein
gene_id_17062	352	100	0	dihydrodipicolinate reductase
gene_id_17063	101	99.01	4.00E-66	2-amino-4-ketopentanoate thiolase subunit alpha
gene_id_17064	97	83.51	1.00E-51	MULTISPECIES: hypothetical protein
gene_id_17065	89	82.02	1.00E-48	membrane protein
gene_id_17067	49	93.88	3.00E-27	dihydrofolate reductase
gene_id_17067	34	73.53	3.00E-27	dihydrofolate reductase
gene_id_17068	155	40.65	1.00E-22	GCN5 family N-acetyltransferase
gene_id_17069	142	73.24	4.00E-72	NUDIX hydrolase
gene_id_17071	274	45.62	7.00E-74	internalin
gene_id_17072	158	93.67	1.00E-101	hypothetical protein
gene_id_17073	205	96.1	2.00E-143	hypothetical protein
gene_id_17074	184	97.28	2.00E-127	hypothetical protein, partial
gene_id_17076	158	94.3	1.00E-106	hypothetical protein, partial
gene_id_17077	115	60.87	6.00E-42	hypothetical protein
gene_id_17078	259	69.5	2.00E-134	hypothetical protein

gene_id_17079	151	59.6	3.00E-62	hypothetical protein
gene_id_17080	37	64.86	3.00E-08	hypothetical protein, partial
gene_id_17088	350	68.86	3.00E-141	ACGS family amino acid carrier protein
gene_id_17089	364	88.74	0	hypothetical protein, partial
gene_id_17089	167	32.93	9.00E-07	hypothetical protein, partial
gene_id_17090	146	97.95	4.00E-97	hypothetical protein, partial
gene_id_17091	178	54.49	7.00E-53	hypothetical protein
gene_id_17092	88	96.59	2.00E-39	hypothetical protein
gene_id_17093	114	98.25	2.00E-75	hypothetical protein
gene_id_17094	63	96.83	5.00E-25	hypothetical protein
gene_id_17095	545	97.25	0	hypothetical protein
gene_id_17096	160	99.38	3.00E-108	hypothetical protein
gene_id_17097	282	97.87	0	hypothetical protein, partial
gene_id_17098	361	96.4	0	hypothetical protein
gene_id_17099	146	97.95	1.00E-98	hypothetical protein
gene_id_17100	123	100	6.00E-83	hypothetical protein
gene_id_17510	24	95.83	7.00E-08	MULTISPECIES: elongation factor Tu, partial
gene_id_17511	193	97.93	8.00E-131	hypothetical protein
gene_id_17512	171	100	3.00E-119	hypothetical protein
gene_id_17513	245	100	4.00E-174	RNA methyltransferase
gene_id_17514	142	100	5.00E-86	Mini-ribonuclease 3
gene_id_17515	469	99.15	0	cysteinyl-tRNA synthetase
gene_id_17516	470	98.94	0	cell wall hydrolase
gene_id_17517	402	99.25	0	hypothetical protein
gene_id_17518	145	100	2.00E-80	hypothetical protein
gene_id_17519	293	99.66	0	hypothetical protein
gene_id_17520	495	99.19	0	hypothetical protein
gene_id_17521	383	59.01	5.00E-157	1-deoxy-D-xylulose 5-phosphate reductoisomerase
gene_id_17756	627	99.36	0	hypothetical protein
gene_id_17757	398	98.24	0	acetylornithine deacetylase
gene_id_17758	455	97.14	0	hypothetical protein
gene_id_17759	468	99.57	0	hypothetical protein
gene_id_17760	494	68.02	0	acetyl-CoA hydrolase
gene_id_17761	169	99.41	7.00E-119	hypothetical protein
gene_id_17762	559	100	0	methylmalonyl-CoA mutase
gene_id_17763	132	100	4.00E-70	methylmalonyl-CoA mutase
gene_id_17764	310	99.35	0	hypothetical protein
gene_id_17765	133	100	2.00E-89	hypothetical protein
gene_id_17766	402	70.15	1.00E-173	sodium ion-translocating decarboxylase subunit beta
gene_id_18040	129	72.09	1.00E-61	DNA-cytosine methyltransferase
gene_id_18041	295	65.08	5.00E-121	DNA methyltransferase
gene_id_18041	213	34.74	3.00E-24	DNA methyltransferase
gene_id_18042	81	82.72	7.00E-34	hypothetical protein
gene_id_18043	200	81.5	8.00E-115	hypothetical protein
gene_id_18044	59	64.41	1.00E-20	BFD-like
gene_id_18046	47	65.96	7.00E-16	hypothetical protein
gene_id_18047	220	38.18	4.00E-38	hypothetical protein

gene_id_18048	108	80.56	2.00E-60	hypothetical protein
gene_id_18049	423	87.23	0	type VI secretion protein
gene_id_18050	109	75.23	6.00E-52	translation initiation inhibitor
gene_id_18050	32	93.75	1.00E-11	translation initiation inhibitor
gene_id_18051	113	89.38	2.00E-69	HxlR family transcriptional regulator
gene_id_18053	189	88.36	4.00E-117	TetR family transcriptional regulator
gene_id_18054	597	92.46	0	myosin-cross-reactive antigen
gene_id_18055	682	85.63	0	hypothetical protein
gene_id_18056	409	77.75	0	hypothetical protein
gene_id_18057	647	86.86	0	hypothetical protein
gene_id_18059	295	78.31	5.00E-179	DegV family EDD domain-containing protein
gene_id_18060	167	44.91	8.00E-43	hypothetical protein
gene_id_18061	54	70.37	2.00E-14	ABC transporter permease
gene_id_18062	57	91.23	2.00E-24	ABC transporter permease
gene_id_18063	269	46.1	2.00E-58	hypothetical protein CLOSCI_00246
gene_id_18064	272	59.56	7.00E-100	hypothetical protein
gene_id_18065	33	69.7	2.00E-06	serine recombinase, partial
gene_id_18066	293	38.57	3.00E-48	hypothetical protein
gene_id_18067	283	46.29	8.00E-67	DNA methylase N-4/N-6 domain-containing protein
gene_id_18068	1009	49.85	0	hypothetical protein
gene_id_18069	243	90.12	4.00E-148	hypothetical protein
gene_id_18070	81	85.19	1.00E-36	hypothetical protein
gene_id_18071	200	65	9.00E-76	putative pancortin-3
gene_id_18072	354	83.33	0	hypothetical protein
gene_id_18073	71	83.1	2.00E-47	hypothetical protein
gene_id_18073	52	80.77	2.00E-47	hypothetical protein
gene_id_18074	254	85.83	4.00E-126	hypothetical protein
gene_id_18075	241	82.16	8.00E-143	lantibiotic ABC transporter permease
gene_id_18076	254	90.94	2.00E-157	ABC transporter ATP-binding protein
gene_id_18077	222	90.99	3.00E-131	chemotaxis protein CheY
gene_id_18078	452	82.96	0	histidine kinase
gene_id_18080	253	80.63	3.00E-157	beta-lactamase
gene_id_18081	210	100	1.00E-147	hypothetical protein
gene_id_18082	176	98.3	3.00E-97	membrane protein
gene_id_18083	189	99.47	1.00E-136	hypothetical protein
gene_id_18084	353	73.94	3.00E-171	hrdc domain-containing protein
gene_id_18085	270	97.78	0	MerR family transcriptional regulator
gene_id_18086	351	93.45	0	hypothetical protein
gene_id_18087	214	95.79	3.00E-150	hypothetical protein
gene_id_18088	253	96.84	0	N-acetyltransferase GCN5
gene_id_18089	305	95.74	0	hypothetical protein
gene_id_18090	295	95.59	0	hypothetical protein
gene_id_18091	318	95.91	0	hypothetical protein
gene_id_18092	274	47.81	1.00E-87	hypothetical protein
gene_id_18093	146	56.16	7.00E-48	hypothetical protein
gene_id_18094	198	86.87	3.00E-122	SAM-dependent methlyltransferase
gene_id_18095	126	99.21	2.00E-87	Rrf2 family transcriptional regulator

gene_id_18096	344	94.48	0	hypothetical protein
gene_id_18097	75	97.33	4.00E-44	hypothetical protein
gene_id_18098	226	70.8	1.00E-123	metal-dependent hydrolase
gene_id_18099	791	97.35	0	valyl-tRNA synthetase
gene_id_18100	435	68.51	0	amidohydrolase
gene_id_18101	272	90.81	0	hypothetical protein
gene_id_18102	116	99.14	1.00E-78	hypothetical protein
gene_id_18103	299	99.33	0	hypothetical protein
gene_id_18104	116	99.14	1.00E-76	HxlR family transcriptional regulator
gene_id_18105	390	96.67	0	hypothetical protein
gene_id_18106	412	93.45	0	sodium:glutamate symporter
gene_id_18107	299	100	0	glutamate formiminotransferase
gene_id_18108	187	95.72	2.00E-84	hypothetical protein
gene_id_18109	525	97.71	0	hypothetical protein
gene_id_18110	447	99.33	0	hypothetical protein
gene_id_18111	457	96.28	0	hypothetical protein
gene_id_18112	414	94.44	0	acetylornithine aminotransferase
gene_id_18113	339	82.3	0	4Fe-4S ferredoxin
gene_id_18114	102	100	7.00E-67	PadR family transcriptional regulator
gene_id_18115	382	98.69	0	chromate transporter
gene_id_18116	104	92.31	2.00E-63	hypothetical protein
gene_id_18117	286	96.85	0	hypothetical protein
gene_id_18118	332	98.49	0	hypothetical protein
gene_id_18119	209	60.77	5.00E-86	hypothetical protein
gene_id_18120	571	39.75	1.00E-155	amidohydrolase
gene_id_18121	148	91.22	2.00E-96	hypothetical protein
gene_id_18122	220	99.09	2.00E-156	hypothetical protein
gene_id_18123	585	51.45	0	hypothetical protein
gene_id_18124	349	98.28	0	16S rRNA methyltransferase
gene_id_18125	300	98.67	0	hypothetical protein
gene_id_18126	190	96.32	5.00E-135	hypothetical protein
gene_id_18127	210	95.24	1.00E-143	TetR family transcriptional regulator
gene_id_18128	417	96.64	0	hypothetical protein
gene_id_18129	775	93.81	0	hypothetical protein
gene_id_18130	244	97.54	3.00E-173	hypothetical protein
gene_id_18131	661	97.13	0	hypothetical protein
gene_id_18132	308	98.38	0	peptidase U61 LD-carboxypeptidase A
gene_id_18133	273	99.63	0	UDP-diphosphatase
gene_id_18864	218	100	5.00E-151	hypothetical protein
gene_id_18865	612	96.9	0	hypothetical protein
gene_id_18866	71	94.37	5.00E-39	hypothetical protein
gene_id_18867	279	97.85	0	hypothetical protein
gene_id_18869	339	97.05	0	radical SAM protein
gene_id_18870	149	96.64	1.00E-103	hypothetical protein
gene_id_18871	253	97.23	9.00E-173	hypothetical protein
gene_id_18872	286	96.5	0	hypothetical protein
gene_id_18873	183	98.91	4.00E-115	hypothetical protein

gene_id_18874	375	96.53	0	hypothetical protein
gene_id_18875	61	98.36	4.00E-34	hypothetical protein
gene_id_18876	331	98.19	0	hypothetical protein
gene_id_18877	78	98.72	2.00E-45	hypothetical protein
gene_id_18878	310	99.03	2.00E-180	cysteine synthase
gene_id_18879	121	98.35	1.00E-80	hypothetical protein
gene_id_18880	199	96.98	4.00E-141	hypothetical protein
gene_id_18881	306	95.75	0	hypothetical protein
gene_id_18882	366	98.91	0	3-methylitaconate isomerase
gene_id_18883	643	98.91	0	hypothetical protein
gene_id_18884	229	97.82	1.00E-144	hypothetical protein
gene_id_18885	718	96.8	0	hypothetical protein
gene_id_18886	290	95.86	0	hypothetical protein
gene_id_18887	126	61.9	3.00E-46	hypothetical protein
gene_id_18888	273	73.63	7.00E-115	ABC transporter
gene_id_18889	226	71.68	5.00E-120	ABC transporter, ATP-binding protein
gene_id_18890	333	58.26	7.00E-116	ABC transporter substrate-binding protein
gene_id_18892	219	98.17	8.00E-141	phosphohydrolase
gene_id_18893	543	96.87	0	hypothetical protein
gene_id_18894	59	100	8.00E-34	hypothetical protein
gene_id_18895	284	93.31	0	hypothetical protein
gene_id_18896	601	79.87	0	hypothetical protein
gene_id_18897	446	54.71	1.00E-132	hypothetical protein
gene_id_18898	218	44.5	5.00E-55	potassium transporter TrkA
gene_id_18899	129	52.71	1.00E-36	hypothetical protein
gene_id_18900	100	48	4.00E-20	hypothetical protein
gene_id_18901	232	62.07	3.00E-85	XRE family transcriptional regulator
gene_id_18902	482	50.41	5.00E-151	integral membrane sensor signal transduction histidi
gene_id_18903	103	97.09	9.00E-66	MarR family transcriptional regulator
gene_id_18904	134	97.76	4.00E-90	hypothetical protein
gene_id_18905	156	84.62	6.00E-93	hypothetical protein
gene_id_18906	205	94.63	3.00E-132	hypothetical protein
gene_id_18907	187	81.82	8.00E-101	hypothetical protein
gene_id_18908	187	94.65	7.00E-131	NADPH-dependent FMN reductase
gene_id_18909	162	98.77	2.00E-113	hypothetical protein
gene_id_18910	185	99.46	5.00E-132	hypothetical protein
gene_id_18911	223	97.76	8.00E-134	hypothetical protein
gene_id_18912	216	96.3	1.00E-141	hypothetical protein, partial
gene_id_18913	335	95.52	0	hypothetical protein
gene_id_18914	117	99.15	6.00E-52	hypothetical protein
gene_id_18915	449	99.11	0	hypothetical protein
gene_id_18916	149	97.32	1.00E-91	hypothetical protein
gene_id_18917	314	97.77	0	hypothetical protein, partial
gene_id_18918	233	95.28	4.00E-159	hypothetical protein
gene_id_18919	323	96.9	0	hypothetical protein
gene_id_18920	637	98.74	0	hypothetical protein
gene_id_18921	632	66.14	0	exported protein of unknown function

gene_id_18922	175	97.71	2.00E-122	diacylglycerol kinase
gene_id_18923	82	98.78	5.00E-52	hypothetical protein
gene_id_18924	329	94.83	0	hypothetical protein
gene_id_18926	231	77.49	4.00E-131	hypothetical protein
gene_id_18927	475	22.74	4.00E-06	hypothetical protein
gene_id_18929	76	96.05	2.00E-40	hypothetical protein
gene_id_18930	151	98.68	3.00E-97	hypothetical protein
gene_id_18931	111	76.58	2.00E-50	hypothetical protein
gene_id_18932	655	97.71	0	chemotaxis protein, partial
gene_id_18933	221	31.22	3.00E-17	membrane protein
gene_id_18934	172	44.19	4.00E-41	RNA polymerase subunit sigma-24
gene_id_18937	91	100	4.00E-58	hypothetical protein
gene_id_18938	131	100	5.00E-87	hypothetical protein, partial
gene_id_18939	353	96.32	0	hypothetical protein
gene_id_18940	96	100	2.00E-60	hypothetical protein
gene_id_18941	94	100	1.00E-61	30S ribosomal protein S18
gene_id_18942	154	100	5.00E-108	single-stranded DNA-binding protein
gene_id_18943	95	100	6.00E-61	30S ribosomal protein S6
gene_id_18944	164	97.56	8.00E-105	hypothetical protein
gene_id_18945	435	97.93	0	phosphomethylpyrimidine synthase
gene_id_18946	273	95.24	0	hypothetical protein
gene_id_18947	214	95.79	3.00E-144	hypothetical protein
gene_id_18948	259	96.91	0	hypothetical protein
gene_id_18949	50	52	2.00E-07	hypothetical protein JCM19045_2349
gene_id_18950	255	56.86	3.00E-102	Zn-dependent hydrolase (beta-lactamase superfamily
gene_id_18951	341	99.41	0	hypothetical protein
gene_id_18952	456	93.86	0	hypothetical protein
gene_id_18953	569	97.89	0	hypothetical protein
gene_id_18954	288	98.61	0	hypothetical protein
gene_id_18955	343	99.71	0	rod shape-determining protein Mbl
gene_id_18956	381	99.21	0	phosphoribosylpyrophosphate synthetase
gene_id_18957	433	97.23	0	hypothetical protein
gene_id_18958	414	99.52	0	hypothetical protein
gene_id_18959	445	99.33	0	multidrug transporter MATE
gene_id_19040	380	99.74	0	hypothetical protein
gene_id_19041	576	97.92	0	hypothetical protein
gene_id_19042	292	98.29	0	hypothetical protein
gene_id_19043	99	96.97	8.00E-63	hypothetical protein, partial
gene_id_19044	568	99.12	0	arginyl-tRNA synthetase
gene_id_19045	359	96.94	0	hypothetical protein
gene_id_19046	524	96.95	0	hypothetical protein
gene_id_19319	222	95.95	3.00E-139	hypothetical protein, partial
gene_id_19320	772	91.84	0	hypothetical protein
gene_id_19321	132	98.48	3.00E-88	hypothetical protein, partial
gene_id_19322	902	96.56	0	hypothetical protein
gene_id_19323	297	98.99	0	hypothetical protein
gene_id_19324	238	100	3.00E-167	sporulation sigma factor SigE

gene_id_19325	257	99.61	0	hypothetical protein
gene_id_19326	90	100	8.00E-44	hypothetical protein
gene_id_19327	177	98.87	2.00E-110	hypothetical protein, partial
gene_id_19327	87	59.77	1.00E-21	hypothetical protein, partial
gene_id_19327	66	69.7	1.00E-18	hypothetical protein, partial
gene_id_19448	425	99.29	0	seryl-tRNA synthetase
gene_id_19449	72	100	4.00E-45	hypothetical protein
gene_id_19450	402	98.01	0	hypothetical protein
gene_id_19451	158	87.97	8.00E-102	transposase
gene_id_19729	638	98.9	0	hypothetical protein
gene_id_19730	574	97.56	0	hypothetical protein
gene_id_19731	164	96.34	1.00E-108	hypothetical protein
gene_id_19732	212	96.7	3.00E-144	hypothetical protein
gene_id_19733	405	97.78	0	hypothetical protein
gene_id_19734	66	98.48	2.00E-38	cold-shock protein
gene_id_19736	382	99.21	0	hypothetical protein
gene_id_19737	268	98.51	0	hypothetical protein
gene_id_19738	326	97.24	0	hypothetical protein
gene_id_19739	459	98.26	0	hypothetical protein
gene_id_19740	109	95.41	2.00E-68	hypothetical protein
gene_id_19741	567	97.88	0	aldehyde ferredoxin oxidoreductase
gene_id_19742	74	97.3	7.00E-45	hypothetical protein
gene_id_19743	234	97.44	1.00E-165	hypothetical protein
gene_id_19744	62	91.94	1.00E-34	hypothetical protein
gene_id_19745	287	96.52	1.00E-178	hypothetical protein
gene_id_19746	76	100	1.00E-43	hypothetical protein
gene_id_19747	319	96.55	0	hypothetical protein
gene_id_19748	106	98.11	6.00E-56	copper amine oxidase, partial
gene_id_19749	301	98.67	0	hypothetical protein
gene_id_19750	669	98.06	0	hypothetical protein
gene_id_19751	464	98.92	0	hypothetical protein
gene_id_19752	380	98.68	0	hypothetical protein
gene_id_19753	185	95.14	3.00E-123	hypothetical protein
gene_id_19754	152	99.34	2.00E-105	hypothetical protein
gene_id_19755	90	100	4.00E-53	hypothetical protein
gene_id_19756	128	32.81	8.00E-16	spore cortex biosynthesis protein YabQ
gene_id_19757	151	99.34	2.00E-87	hypothetical protein
gene_id_19758	527	99.05	0	hypothetical protein
gene_id_19759	461	99.13	0	tRNA(Ile)-lysidine synthetase
gene_id_19760	179	100	4.00E-123	hypothetical protein
gene_id_19761	603	100	0	cell division protein FtsH
gene_id_19994	378	100	0	glutaconyl-CoA decarboxylase subunit beta
gene_id_19995	126	99.21	1.00E-57	hypothetical protein
gene_id_19996	101	100	1.00E-46	hypothetical protein
gene_id_19997	458	99.78	0	oxaloacetate decarboxylase
gene_id_19998	320	97.81	0	hypothetical protein
gene_id_19999	741	95.01	0	hypothetical protein

gene_id_20000	343	95.63	0	hypothetical protein
gene_id_20001	87	98.85	1.00E-50	30S ribosomal protein S20
gene_id_20002	309	100	0	hypothetical protein
gene_id_20003	390	97.44	0	hypothetical protein
gene_id_20004	601	99	0	elongation factor 4
gene_id_20005	168	97.62	6.00E-104	hypothetical protein
gene_id_20006	223	93.27	6.00E-124	hypothetical protein
gene_id_20007	551	100	0	hypothetical protein
gene_id_20008	625	96.96	0	hypothetical protein
gene_id_20009	160	97.5	4.00E-109	hypothetical protein
gene_id_20010	114	97.37	5.00E-70	hypothetical protein
gene_id_20011	167	96.41	4.00E-84	hypothetical protein
gene_id_20012	242	92.15	5.00E-146	hypothetical protein
gene_id_20013	531	99.44	0	hypothetical protein, partial
gene_id_20014	641	99.53	0	threonyl-tRNA synthetase
gene_id_20015	292	98.97	0	hypothetical protein
gene_id_20016	349	99.43	0	hypothetical protein
gene_id_20017	260	98.85	6.00E-178	uridine phosphorylase
gene_id_20018	418	99.04	0	hypothetical protein
gene_id_20019	151	99.34	1.00E-89	hypothetical protein
gene_id_20020	446	98.43	0	hypothetical protein
gene_id_20021	228	99.56	1.00E-145	hypothetical protein
gene_id_20022	459	96.08	0	hypothetical protein
gene_id_20023	101	99.01	5.00E-60	hypothetical protein
gene_id_20024	142	100	1.00E-97	hypothetical protein
gene_id_20025	146	100	3.00E-84	hypothetical protein
gene_id_20026	332	99.7	0	hypothetical protein
gene_id_20027	118	100	3.00E-51	hypothetical protein
gene_id_20412	125	96.8	1.00E-77	hypothetical protein
gene_id_20413	205	99.02	6.00E-132	hypothetical protein, partial
gene_id_20414	352	98.58	0	dihydrodipicolinate reductase
gene_id_20416	355	98.87	0	hypothetical protein
gene_id_20417	452	99.34	0	hypothetical protein
gene_id_20418	731	99.86	0	LuxR family transcriptional regulator
gene_id_20419	116	100	8.00E-77	hypothetical protein
gene_id_20420	289	78.55	5.00E-157	2-amino-4-ketopentanoate thiolase
gene_id_20535	182	99.45	7.00E-126	hypothetical protein
gene_id_20536	288	99.31	0	dimethyladenosine transferase
gene_id_20537	187	98.93	6.00E-127	hypothetical protein
gene_id_20538	215	100	3.00E-139	hypothetical protein
gene_id_20539	185	98.38	2.00E-113	hypothetical protein, partial
gene_id_20540	288	97.57	0	hypothetical protein
gene_id_20541	149	99.33	7.00E-101	hypothetical protein
gene_id_20542	608	75.49	0	hypothetical protein
gene_id_20543	496	99.4	0	inosine 5'-monophosphate dehydrogenase
gene_id_20544	107	99.07	2.00E-41	hypothetical protein
gene_id_20545	692	35.69	5.00E-87	hypothetical protein

gene_id_20546	388	97.16	0	hypothetical protein
gene_id_20547	129	27.91	3.00E-07	hypothetical protein, partial
gene_id_20548	216	95.37	2.00E-147	hypothetical protein
gene_id_20794	118	35.59	5.00E-14	hTH domain-containing protein
gene_id_20800	95	30.53	4.00E-07	hypothetical protein
gene_id_20804	71	46.48	6.00E-11	hypothetical protein
gene_id_20807	100	28	4.00E-06	hypothetical protein
gene_id_20808	180	38.33	7.00E-24	hypothetical protein
gene_id_20809	77	54.55	5.00E-08	membrane protein
gene_id_20809	38	65.79	2.00E-06	membrane protein
gene_id_20810	133	33.08	1.00E-09	hypothetical protein
gene_id_20812	389	29.31	3.00E-38	putative Phage replication protein CRI
gene_id_20814	315	41.27	2.00E-52	recombinase
gene_id_21002	202	79.7	3.00E-114	methylmalonyl-CoA carboxyltransferase
gene_id_21004	72	100	2.00E-40	hypothetical protein, partial
gene_id_21005	298	100	0	hypothetical protein
gene_id_21006	298	98.32	0	hypothetical protein
gene_id_21007	354	99.72	0	hypothetical protein
gene_id_21008	177	94.92	1.00E-115	hypothetical protein
gene_id_21009	166	94.58	3.00E-110	hypothetical protein
gene_id_21010	132	96.97	7.00E-75	hypothetical protein
gene_id_21011	93	97.85	2.00E-58	hypothetical protein
gene_id_21012	334	98.8	0	hypothetical protein
gene_id_21362	139	98.56	5.00E-95	hypothetical protein
gene_id_21363	302	99.34	0	hypothetical protein
gene_id_21364	421	100	0	preprotein translocase subunit SecD
gene_id_21365	130	100	1.00E-86	hypothetical protein
gene_id_21367	358	99.72	0	glutaconyl-CoA decarboxylase subunit beta
gene_id_21368	710	98.45	0	hypothetical protein
gene_id_21369	351	39.89	6.00E-86	ATPase
gene_id_21370	420	98.33	0	hypothetical protein
gene_id_21371	938	99.25	0	hypothetical protein
gene_id_21372	660	99.7	0	excinuclease ABC subunit B
gene_id_21373	160	95.62	6.00E-108	hypothetical protein
gene_id_21374	204	99.51	2.00E-133	hypothetical protein
gene_id_21375	247	95.14	3.00E-171	hypothetical protein
gene_id_21376	255	98.82	1.00E-165	hypothetical protein
gene_id_21377	386	98.19	0	hypothetical protein
gene_id_21378	83	98.8	3.00E-52	hypothetical protein
gene_id_21379	614	98.86	0	hypothetical protein
gene_id_21622	696	59.77	0	ferrous iron transport protein B
gene_id_21623	73	73.97	2.00E-29	feoA family protein
gene_id_21624	70	71.43	2.00E-24	fe2+ transport system protein A
gene_id_21625	454	97.58	0	hypothetical protein
gene_id_21626	357	91.6	0	hypothetical protein
gene_id_21627	140	92.86	9.00E-89	hypothetical protein
gene_id_21628	145	100	1.00E-101	hypothetical protein, partial

gene_id_21629	226	99.12	1.00E-164	manganese catalase
gene_id_21630	228	96.05	8.00E-158	peptide ABC transporter ATP-binding protein
gene_id_21631	386	95.85	0	hypothetical protein
gene_id_21632	215	92.56	4.00E-145	hypothetical protein
gene_id_21633	422	94.08	0	hypothetical protein
gene_id_21634	418	92.82	0	hypothetical protein
gene_id_21635	275	94.18	8.00E-144	ferredoxin
gene_id_21636	292	98.97	0	multidrug transporter, partial
gene_id_21637	91	98.9	4.00E-59	ArsR family transcriptional regulator
gene_id_21638	212	100	1.00E-135	hypothetical protein
gene_id_21639	400	99.25	0	hypothetical protein
gene_id_21640	228	98.25	4.00E-153	hypothetical protein
gene_id_21641	460	94.35	0	hypothetical protein
gene_id_21642	295	97.29	0	hypothetical protein
gene_id_21643	449	98	0	hypothetical protein
gene_id_21644	790	98.86	0	hypothetical protein
gene_id_21645	299	97.99	0	hypothetical protein
gene_id_21646	465	98.06	0	hypothetical protein
gene_id_21647	311	97.11	0	hypothetical protein
gene_id_21719	462	99.13	0	hypothetical protein
gene_id_21721	234	99.15	4.00E-164	hypothetical protein
gene_id_21722	262	98.47	0	electron transfer flavoprotein subunit beta
gene_id_21723	396	98.48	0	electron transfer flavoprotein subunit alpha
gene_id_21724	467	99.14	0	2-hydroxy-acid oxidase
gene_id_21725	103	96.12	2.00E-45	hypothetical protein
gene_id_21726	230	96.09	4.00E-130	hypothetical protein
gene_id_21793	37	64.86	5.00E-08	hypothetical protein, partial
gene_id_21794	175	94.29	8.00E-113	GNAT family acetyltransferase
gene_id_21795	198	100	2.00E-141	hypothetical protein
gene_id_21796	80	100	4.00E-45	hypothetical protein
gene_id_21797	566	99.47	0	DNA polymerase III subunit gamma/tau
gene_id_21798	440	97.5	0	hypothetical protein
gene_id_21799	246	97.97	6.00E-158	hypothetical protein
gene_id_21801	68	100	5.00E-42	50S ribosomal protein L31
gene_id_21802	398	76.63	0	transcription termination factor Rho
gene_id_21803	85	100	3.00E-53	hypothetical protein
gene_id_21804	551	98.73	0	hypothetical protein
gene_id_21805	388	97.94	0	serine/threonine protein phosphatase
gene_id_21806	653	98.93	0	hypothetical protein
gene_id_21807	325	100	0	hypothetical protein
gene_id_21808	272	99.26	0	3-keto-5-aminohexanoate cleavage enzyme
gene_id_21809	353	98.87	0	hypothetical protein
gene_id_21810	465	98.92	0	hypothetical protein
gene_id_21811	370	98.11	0	hypothetical protein
gene_id_21988	74	94.59	7.00E-29	hypothetical protein
gene_id_21990	460	99.13	0	hypothetical protein
gene_id_21991	483	99.79	0	4-hydroxybutyryl-CoA dehydratase

gene_id_21992	92	98.91	2.00E-56	hypothetical protein
gene_id_21993	432	99.07	0	4-hydroxybutyrate CoA-transferase
gene_id_21994	443	99.32	0	hypothetical protein
gene_id_21995	397	96.98	0	hypothetical protein
gene_id_21996	552	96.92	0	hypothetical protein
gene_id_21997	306	98.04	0	hypothetical protein
gene_id_21998	302	98.68	0	hypothetical protein
gene_id_21999	328	98.78	0	peptide ABC transporter ATP-binding protein
gene_id_22000	325	97.54	0	hypothetical protein
gene_id_22001	453	98.68	0	hypothetical protein
gene_id_22002	141	100	1.00E-96	hypothetical protein
gene_id_22003	533	99.44	0	hypothetical protein
gene_id_22004	380	98.42	0	hypothetical protein
gene_id_22005	919	99.46	0	preprotein translocase subunit SecA
gene_id_22006	349	99.14	0	hypothetical protein
gene_id_22007	762	99.34	0	hypothetical protein
gene_id_22008	210	98.1	1.00E-137	hypothetical protein
gene_id_22009	257	99.61	3.00E-172	hypothetical protein
gene_id_22336	154	96.1	3.00E-87	hypothetical protein
gene_id_22337	257	95.72	3.00E-174	hypothetical protein
gene_id_22338	249	92.77	5.00E-157	hypothetical protein
gene_id_22339	233	94.42	6.00E-156	hypothetical protein
gene_id_22340	365	90.41	0	hypothetical protein
gene_id_22341	201	99	9.00E-122	hypothetical protein
gene_id_22342	160	98.12	8.00E-109	hypothetical protein
gene_id_22343	90	94.44	5.00E-55	hypothetical protein
gene_id_22344	578	92.56	0	hypothetical protein
gene_id_22345	210	92.86	5.00E-127	hypothetical protein
gene_id_22346	95	97.89	6.00E-58	hypothetical protein
gene_id_22347	304	96.71	0	hypothetical protein
gene_id_22348	675	97.63	0	hypothetical protein
gene_id_22349	267	98.88	0	hypothetical protein
gene_id_22350	340	98.53	0	hypothetical protein
gene_id_22351	747	91.83	0	hypothetical protein
gene_id_22352	125	100	2.00E-82	hypothetical protein
gene_id_22353	117	85.47	4.00E-60	hypothetical protein
gene_id_22354	557	97.49	0	hypothetical protein, partial
gene_id_22355	621	97.42	0	hypothetical protein, partial
gene_id_22356	134	99.25	1.00E-91	hemerythrin
gene_id_22357	678	96.61	0	hypothetical protein
gene_id_22358	131	54.96	3.00E-41	hypothetical protein
gene_id_22359	202	42.57	5.00E-41	hypothetical protein
gene_id_22360	619	55.57	0	hypothetical protein
gene_id_22361	326	85.58	0	NAD-dependent dehydratase
gene_id_22362	386	77.72	0	aminotransferase DegT
gene_id_22363	339	76.7	1.00E-166	nucleotidyltransferase
gene_id_22364	217	64.98	5.00E-90	sugar O-acyltransferase, sialic acid O-acetyltransferas

gene_id_22365	329	75.68	4.00E-177	hypothetical protein
gene_id_22366	387	59.43	7.00E-157	UDP-N-acetylglucosamine 2-epimerase
gene_id_22367	314	39.81	8.00E-67	hypothetical protein
gene_id_22368	221	54.75	1.00E-77	GlcNAc-PI de-N-acetylase
gene_id_22369	230	60.43	2.00E-95	N-acylneuraminate cytidylyltransferase
gene_id_22370	252	68.65	8.00E-104	flagellin
gene_id_22371	443	95.03	0	hypothetical protein, partial
gene_id_22372	133	98.5	6.00E-90	hypothetical protein
gene_id_22373	643	96.27	0	hypothetical protein, partial
gene_id_22374	191	100	2.00E-131	hypothetical protein, partial
gene_id_22375	278	97.84	0	hypothetical protein, partial
gene_id_22376	267	99.63	0	hypothetical protein
gene_id_22377	294	97.96	0	hypothetical protein
gene_id_22378	332	98.49	0	hypothetical protein
gene_id_22379	265	98.87	0	hypothetical protein
gene_id_22817	547	98.72	0	hypothetical protein, partial
gene_id_22818	107	98.13	5.00E-73	hypothetical protein
gene_id_22819	440	97.27	0	hypothetical protein
gene_id_22820	368	97.83	0	hypothetical protein
gene_id_22821	764	98.04	0	hypothetical protein, partial
gene_id_22822	154	100	1.00E-99	hypothetical protein
gene_id_22862	200	98	8.00E-141	hypothetical protein
gene_id_22863	275	97.09	3.00E-161	hypothetical protein
gene_id_22864	283	98.94	0	hypothetical protein
gene_id_22886	278	98.56	0	hypothetical protein
gene_id_22887	267	99.63	0	hypothetical protein
gene_id_22888	313	99.36	0	hypothetical protein
gene_id_22889	327	96.64	0	hypothetical protein
gene_id_22890	884	99.21	0	valyl-tRNA synthetase
gene_id_22891	338	98.82	0	hypothetical protein
gene_id_22978	144	63.89	1.00E-48	acyl-CoA thioester hydrolase
gene_id_22979	218	94.5	1.00E-148	hypothetical protein
gene_id_22980	155	99.35	9.00E-96	6,7-dimethyl-8-ribityllumazine synthase
gene_id_22981	397	99.75	0	hypothetical protein
gene_id_22982	217	100	1.00E-152	hypothetical protein
gene_id_22983	369	98.37	0	hypothetical protein
gene_id_22984	191	95.81	2.00E-129	hypothetical protein
gene_id_22985	201	98.01	6.00E-145	phosphohydrolase
gene_id_22986	314	99.36	0	2-hydroxyacid dehydrogenase
gene_id_22987	158	95.57	9.00E-87	hypothetical protein
gene_id_22988	145	100	3.00E-101	hypothetical protein
gene_id_22989	343	99.42	0	hypothetical protein
gene_id_22990	103	98.06	2.00E-51	hypothetical protein
gene_id_22991	482	98.13	0	hypothetical protein
gene_id_22992	135	100	4.00E-88	potassium transporter TrkA, partial
gene_id_22993	221	98.19	7.00E-143	hypothetical protein
gene_id_22995	512	99.61	0	hypothetical protein

gene_id_22996	168	93.45	7.00E-100	hypothetical protein
gene_id_22997	455	97.58	0	hypothetical protein
gene_id_22998	225	98.22	6.00E-160	hypothetical protein
gene_id_22999	147	99.32	2.00E-89	hypothetical protein
gene_id_23000	130	96.92	2.00E-74	hypothetical protein
gene_id_23883	104	99.04	1.00E-60	hypothetical protein
gene_id_23884	581	97.42	0	hypothetical protein
gene_id_23885	304	98.68	0	ATPase
gene_id_23886	452	98.23	0	hypothetical protein
gene_id_23887	178	100	2.00E-129	hypothetical protein
gene_id_23888	346	99.71	0	hypothetical protein
gene_id_23889	99	100	3.00E-48	hypothetical protein
gene_id_23890	144	98.61	1.00E-77	hypothetical protein
gene_id_23891	265	98.49	6.00E-174	hypothetical protein
gene_id_23892	346	98.84	0	hypothetical protein
gene_id_23893	260	97.69	2.00E-130	hypothetical protein
gene_id_23894	244	96.72	3.00E-171	hypothetical protein
gene_id_23895	114	96.49	1.00E-65	hypothetical protein
gene_id_23896	352	98.86	0	hypothetical protein
gene_id_23897	228	99.12	6.00E-137	molybdate ABC transporter permease
gene_id_23898	275	94.55	1.00E-166	molybdenum ABC transporter substrate-binding prot
gene_id_23899	340	94.12	0	hypothetical protein
gene_id_23900	341	96.19	0	molybdopterin-binding protein
gene_id_25103	125	82.4	2.00E-70	MULTISPECIES: hypothetical protein
gene_id_25104	131	66.41	6.00E-59	hypothetical protein
gene_id_25105	87	39.08	1.00E-18	hypothetical protein
gene_id_25106	186	38.71	2.00E-26	sigma-70 protein
gene_id_25107	241	29.05	2.00E-22	hypothetical protein
gene_id_25109	245	39.59	2.00E-47	MULTISPECIES: hypothetical protein
gene_id_25110	77	45.45	4.00E-09	hypothetical protein
gene_id_25670	1174	99.15	0	MULTISPECIES: Pyruvate-flavodoxin oxidoreductase
gene_id_25671	55	80	1.00E-21	hypothetical protein
gene_id_25672	126	98.41	6.00E-81	MULTISPECIES: hypothetical protein
gene_id_25673	491	100	0	MULTISPECIES: hypothetical protein
gene_id_25674	451	96.9	0	MULTISPECIES: hypothetical protein
gene_id_25675	228	96.05	7.00E-141	MULTISPECIES: hypothetical protein
gene_id_25676	48	70.83	2.00E-13	hypothetical protein DEHRE_07460
gene_id_25677	160	98.75	2.00E-109	MULTISPECIES: hypothetical protein
gene_id_26476	402	90.55	0	hypothetical protein
gene_id_26477	335	95.82	0	hypothetical protein, partial
gene_id_26478	383	36.55	5.00E-49	hypothetical protein
gene_id_27736	238	99.16	1.00E-170	hypothetical protein
gene_id_27737	713	49.51	0	hypothetical protein EAL2_808p07060

o short-chain alcohol dehydrogenases)

rotein domain-containing protein

r oxidoreductase, gamma subunit

Gene ID	Length (aa)	Identity	e-value
gene_id_793	209	81.34	7.00E-109
gene_id_794	167	75.45	6.00E-86
gene_id_795	348	73.56	0
gene_id_797	134	68.66	2.00E-61
gene_id_798	958	75.99	0
gene_id_799	472	78.39	0
gene_id_800	98	94.9	4.00E-60
gene_id_801	608	86.51	0
gene_id_802	88	90.91	6.00E-53
gene_id_803	187	82.89	5.00E-114
gene_id_805	401	67.33	0
gene_id_806	124	62.1	8.00E-48
gene_id_807	774	68.48	0
gene_id_808	64	48.44	5.00E-15
gene_id_809	93	56.99	2.00E-28
gene_id_811	592	66.22	0
gene_id_812	384	40.62	2.00E-77
gene_id_813	246	60.57	8.00E-104
gene_id_814	573	40.84	8.00E-153
gene_id_815	320	54.69	6.00E-126
gene_id_816	279	59.86	3.00E-104
gene_id_817	318	54.72	1.00E-119
gene_id_818	294	51.02	7.00E-100
gene_id_819	371	62.26	4.00E-172
gene_id_820	59	62.71	2.00E-16
gene_id_821	597	85.09	0
gene_id_822	55	47.27	7.00E-06
gene_id_824	87	93.1	2.00E-52
gene_id_825	138	81.88	3.00E-78
gene_id_826	112	63.39	1.00E-43
gene_id_827	53	60.38	2.00E-07
gene_id_828	101	42.57	5.00E-13
gene_id_829	529	67.67	0
gene_id_830	292	59.93	2.00E-118
gene_id_831	545	71.74	0
gene_id_832	162	45.68	1.00E-42
gene_id_834	93	44.09	2.00E-19
gene_id_835	181	48.62	8.00E-57
gene_id_836	76	52.63	2.00E-19
gene_id_837	56	67.86	3.00E-18
gene_id_838	435	70.57	0
gene_id_839	146	78.77	6.00E-82
gene_id_840	564	44.5	3.00E-165
gene_id_841	350	44.57	1.00E-101
gene_id_842	544	58.09	0
gene_id_843	310	30.65	8.00E-22

gene_id_844	272	59.93	4.00E-112
gene_id_845	476	44.54	3.00E-142
gene_id_846	1077	48.75	0
gene_id_847	326	65.03	7.00E-157
gene_id_848	396	40.66	5.00E-90
gene_id_849	333	40.54	2.00E-74
gene_id_850	465	45.16	4.00E-133
gene_id_851	347	43.23	2.00E-94
gene_id_852	468	27.56	1.00E-49
gene_id_854	122	97.54	2.00E-82
gene_id_855	73	95.89	1.00E-31
gene_id_856	614	98.53	0
gene_id_857	238	53.78	9.00E-80
gene_id_858	369	38.48	2.00E-81
gene_id_859	96	53.12	1.00E-24
gene_id_860	95	29.47	6.00E-07
gene_id_861	97	50.52	6.00E-25
gene_id_862	270	85.19	2.00E-171
gene_id_863	165	41.82	2.00E-40
gene_id_864	185	57.84	1.00E-71
gene_id_865	75	76	5.00E-19
gene_id_866	1321	63.74	0
gene_id_867	76	71.05	2.00E-15
gene_id_868	141	50.35	6.00E-30
gene_id_869	242	82.23	1.00E-139
gene_id_870	271	77.12	3.00E-158
gene_id_871	520	73.46	0
gene_id_872	298	77.52	2.00E-175
gene_id_873	271	78.23	6.00E-129
gene_id_874	129	83.72	3.00E-74
gene_id_875	179	77.09	4.00E-96
gene_id_876	102	62.75	7.00E-32
gene_id_877	565	72.39	0
gene_id_878	113	78.76	3.00E-58
gene_id_879	300	87.67	1.00E-163
gene_id_880	104	61.54	9.00E-44
gene_id_881	83	83.13	2.00E-42
gene_id_4209	204	62.25	6.00E-86
gene_id_4210	124	66.94	1.00E-53
gene_id_4211	368	75	0
gene_id_4212	221	68.78	1.00E-101
gene_id_4213	405	80.74	0
gene_id_4214	155	86.45	9.00E-92
gene_id_4215	431	70.77	0
gene_id_4216	267	80.52	1.00E-155
gene_id_4217	274	85.04	4.00E-170
gene_id_4218	199	79.4	2.00E-95

gene_id_4219	241	74.27	3.00E-114
gene_id_4220	476	56.51	0
gene_id_4221	269	46.84	1.00E-68
gene_id_4222	659	82.4	0
gene_id_4223	111	38.74	2.00E-19
gene_id_4224	341	66.28	3.00E-152
gene_id_4224	63	60.32	2.00E-14
gene_id_4225	333	60.06	7.00E-133
gene_id_4226	49	61.22	3.00E-10
gene_id_4227	452	61.5	0
gene_id_4228	329	54.71	9.00E-131
gene_id_4230	772	44.04	0
gene_id_4231	388	41.49	2.00E-85
gene_id_4232	266	46.62	8.00E-74
gene_id_4233	250	56	1.00E-78
gene_id_4234	227	33.92	6.00E-25
gene_id_4235	614	36.16	2.00E-105
gene_id_4236	456	38.6	1.00E-62
gene_id_4237	223	62.78	6.00E-88
gene_id_4239	144	46.53	5.00E-30
gene_id_4240	418	61.24	2.00E-178
gene_id_4241	640	65.31	0
gene_id_4242	444	77.93	0
gene_id_4244	275	47.64	1.00E-82
gene_id_4245	319	37.93	5.00E-43
gene_id_4246	497	63.58	0
gene_id_4247	335	66.27	1.00E-139
gene_id_4248	269	73.23	3.00E-117
gene_id_4249	333	64.56	1.00E-147
gene_id_4250	315	64.13	2.00E-138
gene_id_4251	489	38.24	5.00E-101
gene_id_4252	54	61.11	9.00E-13
gene_id_4253	221	48.42	3.00E-43
gene_id_4254	289	59.86	1.00E-120
gene_id_4255	79	49.37	2.00E-21
gene_id_4256	222	59.01	7.00E-80
gene_id_4257	76	53.95	3.00E-21
gene_id_4258	245	58.78	1.00E-92
gene_id_6173	178	41.01	7.00E-34
gene_id_6174	67	46.27	7.00E-14
gene_id_6175	373	62.47	2.00E-164
gene_id_6176	498	64.86	0
gene_id_6177	353	68.84	1.00E-135
gene_id_6178	314	69.75	7.00E-145
gene_id_6179	567	43.92	6.00E-175
gene_id_6180	497	38.23	1.00E-94
gene_id_6181	735	49.8	0

gene_id_6182	468	37.18	1.00E-91
gene_id_6183	1083	41.18	0
gene_id_6184	473	46.09	3.00E-153
gene_id_6185	398	70.6	0
gene_id_6186	392	59.18	5.00E-148
gene_id_6187	174	68.97	1.00E-86
gene_id_8536	497	75.45	0
gene_id_8537	272	47.06	2.00E-69
gene_id_8538	199	62.31	2.00E-66
gene_id_8539	254	36.22	1.00E-38
gene_id_8540	662	63.9	0
gene_id_8541	593	53.63	0
gene_id_8542	174	41.95	5.00E-44
gene_id_8543	328	60.67	7.00E-141
gene_id_8544	114	66.67	1.00E-48
gene_id_8545	385	42.86	4.00E-81
gene_id_8546	565	63.54	0
gene_id_8547	148	67.57	1.00E-64
gene_id_8549	386	47.67	4.00E-122
gene_id_8551	359	54.04	9.00E-128
gene_id_8552	216	59.26	6.00E-83
gene_id_8554	123	34.96	5.00E-17
gene_id_8555	206	44.66	9.00E-36
gene_id_8556	355	50.14	2.00E-100
gene_id_8557	297	33	6.00E-34
gene_id_8558	271	46.13	6.00E-69
gene_id_8560	82	42.68	7.00E-06
gene_id_8561	260	31.92	1.00E-20
gene_id_8562	279	44.09	3.00E-75
gene_id_8563	118	39.83	4.00E-22
gene_id_8564	181	41.44	2.00E-42
gene_id_8565	435	49.66	3.00E-129
gene_id_8567	401	28.68	2.00E-26
gene_id_8568	506	26.28	2.00E-24
gene_id_8569	748	35.56	2.00E-103
gene_id_8570	159	28.3	1.00E-07
gene_id_8571	489	52.35	1.00E-173
gene_id_8572	194	29.38	7.00E-11
gene_id_8573	784	23.21	9.00E-22
gene_id_8574	251	36.25	2.00E-46
gene_id_8575	319	67.4	3.00E-150
gene_id_8576	404	58.42	5.00E-156
gene_id_8577	403	43.18	6.00E-95
gene_id_8578	327	40.06	2.00E-75
gene_id_8579	438	24.43	2.00E-08
gene_id_8580	281	35.94	7.00E-48
gene_id_8582	211	54.98	4.00E-70

gene_id_8583	246	49.59	8.00E-77
gene_id_8584	350	62.86	3.00E-145
gene_id_8585	502	59.56	0
gene_id_8586	398	58.54	1.00E-143
gene_id_8587	276	60.14	1.00E-107
gene_id_8588	339	54.57	1.00E-105
gene_id_8589	160	48.75	8.00E-36
gene_id_8590	245	52.24	2.00E-62
gene_id_8591	211	50.24	9.00E-66
gene_id_8592	121	57.02	3.00E-47
gene_id_8593	273	60.81	4.00E-94
gene_id_8594	282	47.16	3.00E-93
gene_id_8595	368	57.07	2.00E-149
gene_id_8596	140	60	1.00E-46
gene_id_8597	219	57.99	5.00E-89
gene_id_8598	256	33.98	2.00E-25
gene_id_8599	342	45.91	7.00E-92
gene_id_8600	209	99.04	7.00E-150
gene_id_8601	265	100	0
gene_id_8602	544	99.45	0
gene_id_8603	414	45.41	8.00E-103
gene_id_8604	123	56.1	3.00E-41
gene_id_8605	410	45.37	5.00E-124
gene_id_8606	148	34.46	5.00E-14
gene_id_8607	238	38.66	3.00E-45
gene_id_8608	620	34.03	5.00E-90
gene_id_8610	247	46.56	3.00E-69
gene_id_8611	191	48.17	3.00E-46
gene_id_8612	405	49.88	4.00E-136
gene_id_8613	440	49.77	6.00E-133
gene_id_8614	425	65.65	0
gene_id_8615	359	71.03	2.00E-180
gene_id_8616	297	76.77	3.00E-138
gene_id_8617	310	70.65	3.00E-143
gene_id_8618	251	70.52	1.00E-127
gene_id_8619	236	75	1.00E-119
gene_id_8620	318	29.56	3.00E-26
gene_id_8621	710	59.15	0
gene_id_8622	420	54.76	7.00E-129
gene_id_8624	352	58.81	7.00E-137
gene_id_8625	447	45.64	1.00E-129
gene_id_8626	250	36.4	2.00E-39
gene_id_8627	320	50.31	9.00E-89
gene_id_8628	279	58.78	3.00E-103
gene_id_8629	248	47.58	3.00E-72
gene_id_8631	106	30.19	3.00E-09
gene_id_8632	254	53.94	1.00E-91

gene_id_8633	139	53.96	4.00E-32
gene_id_8635	449	50.56	6.00E-149
gene_id_8636	292	62.33	1.00E-124
gene_id_8637	364	55.22	5.00E-145
gene_id_8784	63	61.9	5.00E-18
gene_id_8785	377	63.13	1.00E-128
gene_id_8786	598	85.12	0
gene_id_8787	146	45.89	4.00E-37
gene_id_8788	96	55.21	5.00E-29
gene_id_8789	476	50.63	1.00E-136
gene_id_8790	435	71.72	0
gene_id_8791	242	56.61	1.00E-91
gene_id_8792	218	56.88	4.00E-66
gene_id_8793	502	57.57	0
gene_id_8794	93	82.8	7.00E-38
gene_id_8795	206	72.33	3.00E-108
gene_id_8797	376	63.3	3.00E-163
gene_id_8798	277	62.09	5.00E-106
gene_id_8799	253	59.68	1.00E-105
gene_id_8800	370	56.76	3.00E-147
gene_id_8801	436	41.06	7.00E-109
gene_id_8802	83	55.42	1.00E-22
gene_id_8803	324	70.37	1.00E-163
gene_id_8804	339	41	7.00E-70
gene_id_8805	324	54.32	8.00E-97
gene_id_8806	290	66.9	2.00E-133
gene_id_8807	254	55.91	3.00E-87
gene_id_8808	455	49.45	3.00E-142
gene_id_8809	732	52.73	0
gene_id_8810	408	37.01	6.00E-72
gene_id_8811	529	50.85	1.00E-178
gene_id_9768	207	80.19	2.00E-118
gene_id_9769	167	71.26	2.00E-83
gene_id_9770	364	57.69	4.00E-146
gene_id_9771	191	61.78	8.00E-81
gene_id_9772	125	76	3.00E-61
gene_id_9773	80	67.5	1.00E-31
gene_id_9774	54	90.74	7.00E-24
gene_id_9775	140	77.14	1.00E-74
gene_id_9776	933	57.88	0
gene_id_9777	467	65.74	0
gene_id_9778	609	86.86	0
gene_id_9779	84	80.95	3.00E-43
gene_id_9782	126	45.24	6.00E-30
gene_id_9783	151	37.09	1.00E-17
gene_id_9783	146	28.77	3.00E-07
gene_id_9784	277	74.73	1.00E-142

gene_id_9785	120	86.67	2.00E-67
gene_id_9787	207	65.22	3.00E-84
gene_id_9789	459	71.46	0
gene_id_9790	262	49.24	5.00E-65
gene_id_9792	162	32.1	4.00E-19
gene_id_9795	137	64.96	9.00E-58
gene_id_9797	288	46.88	4.00E-59
gene_id_9799	425	61.18	0
gene_id_9800	259	46.33	4.00E-57
gene_id_9801	213	39.91	7.00E-39
gene_id_9802	250	57.6	5.00E-96
gene_id_9803	195	37.44	2.00E-35
gene_id_9804	88	52.27	3.00E-19
gene_id_9805	431	58.47	0
gene_id_9806	117	36.75	1.00E-10
gene_id_9807	422	51.42	2.00E-139
gene_id_9808	556	46.94	1.00E-180
gene_id_9809	109	77.98	1.00E-43
gene_id_9810	136	55.15	9.00E-49
gene_id_9811	171	57.31	2.00E-56
gene_id_9812	124	58.87	1.00E-45
gene_id_9813	159	50.31	7.00E-53
gene_id_9815	133	67.67	1.00E-54
gene_id_9817	70	65.71	2.00E-22
gene_id_9818	532	75.19	0
gene_id_9819	317	56.78	6.00E-102
gene_id_9820	551	88.38	0
gene_id_9821	238	47.9	3.00E-75
gene_id_9822	379	82.59	0
gene_id_9824	76	78.95	2.00E-35
gene_id_9825	299	62.88	1.00E-131
gene_id_9826	846	59.34	0
gene_id_9827	372	71.24	0
gene_id_9828	169	40.83	7.00E-36
gene_id_9830	702	35.33	1.00E-113
gene_id_9831	145	60.69	8.00E-60
gene_id_9832	384	62.24	6.00E-180
gene_id_9833	279	91.04	0
gene_id_9834	751	96.27	0
gene_id_9835	565	95.04	0
gene_id_9837	567	40.92	8.00E-121
gene_id_9838	210	45.71	4.00E-39
gene_id_9839	555	72.61	0
gene_id_9840	282	97.87	0
gene_id_9841	556	96.76	0
gene_id_9842	75	98.67	7.00E-45
gene_id_9843	147	97.28	3.00E-99

gene_id_9844	194	95.88	1.00E-136
gene_id_9845	220	96.36	9.00E-157
gene_id_9846	139	97.84	2.00E-92
gene_id_9847	197	86.8	3.00E-123
gene_id_9848	438	93.61	0
gene_id_9849	426	98.36	0
gene_id_9850	285	97.89	0
gene_id_9851	148	98.65	2.00E-100
gene_id_9853	309	87.38	0
gene_id_9854	452	97.79	0
gene_id_9855	655	93.44	0
gene_id_9856	417	97.6	0
gene_id_9857	241	97.93	2.00E-167
gene_id_9858	247	77.73	1.00E-104
gene_id_9859	392	98.47	0
gene_id_9860	213	98.12	8.00E-151
gene_id_9861	138	99.28	1.00E-82
gene_id_9862	146	99.32	2.00E-85
gene_id_9863	152	99.34	2.00E-91
gene_id_9864	157	92.36	2.00E-104
gene_id_9865	253	97.23	0
gene_id_9866	255	96.86	0
gene_id_9867	210	72.86	1.00E-113
gene_id_9868	222	95.95	1.00E-155
gene_id_9869	154	95.45	4.00E-95
gene_id_9870	162	97.53	1.00E-96
gene_id_9871	229	82.53	4.00E-124
gene_id_9872	482	83.2	0
gene_id_9873	309	38.19	3.00E-63
gene_id_9873	104	41.35	1.00E-07
gene_id_9874	170	92.94	3.00E-93
gene_id_9875	445	92.58	0
gene_id_9876	366	91.8	0
gene_id_9877	181	96.69	1.00E-126
gene_id_9878	168	92.26	7.00E-108
gene_id_9879	195	95.9	2.00E-120
gene_id_9880	329	98.48	0
gene_id_9881	217	94.01	4.00E-149
gene_id_9882	182	71.98	2.00E-95
gene_id_9883	149	75.17	2.00E-78
gene_id_9884	123	86.18	4.00E-64
gene_id_9885	370	97.84	0
gene_id_9886	193	94.82	4.00E-133
gene_id_9887	869	93.44	0
gene_id_9888	340	96.18	0
gene_id_9889	246	98.78	5.00E-164
gene_id_9890	814	98.03	0

gene_id_9891	119	99.16	1.00E-80
gene_id_9892	280	97.5	5.00E-171
gene_id_9893	232	99.57	8.00E-162
gene_id_9894	257	98.05	0
gene_id_9895	144	97.22	3.00E-93
gene_id_9896	373	97.86	0
gene_id_9897	380	97.11	0
gene_id_9898	101	56.44	6.00E-35
gene_id_9899	173	60.12	9.00E-69
gene_id_9900	103	62.14	2.00E-39
gene_id_9901	404	58.42	2.00E-168
gene_id_9902	95	74.74	4.00E-46
gene_id_9903	109	75.23	2.00E-54
gene_id_9904	272	87.5	3.00E-179
gene_id_9905	184	55.98	5.00E-56
gene_id_9906	184	69.02	5.00E-90
gene_id_9907	73	61.64	1.00E-24
gene_id_9908	119	77.31	9.00E-62
gene_id_9909	1312	77.29	0
gene_id_9910	142	56.34	2.00E-39
gene_id_9911	274	78.1	2.00E-154
gene_id_9912	270	81.85	3.00E-153
gene_id_9913	447	84.12	0
gene_id_9914	309	85.76	0
gene_id_9915	290	83.45	2.00E-147
gene_id_9916	218	66.51	3.00E-97
gene_id_9917	131	81.68	1.00E-73
gene_id_9918	182	70.33	3.00E-82
gene_id_9919	181	58.56	3.00E-51
gene_id_9920	515	79.03	0
gene_id_9921	86	74.42	1.00E-40
gene_id_9922	53	73.58	9.00E-18
gene_id_9923	90	93.33	8.00E-53
gene_id_9924	104	45.19	8.00E-20
gene_id_9926	141	49.65	3.00E-48
gene_id_9927	135	33.33	2.00E-20
gene_id_9928	301	89.04	0
gene_id_9929	240	37.92	7.00E-55
gene_id_9929	109	48.62	6.00E-26
gene_id_9930	80	86.25	9.00E-42
gene_id_10479	287	56.45	2.00E-99
gene_id_10481	426	71.83	0
gene_id_10482	246	81.3	2.00E-137
gene_id_10483	289	69.2	2.00E-122
gene_id_10484	396	78.03	0
gene_id_10485	265	54.34	1.00E-90
gene_id_10486	481	70.48	0

gene_id_10487	365	66.58	1.00E-179
gene_id_10488	342	63.16	2.00E-122
gene_id_10489	350	64.57	2.00E-157
gene_id_10490	551	42.83	1.00E-131
gene_id_10491	582	58.76	0
gene_id_10492	527	66.98	0
gene_id_10493	986	45.33	0
gene_id_10494	270	69.63	4.00E-130
gene_id_10495	81	55.56	9.00E-19
gene_id_10553	254	57.87	1.00E-87
gene_id_10554	395	32.41	8.00E-47
gene_id_10555	221	52.94	1.00E-75
gene_id_10556	438	34.93	1.00E-57
gene_id_10557	328	79.88	1.00E-179
gene_id_10558	155	50.97	2.00E-44
gene_id_10559	237	55.7	1.00E-88
gene_id_10560	173	65.32	1.00E-72
gene_id_10561	239	48.12	4.00E-69
gene_id_10562	237	47.68	4.00E-55
gene_id_10563	567	66.31	0
gene_id_10564	504	60.32	0
gene_id_10565	242	31.82	2.00E-18
gene_id_10567	785	42.93	0
gene_id_10568	439	49.66	4.00E-119
gene_id_10569	581	53.7	0
gene_id_10570	135	35.56	3.00E-13
gene_id_10571	231	41.13	2.00E-57
gene_id_10572	337	76.56	1.00E-172
gene_id_10573	285	35.09	5.00E-37
gene_id_10574	232	44.83	3.00E-44
gene_id_10575	579	68.39	0
gene_id_10576	610	41.31	9.00E-143
gene_id_10577	287	45.64	9.00E-85
gene_id_10578	140	48.57	2.00E-40
gene_id_11245	884	51.36	0
gene_id_11246	158	34.18	6.00E-18
gene_id_11247	152	43.42	3.00E-33
gene_id_11248	304	65.13	6.00E-129
gene_id_11249	258	56.59	8.00E-95
gene_id_11250	292	43.49	9.00E-69
gene_id_11251	153	33.33	2.00E-26
gene_id_11253	114	30.7	1.00E-07
gene_id_11254	615	60.81	0
gene_id_11255	596	70.13	0
gene_id_11256	652	40.49	1.00E-133
gene_id_11257	421	67.46	0
gene_id_11258	161	59.63	6.00E-58

gene_id_11259	293	61.43	2.00E-123
gene_id_11260	491	61.51	0
gene_id_11261	421	57.96	3.00E-171
gene_id_11262	365	46.85	7.00E-108
gene_id_11263	327	43.12	2.00E-97
gene_id_11264	270	64.44	2.00E-112
gene_id_11265	280	62.86	6.00E-116
gene_id_11266	33	72.73	3.00E-07
gene_id_11275	207	49.28	7.00E-35
gene_id_11276	312	42.63	5.00E-88
gene_id_11277	624	44.39	0
gene_id_11278	542	46.31	7.00E-166
gene_id_11279	603	81.43	0
gene_id_11280	329	54.1	7.00E-113
gene_id_11281	289	62.28	7.00E-74
gene_id_11282	144	79.86	3.00E-74
gene_id_11283	308	45.13	4.00E-78
gene_id_11284	290	77.59	3.00E-154
gene_id_11285	312	68.91	4.00E-112
gene_id_11286	501	66.07	0
gene_id_11287	248	62.5	1.00E-102
gene_id_11288	483	43.48	1.00E-93
gene_id_11289	480	53.54	4.00E-162
gene_id_11290	778	71.98	0
gene_id_11297	611	68.41	0
gene_id_11298	226	40.27	6.00E-39
gene_id_11299	181	41.44	3.00E-46
gene_id_11300	93	70.97	5.00E-43
gene_id_11301	298	40.27	4.00E-43
gene_id_11303	106	40.57	3.00E-22
gene_id_11304	370	32.16	3.00E-58
gene_id_11305	194	35.57	1.00E-28
gene_id_11306	189	46.03	2.00E-48
gene_id_11307	331	66.77	4.00E-142
gene_id_11308	69	68.12	5.00E-25
gene_id_11309	103	56.31	3.00E-33
gene_id_11310	594	57.24	0
gene_id_11311	74	48.65	2.00E-14
gene_id_11312	642	58.1	0
gene_id_11313	179	39.66	4.00E-36
gene_id_11314	680	26.32	4.00E-53
gene_id_11315	148	29.73	7.00E-19
gene_id_11316	255	30.59	6.00E-27
gene_id_11317	238	39.92	1.00E-39
gene_id_11318	1132	54.86	0
gene_id_11320	97	59.79	8.00E-32
gene_id_11321	352	59.09	3.00E-133

gene_id_11322	135	68.15	1.00E-35
gene_id_11323	647	38.33	1.00E-116
gene_id_11324	188	53.19	6.00E-54
gene_id_11325	428	81.31	0
gene_id_11326	583	70.5	0
gene_id_11327	179	31.84	1.00E-12
gene_id_11328	202	35.15	5.00E-18
gene_id_11345	207	28.99	1.00E-08
gene_id_11346	647	56.26	0
gene_id_11347	351	34.47	1.00E-51
gene_id_11348	60	66.67	7.00E-22
gene_id_11349	77	72.73	5.00E-32
gene_id_11350	168	33.33	3.00E-21
gene_id_11351	244	57.38	1.00E-99
gene_id_11352	117	68.38	7.00E-50
gene_id_11353	112	43.75	5.00E-26
gene_id_11355	127	39.37	7.00E-19
gene_id_11356	402	75.37	0
gene_id_11357	342	66.96	9.00E-164
gene_id_11358	283	43.11	7.00E-62
gene_id_11359	726	50.28	0
gene_id_11572	259	46.72	3.00E-78
gene_id_11573	517	54.74	0
gene_id_11574	415	38.55	1.00E-69
gene_id_11575	217	37.79	6.00E-39
gene_id_11576	268	52.61	4.00E-66
gene_id_11577	634	40.69	4.00E-125
gene_id_11578	221	47.51	5.00E-71
gene_id_11579	554	30.14	5.00E-71
gene_id_11580	322	60.25	1.00E-140
gene_id_11581	319	65.52	3.00E-148
gene_id_11582	325	62.46	2.00E-123
gene_id_11583	326	66.87	3.00E-163
gene_id_11584	548	53.1	0
gene_id_11585	552	39.49	9.00E-121
gene_id_11586	324	36.11	8.00E-52
gene_id_11872	96	72.92	2.00E-45
gene_id_11873	343	72.01	0
gene_id_11874	206	61.65	3.00E-87
gene_id_11875	388	52.58	6.00E-136
gene_id_11877	285	84.21	8.00E-168
gene_id_11878	621	67.79	0
gene_id_11879	223	77.58	4.00E-124
gene_id_11880	752	66.36	0
gene_id_11881	323	31.27	3.00E-44
gene_id_11882	683	58.86	0
gene_id_11883	217	46.08	8.00E-51

gene_id_11885	192	43.23	1.00E-50
gene_id_11886	192	44.79	1.00E-43
gene_id_11887	74	51.35	3.00E-20
gene_id_11888	616	41.23	3.00E-129
gene_id_11889	451	51.44	1.00E-162
gene_id_11890	287	51.57	1.00E-75
gene_id_11893	1185	74.01	0
gene_id_11894	302	40.4	2.00E-73
gene_id_11895	203	51.23	1.00E-60
gene_id_11896	160	44.38	5.00E-36
gene_id_11897	281	69.4	5.00E-132
gene_id_11898	492	66.26	0
gene_id_11899	203	40.39	4.00E-38
gene_id_11900	411	41.12	6.00E-106
gene_id_11901	433	43.19	5.00E-119
gene_id_11902	306	44.12	2.00E-68
gene_id_11903	327	47.71	4.00E-87
gene_id_11904	516	53.68	0
gene_id_11905	332	40.66	4.00E-66
gene_id_11906	421	42.76	4.00E-96
gene_id_11907	191	35.08	3.00E-21
gene_id_11908	254	64.17	6.00E-113
gene_id_11909	366	48.91	3.00E-115
gene_id_11910	531	56.12	0
gene_id_11911	221	39.37	3.00E-49
gene_id_11914	233	67.81	2.00E-113
gene_id_11915	246	30.49	3.00E-24
gene_id_11916	66	68.18	4.00E-24
gene_id_11917	138	53.62	1.00E-38
gene_id_11918	157	48.41	2.00E-50
gene_id_11919	332	47.89	2.00E-86
gene_id_11920	325	43.08	4.00E-83
gene_id_11921	382	45.03	1.00E-98
gene_id_11922	787	42.44	0
gene_id_11923	176	67.61	7.00E-77
gene_id_11924	402	50.5	2.00E-133
gene_id_11925	491	53.16	1.00E-158
gene_id_11926	447	29.98	1.00E-63
gene_id_11927	445	38.88	6.00E-74
gene_id_11928	234	39.32	2.00E-41
gene_id_11929	396	64.14	1.00E-174
gene_id_11930	210	52.86	1.00E-70
gene_id_11931	191	84.29	3.00E-103
gene_id_11932	124	74.19	2.00E-55
gene_id_11933	53	83.02	3.00E-22
gene_id_11934	96	55.21	3.00E-29
gene_id_11935	414	46.86	1.00E-100

gene_id_11936	121	52.89	2.00E-29
gene_id_11937	273	38.83	7.00E-65
gene_id_11938	273	38.83	2.00E-66
gene_id_11939	293	40.27	2.00E-79
gene_id_11940	109	43.12	5.00E-08
gene_id_11941	379	57.78	1.00E-135
gene_id_11942	691	39.94	9.00E-148
gene_id_11943	320	48.12	3.00E-73
gene_id_11944	130	70	2.00E-63
gene_id_11945	78	67.95	3.00E-31
gene_id_11946	337	38.28	3.00E-37
gene_id_11947	164	45.73	2.00E-50
gene_id_11948	178	67.98	7.00E-72
gene_id_11949	374	32.35	6.00E-44
gene_id_11950	424	73.35	0
gene_id_11951	224	35.27	6.00E-19
gene_id_11952	467	49.25	2.00E-128
gene_id_11953	255	67.45	2.00E-106
gene_id_11954	224	41.07	5.00E-48
gene_id_11955	204	54.41	2.00E-63
gene_id_11956	243	40.74	3.00E-52
gene_id_11957	523	52.77	9.00E-164
gene_id_11958	58	79.31	3.00E-14
gene_id_11959	41	70.73	1.00E-12
gene_id_11960	185	67.57	2.00E-89
gene_id_11961	142	84.51	2.00E-70
gene_id_11962	226	69.47	4.00E-113
gene_id_11963	182	58.24	8.00E-66
gene_id_11964	130	76.92	5.00E-41
gene_id_11965	1163	77.3	0
gene_id_11966	1427	75.47	0
gene_id_11967	124	88.71	6.00E-74
gene_id_11968	156	73.08	6.00E-79
gene_id_11969	695	35.97	7.00E-134
gene_id_11970	395	84.56	0
gene_id_11971	102	82.35	4.00E-55
gene_id_11972	206	64.08	2.00E-81
gene_id_11973	214	68.22	1.00E-99
gene_id_11974	93	62.37	3.00E-32
gene_id_11975	259	71.43	8.00E-126
gene_id_11976	93	82.8	2.00E-51
gene_id_11977	119	72.27	1.00E-48
gene_id_11978	225	73.33	3.00E-106
gene_id_11979	138	77.54	5.00E-71
gene_id_11980	65	60	2.00E-19
gene_id_11981	92	68.48	2.00E-33
gene_id_11982	122	89.34	2.00E-73

gene_id_11983	106	69.81	1.00E-43
gene_id_11984	182	76.92	5.00E-99
gene_id_11985	132	80.3	1.00E-73
gene_id_11986	173	58.96	2.00E-68
gene_id_11987	96	70.83	4.00E-41
gene_id_11988	169	65.09	3.00E-77
gene_id_11989	149	67.11	1.00E-61
gene_id_11990	435	73.79	0
gene_id_11991	121	83.47	3.00E-67
gene_id_11992	115	88.7	3.00E-69
gene_id_11993	211	68.25	8.00E-102
gene_id_11994	351	70.37	9.00E-165
gene_id_11995	116	71.55	1.00E-39
gene_id_11996	56	69.64	2.00E-20
gene_id_11997	233	63.95	1.00E-100
gene_id_11998	252	65.87	4.00E-111
gene_id_11999	330	56.97	4.00E-92
gene_id_12000	305	62.62	5.00E-110
gene_id_12001	349	71.63	1.00E-176
gene_id_12002	259	48.65	2.00E-69
gene_id_12003	409	55.5	7.00E-136
gene_id_12004	1151	59.51	0
gene_id_12005	511	59.88	0
gene_id_12006	280	48.57	1.00E-72
gene_id_12007	429	78.09	0
gene_id_12008	231	38.96	3.00E-43
gene_id_12009	384	38.54	6.00E-84
gene_id_12010	384	43.75	2.00E-97
gene_id_12011	250	50	1.00E-81
gene_id_12012	285	56.49	2.00E-102
gene_id_12013	391	52.17	4.00E-137
gene_id_12014	305	66.56	1.00E-131
gene_id_12015	277	44.77	1.00E-81
gene_id_12016	474	32.7	5.00E-61
gene_id_12017	139	62.59	1.00E-48
gene_id_12855	930	71.29	0
gene_id_12856	901	42.95	0
gene_id_12857	562	63.7	0
gene_id_12858	262	40.46	2.00E-36
gene_id_12859	301	78.07	5.00E-166
gene_id_12860	613	71.29	0
gene_id_12861	446	77.8	0
gene_id_12862	604	63.25	0
gene_id_12863	699	58.8	0
gene_id_12864	179	69.83	7.00E-80
gene_id_12865	272	37.13	1.00E-58
gene_id_12866	175	37.71	2.00E-28

gene_id_12867	74	70.27	2.00E-32
gene_id_13948	120	84.17	6.00E-67
gene_id_13949	825	43.64	0
gene_id_13950	311	46.95	2.00E-90
gene_id_13951	258	33.72	1.00E-28
gene_id_13952	62	48.39	3.00E-08
gene_id_13953	196	39.8	3.00E-40
gene_id_13954	186	50	1.00E-53
gene_id_13955	404	39.6	3.00E-85
gene_id_13956	301	37.87	5.00E-51
gene_id_13958	324	51.54	5.00E-110
gene_id_13959	542	30.26	8.00E-53
gene_id_13960	126	67.46	3.00E-59
gene_id_13961	177	58.19	6.00E-66
gene_id_13962	359	69.64	0
gene_id_13963	335	53.73	3.00E-111
gene_id_13964	187	45.99	2.00E-39
gene_id_13965	748	56.15	0
gene_id_13966	424	67.22	0
gene_id_13967	203	64.53	6.00E-93
gene_id_13968	506	49.21	2.00E-152
gene_id_13969	247	63.56	9.00E-113
gene_id_13970	140	57.86	4.00E-53
gene_id_13971	337	38.87	4.00E-59
gene_id_13972	270	38.15	7.00E-38
gene_id_13973	94	38.3	2.00E-08
gene_id_13975	248	68.95	3.00E-119
gene_id_13976	210	56.67	6.00E-71
gene_id_13977	294	66.67	1.00E-123
gene_id_13978	417	74.82	0
gene_id_13979	356	85.11	0
gene_id_13980	744	59.81	0
gene_id_13983	423	34.52	2.00E-61
gene_id_13984	259	37.07	4.00E-57
gene_id_13986	183	25.14	1.00E-12
gene_id_13988	533	65.29	0
gene_id_13989	261	27.97	4.00E-17
gene_id_13990	453	40.84	4.00E-81
gene_id_13991	96	53.12	1.00E-25
gene_id_13991	67	46.27	6.00E-09
gene_id_13994	292	36.64	2.00E-34
gene_id_13995	166	57.23	6.00E-39
gene_id_13996	463	72.35	0
gene_id_13997	365	43.56	1.00E-95
gene_id_13998	434	70.05	1.00E-146
gene_id_13999	162	40.12	1.00E-21
gene_id_14000	341	58.94	9.00E-141

gene_id_14001	256	46.09	3.00E-68
gene_id_14002	194	69.07	1.00E-88
gene_id_14003	386	65.54	3.00E-165
gene_id_14004	133	41.35	1.00E-24
gene_id_14005	354	52.26	9.00E-116
gene_id_14006	698	46.42	0
gene_id_14007	495	46.06	1.00E-140
gene_id_14008	281	41.99	5.00E-57
gene_id_14010	309	70.55	2.00E-162
gene_id_14011	393	38.17	6.00E-72
gene_id_14012	724	33.84	5.00E-101
gene_id_14013	72	47.22	1.00E-13
gene_id_14208	224	36.61	1.00E-28
gene_id_14209	465	36.56	2.00E-79
gene_id_14210	601	75.37	0
gene_id_14211	90	60	2.00E-32
gene_id_14212	106	61.32	6.00E-44
gene_id_14213	391	40.92	2.00E-90
gene_id_14214	381	47.77	4.00E-108
gene_id_14215	410	46.59	4.00E-118
gene_id_14217	317	47.63	4.00E-97
gene_id_14218	1246	63.08	0
gene_id_14219	423	40.66	3.00E-90
gene_id_14220	431	71.23	0
gene_id_14221	236	40.25	7.00E-50
gene_id_14222	193	33.68	2.00E-14
gene_id_14223	715	49.09	0
gene_id_14224	575	52.17	0
gene_id_14225	165	50.3	3.00E-41
gene_id_14226	473	37.42	4.00E-60
gene_id_14227	208	36.06	6.00E-25
gene_id_14228	303	44.55	5.00E-64
gene_id_14229	220	49.55	2.00E-77
gene_id_14229	90	61.11	2.00E-77
gene_id_14230	213	39.91	1.00E-38
gene_id_14231	289	71.63	3.00E-136
gene_id_14232	282	55.32	1.00E-103
gene_id_14233	183	68.85	5.00E-86
gene_id_14234	228	60.96	5.00E-95
gene_id_14235	236	36.86	2.00E-21
gene_id_14236	375	47.2	2.00E-97
gene_id_14237	438	43.84	7.00E-120
gene_id_14296	95	47.37	2.00E-22
gene_id_14297	225	57.33	1.00E-86
gene_id_14298	415	32.53	8.00E-55
gene_id_14299	389	40.1	7.00E-83
gene_id_14300	220	39.09	2.00E-51

gene_id_14302	1056	70.83	0
gene_id_14303	128	35.16	1.00E-09
gene_id_14304	206	38.35	3.00E-27
gene_id_14305	433	42.26	9.00E-109
gene_id_14306	94	41.49	5.00E-13
gene_id_14307	450	56.44	6.00E-180
gene_id_14308	561	49.38	0
gene_id_14309	254	44.09	2.00E-76
gene_id_14310	379	41.69	1.00E-91
gene_id_14311	504	41.27	8.00E-118
gene_id_14312	171	47.95	3.00E-40
gene_id_14313	275	47.64	3.00E-79
gene_id_14314	433	70.44	0
gene_id_14315	294	63.27	2.00E-134
gene_id_14316	277	71.12	2.00E-125
gene_id_14317	488	48.36	8.00E-166
gene_id_14318	275	57.09	6.00E-92
gene_id_14319	432	74.77	0
gene_id_14320	150	50.67	3.00E-45
gene_id_14321	334	68.56	5.00E-154
gene_id_14322	175	40	7.00E-26
gene_id_14323	427	37	5.00E-63
gene_id_14324	416	53.85	4.00E-124
gene_id_14325	434	55.76	1.00E-161
gene_id_14326	478	32.64	2.00E-60
gene_id_14327	227	50.66	7.00E-68
gene_id_14328	222	36.94	1.00E-29
gene_id_14329	226	46.02	1.00E-65
gene_id_14330	233	30.47	3.00E-29
gene_id_14330	160	33.12	9.00E-10
gene_id_14331	503	33	1.00E-38
gene_id_14332	231	64.94	5.00E-95
gene_id_14333	484	70.66	0
gene_id_14334	277	55.6	3.00E-73
gene_id_14335	194	52.06	2.00E-60
gene_id_14336	307	44.95	2.00E-82
gene_id_14337	221	47.51	4.00E-58
gene_id_14338	363	65.29	8.00E-155
gene_id_14339	734	61.44	0
gene_id_14340	329	64.74	1.00E-152
gene_id_14341	139	36.69	3.00E-22
gene_id_14342	77	54.55	4.00E-21
gene_id_14384	397	43.58	6.00E-83
gene_id_14384	258	29.07	3.00E-19
gene_id_14385	255	99.61	0
gene_id_14386	433	100	0
gene_id_14387	442	100	0

gene_id_14388	232	100	3.00E-167
gene_id_14389	492	100	0
gene_id_14390	449	100	0
gene_id_14391	226	100	6.00E-163
gene_id_14392	439	100	0
gene_id_14393	230	100	2.00E-145
gene_id_14394	432	100	0
gene_id_14395	75	100	1.00E-44
gene_id_14396	198	100	5.00E-143
gene_id_14397	388	99.74	0
gene_id_14398	427	100	0
gene_id_14399	165	100	8.00E-104
gene_id_14400	265	100	0
gene_id_14401	341	100	0
gene_id_14402	291	100	0
gene_id_14403	262	100	1.00E-164
gene_id_14404	279	100	0
gene_id_14405	249	99.6	2.00E-176
gene_id_14406	74	100	2.00E-44
gene_id_14407	126	99.21	1.00E-85
gene_id_14408	208	59.13	2.00E-88
gene_id_14409	303	60.07	1.00E-117
gene_id_14410	382	37.43	3.00E-81
gene_id_14412	211	41.23	4.00E-38
gene_id_14413	727	68.23	0
gene_id_14413	357	40.34	3.00E-75
gene_id_14414	335	66.57	1.00E-152
gene_id_14415	487	67.56	0
gene_id_14416	220	29.55	2.00E-19
gene_id_14418	135	68.15	2.00E-58
gene_id_14419	199	43.72	3.00E-48
gene_id_14420	210	43.33	9.00E-49
gene_id_14421	98	53.06	6.00E-07
gene_id_14422	214	37.38	7.00E-46
gene_id_14423	377	40.85	1.00E-75
gene_id_14424	452	68.36	0
gene_id_14740	109	78.9	4.00E-49
gene_id_14741	347	52.74	5.00E-119
gene_id_14742	311	79.1	0
gene_id_14743	566	76.33	0
gene_id_14744	371	66.31	3.00E-169
gene_id_14745	471	47.98	5.00E-106
gene_id_14746	366	41.53	1.00E-77
gene_id_14747	138	49.28	4.00E-36
gene_id_14748	401	37.66	1.00E-70
gene_id_14749	254	66.54	1.00E-107
gene_id_14750	95	49.47	2.00E-14

gene_id_14751	283	63.6	3.00E-128
gene_id_14753	414	45.65	3.00E-104
gene_id_14754	380	58.95	1.00E-162
gene_id_14755	78	57.69	3.00E-23
gene_id_14756	372	54.03	2.00E-145
gene_id_14757	218	34.86	3.00E-36
gene_id_14758	100	49	4.00E-26
gene_id_14759	301	41.86	6.00E-71
gene_id_14760	362	45.86	5.00E-87
gene_id_14761	288	71.88	7.00E-142
gene_id_14762	321	59.19	9.00E-123
gene_id_14763	231	66.23	2.00E-94
gene_id_14764	506	58.89	0
gene_id_14765	252	69.05	6.00E-106
gene_id_14766	588	66.67	0
gene_id_14767	223	31.84	2.00E-22
gene_id_14768	523	52.01	0
gene_id_14769	408	67.4	6.00E-167
gene_id_14770	553	61.84	0
gene_id_14771	349	44.41	1.00E-89
gene_id_14772	157	59.87	4.00E-61
gene_id_14773	63	53.97	7.00E-14
gene_id_14774	850	70.24	0
gene_id_14775	175	32	1.00E-19
gene_id_15088	210	40.95	6.00E-40
gene_id_15091	179	35.75	8.00E-20
gene_id_15092	555	74.05	0
gene_id_15093	176	64.77	4.00E-74
gene_id_15094	74	36.49	4.00E-11
gene_id_15095	249	49.4	2.00E-69
gene_id_15096	320	25.62	4.00E-15
gene_id_15097	269	26.39	1.00E-16
gene_id_15098	129	66.67	1.00E-44
gene_id_15099	562	46.8	4.00E-154
gene_id_15100	279	43.01	4.00E-61
gene_id_15101	340	40.29	1.00E-69
gene_id_15313	808	69.93	0
gene_id_15314	633	75.36	0
gene_id_15315	477	45.28	1.00E-139
gene_id_15316	366	54.92	9.00E-142
gene_id_15317	369	46.34	4.00E-86
gene_id_15318	90	43.33	9.00E-19
gene_id_15319	51	92.16	5.00E-23
gene_id_15320	69	47.83	5.00E-13
gene_id_15321	69	65.22	1.00E-25
gene_id_15322	521	49.52	7.00E-165
gene_id_15323	231	60.17	4.00E-96

gene_id_15324	448	64.51	0
gene_id_15325	330	61.21	7.00E-108
gene_id_15326	189	55.56	4.00E-58
gene_id_15327	201	73.63	2.00E-101
gene_id_15328	191	66.49	1.00E-80
gene_id_15329	245	66.12	2.00E-111
gene_id_15330	165	38.18	5.00E-29
gene_id_15331	81	76.54	1.00E-38
gene_id_15332	86	74.42	6.00E-40
gene_id_15333	276	38.04	2.00E-55
gene_id_15335	111	67.57	8.00E-43
gene_id_15336	71	54.93	2.00E-12
gene_id_15338	1008	50.89	0
gene_id_15338	170	40	2.00E-21
gene_id_15339	93	56.99	1.00E-29
gene_id_15340	99	55.56	1.00E-31
gene_id_15341	114	47.37	6.00E-26
gene_id_15342	70	70	1.00E-24
gene_id_15342	87	63.22	2.00E-24
gene_id_15343	388	71.65	0
gene_id_15344	379	36.41	5.00E-62
gene_id_15345	493	44.22	1.00E-138
gene_id_15346	146	76.03	5.00E-78
gene_id_15347	243	79.01	8.00E-135
gene_id_15348	260	79.62	6.00E-122
gene_id_15349	226	73.01	3.00E-115
gene_id_15350	500	61.4	0
gene_id_15351	215	78.6	1.00E-115
gene_id_15352	109	64.22	3.00E-47
gene_id_15353	441	51.93	5.00E-161
gene_id_15354	84	44.05	1.00E-06
gene_id_15355	464	48.49	9.00E-132
gene_id_15356	231	58.87	6.00E-93
gene_id_15357	68	58.82	6.00E-18
gene_id_15358	747	66.8	0
gene_id_15359	533	43.53	1.00E-117
gene_id_15360	259	47.49	7.00E-46
gene_id_15361	753	52.06	0
gene_id_15362	313	40.58	3.00E-64
gene_id_15363	221	26.24	7.00E-17
gene_id_15364	140	40.71	7.00E-32
gene_id_15365	54	46.3	2.00E-06
gene_id_15366	491	63.34	0
gene_id_15367	73	32.88	1.00E-08
gene_id_15368	172	52.91	5.00E-52
gene_id_15369	413	55.21	5.00E-168
gene_id_15371	79	64.56	2.00E-30

gene_id_15372	178	65.73	3.00E-71
gene_id_15373	86	55.81	3.00E-19
gene_id_15374	638	48.59	0
gene_id_15375	1231	53.21	0
gene_id_15376	137	51.09	3.00E-45
gene_id_15377	381	62.47	2.00E-178
gene_id_15378	405	60	5.00E-169
gene_id_15379	442	54.07	3.00E-145
gene_id_15380	321	63.86	7.00E-141
gene_id_15381	465	68.17	0
gene_id_15382	95	64.21	4.00E-33
gene_id_15503	768	80.73	0
gene_id_15504	755	60.26	0
gene_id_15505	442	51.81	3.00E-144
gene_id_15506	349	71.06	4.00E-170
gene_id_15507	537	86.22	0
gene_id_15508	55	61.82	5.00E-18
gene_id_15510	284	42.25	6.00E-68
gene_id_15511	95	66.32	1.00E-37
gene_id_15512	68	66.18	2.00E-26
gene_id_15513	101	51.49	9.00E-20
gene_id_15514	612	70.75	0
gene_id_15514	291	39.52	3.00E-58
gene_id_15515	48	47.92	2.00E-07
gene_id_15516	111	30.63	2.00E-09
gene_id_15517	121	34.71	1.00E-18
gene_id_15518	131	25.95	9.00E-12
gene_id_15519	345	68.99	7.00E-165
gene_id_15520	119	42.86	5.00E-24
gene_id_15521	134	39.55	2.00E-23
gene_id_15522	213	79.34	3.00E-123
gene_id_15523	237	85.23	2.00E-143
gene_id_15524	260	82.69	9.00E-146
gene_id_15525	419	74.22	1.00E-178
gene_id_15526	300	82.67	2.00E-168
gene_id_15527	361	85.32	0
gene_id_15528	292	60.96	5.00E-123
gene_id_15529	297	54.55	4.00E-83
gene_id_15530	262	57.63	2.00E-92
gene_id_15531	197	72.08	6.00E-99
gene_id_15532	270	71.48	3.00E-143
gene_id_15533	161	44.72	1.00E-37
gene_id_15534	432	53.94	3.00E-124
gene_id_15535	118	36.44	6.00E-12
gene_id_15537	387	54.01	5.00E-139
gene_id_15539	97	67.01	9.00E-44
gene_id_15638	259	43.63	1.00E-60

gene_id_15640	248	47.18	2.00E-60
gene_id_15642	298	34.9	3.00E-37
gene_id_15643	411	35.77	3.00E-73
gene_id_15644	418	38.28	1.00E-65
gene_id_15645	341	69.79	4.00E-167
gene_id_15646	280	38.57	5.00E-58
gene_id_15647	273	47.99	3.00E-78
gene_id_15648	253	43.48	2.00E-57
gene_id_15649	519	62.04	0
gene_id_15650	397	35.01	7.00E-64
gene_id_15651	473	58.99	0
gene_id_15652	139	59.71	1.00E-56
gene_id_15654	99	72.73	9.00E-48
gene_id_15655	77	62.34	4.00E-20
gene_id_15658	811	76.7	0
gene_id_15659	152	50.66	1.00E-33
gene_id_15659	106	27.36	8.00E-06
gene_id_15660	117	43.59	4.00E-23
gene_id_15661	151	58.28	6.00E-55
gene_id_15662	469	79.53	0
gene_id_15663	86	65.12	1.00E-29
gene_id_15664	91	71.43	2.00E-42
gene_id_15665	539	43.04	7.00E-107
gene_id_15666	246	51.22	1.00E-67
gene_id_15667	241	37.34	8.00E-32
gene_id_15668	218	52.29	1.00E-76
gene_id_15669	127	48.82	9.00E-36
gene_id_15670	1043	70.47	0
gene_id_15671	207	59.9	4.00E-74
gene_id_15672	396	83.33	0
gene_id_15674	1266	57.03	0
gene_id_15675	305	55.41	1.00E-111
gene_id_15677	384	76.56	0
gene_id_15678	78	84.62	6.00E-38
gene_id_15679	527	79.89	0
gene_id_15680	356	55.06	5.00E-127
gene_id_15681	164	52.44	2.00E-49
gene_id_15683	58	74.14	4.00E-23
gene_id_15684	138	52.17	8.00E-27
gene_id_15685	300	54	1.00E-107
gene_id_15686	430	52.33	3.00E-148
gene_id_15687	158	37.34	6.00E-32
gene_id_15688	308	54.87	2.00E-119
gene_id_15689	258	46.12	5.00E-61
gene_id_15690	320	70	6.00E-165
gene_id_15691	652	58.13	0
gene_id_15692	108	50	2.00E-31

gene_id_15694	135	50.37	2.00E-32
gene_id_15695	362	49.17	4.00E-114
gene_id_15696	548	36.13	4.00E-85
gene_id_15697	286	65.38	3.00E-125
gene_id_15698	324	62.96	7.00E-141
gene_id_15699	335	53.13	1.00E-121
gene_id_15700	307	75.24	7.00E-156
gene_id_15701	485	58.76	0
gene_id_15702	326	56.13	2.00E-99
gene_id_15703	322	58.39	8.00E-96
gene_id_15704	335	68.66	8.00E-155
gene_id_15705	210	52.38	2.00E-63
gene_id_15706	269	40.89	2.00E-69
gene_id_15707	147	32.65	7.00E-20
gene_id_15708	150	50	1.00E-40
gene_id_15709	283	78.09	2.00E-127
gene_id_15710	307	76.87	6.00E-159
gene_id_15711	489	75.87	0
gene_id_15712	609	69.29	0
gene_id_15713	395	64.05	5.00E-167
gene_id_15714	288	44.1	2.00E-82
gene_id_15715	489	52.35	4.00E-139
gene_id_15716	1560	44.55	0
gene_id_15717	97	56.7	2.00E-25
gene_id_15718	60	56.67	5.00E-18
gene_id_15718	46	47.83	5.00E-18
gene_id_15720	384	58.59	5.00E-161
gene_id_15721	247	60.73	9.00E-112
gene_id_15722	399	46.37	6.00E-118
gene_id_15723	104	75	2.00E-35
gene_id_15724	111	79.28	4.00E-48
gene_id_15725	200	53.5	4.00E-62
gene_id_15726	287	28.57	3.00E-16
gene_id_15726	290	24.14	3.00E-08
gene_id_15727	603	49.75	0
gene_id_15728	356	55.06	4.00E-136
gene_id_15730	72	52.78	5.00E-15
gene_id_15731	416	60.1	0
gene_id_15732	379	44.06	5.00E-93
gene_id_15733	104	73.08	1.00E-50
gene_id_15734	326	70.55	1.00E-153
gene_id_15735	299	59.87	6.00E-114
gene_id_15736	332	62.05	3.00E-102
gene_id_15737	494	61.94	0
gene_id_15738	470	62.34	0
gene_id_15739	286	52.1	4.00E-102
gene_id_15740	385	35.84	2.00E-61

gene_id_15741	155	39.35	1.00E-27
gene_id_15742	152	74.34	7.00E-80
gene_id_15743	180	47.22	5.00E-46
gene_id_15744	129	66.67	3.00E-57
gene_id_15745	596	81.38	0
gene_id_15746	594	69.53	0
gene_id_15747	396	26.52	2.00E-22
gene_id_15748	465	34.62	2.00E-83
gene_id_15749	348	77.3	0
gene_id_15750	299	44.15	4.00E-69
gene_id_15751	132	52.27	2.00E-33
gene_id_15752	265	46.42	7.00E-80
gene_id_15753	670	62.09	0
gene_id_15755	349	50.43	1.00E-122
gene_id_15756	405	61.98	2.00E-179
gene_id_15757	281	58.36	7.00E-100
gene_id_15758	386	52.85	5.00E-121
gene_id_15791	120	44.17	7.00E-20
gene_id_15792	205	56.59	4.00E-76
gene_id_15793	367	35.69	2.00E-51
gene_id_15794	565	53.98	0
gene_id_15795	218	33.03	5.00E-19
gene_id_15796	177	62.71	4.00E-74
gene_id_15797	251	78.09	2.00E-148
gene_id_15798	355	68.17	3.00E-168
gene_id_15799	71	64.79	1.00E-23
gene_id_15800	295	62.71	2.00E-113
gene_id_15801	355	58.87	3.00E-142
gene_id_15802	288	62.85	6.00E-106
gene_id_15803	658	42.71	2.00E-180
gene_id_15804	183	56.28	5.00E-47
gene_id_15805	150	35.33	2.00E-16
gene_id_15806	290	66.9	1.00E-125
gene_id_15807	280	37.5	2.00E-51
gene_id_15808	289	40.14	3.00E-61
gene_id_15809	118	59.32	2.00E-37
gene_id_15810	46	89.13	1.00E-18
gene_id_15811	136	40.44	3.00E-22
gene_id_15812	104	38.46	7.00E-15
gene_id_15815	472	51.48	3.00E-130
gene_id_15816	236	34.32	3.00E-37
gene_id_15817	185	47.03	6.00E-44
gene_id_15818	352	71.31	0
gene_id_15819	192	55.21	2.00E-65
gene_id_15820	249	43.78	3.00E-55
gene_id_15821	491	39.92	1.00E-87
gene_id_15822	313	44.41	1.00E-86

gene_id_15823	146	35.62	1.00E-21
gene_id_15824	308	49.35	2.00E-105
gene_id_15825	519	38.54	6.00E-115
gene_id_15826	297	39.39	1.00E-55
gene_id_15827	259	42.86	2.00E-34
gene_id_15828	209	50.72	9.00E-62
gene_id_15830	243	43.62	3.00E-50
gene_id_15831	158	31.01	9.00E-17
gene_id_15832	435	64.37	0
gene_id_15833	739	42.22	0
gene_id_15834	566	28.09	1.00E-42
gene_id_15836	72	38.89	1.00E-06
gene_id_15837	201	37.81	7.00E-20
gene_id_15838	157	67.52	1.00E-70
gene_id_15839	407	43.24	5.00E-78
gene_id_15840	230	24.35	8.00E-10
gene_id_15841	122	37.7	6.00E-11
gene_id_15842	438	66.67	0
gene_id_15843	310	70.97	2.00E-157
gene_id_15844	123	44.72	3.00E-25
gene_id_15845	631	78.76	0
gene_id_15846	819	56.04	0
gene_id_15847	372	70.43	8.00E-178
gene_id_15848	62	64.52	1.00E-18
gene_id_15851	514	70.23	0
gene_id_15852	133	69.17	8.00E-61
gene_id_15853	375	44.8	1.00E-88
gene_id_15854	130	81.54	1.00E-72
gene_id_15855	553	77.03	0
gene_id_15856	166	55.42	1.00E-35
gene_id_15857	233	65.24	3.00E-99
gene_id_15869	316	51.9	2.00E-105
gene_id_15870	1027	36.61	0
gene_id_15870	1131	30.86	3.00E-137
gene_id_15870	974	29.36	3.00E-98
gene_id_15870	837	28.91	4.00E-90
gene_id_15870	702	24.93	6.00E-37
gene_id_15871	659	25.34	2.00E-36
gene_id_15872	311	43.73	5.00E-78
gene_id_15873	477	68.97	0
gene_id_15874	187	48.13	8.00E-51
gene_id_15875	47	53.19	5.00E-11
gene_id_15877	537	27.93	1.00E-56
gene_id_15878	409	68.95	0
gene_id_15879	260	32.69	4.00E-25
gene_id_15880	93	63.44	4.00E-38
gene_id_15881	83	59.04	1.00E-24

gene_id_15882	118	45.76	2.00E-28
gene_id_15883	333	47.75	2.00E-97
gene_id_15884	187	72.73	9.00E-96
gene_id_15885	475	28.42	3.00E-34
gene_id_15886	163	33.13	7.00E-23
gene_id_15887	711	53.59	0
gene_id_15888	508	49.21	2.00E-158
gene_id_15889	381	47.51	1.00E-97
gene_id_15890	428	52.1	5.00E-129
gene_id_15891	252	56.75	7.00E-91
gene_id_15892	218	41.74	1.00E-48
gene_id_15893	168	54.17	2.00E-55
gene_id_15894	337	27.3	6.00E-33
gene_id_15895	294	51.02	2.00E-87
gene_id_15896	251	41.43	4.00E-44
gene_id_15897	278	52.16	2.00E-78
gene_id_15898	351	34.76	1.00E-55
gene_id_15899	219	62.1	9.00E-93
gene_id_15900	280	43.93	2.00E-56
gene_id_15901	224	33.93	3.00E-29
gene_id_15909	176	40.91	3.00E-40
gene_id_15910	525	81.71	0
gene_id_15911	358	66.48	2.00E-160
gene_id_15912	152	40.13	4.00E-36
gene_id_15914	82	64.63	3.00E-30
gene_id_15915	131	64.89	3.00E-55
gene_id_15916	580	66.38	0
gene_id_15917	417	63.07	0
gene_id_15918	140	47.14	2.00E-40
gene_id_15920	83	75.9	4.00E-38
gene_id_15921	386	56.74	3.00E-136
gene_id_15922	488	66.19	0
gene_id_15923	279	75.99	4.00E-139
gene_id_15924	274	74.82	4.00E-146
gene_id_15925	328	61.89	9.00E-142
gene_id_15926	334	65.57	9.00E-160
gene_id_15927	98	51.02	7.00E-28
gene_id_15928	382	39.01	1.00E-73
gene_id_15929	327	63	8.00E-147
gene_id_15930	523	62.52	0
gene_id_15931	377	61.27	2.00E-150
gene_id_15932	268	66.42	7.00E-114
gene_id_15933	308	46.1	9.00E-63
gene_id_15935	225	32.44	3.00E-28
gene_id_15936	472	56.99	1.00E-180
gene_id_15937	138	65.22	1.00E-60
gene_id_15938	172	55.23	5.00E-57

gene_id_15939	406	52.22	2.00E-103
gene_id_15940	96	64.58	1.00E-36
gene_id_15941	76	68.42	3.00E-29
gene_id_15942	394	75.13	2.00E-166
gene_id_15943	277	49.1	3.00E-83
gene_id_15944	114	54.39	4.00E-32
gene_id_15945	213	48.36	7.00E-62
gene_id_15946	142	53.52	3.00E-46
gene_id_15947	383	31.85	3.00E-39
gene_id_15948	634	46.69	0
gene_id_15949	284	61.62	4.00E-107
gene_id_15950	289	68.17	2.00E-125
gene_id_15951	472	45.55	9.00E-130
gene_id_15952	636	44.03	2.00E-169
gene_id_15953	833	76.23	0
gene_id_15954	346	76.88	3.00E-175
gene_id_15955	469	61.83	0
gene_id_15956	323	76.47	4.00E-172
gene_id_15957	333	76.88	0
gene_id_15958	67	46.27	6.00E-11
gene_id_15959	504	75	0
gene_id_15960	394	69.29	0
gene_id_15961	166	68.67	3.00E-77
gene_id_15962	407	63.14	8.00E-157
gene_id_15963	228	64.04	2.00E-89
gene_id_15964	101	64.36	1.00E-36
gene_id_15965	166	35.54	3.00E-16
gene_id_15966	104	45.19	1.00E-25
gene_id_15967	184	75.54	5.00E-102
gene_id_15968	163	60.74	6.00E-65
gene_id_15969	570	53.33	0
gene_id_15970	409	56.72	4.00E-148
gene_id_15971	84	42.86	6.00E-18
gene_id_15972	522	47.89	4.00E-128
gene_id_15973	1116	68.73	0
gene_id_15974	369	60.16	4.00E-152
gene_id_15975	313	53.04	3.00E-111
gene_id_15976	248	52.02	1.00E-74
gene_id_15978	252	46.43	4.00E-61
gene_id_15978	238	45.38	2.00E-52
gene_id_15978	191	48.69	1.00E-43
gene_id_15978	201	45.27	2.00E-41
gene_id_15979	87	52.87	1.00E-20
gene_id_15981	101	43.56	1.00E-23
gene_id_15982	473	68.08	0
gene_id_15983	530	69.43	0
gene_id_15984	476	49.37	2.00E-119

gene_id_15985	412	77.43	0
gene_id_15986	238	57.14	6.00E-67
gene_id_15987	433	49.19	3.00E-152
gene_id_15988	203	34.48	2.00E-30
gene_id_15989	729	30.32	2.00E-81
gene_id_15990	404	27.23	2.00E-11
gene_id_15991	249	39.76	4.00E-53
gene_id_15992	270	48.15	7.00E-65
gene_id_16551	209	41.15	2.00E-43
gene_id_16552	262	43.13	3.00E-55
gene_id_16553	142	40.85	3.00E-27
gene_id_16555	326	50.61	2.00E-84
gene_id_16555	316	49.68	2.00E-82
gene_id_16555	307	48.21	1.00E-76
gene_id_16555	308	49.68	3.00E-76
gene_id_16555	304	48.68	1.00E-73
gene_id_16555	305	47.21	2.00E-70
gene_id_16555	255	45.1	2.00E-46
gene_id_16555	156	45.51	1.00E-28
gene_id_16556	326	34.66	4.00E-59
gene_id_16557	308	64.61	6.00E-113
gene_id_16558	511	64.97	0
gene_id_16559	277	59.21	9.00E-106
gene_id_16560	333	50.75	9.00E-111
gene_id_16561	400	70.5	0
gene_id_16562	410	49.27	9.00E-137
gene_id_16563	285	55.09	1.00E-107
gene_id_16564	505	59.21	0
gene_id_16565	105	60.95	3.00E-35
gene_id_16566	91	75.82	5.00E-39
gene_id_16567	174	52.87	1.00E-57
gene_id_16568	476	63.45	0
gene_id_16569	191	57.59	3.00E-65
gene_id_16571	60	83.33	6.00E-29
gene_id_16626	333	34.53	1.00E-38
gene_id_16627	155	44.52	7.00E-39
gene_id_16628	535	48.04	4.00E-144
gene_id_16629	295	49.83	2.00E-94
gene_id_16630	841	61.71	0
gene_id_16631	248	70.97	5.00E-120
gene_id_16632	219	48.4	1.00E-68
gene_id_16633	143	53.15	9.00E-41
gene_id_16634	350	83.14	0
gene_id_16635	347	82.71	4.00E-180
gene_id_16636	525	78.48	0
gene_id_16637	376	88.3	0
gene_id_16638	461	26.46	2.00E-30

gene_id_16639	233	27.47	1.00E-09
gene_id_16640	192	40.62	3.00E-38
gene_id_16641	109	49.54	5.00E-31
gene_id_16642	216	59.72	2.00E-92
gene_id_16643	474	28.9	1.00E-38
gene_id_16644	97	59.79	3.00E-39
gene_id_16645	592	75	0
gene_id_16647	65	53.85	9.00E-12
gene_id_16649	640	56.72	0
gene_id_16650	335	53.73	7.00E-113
gene_id_16651	471	73.46	0
gene_id_16654	476	26.05	2.00E-36
gene_id_16655	304	41.12	2.00E-70
gene_id_16656	301	78.41	4.00E-160
gene_id_16657	186	52.69	2.00E-58
gene_id_16658	410	44.15	1.00E-109
gene_id_16659	323	38.7	2.00E-61
gene_id_16661	190	57.89	2.00E-85
gene_id_16662	165	53.33	9.00E-41
gene_id_16663	516	44.19	1.00E-135
gene_id_16664	274	38.69	1.00E-47
gene_id_16665	88	54.55	6.00E-24
gene_id_16666	264	40.91	3.00E-62
gene_id_16667	67	44.78	1.00E-10
gene_id_16680	155	54.19	3.00E-52
gene_id_16681	1054	56.17	0
gene_id_16682	590	59.49	0
gene_id_16683	216	38.43	2.00E-40
gene_id_16684	248	24.19	2.00E-10
gene_id_16685	1166	60.89	0
gene_id_16686	261	50.57	7.00E-82
gene_id_16687	148	72.3	3.00E-72
gene_id_16688	299	69.9	9.00E-126
gene_id_16689	334	46.41	1.00E-95
gene_id_16691	375	40.53	3.00E-68
gene_id_16693	337	50.15	4.00E-117
gene_id_16694	287	50.87	5.00E-87
gene_id_16695	499	60.92	0
gene_id_16696	327	51.38	7.00E-70
gene_id_16697	286	51.05	1.00E-91
gene_id_16698	338	65.98	6.00E-159
gene_id_16699	266	49.25	2.00E-83
gene_id_16700	610	71.31	0
gene_id_16701	295	73.22	5.00E-161
gene_id_16702	327	81.96	0
gene_id_16705	114	42.98	6.00E-23
gene_id_16707	519	63.97	0

gene_id_16708	215	47.91	5.00E-69
gene_id_16709	236	29.66	1.00E-19
gene_id_16709	92	38.04	2.00E-12
gene_id_16710	444	51.8	6.00E-154
gene_id_16711	771	49.03	0
gene_id_16712	255	28.63	1.00E-19
gene_id_16713	505	38.02	6.00E-85
gene_id_16714	489	59.51	0
gene_id_16716	272	43.01	2.00E-42
gene_id_16717	477	63.94	0
gene_id_16718	440	60	4.00E-178
gene_id_16719	127	55.91	7.00E-46
gene_id_16720	354	61.02	4.00E-151
gene_id_16721	177	43.5	4.00E-36
gene_id_16722	289	41.18	4.00E-48
gene_id_16723	373	41.29	2.00E-85
gene_id_16724	257	37.35	9.00E-28
gene_id_16725	390	63.85	5.00E-179
gene_id_16799	570	67.37	0
gene_id_16800	892	64.57	0
gene_id_16801	180	65	6.00E-75
gene_id_16802	220	65.91	1.00E-83
gene_id_16803	315	81.27	0
gene_id_16804	323	53.25	6.00E-102
gene_id_16805	256	48.83	7.00E-69
gene_id_16806	217	47	6.00E-66
gene_id_16807	499	75.15	0
gene_id_16808	354	66.67	2.00E-133
gene_id_16809	315	73.02	1.00E-136
gene_id_16810	628	63.69	0
gene_id_16811	450	47.11	8.00E-137
gene_id_16812	144	55.56	9.00E-50
gene_id_16813	258	33.33	2.00E-40
gene_id_16814	384	40.89	5.00E-88
gene_id_16815	366	45.9	2.00E-101
gene_id_17178	327	43.43	8.00E-75
gene_id_17179	576	69.1	0
gene_id_17180	84	64.29	1.00E-34
gene_id_17181	778	63.62	0
gene_id_17182	225	51.11	7.00E-73
gene_id_17183	490	34.29	8.00E-80
gene_id_17184	328	45.43	3.00E-94
gene_id_17185	903	33.44	2.00E-123
gene_id_17186	306	52.29	5.00E-109
gene_id_17187	103	49.51	3.00E-27
gene_id_17194	642	25.23	3.00E-49
gene_id_17195	822	41.85	0

gene_id_17196	890	48.54	0
gene_id_17197	235	34.04	3.00E-29
gene_id_17198	119	36.13	2.00E-22
gene_id_17199	490	56.73	4.00E-178
gene_id_17200	592	70.1	0
gene_id_17201	97	49.48	2.00E-19
gene_id_17202	258	45.35	3.00E-62
gene_id_17203	236	36.86	7.00E-39
gene_id_17204	87	63.22	1.00E-31
gene_id_17205	694	67.29	0
gene_id_17206	397	32.24	3.00E-62
gene_id_17207	134	59.7	3.00E-52
gene_id_17208	367	37.06	4.00E-57
gene_id_17209	343	32.07	5.00E-39
gene_id_17210	375	63.47	2.00E-172
gene_id_17211	897	53.85	0
gene_id_17212	299	42.47	6.00E-67
gene_id_17213	195	55.38	5.00E-72
gene_id_17214	194	28.35	5.00E-18
gene_id_17215	346	27.17	6.00E-28
gene_id_17216	126	62.7	5.00E-47
gene_id_17217	885	74.92	0
gene_id_17218	193	27.46	1.00E-17
gene_id_17219	95	47.37	7.00E-25
gene_id_17220	773	67.14	0
gene_id_17221	67	49.25	3.00E-06
gene_id_17345	52	48.08	1.00E-08
gene_id_17346	658	69.45	0
gene_id_17347	324	41.05	1.00E-75
gene_id_17348	145	44.14	1.00E-31
gene_id_17349	257	45.14	2.00E-64
gene_id_17350	518	37.64	6.00E-70
gene_id_17351	303	49.17	2.00E-98
gene_id_17352	417	69.78	0
gene_id_17353	200	76	7.00E-110
gene_id_17354	450	44.22	7.00E-118
gene_id_17355	265	46.04	6.00E-78
gene_id_17356	84	39.29	1.00E-11
gene_id_17389	348	36.21	2.00E-48
gene_id_17390	277	68.59	2.00E-124
gene_id_17391	219	36.53	3.00E-34
gene_id_17392	719	59.11	0
gene_id_17393	396	55.05	3.00E-138
gene_id_17394	235	57.87	5.00E-89
gene_id_17395	288	50.69	3.00E-86
gene_id_17396	156	36.54	1.00E-21
gene_id_17397	298	42.95	9.00E-63

gene_id_17398	186	56.45	1.00E-65
gene_id_17399	288	53.12	2.00E-89
gene_id_17400	496	45.56	2.00E-136
gene_id_17401	200	31.5	3.00E-19
gene_id_17402	231	40.26	6.00E-41
gene_id_17403	312	54.17	2.00E-105
gene_id_17404	307	36.81	2.00E-57
gene_id_17405	160	36.25	3.00E-21
gene_id_17407	177	41.24	2.00E-45
gene_id_17408	166	50.6	3.00E-43
gene_id_17409	377	57.29	5.00E-145
gene_id_17410	127	63.78	4.00E-43
gene_id_17411	182	52.75	2.00E-54
gene_id_17412	241	61.41	1.00E-63
gene_id_17413	431	79.58	0
gene_id_17414	182	33.52	2.00E-20
gene_id_17415	270	51.48	4.00E-52
gene_id_17416	248	64.52	7.00E-116
gene_id_17417	71	67.61	3.00E-27
gene_id_17418	255	62.35	5.00E-114
gene_id_17419	275	62.91	2.00E-128
gene_id_17420	254	79.53	2.00E-143
gene_id_17421	153	35.29	1.00E-25
gene_id_17422	210	77.14	1.00E-116
gene_id_17423	341	56.3	7.00E-136
gene_id_17424	206	36.89	2.00E-40
gene_id_17425	384	66.41	0
gene_id_17426	232	36.21	9.00E-38
gene_id_17427	157	37.58	9.00E-28
gene_id_17428	646	50.62	0
gene_id_17429	556	37.41	8.00E-106
gene_id_17430	239	52.3	3.00E-68
gene_id_17431	203	26.6	3.00E-13
gene_id_17432	480	63.33	0
gene_id_17433	439	45.56	9.00E-109
gene_id_17434	133	60.15	1.00E-48
gene_id_17435	111	62.16	2.00E-43
gene_id_17436	198	57.58	4.00E-76
gene_id_17437	96	45.83	3.00E-22
gene_id_17438	390	61.03	7.00E-151
gene_id_17439	327	40.98	9.00E-68
gene_id_17440	406	27.83	1.00E-35
gene_id_17441	310	51.94	4.00E-104
gene_id_17442	257	76.26	3.00E-142
gene_id_17443	239	64.85	9.00E-107
gene_id_17444	179	34.64	4.00E-32
gene_id_17445	165	24.24	2.00E-07

gene_id_17446	509	64.05	0
gene_id_17447	231	40.26	6.00E-41
gene_id_17448	116	39.66	2.00E-19
gene_id_17456	452	44.03	5.00E-114
gene_id_17457	644	59.78	0
gene_id_17458	212	40.57	4.00E-32
gene_id_17459	221	42.53	1.00E-41
gene_id_17460	195	46.67	3.00E-47
gene_id_17461	585	66.84	0
gene_id_17462	553	70.52	0
gene_id_17463	166	87.95	1.00E-93
gene_id_17523	138	62.32	2.00E-57
gene_id_17524	694	80.12	0
gene_id_17525	234	57.26	5.00E-96
gene_id_17526	228	35.09	3.00E-34
gene_id_17527	208	36.06	9.00E-18
gene_id_17528	464	50	1.00E-151
gene_id_17529	437	34.78	2.00E-83
gene_id_17530	389	47.3	4.00E-119
gene_id_17531	304	31.58	3.00E-22
gene_id_17532	261	59.77	8.00E-109
gene_id_17533	289	43.94	9.00E-75
gene_id_17534	294	52.04	9.00E-88
gene_id_17535	206	52.91	2.00E-60
gene_id_17538	122	43.44	3.00E-19
gene_id_17542	406	50.99	4.00E-95
gene_id_17543	561	63.81	0
gene_id_17544	84	71.43	3.00E-34
gene_id_17545	315	59.68	8.00E-90
gene_id_17546	322	40.99	2.00E-71
gene_id_17547	178	51.12	5.00E-51
gene_id_17548	186	77.96	5.00E-102
gene_id_17549	164	60.37	8.00E-70
gene_id_17550	314	67.83	1.00E-110
gene_id_17551	324	61.73	3.00E-93
gene_id_17552	507	65.68	0
gene_id_17553	304	67.43	5.00E-143
gene_id_17554	240	48.75	7.00E-78
gene_id_17555	61	40.98	2.00E-08
gene_id_17556	374	40.64	4.00E-73
gene_id_17557	1060	40.57	0
gene_id_17558	183	28.42	2.00E-09
gene_id_17559	329	41.34	8.00E-80
gene_id_17561	372	33.06	1.00E-45
gene_id_17562	228	50.88	5.00E-63
gene_id_17563	215	44.65	2.00E-44
gene_id_17564	251	64.94	1.00E-115

gene_id_17565	304	60.2	7.00E-113
gene_id_17566	302	38.08	6.00E-48
gene_id_17567	302	43.71	4.00E-56
gene_id_17568	263	50.19	7.00E-75
gene_id_17583	322	31.37	2.00E-43
gene_id_17586	54	44.44	2.00E-07
gene_id_17588	464	32.54	2.00E-63
gene_id_17589	327	27.52	1.00E-14
gene_id_17599	145	42.76	4.00E-24
gene_id_17600	159	69.18	3.00E-68
gene_id_17601	240	30.42	7.00E-20
gene_id_17602	804	61.44	0
gene_id_17603	277	64.62	3.00E-125
gene_id_17605	399	43.36	1.00E-105
gene_id_17606	193	40.41	2.00E-27
gene_id_17607	190	24.74	5.00E-07
gene_id_17608	490	65.92	0
gene_id_17610	190	31.58	4.00E-20
gene_id_17611	104	30.77	1.00E-05
gene_id_17614	76	47.37	2.00E-13
gene_id_17615	202	31.68	4.00E-24
gene_id_17616	88	38.64	3.00E-06
gene_id_17618	259	30.89	9.00E-31
gene_id_17619	1006	47.42	0
gene_id_17620	443	48.08	1.00E-127
gene_id_17621	525	53.52	5.00E-178
gene_id_17622	174	61.49	2.00E-77
gene_id_17623	136	45.59	5.00E-30
gene_id_17624	88	48.86	7.00E-19
gene_id_17625	709	55.71	0
gene_id_17626	462	37.45	3.00E-92
gene_id_17627	622	66.88	0
gene_id_17628	176	62.5	1.00E-60
gene_id_17629	126	42.86	4.00E-25
gene_id_17630	418	67.46	0
gene_id_17631	474	70.89	0
gene_id_17632	845	60.71	0
gene_id_17633	281	25.98	2.00E-11
gene_id_17634	668	53.44	0
gene_id_17635	332	41.27	2.00E-81
gene_id_17636	334	47.6	4.00E-101
gene_id_17637	86	58.14	3.00E-24
gene_id_17638	437	64.76	0
gene_id_17639	784	52.93	0
gene_id_17639	64	51.56	3.00E-10
gene_id_17729	423	67.14	0
gene_id_17730	223	70.4	6.00E-95

gene_id_17731	120	55	2.00E-37
gene_id_17732	153	27.45	4.00E-14
gene_id_17733	248	42.34	4.00E-47
gene_id_17734	244	47.95	5.00E-69
gene_id_17735	197	31.47	5.00E-20
gene_id_17736	247	35.22	2.00E-28
gene_id_17737	471	47.13	1.00E-120
gene_id_17739	332	53.31	8.00E-122
gene_id_17740	599	51.75	0
gene_id_17741	255	41.96	8.00E-52
gene_id_17743	68	45.59	3.00E-12
gene_id_17744	204	52.45	7.00E-62
gene_id_17812	292	38.01	5.00E-64
gene_id_17813	467	35.12	8.00E-81
gene_id_17814	310	27.1	1.00E-19
gene_id_17815	158	50.63	7.00E-46
gene_id_17816	142	38.73	5.00E-17
gene_id_17817	209	36.84	2.00E-26
gene_id_17818	156	44.87	6.00E-32
gene_id_17819	180	40.56	1.00E-36
gene_id_17821	57	42.11	8.00E-09
gene_id_17823	794	23.93	5.00E-25
gene_id_17824	165	30.91	3.00E-17
gene_id_17825	270	40	2.00E-58
gene_id_17828	468	53.42	2.00E-167
gene_id_17829	443	34.99	2.00E-75
gene_id_17830	392	58.93	5.00E-160
gene_id_17831	305	77.38	4.00E-166
gene_id_17832	260	68.08	1.00E-132
gene_id_17975	662	35.95	1.00E-97
gene_id_17976	786	37.53	7.00E-142
gene_id_17977	186	57.53	6.00E-56
gene_id_17978	575	52.17	0
gene_id_17979	450	60.67	0
gene_id_18148	541	66.54	0
gene_id_18149	156	55.77	1.00E-51
gene_id_18150	421	57.01	7.00E-141
gene_id_18152	346	70.81	0
gene_id_18153	808	52.35	0
gene_id_18154	322	72.05	1.00E-166
gene_id_18155	358	40.78	4.00E-63
gene_id_18156	221	47.96	8.00E-45
gene_id_18156	553	27.85	1.00E-35
gene_id_18157	408	42.65	5.00E-88
gene_id_18158	481	40.33	4.00E-73
gene_id_18159	499	58.52	0
gene_id_18160	309	68.93	2.00E-128

gene_id_18161	408	60.05	2.00E-161
gene_id_18162	328	81.71	0
gene_id_18163	328	74.7	1.00E-179
gene_id_18164	329	43.77	1.00E-88
gene_id_18165	157	43.31	5.00E-36
gene_id_18166	77	45.45	9.00E-14
gene_id_18167	75	46.67	6.00E-18
gene_id_18168	75	48	2.00E-10
gene_id_18169	235	42.98	8.00E-27
gene_id_18170	109	51.38	4.00E-30
gene_id_18171	432	44.91	4.00E-76
gene_id_18172	556	39.75	1.00E-120
gene_id_18173	287	49.83	2.00E-89
gene_id_18174	166	71.69	4.00E-85
gene_id_18175	163	44.79	9.00E-44
gene_id_18176	375	61.33	5.00E-163
gene_id_18177	593	58.01	0
gene_id_18183	147	67.35	7.00E-67
gene_id_18184	327	49.54	5.00E-87
gene_id_18186	440	48.18	3.00E-106
gene_id_18187	360	61.11	6.00E-130
gene_id_18188	352	40.34	5.00E-57
gene_id_18189	224	33.04	4.00E-27
gene_id_18190	412	48.54	3.00E-124
gene_id_18191	414	57.97	1.00E-134
gene_id_18192	287	50.52	3.00E-96
gene_id_18193	280	41.43	2.00E-63
gene_id_18194	701	61.48	0
gene_id_18195	295	48.81	9.00E-87
gene_id_18196	196	66.84	1.00E-72
gene_id_18197	470	59.36	6.00E-174
gene_id_18198	253	66.4	1.00E-109
gene_id_18199	453	66.45	0
gene_id_18200	396	46.46	8.00E-103
gene_id_18201	318	43.71	4.00E-67
gene_id_18202	146	34.93	5.00E-14
gene_id_18203	331	54.08	3.00E-97
gene_id_18204	521	62.19	0
gene_id_18205	396	45.45	5.00E-107
gene_id_18206	199	46.73	8.00E-59
gene_id_18207	313	73.8	3.00E-170
gene_id_18208	327	46.18	4.00E-105
gene_id_18210	249	26.1	2.00E-11
gene_id_18211	195	55.38	2.00E-70
gene_id_18212	70	82.86	1.00E-36
gene_id_18213	436	86.01	0
gene_id_18214	100	33	3.00E-09

gene_id_18215	100	57	4.00E-34
gene_id_18216	82	56.1	7.00E-13
gene_id_18217	180	42.78	3.00E-32
gene_id_18218	39	89.74	3.00E-17
gene_id_18433	321	46.73	2.00E-78
gene_id_18434	264	52.27	3.00E-66
gene_id_18435	282	64.54	5.00E-118
gene_id_18436	153	50.33	1.00E-48
gene_id_18437	461	55.97	4.00E-165
gene_id_18438	795	44.03	0
gene_id_18439	196	50	1.00E-59
gene_id_18440	595	48.4	9.00E-152
gene_id_18441	480	63.54	1.00E-171
gene_id_18442	290	56.9	9.00E-90
gene_id_18443	114	63.16	7.00E-37
gene_id_18444	325	72	8.00E-170
gene_id_18445	155	71.61	3.00E-76
gene_id_18446	267	48.69	8.00E-75
gene_id_18447	301	67.77	2.00E-137
gene_id_18448	236	65.25	5.00E-108
gene_id_18449	219	64.38	3.00E-84
gene_id_18450	233	56.22	2.00E-76
gene_id_18451	150	29.33	1.00E-12
gene_id_18452	65	73.85	2.00E-25
gene_id_18608	87	71.26	6.00E-38
gene_id_18609	388	89.95	0
gene_id_18610	306	82.35	4.00E-173
gene_id_18611	285	80.35	3.00E-140
gene_id_18612	213	39.44	1.00E-42
gene_id_18613	136	27.94	2.00E-08
gene_id_18615	635	35.91	6.00E-110
gene_id_18616	34	76.47	5.00E-07
gene_id_18617	142	74.65	3.00E-71
gene_id_18618	132	68.18	2.00E-59
gene_id_18620	216	75	1.00E-108
gene_id_18621	967	54.29	0
gene_id_18622	257	44.36	4.00E-54
gene_id_18623	381	63.25	7.00E-166
gene_id_18624	507	41.62	3.00E-129
gene_id_18625	179	45.25	4.00E-45
gene_id_18981	320	67.5	5.00E-145
gene_id_18983	341	48.39	3.00E-104
gene_id_18984	260	44.62	2.00E-67
gene_id_18985	165	55.15	2.00E-57
gene_id_18986	289	42.91	1.00E-73
gene_id_18987	507	52.27	7.00E-166
gene_id_18988	603	27.86	3.00E-66

gene_id_18989	146	54.11	7.00E-38
gene_id_18990	316	40.19	2.00E-61
gene_id_18991	287	71.78	7.00E-149
gene_id_18992	306	64.71	1.00E-144
gene_id_18993	228	38.6	2.00E-26
gene_id_18994	444	65.09	0
gene_id_18995	289	70.93	3.00E-115
gene_id_18996	335	68.96	1.00E-117
gene_id_18997	504	66.67	0
gene_id_18998	324	71.3	5.00E-138
gene_id_18999	251	66.53	2.00E-108
gene_id_19000	417	70.26	0
gene_id_19001	94	53.19	7.00E-27
gene_id_19002	450	82.22	0
gene_id_19003	570	74.04	0
gene_id_19004	491	62.32	0
gene_id_19006	65	75.38	3.00E-27
gene_id_19007	206	42.23	7.00E-41
gene_id_19008	443	49.44	3.00E-132
gene_id_19009	233	53.22	5.00E-75
gene_id_19010	59	84.75	4.00E-29
gene_id_19011	155	43.87	2.00E-38
gene_id_19012	557	41.65	5.00E-133
gene_id_19364	128	49.22	2.00E-41
gene_id_19365	300	28	2.00E-13
gene_id_19366	150	41.33	2.00E-30
gene_id_19367	442	59.95	0
gene_id_19368	199	32.66	2.00E-21
gene_id_19369	94	46.81	8.00E-17
gene_id_19370	438	39.04	2.00E-109
gene_id_19371	157	59.87	4.00E-59
gene_id_19372	388	36.86	1.00E-70
gene_id_19373	642	33.18	9.00E-86
gene_id_19374	234	45.73	9.00E-70
gene_id_19375	221	45.7	6.00E-57
gene_id_19376	269	44.61	2.00E-75
gene_id_19377	469	39.45	9.00E-108
gene_id_19378	940	65.85	0
gene_id_19379	382	25.92	1.00E-26
gene_id_19380	543	30.39	1.00E-44
gene_id_19381	130	47.69	2.00E-16
gene_id_19382	72	47.22	6.00E-15
gene_id_19383	390	50.77	5.00E-115
gene_id_19384	890	55.84	0
gene_id_19385	48	62.5	7.00E-10
gene_id_19386	93	58.06	1.00E-33
gene_id_19387	430	55.35	2.00E-150

gene_id_19413	94	41.49	1.00E-14
gene_id_19414	212	58.02	4.00E-78
gene_id_19415	410	41.22	3.00E-91
gene_id_19416	250	28.8	2.00E-26
gene_id_19417	368	54.62	2.00E-136
gene_id_19420	66	59.09	7.00E-21
gene_id_19421	45	60	8.00E-10
gene_id_19422	55	61.82	9.00E-20
gene_id_19422	50	46	9.00E-20
gene_id_19423	305	57.38	6.00E-118
gene_id_19424	470	45.96	2.00E-147
gene_id_19425	207	35.75	2.00E-38
gene_id_19426	72	47.22	3.00E-11
gene_id_19427	503	67.4	0
gene_id_19429	294	74.15	7.00E-153
gene_id_19430	111	100	3.00E-72
gene_id_19431	426	99.53	0
gene_id_19432	210	99.52	3.00E-134
gene_id_19433	217	100	4.00E-141
gene_id_19434	339	100	0
gene_id_19435	315	99.68	0
gene_id_19437	186	55.91	3.00E-61
gene_id_19438	127	52.76	5.00E-34
gene_id_19439	214	42.99	1.00E-53
gene_id_19770	234	36.32	4.00E-32
gene_id_19771	346	64.74	2.00E-169
gene_id_19772	173	57.8	2.00E-61
gene_id_19773	201	57.21	9.00E-74
gene_id_19774	805	58.76	0
gene_id_19775	78	69.23	2.00E-30
gene_id_19776	132	61.36	3.00E-46
gene_id_19777	141	45.39	3.00E-33
gene_id_19778	370	38.92	7.00E-71
gene_id_19779	595	29.58	3.00E-54
gene_id_19780	282	37.94	6.00E-42
gene_id_19781	368	37.23	1.00E-75
gene_id_19782	231	28.57	4.00E-16
gene_id_19783	383	37.86	6.00E-55
gene_id_20315	186	51.61	2.00E-54
gene_id_20316	381	49.61	8.00E-128
gene_id_20317	324	69.44	2.00E-145
gene_id_20318	201	46.77	4.00E-58
gene_id_20319	113	57.52	9.00E-34
gene_id_20320	101	63.37	2.00E-37
gene_id_20321	289	60.9	2.00E-132
gene_id_20322	377	47.75	2.00E-105
gene_id_20323	336	74.11	1.00E-172

gene_id_20325	380	62.37	9.00E-150
gene_id_20326	284	57.39	4.00E-91
gene_id_20327	287	51.22	7.00E-79
gene_id_20328	237	64.56	7.00E-99
gene_id_20329	234	60.26	2.00E-93
gene_id_20330	256	57.81	2.00E-89
gene_id_20331	235	44.68	4.00E-63
gene_id_20332	403	67	0
gene_id_20333	386	64.77	5.00E-154
gene_id_20334	83	38.55	1.00E-07
gene_id_20421	287	69.69	1.00E-143
gene_id_20422	238	73.53	4.00E-126
gene_id_20423	177	54.24	3.00E-49
gene_id_20424	155	58.06	3.00E-37
gene_id_20425	110	36.36	2.00E-09
gene_id_20426	108	74.07	1.00E-55
gene_id_20427	51	58.82	3.00E-12
gene_id_20428	332	70.78	1.00E-150
gene_id_20429	170	58.82	5.00E-66
gene_id_20430	105	66.67	1.00E-42
gene_id_20431	113	44.25	1.00E-18
gene_id_20432	592	64.36	0
gene_id_20433	576	58.33	0
gene_id_20434	143	27.27	1.00E-09
gene_id_20435	276	54.35	3.00E-106
gene_id_20436	494	69.23	0
gene_id_20437	445	79.55	0
gene_id_20438	327	79.51	0
gene_id_20439	505	69.11	0
gene_id_20440	390	71.03	4.00E-167
gene_id_20441	380	68.42	0
gene_id_20442	389	44.22	3.00E-96
gene_id_20443	74	75.68	9.00E-30
gene_id_20444	187	48.66	1.00E-54
gene_id_20446	281	62.99	3.00E-125
gene_id_20447	295	55.25	9.00E-113
gene_id_20448	193	77.72	5.00E-100
gene_id_20450	412	47.09	5.00E-133
gene_id_20451	362	41.16	1.00E-69
gene_id_20452	298	84.23	3.00E-169
gene_id_20463	125	58.4	8.00E-43
gene_id_20464	504	55.56	0
gene_id_20465	378	52.12	3.00E-126
gene_id_20466	399	57.89	9.00E-165
gene_id_20467	424	25.47	1.00E-16
gene_id_20468	230	27.83	8.00E-06
gene_id_20469	440	53.64	1.00E-173

gene_id_20471	253	65.22	2.00E-118
gene_id_20472	286	64.34	2.00E-126
gene_id_20473	381	43.31	4.00E-90
gene_id_20474	564	60.28	0
gene_id_20475	90	66.67	2.00E-28
gene_id_20476	355	68.73	5.00E-171
gene_id_20477	276	60.51	3.00E-98
gene_id_20478	287	67.94	2.00E-129
gene_id_20479	378	63.49	1.00E-168
gene_id_20480	531	52.17	6.00E-175
gene_id_20481	237	42.19	1.00E-45
gene_id_20482	52	65.38	4.00E-08
gene_id_20483	186	31.72	4.00E-14
gene_id_20484	122	29.51	6.00E-09
gene_id_20485	212	68.4	5.00E-101
gene_id_20487	136	39.71	3.00E-28
gene_id_20488	487	50.51	2.00E-145
gene_id_20489	444	43.47	3.00E-112
gene_id_20490	589	37.52	1.00E-107
gene_id_20491	222	47.75	6.00E-67
gene_id_20492	288	53.82	4.00E-109
gene_id_20549	198	47.47	1.00E-51
gene_id_20550	264	45.08	5.00E-70
gene_id_20551	161	67.7	2.00E-76
gene_id_20552	254	45.28	8.00E-61
gene_id_20553	496	64.92	0
gene_id_20554	81	71.6	3.00E-35
gene_id_20555	84	71.43	3.00E-39
gene_id_20556	353	54.11	2.00E-116
gene_id_20557	214	42.52	3.00E-32
gene_id_20558	151	57.62	3.00E-64
gene_id_20559	283	32.86	3.00E-26
gene_id_20560	483	46.79	6.00E-128
gene_id_20561	157	53.5	2.00E-50
gene_id_20562	378	65.34	0
gene_id_20563	197	74.62	3.00E-76
gene_id_20564	195	67.69	1.00E-79
gene_id_20565	201	46.27	7.00E-48
gene_id_20566	292	57.88	5.00E-102
gene_id_20567	120	50	3.00E-35
gene_id_20568	288	64.58	1.00E-103
gene_id_20569	256	47.27	4.00E-64
gene_id_20570	269	48.7	4.00E-59
gene_id_20571	141	26.24	1.00E-08
gene_id_20761	473	71.25	0
gene_id_20762	369	38.21	2.00E-56
gene_id_20763	213	38.03	1.00E-31

gene_id_20764	441	40.36	3.00E-103
gene_id_20765	235	69.36	8.00E-115
gene_id_20766	257	63.81	8.00E-106
gene_id_20767	305	65.57	1.00E-92
gene_id_20768	292	76.03	2.00E-139
gene_id_20769	367	65.94	2.00E-176
gene_id_20770	216	50.93	7.00E-45
gene_id_20771	55	58.18	6.00E-11
gene_id_20921	392	39.54	2.00E-59
gene_id_20922	831	41.88	0
gene_id_20924	393	38.68	5.00E-72
gene_id_20925	256	59.38	4.00E-109
gene_id_20926	187	52.41	6.00E-50
gene_id_20927	409	65.04	0
gene_id_20928	57	71.93	4.00E-23
gene_id_20929	284	41.2	7.00E-70
gene_id_20930	324	54.63	1.00E-130
gene_id_20931	98	46.94	5.00E-23
gene_id_20932	232	43.1	4.00E-64
gene_id_20933	432	82.64	0
gene_id_20934	307	44.63	5.00E-79
gene_id_20935	398	68.59	0
gene_id_20936	443	53.95	3.00E-135
gene_id_20937	217	65.44	5.00E-96
gene_id_21024	306	66.34	6.00E-156
gene_id_21025	466	49.14	1.00E-156
gene_id_21026	363	77.13	0
gene_id_21027	371	63.88	2.00E-180
gene_id_21028	181	74.03	9.00E-96
gene_id_21029	440	78.41	0
gene_id_21030	374	34.22	6.00E-49
gene_id_21031	368	63.59	1.00E-171
gene_id_21032	210	27.62	9.00E-09
gene_id_21033	372	44.89	5.00E-77
gene_id_21034	317	44.79	3.00E-86
gene_id_21035	334	70.06	1.00E-176
gene_id_21036	369	52.3	9.00E-132
gene_id_21037	372	67.47	0
gene_id_21038	378	44.44	1.00E-104
gene_id_21039	61	52.46	5.00E-16
gene_id_21040	58	56.9	2.00E-16
gene_id_21041	375	72.27	0
gene_id_21042	375	60	5.00E-150
gene_id_21043	156	50.64	2.00E-46
gene_id_21044	541	56.38	0
gene_id_21045	395	31.14	1.00E-53
gene_id_21046	502	52.59	0

gene_id_21047	713	48.81	0
gene_id_21048	257	75.1	1.00E-135
gene_id_21049	386	57.25	2.00E-151
gene_id_21051	211	43.13	7.00E-50
gene_id_21052	236	59.32	1.00E-97
gene_id_21053	161	64.6	1.00E-47
gene_id_21054	242	55.37	6.00E-87
gene_id_21055	107	36.45	1.00E-06
gene_id_21056	264	50.38	5.00E-86
gene_id_21057	160	79.38	1.00E-94
gene_id_21058	310	60	7.00E-119
gene_id_21123	117	71.79	3.00E-54
gene_id_21124	166	75.9	7.00E-80
gene_id_21125	594	89.9	0
gene_id_21126	195	85.64	3.00E-116
gene_id_21127	84	78.57	3.00E-38
gene_id_21128	522	62.64	0
gene_id_21337	322	50.62	3.00E-96
gene_id_21340	293	48.12	2.00E-90
gene_id_21341	148	37.84	4.00E-17
gene_id_21380	833	82.23	0
gene_id_21381	256	77.34	2.00E-152
gene_id_21382	698	60.6	0
gene_id_21383	102	64.71	2.00E-38
gene_id_21384	309	62.46	3.00E-114
gene_id_21385	105	40.95	1.00E-13
gene_id_21386	211	44.55	5.00E-55
gene_id_21387	588	63.78	0
gene_id_21388	171	42.11	3.00E-31
gene_id_21389	122	36.07	7.00E-14
gene_id_21390	380	38.16	7.00E-71
gene_id_21391	541	43.81	1.00E-134
gene_id_21392	734	36.78	3.00E-129
gene_id_21393	790	70.89	0
gene_id_21394	100	47	7.00E-21
gene_id_21464	32	81.25	2.00E-09
gene_id_21465	435	77.01	0
gene_id_21466	224	31.7	5.00E-17
gene_id_21467	91	52.75	3.00E-24
gene_id_21469	268	36.94	1.00E-47
gene_id_21470	239	39.75	8.00E-35
gene_id_21471	419	41.53	9.00E-106
gene_id_21472	424	42.45	1.00E-103
gene_id_21473	294	41.5	7.00E-60
gene_id_21474	130	33.08	1.00E-08
gene_id_21475	420	35.71	1.00E-67
gene_id_21476	393	35.11	7.00E-52

gene_id_21478	467	42.83	1.00E-118
gene_id_21479	51	47.06	2.00E-07
gene_id_21480	465	26.24	2.00E-33
gene_id_21546	382	69.11	0
gene_id_21548	231	65.37	2.00E-108
gene_id_21549	488	63.11	0
gene_id_21550	617	55.27	0
gene_id_21551	496	61.49	0
gene_id_21552	314	77.71	3.00E-112
gene_id_21553	208	86.06	3.00E-109
gene_id_21567	387	32.56	2.00E-55
gene_id_21568	330	45.45	3.00E-80
gene_id_21569	277	47.29	9.00E-63
gene_id_21570	42	61.9	1.00E-08
gene_id_21571	423	53.19	2.00E-139
gene_id_21572	373	63	4.00E-166
gene_id_21573	131	64.12	2.00E-60
gene_id_21574	368	36.41	7.00E-62
gene_id_21575	332	51.81	1.00E-90
gene_id_21576	278	57.19	5.00E-108
gene_id_21577	288	73.26	3.00E-155
gene_id_21579	164	39.02	3.00E-27
gene_id_21580	51	58.82	7.00E-12
gene_id_21581	409	36.92	2.00E-77
gene_id_21583	600	71	0
gene_id_21584	632	61.23	0
gene_id_21594	370	69.46	0
gene_id_21595	1045	43.92	0
gene_id_21596	957	48.38	0
gene_id_21597	332	36.75	5.00E-60
gene_id_21597	250	40	7.00E-46
gene_id_21598	565	76.64	0
gene_id_21599	90	56.67	2.00E-12
gene_id_21600	297	50.51	2.00E-98
gene_id_21601	200	44	2.00E-52
gene_id_21602	80	32.5	4.00E-10
gene_id_21603	138	34.06	1.00E-18
gene_id_21604	460	30.65	5.00E-54
gene_id_21605	125	34.4	1.00E-13
gene_id_21606	347	42.36	2.00E-64
gene_id_21607	766	38.12	5.00E-151
gene_id_21608	363	43.8	3.00E-92
gene_id_21609	442	42.31	1.00E-123
gene_id_21610	213	57.28	3.00E-72
gene_id_21648	367	77.93	0
gene_id_21649	207	48.79	3.00E-59
gene_id_21650	158	51.9	1.00E-37

gene_id_21651	425	26.35	2.00E-27
gene_id_21652	132	50.76	6.00E-39
gene_id_21653	121	47.11	9.00E-27
gene_id_21824	103	53.4	7.00E-29
gene_id_21825	266	42.86	2.00E-74
gene_id_21826	292	48.29	7.00E-81
gene_id_21828	332	87.05	0
gene_id_21829	170	71.18	4.00E-77
gene_id_21830	66	72.73	7.00E-10
gene_id_21831	117	73.5	9.00E-52
gene_id_21833	77	42.86	5.00E-10
gene_id_21834	63	49.21	5.00E-16
gene_id_21835	267	52.06	2.00E-79
gene_id_21836	126	53.17	7.00E-35
gene_id_21837	670	52.69	0
gene_id_21838	311	57.23	6.00E-118
gene_id_21839	410	46.59	2.00E-119
gene_id_21840	223	36.32	4.00E-32
gene_id_21881	141	58.16	3.00E-48
gene_id_21882	597	69.35	0
gene_id_21883	142	34.51	6.00E-07
gene_id_21884	381	57.48	2.00E-136
gene_id_21886	155	35.48	1.00E-09
gene_id_21890	266	32.71	3.00E-32
gene_id_21891	291	28.87	3.00E-13
gene_id_21892	335	31.04	2.00E-39
gene_id_21894	102	33.33	6.00E-09
gene_id_22024	282	51.06	2.00E-85
gene_id_22025	443	68.85	0
gene_id_22026	240	26.67	3.00E-09
gene_id_22028	126	38.1	8.00E-20
gene_id_22029	227	49.78	7.00E-61
gene_id_22030	631	53.25	0
gene_id_22031	310	37.42	8.00E-71
gene_id_22032	96	33.33	5.00E-13
gene_id_22033	246	57.32	1.00E-98
gene_id_22034	260	57.31	2.00E-87
gene_id_22035	138	31.16	6.00E-08
gene_id_22036	226	43.81	2.00E-44
gene_id_22037	606	70.63	0
gene_id_22038	150	59.33	4.00E-58
gene_id_22039	221	44.34	2.00E-54
gene_id_22040	298	71.81	2.00E-157
gene_id_22041	163	48.47	1.00E-40
gene_id_22042	425	70.59	1.00E-153
gene_id_22043	534	74.16	0
gene_id_22047	61	68.85	4.00E-22

gene_id_22048	443	52.37	2.00E-135
gene_id_22049	270	67.41	3.00E-130
gene_id_22050	497	51.51	0
gene_id_22051	420	78.81	0
gene_id_22111	411	57.66	5.00E-150
gene_id_22112	390	73.08	1.00E-169
gene_id_22113	508	75.98	0
gene_id_22114	366	87.16	0
gene_id_22115	322	67.7	2.00E-157
gene_id_22116	540	40.74	3.00E-125
gene_id_22117	464	57.54	9.00E-171
gene_id_22118	315	43.17	2.00E-75
gene_id_22119	610	69.34	0
gene_id_22121	294	44.9	3.00E-75
gene_id_22122	404	52.97	2.00E-108
gene_id_22123	455	64.4	0
gene_id_22124	292	46.58	1.00E-91
gene_id_22125	244	46.31	3.00E-76
gene_id_22127	530	87.17	0
gene_id_22128	590	65.08	0
gene_id_22129	793	49.18	0
gene_id_22130	105	42.86	4.00E-21
gene_id_22131	471	46.07	4.00E-145
gene_id_22132	442	50.23	2.00E-147
gene_id_22133	265	61.51	4.00E-114
gene_id_22134	361	44.04	2.00E-73
gene_id_22135	421	50.83	2.00E-136
gene_id_22136	359	48.19	6.00E-92
gene_id_22137	930	43.66	0
gene_id_22138	451	54.1	2.00E-156
gene_id_22139	107	67.29	2.00E-49
gene_id_22140	328	30.49	9.00E-30
gene_id_22141	276	63.04	2.00E-108
gene_id_22142	312	58.97	5.00E-129
gene_id_22143	162	77.78	1.00E-92
gene_id_22144	466	61.16	0
gene_id_22145	369	55.01	4.00E-137
gene_id_22146	308	62.34	2.00E-125
gene_id_22147	425	47.53	5.00E-116
gene_id_22148	442	52.71	2.00E-160
gene_id_22149	142	54.93	1.00E-42
gene_id_22150	157	39.49	6.00E-26
gene_id_22151	155	39.35	5.00E-30
gene_id_22155	133	99.25	2.00E-91
gene_id_22156	273	99.27	0
gene_id_22157	106	99.06	2.00E-68
gene_id_22158	382	99.48	0

gene_id_22159	266	99.62	0
gene_id_22208	275	74.18	1.00E-132
gene_id_22209	396	70.96	0
gene_id_22210	270	52.22	1.00E-83
gene_id_22211	410	65.37	0
gene_id_22212	218	22.48	2.00E-08
gene_id_22213	271	29.52	3.00E-26
gene_id_22214	517	61.9	0
gene_id_22215	242	57.44	2.00E-92
gene_id_22216	492	61.59	0
gene_id_22217	216	57.87	2.00E-74
gene_id_22218	218	70.64	2.00E-107
gene_id_22219	126	68.25	2.00E-57
gene_id_22220	401	64.09	0
gene_id_22221	202	56.93	1.00E-67
gene_id_22222	464	86.42	0
gene_id_22223	262	76.72	2.00E-132
gene_id_22224	101	63.37	4.00E-38
gene_id_22225	207	58.94	6.00E-84
gene_id_22226	405	57.28	8.00E-167
gene_id_22227	285	58.6	4.00E-119
gene_id_22228	305	39.02	1.00E-47
gene_id_22229	167	55.69	1.00E-53
gene_id_22230	185	48.11	9.00E-41
gene_id_22254	82	67.07	4.00E-32
gene_id_22255	426	61.74	5.00E-165
gene_id_22256	139	49.64	1.00E-40
gene_id_22257	411	59.12	2.00E-165
gene_id_22258	254	39.37	4.00E-48
gene_id_22259	594	61.28	0
gene_id_22260	335	46.57	6.00E-102
gene_id_22261	560	53.39	0
gene_id_22262	307	67.75	3.00E-137
gene_id_22263	341	70.97	0
gene_id_22264	301	58.8	4.00E-119
gene_id_22265	497	45.67	3.00E-140
gene_id_22266	632	45.89	1.00E-175
gene_id_22269	261	48.28	2.00E-86
gene_id_22270	484	76.24	0
gene_id_22383	364	76.92	0
gene_id_22385	428	61.45	1.00E-169
gene_id_22386	372	51.61	2.00E-121
gene_id_22387	156	55.77	2.00E-53
gene_id_22488	217	64.52	8.00E-96
gene_id_22489	308	65.91	2.00E-140
gene_id_22490	64	45.31	3.00E-10
gene_id_22492	149	34.9	1.00E-18

gene_id_22493	317	41.01	3.00E-66
gene_id_22562	444	55.41	4.00E-156
gene_id_22563	576	57.12	0
gene_id_22564	394	32.74	6.00E-50
gene_id_22565	365	54.25	6.00E-118
gene_id_22566	343	44.31	1.00E-92
gene_id_22567	286	48.6	4.00E-72
gene_id_22568	393	33.59	2.00E-50
gene_id_22569	426	45.31	5.00E-129
gene_id_22570	281	28.83	3.00E-28
gene_id_22571	500	47	2.00E-146
gene_id_22572	290	47.59	1.00E-76
gene_id_22573	374	58.29	2.00E-137
gene_id_22574	491	63.14	0
gene_id_22575	351	57.83	7.00E-149
gene_id_22576	314	48.09	5.00E-86
gene_id_22577	121	53.72	2.00E-25
gene_id_22718	109	62.39	2.00E-42
gene_id_22719	784	38.01	2.00E-169
gene_id_22720	41	58.54	1.00E-06
gene_id_22721	294	56.12	9.00E-103
gene_id_22722	207	64.25	3.00E-97
gene_id_22723	180	45	1.00E-44
gene_id_22724	534	64.23	0
gene_id_22725	140	35.71	3.00E-12
gene_id_22726	1080	41.85	0
gene_id_22780	386	46.11	1.00E-105
gene_id_22781	149	43.62	3.00E-34
gene_id_22782	1033	98.16	0
gene_id_22783	373	49.33	1.00E-112
gene_id_22784	522	99.43	0
gene_id_22785	73	100	2.00E-43
gene_id_22796	119	63.03	9.00E-48
gene_id_22798	356	47.47	6.00E-97
gene_id_22799	481	45.32	2.00E-110
gene_id_22800	353	47.88	6.00E-93
gene_id_22801	226	42.48	2.00E-54
gene_id_22803	147	62.59	6.00E-70
gene_id_22804	434	39.86	6.00E-83
gene_id_22806	72	40.28	4.00E-12
gene_id_22808	352	41.19	1.00E-84
gene_id_22809	358	49.16	2.00E-106
gene_id_22810	362	71.55	3.00E-145
gene_id_22812	382	70.94	0
gene_id_22813	509	31.43	5.00E-54
gene_id_22814	234	44.87	6.00E-70
gene_id_22815	414	39.37	2.00E-81

gene_id_22816	337	35.31	3.00E-44
gene_id_22843	321	31.78	6.00E-39
gene_id_22845	62	51.61	4.00E-14
gene_id_22847	354	38.7	5.00E-71
gene_id_23136	177	40.68	9.00E-27
gene_id_23137	135	44.44	1.00E-35
gene_id_23138	208	57.69	8.00E-65
gene_id_23139	455	57.14	1.00E-174
gene_id_23140	127	55.12	7.00E-45
gene_id_23141	244	39.75	1.00E-43
gene_id_23142	706	51.13	0
gene_id_23143	673	68.05	0
gene_id_23145	152	34.87	1.00E-19
gene_id_23146	775	46.84	0
gene_id_23178	197	31.47	2.00E-15
gene_id_23179	228	69.3	2.00E-113
gene_id_23180	407	47.42	2.00E-122
gene_id_23181	369	70.46	0
gene_id_23182	179	35.2	2.00E-29
gene_id_23183	945	76.3	0
gene_id_23183	198	37.88	1.00E-31
gene_id_23184	536	34.14	2.00E-63
gene_id_23185	304	56.25	2.00E-119
gene_id_23186	357	45.94	1.00E-86
gene_id_23186	247	27.53	6.00E-23
gene_id_23187	137	48.91	9.00E-28
gene_id_23188	191	53.93	1.00E-65
gene_id_23455	62	66.13	5.00E-24
gene_id_23456	373	59.52	3.00E-154
gene_id_23457	71	53.52	6.00E-19
gene_id_23458	518	60.81	0
gene_id_23459	376	37.5	4.00E-66
gene_id_23460	490	62.45	0
gene_id_23461	265	39.62	8.00E-59
gene_id_23462	208	32.69	2.00E-21
gene_id_23463	258	42.25	9.00E-65
gene_id_23464	131	32.06	4.00E-12
gene_id_23465	149	61.07	2.00E-60
gene_id_23466	355	35.77	7.00E-50
gene_id_23467	169	44.97	5.00E-28
gene_id_23467	88	43.18	9.00E-06
gene_id_23469	137	43.8	1.00E-30
gene_id_23470	362	42.27	3.00E-89
gene_id_23488	377	49.07	3.00E-111
gene_id_23489	87	64.37	4.00E-34
gene_id_23490	105	49.52	1.00E-29
gene_id_23630	61	85.25	2.00E-18

gene_id_23631	321	61.06	2.00E-133
gene_id_23632	347	49.28	2.00E-84
gene_id_23633	356	49.44	1.00E-81
gene_id_23634	246	69.51	7.00E-119
gene_id_23635	734	34.06	1.00E-125
gene_id_23636	466	51.5	2.00E-148
gene_id_23637	411	47.69	8.00E-115
gene_id_23638	377	54.91	2.00E-133
gene_id_23639	130	60	4.00E-55
gene_id_23640	81	66.67	9.00E-31
gene_id_23677	597	78.56	0
gene_id_23678	270	27.04	1.00E-25
gene_id_23679	351	38.46	3.00E-67
gene_id_23680	202	34.65	6.00E-29
gene_id_23681	159	61.01	7.00E-70
gene_id_23683	151	42.38	2.00E-34
gene_id_23684	197	49.24	7.00E-49
gene_id_23685	876	52.97	0
gene_id_23686	749	22.43	1.00E-23
gene_id_23687	1109	29.94	3.00E-96
gene_id_23691	200	57	2.00E-69
gene_id_23692	342	34.8	2.00E-45
gene_id_23693	394	60.15	5.00E-134
gene_id_23694	546	54.4	0
gene_id_23695	476	40.55	4.00E-108
gene_id_23696	270	72.22	5.00E-134
gene_id_23697	461	38.18	6.00E-83
gene_id_23698	287	59.58	4.00E-119
gene_id_23699	429	54.31	3.00E-148
gene_id_23700	387	59.43	1.00E-157
gene_id_23701	339	45.72	3.00E-97
gene_id_23702	72	45.83	2.00E-06
gene_id_23717	231	39.83	5.00E-38
gene_id_23718	303	60.4	4.00E-112
gene_id_23719	352	52.56	4.00E-128
gene_id_23720	246	56.5	1.00E-95
gene_id_23721	502	54.78	1.00E-156
gene_id_23722	107	38.32	1.00E-13
gene_id_23745	442	68.33	0
gene_id_23746	176	67.05	3.00E-81
gene_id_23747	610	46.39	8.00E-179
gene_id_23748	111	36.94	5.00E-18
gene_id_23749	279	43.73	3.00E-76
gene_id_23750	262	45.04	9.00E-72
gene_id_23751	240	48.75	1.00E-66
gene_id_23752	305	65.25	4.00E-142
gene_id_23753	374	50.27	4.00E-116

gene_id_23754	524	74.62	0
gene_id_23755	598	52.34	0
gene_id_23756	147	64.63	2.00E-70
gene_id_23757	271	38.75	4.00E-51
gene_id_23759	287	35.54	2.00E-37
gene_id_23760	167	55.69	5.00E-58
gene_id_23876	89	78.65	2.00E-44
gene_id_23877	423	43.5	1.00E-101
gene_id_23878	240	61.67	6.00E-100
gene_id_23879	108	86.11	3.00E-56
gene_id_23879	29	93.1	3.00E-56
gene_id_23880	218	83.03	4.00E-133
gene_id_23881	124	100	7.00E-84
gene_id_23882	865	97.23	0
gene_id_24052	117	78.63	1.00E-60
gene_id_24053	159	33.33	2.00E-27
gene_id_24054	597	89.78	0
gene_id_24055	322	76.71	0
gene_id_24056	154	96.1	4.00E-97
gene_id_24057	372	84.14	0
gene_id_24058	189	84.13	2.00E-111
gene_id_24059	81	80.25	3.00E-33
gene_id_24060	447	57.94	4.00E-174
gene_id_24426	197	76.65	3.00E-93
gene_id_24427	277	68.59	2.00E-130
gene_id_24428	353	47.88	2.00E-106
gene_id_24429	1017	45.82	0
gene_id_24430	569	42.53	2.00E-158
gene_id_24433	297	52.53	6.00E-102
gene_id_24434	407	52.58	1.00E-143
gene_id_24435	899	76.75	0
gene_id_24436	381	48.56	1.00E-119
gene_id_24437	986	59.43	0
gene_id_24438	558	60.39	0
gene_id_24439	191	73.82	3.00E-101
gene_id_24440	959	79.67	0
gene_id_24441	312	45.19	2.00E-95
gene_id_24442	94	50	1.00E-19
gene_id_24443	136	63.97	3.00E-59
gene_id_24444	100	68	1.00E-33
gene_id_24445	159	71.07	3.00E-71
gene_id_24762	90	35.56	2.00E-07
gene_id_24763	439	58.31	0
gene_id_24764	150	58.67	4.00E-53
gene_id_24765	323	27.24	4.00E-07
gene_id_24766	62	83.87	5.00E-29
gene_id_24767	167	52.1	2.00E-44

gene_id_24768	93	51.61	4.00E-23
gene_id_25011	87	50.57	5.00E-21
gene_id_25012	124	58.87	5.00E-42
gene_id_25013	68	67.65	3.00E-26
gene_id_25014	839	78.07	0
gene_id_25015	321	81.93	0
gene_id_25016	503	64.61	0
gene_id_25017	218	70.64	5.00E-107
gene_id_25018	118	54.24	2.00E-37
gene_id_25194	287	51.57	7.00E-73
gene_id_25195	400	49.25	2.00E-123
gene_id_25197	228	45.61	5.00E-62
gene_id_25198	82	62.2	2.00E-28
gene_id_25411	194	30.93	9.00E-30
gene_id_25412	1176	78.06	0
gene_id_25413	209	52.15	6.00E-67
gene_id_25626	196	57.14	4.00E-77
gene_id_25627	93	37.63	3.00E-12
gene_id_25629	441	32.2	3.00E-49
gene_id_25630	408	30.88	5.00E-31
gene_id_25631	149	63.09	3.00E-61
gene_id_25632	87	74.71	4.00E-38
gene_id_25633	613	69.66	0
gene_id_25634	282	52.48	8.00E-87
gene_id_25870	84	83.33	1.00E-41
gene_id_25871	88	60.23	5.00E-22
gene_id_25872	263	67.68	1.00E-131
gene_id_25873	384	60.94	4.00E-173
gene_id_25874	345	23.19	5.00E-07
gene_id_25875	207	29.47	3.00E-27
gene_id_25876	213	61.03	2.00E-92
gene_id_25877	381	48.29	3.00E-122
gene_id_25878	230	51.74	1.00E-73
gene_id_25879	407	80.1	0
gene_id_25880	141	45.39	9.00E-30
gene_id_26203	666	74.02	0
gene_id_26204	118	77.97	2.00E-61
gene_id_26205	361	63.71	2.00E-149
gene_id_26359	194	59.28	3.00E-74
gene_id_26360	144	47.92	4.00E-41
gene_id_26361	127	58.27	8.00E-45
gene_id_26362	293	38.91	8.00E-42
gene_id_26543	169	42.01	3.00E-23
gene_id_26544	248	53.23	1.00E-88
gene_id_26545	127	54.33	3.00E-44
gene_id_26546	314	35.67	4.00E-62
gene_id_26547	244	54.92	3.00E-95

gene_id_26548	265	53.58	6.00E-78
gene_id_26549	633	53.87	0
gene_id_26821	421	52.73	2.00E-143
gene_id_26822	238	62.18	1.00E-71
gene_id_26876	268	46.27	5.00E-75
gene_id_26877	504	75.99	0
gene_id_26878	84	70.24	4.00E-29
gene_id_26879	398	60.55	9.00E-169
gene_id_27271	97	63.92	3.00E-34
gene_id_27968	85	75.29	6.00E-38
gene_id_27969	303	54.46	2.00E-94
gene_id_27970	240	40.83	1.00E-52
gene_id_27971	65	52.31	2.00E-11

Annotation
virulence associated protein
MULTISPECIES: gamma-glutamyl cyclotransferase
peptidase M23
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
conjugal transfer protein TraG
transcriptional regulator
TetR family transcriptional regulator
MATE efflux family protein
transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
ATPase
peptidase M20/M25/M40 family
GlcNAc-PI de-N-acetylase
peptide ABC transporter substrate-binding protein
MULTISPECIES: peptide ABC transporter permease
ABC transporter permease
peptide ABC transporter ATPase
peptide ABC transporter ATPase
aminopeptidase
hypothetical protein
cation transporter
hypothetical protein
metal-sensitive transcriptional repressor
RNA polymerase subunit sigma-24
growth inhibitor PemK
hypothetical protein
resolvase
resolvase
recombinase
resolvase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
Eco57I restriction endonuclease
BsuBIPstI restriction endonuclease domain-containing protein
hypothetical protein
hypothetical protein

hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
MULTISPECIES: ArsR family transcriptional regulator
hypothetical protein
zinc ABC transporter ATPase
hypothetical protein HMPREF9225_0440
Antirestriction protein (ArdA)
hypothetical protein
hypothetical protein
hypothetical protein
DNA methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
S-layer protein
hypothetical protein
peptidase A24A prepilin type IV
Flp pilus assembly protein CpaB
MULTISPECIES: ATPase AAA
MULTISPECIES: type II secretion system protein E
membrane protein
Hypothetical protein DPCES_0138
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
Hypothetical protein DPCES_0133
hypothetical protein
hypothetical protein
hypothetical protein
C-5 cytosine-specific DNA methylase
transporter
7-cyano-7-deazaguanine reductase
riboflavin biosynthesis protein RibD
riboflavin synthase subunit alpha
GTP cyclohydrolase
6,7-dimethyl-8-ribityllumazine synthase
phosphomethylpyrimidine synthase
phosphomethylpyrimidine kinase
hydroxyethylthiazole kinase
Thiamine-phosphate pyrophosphorylase

Haloacid dehalogenase domain-containing protein hydrolase
von Willebrand factor A, partial
radical SAM domain-containing protein
ribonucleoside triphosphate reductase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
alpha-glucosidase
LacI family transcriptional regulator
glycoside hydrolase family protein
sugar ABC transporter substrate-binding protein
sugar ABC transporter permease
sugar ABC transporter permease
deacetylase
glycogen debranching protein
signal transduction histidine kinase
two component transcriptional regulator, winged helix family
Lipase class 3 family protein
isocitrate dehydrogenase
aconitate hydratase
citrate synthase
polysaccharide deacetylase
D-alanine--D-alanine ligase
extracellular solute-binding protein family 5
peptide ABC transporter permease
D-ala-D-ala transporter subunit
oligopeptide/dipeptide ABC transporter, ATPase subunit
peptide ABC transporter ATP-binding protein
beta-lactamase
hypothetical protein
hypothetical protein
beta-lactamase
hypothetical protein
type 11 methyltransferase
ATPase AAA
NAD-dependent deacetylase
dephospho-CoA kinase
sporulation domain-containing protein
ABC transporter substrate-binding protein
ABC transporter
ABC transporter permease
ABC transporter permease
adenine deaminase
hypothetical protein
Xanthine dehydrogenase, molybdenum binding subunit

MULTISPECIES: hypothetical protein
selenate reductase subunit YgfK
amidohydrolase
peptidase
pyridoxal-5'-phosphate-dependent protein beta subunit
pyridoxal-5-phosphate-dependent protein subunit beta
heme ABC transporter ATP-binding protein
hypothetical protein
membrane protein
PAS domain S-box
transketolase
excinuclease ABC subunit C
NUDIX hydrolase
oxidoreductase
cupin
major facilitator superfamily protein
hypothetical protein
hypothetical protein, partial
ATPase AAA
MULTISPECIES: hypothetical protein, partial
hypothetical protein, partial
hypothetical protein
tRNA synthetase subunit beta
translation factor Sua5
hypothetical protein
type 11 methyltransferase
hypothetical protein
hypothetical protein
dimethyladenosine transferase
hypothetical protein
hypothetical protein
2-methylthioadenine synthetase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein TcarDRAFT_0067
4-alpha-glucanotransferase
hypothetical protein OM95_08140
fimbrial biogenesis outer membrane usher protein
hypothetical protein
UDP-glucose 4-epimerase
acetylornithine deacetylase
hypothetical protein
hypothetical protein
membrane protein
hypothetical protein
aldolase

DeoR faimly transcriptional regulator
methylthioribose-1-phosphate isomerase
hypothetical protein
inner-membrane translocator
inner-membrane translocator
hypothetical protein
cupin
short-chain dehydrogenase
pseudouridine synthase
MULTISPECIES: hypothetical protein
mechanosensitive ion channel MscS
hypothetical protein
aminotransferase class V
dinitrogenase iron-molybdenum cofactor biosynthesis protein
ATPase
type 11 methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
1-pyrroline-5-carboxylate dehydrogenase
hypothetical protein
hypothetical protein
hypothetical protein, partial
peptide-binding protein
hypothetical protein
hypothetical protein
cobalt ABC transporter ATP-binding protein
biotin permease
aspartate-ammonia ligase
hypothetical protein
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
branched-chain amino acid ABC transporter substrate-binding protein
branched-chain amino acid ABC transporter permease
ABC transporter permease
ABC transporter
amino acid ABC transporter ATPase
hypothetical protein
glutamine synthetase
ATPase AAA
hypothetical protein
aspartate kinase
dihydrodipicolinate reductase
dihydrodipicolinate synthase
2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase
pyrroline-5-carboxylate reductase
hypothetical protein
hypothetical protein

signal peptidase
hypothetical protein
hydroxyacid dehydrogenase
MFS transporter
Heavy metal transport/detoxification protein
molecular chaperone DnaJ
chaperone protein DnaK
co-chaperone GrpE
ethanolamine utilization protein EutN
ethanolamine utilization protein EutA
ethanolamine transporter
ethanolamine ammonia-lyase
ethanolamine utilization protein EutL
acetaldehyde dehydrogenase
carboxysome shell protein
hypothetical protein
iron ABC transporter substrate-binding protein
ABC transporter
spermidine/putrescine ABC transporter permease
spermidine/putrescine ABC transporter ATPase
RNA polymerase sigma54 factor
ribosomal biogenesis protein
aldolase
hypothetical protein
ADP-ribosylation/crystallin J1
protein lplB
ABC transporter permease
ABC transporter substrate-binding protein
crystallin
citrate lyase ACP
citrate lyase subunit alpha
hypothetical protein
gamma-glutamyl cyclotransferase
peptidase M23
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
Sel1 domain-containing protein repeat-containing protein
hypothetical protein
conjugal transfer protein TraG
transcriptional regulator
hypothetical protein
hypothetical protein
hypothetical protein
peptidase M56, partial

transcriptional repressor, CopY family
polysaccharide deacetylase, partial
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
histidine kinase
MULTISPECIES: hypothetical protein
hypothetical protein
diguanylate cyclase, partial
hypothetical protein
RNA-directed DNA polymerase (Reverse transcriptase)
hypothetical protein
XRE family transcriptional regulator
hypothetical protein
FliA/WhiG subfamily RNA polymerase sigma-28 subunit
hypothetical protein
resolvase
recombinase
resolvase
hypothetical protein
putative phage DNA-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
glucosyltransferase
DNA-binding protein
peptidase U32
ABC transporter
hypothetical protein
hypothetical protein
2-oxoacid:ferredoxin oxidoreductase subunit alpha
2-oxoacid ferredoxin oxidoreductase subunit beta
hypothetical protein
hypothetical protein
hypothetical protein

hypothetical protein
chloramphenicol acetyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
Membrane spanning protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
AraC family transcriptional regulator
hypothetical protein
methyltransferase
hypothetical protein
hypothetical protein
pyridoxamine 5-phosphate oxidase
hypothetical protein
hypothetical protein
polysaccharide deacetylase
polysaccharide deacetylase
hypothetical protein
hypothetical protein
hypothetical protein
GNAT family acetyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
3-methyladenine DNA glycosylase
AraC family transcriptional regulator
methylated-DNA-protein-cysteine methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
phosphoenolpyruvate synthase
hypothetical protein
DNA repair protein
DNA ligase

hypothetical protein
UDP pyrophosphate phosphatase
1-acyl-sn-glycerol-3-phosphate acyltransferase
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein
RNA methyltransferase
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
Hypothetical protein DPCES_0152
DNA methyltransferase
hypothetical protein
YodL-like
hypothetical protein
SpoVG family protein
S-layer protein
peptidase A24
Flp pilus assembly protein CpaB
ATPase AAA
MULTISPECIES: type II secretion system protein E
MULTISPECIES: membrane protein
Hypothetical protein DPCES_0138
MULTISPECIES: hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein HMPREF9460_02825
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
C-5 cytosine-specific DNA methylase
cation diffusion facilitator family transporter
tryptophan synthase subunit beta
sugar ABC transporter permease
ABC transporter permease
extracellular solute-binding protein family 1
RpiR family transcriptional regulator
6-phosphogluconate dehydrogenase

ribokinase
alcohol dehydrogenase GroES domain protein
oxidoreductase
Mg chelatase-like protein
phenylalanyl-tRNA synthetase subunit beta
phenylalanyl-tRNA synthetase subunit alpha
pyruvate phosphate dikinase
3-deoxy-7-phosphoheptulonate synthase, partial
hypothetical protein, partial
cell division protein FtsY
hypothetical protein
ABC transporter ATP-binding protein
lipoprotein releasing system permease
recombinase RecA, partial
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
Segregation and condensation protein A
segregation and condensation protein B
pseudouridine synthase
cytidylate kinase
30S ribosomal protein S1
Fis family transcriptional regulator
hypothetical protein JO40_07740
radical SAM protein
rod shape-determining protein RodA
penicillin-binding protein
rod shape-determining protein MreD
rod shape-determining protein MreC
rod shape-determining protein Mbl
hypothetical protein
hypothetical protein
RNA polymerase sigma factor RpoD
DNA primase
hypothetical protein
Fe-S oxidoreductase
DNA polymerase I
hypothetical protein
kinase
pseudouridine-5'-phosphate glycosidase
hypothetical protein
hypothetical protein
transposase, partial
dinitrogenase iron-molybdenum cofactor biosynthesis protein
DNA topoisomerase IV subunit A
DNA topoisomerase IV subunit B
sigma54 specific transcriptional regulator, Fis family
3-isopropylmalate dehydratase large subunit
3-isopropylmalate dehydratase, small subunit

C4-dicarboxylate ABC transporter substrate-binding protein
C4-dicarboxylate ABC transporter permease, partial
transcriptional regulator
oxidoreductase
oxidoreductase
sugar ABC transporter permease
ABC transporter permease
MULTISPECIES: sugar ABC transporter substrate-binding protein
transport system permease protein
periplasmic binding protein
MULTISPECIES: hypothetical protein
xenobiotic-transporting ATPase
fucose isomerase
LacI family transcriptional regulator
hypothetical protein
L-fucose mutarotase
hypothetical protein
LacI family transcriptional regulator
ribose ABC transporter permease
MULTISPECIES: D-ribose transporter ATP binding protein
DeoR faimly transcriptional regulator
pyruvate dehydrogenase E2 component
pyridine nucleotide-disulfide oxidoreductase
dehydrogenase
ATP-dependent metalloprotease
Bifunctional protein tilS/hprT
50S ribosomal protein L25
Protein of unknown function identified by role in sporulation (SpoVG)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
iojap family protein
hypothetical protein
hypothetical protein
nicotinate
GTPase CgtA
50S ribosomal protein L27
50S ribosomal protein L21
arginyl-tRNA synthetase
hypothetical conserved protein
NAD-dependent DNA ligase LigA
hypothetical protein
xanthine dehydrogenase
hypothetical protein
hypothetical protein
SAM-dependent methyltransferase
transcription-repair coupling factor
ArsR family transcriptional regulator
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase

V-type sodium ATPase, K subunit
hypothetical protein
ATP synthase subunit D
ATP synthase subunit B
ATP synthase subunit A
hypothetical protein
ATP synthase subunit E
hypothetical protein
AMP-dependent synthetase
hypothetical protein
30S ribosomal protein S16
MULTISPECIES: hypothetical protein
16S rRNA processing protein RimM
tRNA (guanine-N1)-methyltransferase
50S ribosomal protein L19
hypothetical protein
hypothetical protein
seryl-tRNA synthetase
peptide chain release factor 1
hypothetical protein
(p)ppGpp synthetase
HyfI
hydrogenase
hydrogenase
NAD-dependent dehydrogenase subunit
hydrogenase
protein HyfB
PTS fructose transporter subunit IIA
hypothetical protein
MULTISPECIES: chemotaxis protein
Oligopeptide transport ATP-binding protein OppD
MULTISPECIES: peptide ABC transporter permease
MULTISPECIES: peptide ABC transporter permease
MULTISPECIES: ABC transporter substrate-binding protein
glycosyl hydrolase family 3 protein
acetyltransferase
CRISPR-associated protein Cas2
CRISPR-associated protein Cas1
CRISPR-associated protein Cas4
ATPase
CRISPR-associated protein Csh2
CRISPR-associated protein Csd1
CRISPR-associated protein
phosphohydrolase
transcriptional regulator
sodium/hydrogen exchanger
ribosomal large subunit pseudouridine synthase C

hypothetical protein
hypothetical protein
hypothetical protein ETSY2_32695
MFS transporter
multidrug transporter MatE
nucleoside triphosphate hydrolase
pyruvate-flavodoxin oxidoreductase
nucleotidyltransferase
UDP-N-acetylglucosamine diphosphorylase
Purine nucleoside phosphorylase DeoD-type
ferredoxin-NADP(+) reductase subunit alpha
dihydropyrimidine dehydrogenase subunit A
hypothetical protein
peptidase M20
amidohydrolase
ABC transporter permease
ABC transporter permease
ABC transporter ATP-binding protein
adenine nucleotide translocator 1
peptidase M20
hypothetical protein ACD_7C00469G0003
ABC transporter substrate-binding protein, partial
hypothetical protein
ABC transporter permease
phosphoglycerate mutase
purine nucleoside phosphorylase
hypothetical protein
30S ribosomal protein S21
hypothetical protein
peptide deformylase
methionyl-tRNA formyltransferase
penicillin-binding protein
hypothetical protein
Beta-galactosidase
uracil-DNA glycosylase, family 4
primosomal protein N'
Trk system potassium transporter TrkH
potassium transporter
H(+)-transporting two-sector ATPase
hypothetical protein
2-amino-3-ketobutyrate CoA ligase
hypothetical protein
rubrerythrin
Desulfoferrodoxin
rubredoxin
hypothetical protein
SAM-dependent methyltransferase

hypothetical protein
hypothetical protein
MULTISPECIES: ATPase
MULTISPECIES: (4Fe-4S)-binding protein
dinitrogenase iron-molybdenum cofactor biosynthesis protein
DNA repair protein RadA
4-alpha-glucanotransferase (amylomaltase)
transporter
twitching motility protein PilT
prevent-host-death protein
Cytochrome c-type biogenesis protein CcdA
thioredoxin
ATP-dependent Clp protease ClpP
endonuclease
gluconate transporter
hypothetical protein
D-glycerate 2-kinase
hypothetical protein
hypothetical protein
peptidase M15B and M15C DD-carboxypeptidase VanY/endolysin
hydrolase
multidrug transporter MurJ
50S ribosomal protein L33
preprotein translocase subunit SecE
transcription termination/antitermination factor NusG
50S ribosomal protein L11
50S ribosomal protein L1
50S ribosomal protein L10
50S ribosomal protein L7/L12
DNA-directed RNA polymerase subunit beta
DNA-directed RNA polymerase subunit beta'
30S ribosomal protein S12
30S ribosomal protein S7
elongation factor P
elongation factor Tu
30S ribosomal protein S10
50S ribosomal protein L3
50S ribosomal protein L4
50S ribosomal protein L23
50S ribosomal protein L2
30S ribosomal protein S19
50S ribosomal protein L22
30S ribosomal protein S3
50S ribosomal protein L16
50S ribosomal protein L29
30S ribosomal protein S17
50S ribosomal protein L14

50S ribosomal protein L24
50S ribosomal protein L5
30S ribosomal protein S8
50S ribosomal protein L6
50S ribosomal protein L18
30S ribosomal protein S5
50S ribosomal protein L15
preprotein translocase subunit SecY
30S ribosomal protein S13
30S ribosomal protein S11
30S ribosomal protein S4
DNA-directed RNA polymerase subunit alpha
50S ribosomal protein L17
hypothetical protein
amino acid ABC transporter ATPase
branched-chain amino acid ABC transporter ATP-binding protein
branched-chain amino acid ABC transporter permease
ABC transporter permease
ethanolamine utilization protein EutJ
transporter
imidazolonepropionase
hypothetical protein
histidine ammonia-lyase
hypothetical protein
adenine permease
hypothetical protein, partial
hypothetical protein
hypothetical protein
ABC transporter permease
MULTISPECIES: ABC transporter permease
ABC transporter substrate-binding protein
N-acetylmuramic acid-6-phosphate etherase
RpiR family transcriptional regulator
hypothetical protein
hypothetical protein
glycoside hydrolase family protein
pullulanase, type I
alpha amylase catalytic region
hypothetical protein
ABC transporter permease
ABC transporter permease
ABC transporter substrate-binding protein
cyclomaltodextrinase
hypothetical protein
hypothetical protein
hypothetical protein
PF08876 domain protein

MULTISPECIES: hypothetical protein
transcriptional regulator
DNA mismatch repair protein MutS
ribosome small subunit-dependent GTPase A
glutamate racemase
hypothetical protein
hypothetical protein
metallo-beta-lactamase domain protein
hypothetical protein
coproporphyrinogen III oxidase
signal peptidase
hypothetical protein
single-stranded DNA-binding protein
methyltransferase
hypothetical protein
50S rRNA methyltransferase
hypothetical protein
ATP-dependent helicase
glucose-1-phosphate adenylyltransferase
phosphoribosyl transferase
serine protease
methionine aminopeptidase
transcription antitermination protein NusB
membrane protein
Chaperone protein DnaJ
hypothetical protein
triosephosphate isomerase
serine acetyltransferase, partial
cysteine synthase A
phosphoglycerate kinase
glyceraldehyde-3-phosphate dehydrogenase
penicillin-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
recombinase RarA
Hydrolase, haloacid dehalogenase-like family
FolC bifunctional protein
YheB protein
YheB protein
peptidase C14 caspase catalytic subunit p20
hypothetical protein
asparaginyl-tRNA synthetase
D-alanyl-D-alanine carboxypeptidase
TRAP dicarboxylate transporter, DctM subunit
tripartite ATP-independent periplasmic transporter DctQ component
C4-dicarboxylate ABC transporter substrate-binding protein

endonuclease III
nitrogen fixation protein NifU
cysteine desulfurase
Rrf2 family transcriptional regulator
sulfurtransferase
MULTISPECIES: hypothetical protein
UDP-N-acetylmuramoylalanine--D-glutamate ligase
dioxygenase
ribonuclease Z
DEAD/DEAH box helicase
Radical SAM domain-containing protein
hypothetical protein
arginyl-tRNA-protein transferase
PpiC-type peptidyl-prolyl cis-trans isomerase
elongation factor 4
glutaredoxin
ferredoxin thioredoxin reductase
cysteine desulfurase
thiamine biosynthesis/tRNA modification protein ThiI
(p)ppGpp synthetase
cell wall hydrolase/autolysin
ribonucleoside diphosphate reductase
arginine deiminase
MULTISPECIES: GTPase
hypothetical protein
ribosomal large subunit pseudouridine synthase D
multidrug ABC transporter ATPase
ABC transporter
ribonuclease H
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
maf-like protein
30S ribosomal protein S2
elongation factor Ts
ribosome recycling factor
UDP diphosphate synthase
hypothetical protein
1-deoxy-D-xylulose 5-phosphate reductoisomerase
RIP metalloprotease RseP
transcriptional regulator
ABC transporter
MULTISPECIES: hypothetical protein
MULTISPECIES: hypothetical protein
negative regulator of sigma E activity

isoleucyl-tRNA synthetase
hypothetical protein
hypothetical protein
putative M18 family aminopeptidase 2
MerR family transcriptional regulator
ribosome-associated GTPase EngA
phosphoenolpyruvate-protein phosphotransferase
hypothetical protein
FeS-binding protein
fumarate hydratase
NUDIX hydrolase
glycerophosphoryl diester phosphodiesterase
sn-glycerol-3-phosphate ABC transporter substrate-binding protein
glycerol-3-phosphate transporter permease
glycerol-3-phosphate transporter membrane protein
glucuronate isomerase
short-chain dehydrogenase
membrane protein
C4-dicarboxylate ABC transporter permease
C4-dicarboxylate ABC transporter
two-component response regulator
integral membrane sensor signal transduction histidine kinase
hypothetical protein
hypothetical protein
integral membrane sensor signal transduction histidine kinase
transcriptional regulator
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
lipoprotein release ABC transporter permease
ABC transporter
hypothetical protein
hypothetical protein
aromatic acid decarboxylase
nitrate/sulfonate/bicarbonate ABC transporter periplasmic protein
ABC transporter
Fe(3+) ions import ATP-binding protein FbpC 1
ABC transporter permease
Extracellular solute-binding protein family 1
spore protein SP21 family protein
ferredoxin
ABC transporter
ABC transporter
hypothetical protein, partial
hypothetical protein
hypothetical protein, partial

ABC transporter
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
transcriptional regulator
hypothetical protein
hypothetical protein
alkylhydroperoxidase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
4-hydroxy-2-oxopentanoic acid aldolase
acetaldehyde dehydrogenase
2-keto-4-pentenoate hydratase
2-hydroxy-6-oxo-2,4-heptadienoate hydrolase
hypothetical protein
hypothetical protein
hypothetical protein
N-acetyltransferase GCN5
ATPase AAA
metal dependent phosphohydrolase
thiamine biosynthesis protein ThiF
peptidoglycan-binding protein
peptidoglycan-binding protein
2-nitropropane dioxygenase
hypothetical protein
PDZ/DHR/GLGF domain-containing protein
3-dehydroquinate dehydratase
methyltransferase
hypothetical protein OP10G_1753
hypothetical protein
hypothetical conserved protein
FAD-dependent pyridine nucleotide-disulphide oxidoreductase
multidrug transporter MatE
LacI family transcriptional regulator
LacI family transcriptional regulator
ABC transporter substrate-binding protein
iron ABC transporter permease
polyamine ABC transporter ATP-binding protein
MULTISPECIES: membrane protein
putative signaling protein
chemotaxis protein CheY
histidine kinase
lipoate--protein ligase
hypothetical protein

lipoic acid synthetase
biotin synthase
cystathionine beta-lyase
hypothetical protein
hypothetical protein
hypothetical protein
ATP-binding protein
alpha/beta hydrolase
polynucleotide adenylyltransferase
hypothetical protein
peptide ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein
hypothetical protein
formate--tetrahydrofolate ligase
hypothetical protein
glycoside hydrolase
adenylosuccinate synthetase
GMP synthase
L-lysine 2,3-aminomutase
ArgR family transcriptional regulator
hypothetical protein
protein disaggregation chaperone
deoxyribonuclease
hypothetical protein, partial
hypothetical protein
phosphoglyceromutase
adenine phosphoribosyltransferase
hypothetical protein
pyridoxal phosphate enzyme, YggS family
hypothetical protein
hypothetical protein
cytidine deaminase
DNA recombination protein RecN
hypothetical protein
DegT/DnrJ/EryC1/StrS aminotransferase family protein
DNA gyrase subunit A
DNA gyrase subunit B
chromosomal replication initiator protein DnaA
DNA polymerase III subunit beta
DNA repair protein RecF
hypothetical protein
MULTISPECIES: 50S ribosomal protein L34
hypothetical protein, partial
hypothetical protein
membrane protein
single-stranded DNA-binding protein

NADH-quinone reductase
NADH-quinone reductase
electron transporter RnfG
electron transporter RsxE
electron transport complex RsxE subunit
ferredoxin
hypothetical protein
prevent-host-death protein
toxin YoeB
integrase
tryptophan synthase subunit beta
pyridoxal-phosphate dependent TrpB-like protein
RNA helicase
RNA helicase
methylglyoxal synthase
transposase IS4 family protein
transposase IS4 family protein
hypothetical protein, partial
hypothetical protein, partial
S-adenosylmethionine synthetase
Zn-dependent protease-like protein
Zn-dependent protease
redox protein
amino acid ABC transporter ATPase
amino acid ABC transporter permease
amino acid ABC transporter substrate-binding protein
hypothetical protein
hypothetical protein
thiol-disulfide isomerase
toxin HipA
transcriptional regulator
signal transduction histidine kinase
response regulator with CheY-like receiver domain and winged-helix DNA-binding domain
copper chaperone
heavy metal translocating P-type ATPase
heavy metal transporter
high-affinity iron transporter
ATPase
sensory transduction system regulatory protein
sagB-type dehydrogenase domain-containing protein
amino acid-binding protein
putative membrane protein
hydrogenase large subunit domain-containing protein
hypothetical protein
hypothetical protein ANME2D_00630
Fe-S oxidoreductase
response regulator SirA

hypothetical protein
ArsR family transcriptional regulator
homocysteine S-methyltransferase
B12-dependent methionine synthase
NIL domain-containing protein
hypothetical protein
GTP-binding protein
aspartate ammonia-lyase
radical SAM protein
thiamine biosynthesis protein ThiH
CopG family transcripitonal regulator
DEAD/DEAH box helicase
hypothetical protein
Putative Type I restriction modification system, specificity protein
conserved hypothetical protein
DNA methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
antitoxin
arsenical resistance operon trans-acting repressor ArsD
putative arsenical pump-driving ATPase
putative arsenical pump-driving ATPase
hypothetical protein U27_03625
hypothetical protein
hypothetical protein
hypothetical protein
arsenic resistance protein ArsB
putative transcriptional regulator
hypothetical protein
hypothetical protein
amino acid ABC transporter ATPase
ABC transporter
ABC transporter permease
branched-chain amino acid transporter permease subunit LivH
branched-chain amino acid ABC transporter substrate-binding protein
ABC transporter substrate-binding protein
ABC transporter permease
ABC transporter ATP-binding protein
putative abortive infection protein AbiGI
uncharacterized protein
hypothetical protein
MFS transporter
hypothetical protein ACD_11C00105G0010
ATPase AAA
hypothetical protein
endonuclease

hypothetical protein, partial
conserved exported hypothetical protein
site-specific recombinase, phage integrase family
hypothetical protein
L-threonine 3-dehydrogenase
hypothetical protein
phospholipid-binding protein
rRNA methyltransferase
aspartate carbamoyltransferase
23S rRNA methyltransferase
metallo-beta-lactamase
ribose 5-phosphate isomerase
potassium ABC transporter ATPase
multidrug transporter MatE
leucyl-tRNA synthetase
hypothetical protein
hypothetical protein
hypothetical protein
peptidyl-prolyl cis-trans isomerase
cell division protein FtsK
antitoxin
toxin
phosphate:sodium symporter
ABC transporter
zinc ABC transporter ATP-binding protein
ABC transporter substrate-binding protein
hypothetical protein
DEAD/DEAH box helicase
MULTISPECIES: hypothetical protein
ATPase
hypothetical protein
hypothetical protein, partial
cell division protein Fic
2-hydroxyacid dehydrogenase
N-6 DNA methylase
helix-turn-helix domain-containing protein
hypothetical protein
hypothetical protein
peptide chain release factor I
hypothetical protein
TRAP transporter, DctM subunit
C4-dicarboxylate ABC transporter permease
DctP family TRAP transporter solute receptor
IclR family transcriptional regulator
C4-dicarboxylate ABC transporter substrate-binding protein
C4-dicarboxylate ABC transporter permease
hypothetical protein

phosphatase
mRNA-binding protein
carbohydrate kinase FGGY
xylose isomerase
xylose isomerase
LacI family transcriptional regulator
ribose/xylose/arabinose/galactoside ABC-type transport system protein
sugar ABC transporter ATPase/substrate-binding protein
putative amino acid or sugar ABC transport system, permease protein
inner-membrane translocator
glycerone kinase
hypothetical protein
2-hydroxy-3-oxopropionate reductase
hypothetical protein
hypothetical protein
glutathione ABC transporter permease GsiD
glutathione ABC transporter permease
protein DppA2
glutathione ABC transporter ATP-binding protein
isoaspartyl dipeptidase
RpiR family transcriptional regulator
amidase
hypothetical protein
N-acetylglucosamine-6-phosphate deacetylase
ferredoxin
ferredoxin
hypothetical protein
purine nucleoside phosphorylase
MULTISPECIES: chlorohydrolase
hypothetical protein
hypothetical protein
protein-L-isoaspartate O-methyltransferase
D-alanine--D-alanine ligase
D-alanine--D-alanine ligase
cobalamin-binding protein
hypothetical protein
hypothetical protein
rhamnose isomerase
alcohol dehydrogenase
L-rhamnose mutarotase
hypothetical protein
branched-chain amino acid ABC transporter permease
branched-chain amino acid ABC transporter permease
D-ribose transporter ATP binding protein
arabinose isomerase
transcriptional regulator
protein kinase family protein

hypothetical protein
NADH dehydrogenase
hypothetical protein
NAD(P)-dependent iron-only hydrogenase iron-sulfur protein
NADH dehydrogenase
ferredoxin
ribosomal small subunit Rsm22
hypothetical protein
tryptophan--tRNA ligase
alpha/beta hydrolase fold protein
thioesterase
hypothetical protein
Pyrophosphate-energized proton pump
N-acetyl-gamma-glutamyl-phosphate reductase
ornithine acetyltransferase
acetylglutamate kinase
acetylornithine aminotransferase
hypothetical protein
glycosyl transferase family protein, partial
hypothetical protein
hypothetical protein
IclR family transcriptional regulator
pyruvate/ketoisovalerate oxidoreductase subunit gamma
MFS transporter
2-ketoisovalerate ferredoxin reductase
tungsten formylmethanofuran dehydrogenase subunit G
phosphate butyryltransferase
butyrate kinase
peptide ABC transporter ATPase
phosphatidylglycerol lysyltransferase
ribonuclease HII
GNAT family acetyltransferase
thioredoxin reductase
signal transduction histidine kinase
histidinol phosphatase
conjugal transfer protein TraR
translation initiation factor IF-1
Smr domain-containing protein
hypothetical protein, partial
sodium:glutamate symporter
Crp/Fnr family transcriptional regulator
hypothetical protein
uracil phosphoribosyltransferase
propanediol utilization protein
DhnA-type fructose-1,6-bisphosphate aldolase-like enzyme
pentulose/hexulose kinase
theronine dehydrogenase-like Zn-dependent dehydrogenase

MerR family transcriptional regulator
putative ABC-type transport system, periplasmic component/surface lipoprotein
LOW QUALITY PROTEIN: ATPase component of uncharacterized ABC-type transporter
ABC transporter permease
ABC transporter permease
5'-nucleotidase
peptidase S9
DNA repair protein recO
pyrimidine-nucleoside phosphorylase
single-stranded DNA exonuclease
TonB-denpendent receptor
TonB family protein
hypothetical protein
CarD family transcriptional regulator
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
hypothetical protein
alpha-glucosidase
fucose isomerase
C4-dicarboxylate ABC transporter substrate-binding protein
hypothetical protein
C4-dicarboxylate ABC transporter
aspartokinase
glutaconyl-CoA decarboxylase subunit beta
biotin attachment protein
methylmalonyl-CoA carboxyltransferase
MULTISPECIES: hypothetical protein
putative periplasmic protein kinase ArgK
methylmalonyl-CoA mutase
methylmalonyl-CoA mutase
2-oxoglutarate ferredoxin oxidoreductase subunit gamma
2-oxoglutarate oxidoreductase, beta subunit
hypothetical protein
cell envelope biogenesis protein OmpA
cell envelope biogenesis protein OmpA
cell envelope biogenesis protein OmpA
cell envelope biogenesis protein OmpA
cell envelope biogenesis protein OmpA
sodium:proton exchanger
UDP-N-acetylenolpyruvoylglucosamine reductase
cysteinyl-tRNA synthetase
Sigma-70 region 2
hypothetical protein
hypothetical protein
serine hydroxymethyltransferase
putative iron-sulfur protein
plasmid stabilization protein
prevent-host-death protein

ATPase AAA
LysR family transcriptional regulator
elongation factor P
methyltransferase small
hypothetical protein
ATP-dependent DNA helicase RecG
carboxypeptidase
hypothetical protein GUITHDRAFT_159625
histidinol dehydrogenase
imidazole glycerol phosphate synthase
hypothetical protein
hypothetical protein M408DRAFT_329238
histidinol-phosphate aminotransferase
hypothetical protein
histidinol dehydrogenase
phosphotransferase
hypothetical protein
16S rRNA methyltransferase
RNA methyltransferase
hypothetical protein
ABC transporter
aBC-type Fe3+ transport system permease component
iron ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein
PilT protein domain-containing protein
ferredoxin
NADH dehydrogenase
NADH-quinone oxidoreductase subunit E
RNA-binding protein
hypothetical protein
ABC transporter periplasmic protein
peptide ABC transporter
glutathione ABC transporter permease GsiD
peptide ABC transporter ATP-binding protein
peptide ABC transporter ATP-binding protein
N-acetyltransferase GCN5
hypothetical protein
ABC transporter substrate-binding protein
hypothetical protein
hypothetical protein
S-adenosylmethionine decarboxylase
Spermidine synthase
lipoyltransferase and lipoate-protein ligase
dihydrolipoamide dehydrogenase
arsenate reductase
NAD(P)H nitroreductase

citrate transporter
ArsR family transcriptional regulator
redox-active disulfide protein 2
permease
cation transporter
cupin
HAD-superfamily hydrolase
hypothetical protein
hypothetical protein
hypothetical protein
aldo/keto reductase
sugar kinase
hypothetical protein
putative glycosidase
ABC transporter substrate-binding protein
peptide ABC transporter permease
ABC transporter permease
peptide ABC transporter ATPase
peptide ABC transporter ATPase
hypothetical protein
2-isopropylmalate synthase
3-isopropylmalate dehydratase, large subunit
MULTISPECIES: 3-isopropylmalate dehydratase small subunit
3-isopropylmalate dehydrogenase
AzlC family protein
branched-chain amino acid transport
GCN5 family acetyltransferase
MULTISPECIES: putative alkylmercury lyase
NADPH-dependent FMN reductase
peptidylprolyl isomerase
Fe-S cluster protein
stage II sporulation protein E
hypothetical protein
hydrogenase assembly protein HupF
carbamoyl phosphate synthase large subunit
carbamoyl phosphate synthase small subunit
MULTISPECIES: malate transporter
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
PadR family transcripitonal regulator
anthranilate synthase
glutamine amidotransferase
indole-3-glycerol phosphate synthase

tryptophan synthase subunit beta
Tryptophan synthase subunit alpha
hypothetical protein
TetR family transcriptional regulator
MULTISPECIES: hypothetical protein
hypothetical protein
hypothetical protein
UDP-diphosphatase
hypothetical protein
hypothetical protein
hypothetical protein, partial
ankyrin
ankyrin
ankyrin
ankyrin
ankyrin
ankyrin
ankyrin
ankyrin
hypothetical protein
monosaccharide-transporting ATPase
ABC-type ribose transport system
monosaccharide-transporting ATPase
periplasmic binding protein/LacI transcriptional regulator
hypothetical protein U27_06219
hypothetical protein
L-xylulose 5-phosphate 3-epimerase
carbohydrate kinase FGGY family protein
shikimate dehydrogenase
shikimate dehydrogenase
LOG family protein
nicotinate phosphoribosyltransferase
isochorismatase hydrolase
YruB family glutaredoxin
hypothetical protein
hypothetical protein
gamma-glutamyltranspeptidase
hypothetical protein
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
MULTISPECIES: phosphoglyceromutase
multiple antibiotic resistance (MarC)-like protein
hypothetical protein
ABC transporter
ABC transporter
sugar ABC transporter ATP-binding protein
hypothetical protein
hypothetical protein

hypothetical protein
hypothetical protein
hypothetical protein
MULTISPECIES: ABC transporter
hypothetical protein
hypothetical protein
phosphoenolpyruvate carboxykinase
hypothetical protein
hypothetical protein
electron transfer flavoprotein subunit alpha
FAD-binding protein
phospholipase D/Transphosphatidylase
PREDICTED: methionine adenosyltransferase 2 subunit beta-like
pyridoxal biosynthesis protein
MULTISPECIES: hypothetical protein
hypothetical protein
patatin
DNA-3-methyladenine glycosylase
ferritin
threonine synthase
hypothetical protein
6-O-methylguanine-DNA methyltransferase
hypothetical protein
hypothetical protein
NADH dehydrogenase
hypothetical protein ACD_77C00487G0002
ferredoxin
HAD family hydrolase
metal-dependent hydrolase
DNA polymerase III subunit alpha
hypothetical protein
(2Fe-2S)-binding protein
aldehyde oxidase
LacI family transcription regulator
MFS transporter
myo-inositol 2-dehydrogenase
hypothetical protein
hypothetical protein
hypothetical protein
xylose isomerase
oxidoreductase
5-deoxyglucuronate isomerase
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase
inosose dehydratase
glyceraldehyde-3-phosphate dehydrogenase
peptidase M23
diphosphate--fructose-6-phosphate 1-phosphotransferase

cell envelope biogenesis protein LolA
hypothetical protein
hypothetical protein
30S ribosomal protein S13
ATPase AAA
hypothetical protein
hypothetical protein
glycogen synthase
UDP-phosphate N-acetylglucosaminyl 1-phosphate transferase
glycine dehydrogenase subunit 2
glycine dehydrogenase subunit 1
glycine cleavage system protein H
glycine cleavage system T protein
hypothetical protein
calcineurin, partial
hypothetical protein
hypothetical protein
ornithine decarboxylase
long-chain fatty acid--CoA ligase
valyl-tRNA synthetase
hypothetical protein
deoxyribose-phosphate aldolase
membrane protein
phosphate ABC transporter substrate-binding protein
hypothetical protein
phosphate transport system permease protein PstA
heme ABC transporter ATP-binding protein
ABC transporter
branched-chain amino acid ABC transporter permease
amylosucrase
diguanylate cyclase
cyclic nucleotide-binding protein
hypothetical protein
hypothetical protein
alanine racemase
Putative dihydropyrimidine dehydrogenase
threonyl-tRNA synthetase
ATP-dependent Clp protease ClpS
ATP-dependent Clp protease ATP-binding protein
hypothetical protein
Fe-S oxidoreductase
2-hydroxyacid dehydrogenase
ankyrin
RNA polymerase sigma70 factor
hypothetical protein
hypothetical protein
outer membrane protein assembly complex, YaeT protein

DNA mismatch repair protein MutS
hypothetical protein
hypothetical protein
transcription termination factor NusA
translation initiation factor IF-2
ribosome-binding factor A
tRNA pseudouridine synthase B
putative riboflavin biosynthesis protein
MULTISPECIES: 30S ribosomal protein S15
polynucleotide phosphorylase
zinc protease
deoxyuridine 5'-triphosphate nucleotidohydrolase
hypothetical protein
hypothetical protein
queuine tRNA-ribosyltransferase
transcription elongation factor GreA
hypothetical protein
ribulose-phosphate 3-epimerase
hypothetical protein
hypothetical protein
D-tyrosyl-tRNA(Tyr) deacylase
Pyruvate, phosphate dikinase
hypothetical protein
hypothetical protein
methionyl-tRNA synthetase
peptidoglycan bridge formation protein FemAB
peptidase S1
excinuclease ABC subunit B
peptidase
shikimate kinase
sulfate-transporting ATPase
ABC transporter permease
thiamine-binding periplasmic protein
ATP-dependent protease
Clp protease proteolytic subunit ClpP
trigger factor
radical SAM protein
inorganic pyrophosphatase
polyprenyl synthetase
RNA polymerase sigma factor rpoD
SEC-C motif domain-containing protein
glycogen debranching protein GlgX
3-oxoacyl-ACP synthase
3-ketoacyl-ACP reductase
malonyl CoA-ACP transacylase
GCN5-like N-acetyltransferase
PHP domain-containing protein

peptidyl-tRNA hydrolase
GTPase Era
3-dehydroquinate dehydratase
DbpA RNA-binding domain-containing protein
beta-lactamase
thiamine biosynthesis lipoprotein ApbE
phosphoesterase PA-phosphatase-like protein
hypothetical protein
flavin reductase
membrane protein
aminotransferase class I and II
endoribonuclease L-PSP
glutamine amidotransferase
membrane protein
enolase
hypothetical protein
chromosome partitioning protein ParB
ParA family ATPase
nitrogen-fixing protein NifU
transcriptional regulator
5-keto-4-deoxyuronate isomerase
2-deoxy-D-gluconate 3-dehydrogenase
hypothetical protein
2-dehydro-3-deoxyphosphogluconate aldolase, partial
2-dehydro-3-deoxygluconokinase
HAD hydrolase, family IA
phosphoribosylpyrophosphate synthetase
hypothetical protein
hypothetical protein
AMP-dependent synthetase
peptidase M20
hypothetical protein
hypothetical protein
hypothetical protein
ferredoxin
MULTISPECIES: putative anti-sigma regulatory factor, serine/threonine protein kinase
hypothetical protein
recombinase RecR
hypothetical protein
DNA polymerase III subunit gamma/tau
radical SAM protein
hypothetical protein
tRNA-dihydrouridine synthase
TatD family hydrolase
ABC transporter
organic solvent tolerance protein OstA
hypothetical protein

CTP synthase
16S rRNA methyltransferase
hypothetical protein
tRNA modification GTPase MnmE
tRNA uridine 5-carboxymethylaminomethyl modification protein
hypothetical protein
CDP-alcohol phosphatidyltransferase
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
acetolactate synthase
transferase
acetolactate synthase
osmotically inducible protein C
elongation factor G 2
hypothetical protein
hypothetical protein, partial
6-phosphogluconolactonase
glucose-6-phosphate dehydrogenase
putative N6-adenine-specific DNA methylase
iron-containing alcohol dehydrogenase
hypothetical protein HMPREF9194_00537
haloacid dehalogenase
hypothetical protein
glycerol-3-phosphate O-acyltransferase
glpG protein
hypothetical protein, partial
protein-export membrane protein SecF
preprotein translocase subunit SecD
preprotein translocase subunit YajC
carbamate kinase
4-hydroxy-3-methylbut-2-enyl diphosphate reductase
nitroreductase
uridine/cytidine kinase
peptide-methionine (S)-S-oxide reductase
ABC transporter permease
ABC transporter permease
ABC transporter
membrane protein
arginosuccinate synthase
integral membrane transport protein
diacylglycerol kinase
histidine kinase
hypothetical protein
phosphohydrolase
hypothetical protein
ArsR family transcriptional regulator
phosphate uptake regulator PhoU
phosphate ABC transporter ATP-binding protein

dihydroorotate dehydrogenase
2-polyprenylphenol 6-hydroxylase
hypothetical protein
hypothetical protein
DNA repair protein RadA
excisionase family DNA binding domain-containing protein
hypothetical protein
pfkB domain protein
hypothetical protein
lipid hydroperoxide peroxidase
acyl-ACP thioesterase
hypothetical protein
nucleotidyltransferase
MFS transporter
phosphatidate cytidylyltransferase
hypothetical protein
prolyl-tRNA synthetase
RNA polymerase sigma factor RpoE
hypothetical protein
glycoside hydrolase family 13
RNA polymerase
hypothetical protein
diguanylate cyclase
peptidase M16C associated domain protein
peptidase M16 domain-containing protein
peptidase M16 domain-containing protein
phosphoribosyltransferase
Fur family transcriptional regulator
FeoA family protein
iron transporter
hypothetical protein
5'-nucleotidase
heat shock protein Hsp20
MULTISPECIES: molybdopterin oxidoreductase
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
FAD-dependent oxidoreductase
alpha-glucan phosphorylase
hypothetical protein
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
heptaprenyl diphosphate synthase
zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase)
acylphosphatase
FAD-dependent pyridine nucleotide-disulfide oxidoreductase
heavy metal translocating P-type ATPase
heavy metal translocating P-type ATPase
UDP-N-acetylglucosamine 1-carboxyvinyltransferase
phage-shock protein

hypothetical protein
anti-sigma F factor antagonist
short-chain dehydrogenase/reductase SDR
Fis family transcriptional regulator
glycosyltransferase WecB/TagA/CpsF family protein
hypothetical protein
peptidase S41
diacylglyceryl transferase
NAD+ synthetase
glycerophosphodiester phosphodiesterase
conserved hypothetical protein
transposase, IS116/IS110/IS902 family
hypothetical protein, partial
hypothetical protein
hypothetical protein
VRR-NUC domain-containing protein
VRR-NUC domain-containing protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
DNA-binding protein
nuclease SbcCD subunit C
hypothetical protein
phage integrase family protein
hypothetical protein
phage-related conserved hypothetical protein
transposase
DNA methyltransferase
hypothetical protein
hypothetical protein
hypothetical protein
indolepyruvate oxidoreductase
thiamine pyrophosphate-binding protein
glutamine synthetase
Gamma-glutamyltranspeptidase
hypothetical protein
hypothetical protein
succinylglutamate desuccinylase
cation-transporting ATPase
NADP-dependent aryl-alcohol dehydrogenase
nuclease SbcCD subunit D
nuclease SbcCD subunit C
nuclease SbcCD subunit C
alcohol dehydrogenase
Cl- channel voltage-gated family protein
ABC transporter substrate-binding protein
ABC transporter

peptide ABC transporter permease
oligopeptide ABC transporter, ATP-binding protein OppD
peptide ABC transporter ATP-binding protein
diguanylate cyclase
cation:proton antiporter
hypothetical protein
cation:proton antiporter
hypothetical protein
cation:proton antiporter
cation:proton antiporter
hypothetical protein
hypothetical protein
NADH dehydrogenase
NADH dehydrogenase subunit B
NADH dehydrogenase
NADH-quinone oxidoreductase subunit D
oxidoreductase
cell division protein MraZ
16S rRNA methyltransferase
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
phospho-N-acetylmuramoyl-pentapeptide-transferase
putative cell division protein FtsW
polypeptide-transport-associated domain-containing protein FtsQ-type
cell division protein FtsA
cell division protein FtsZ
recombinase XerD
DNA-binding protein, partial
DNA topoisomerase I
tyrosine recombinase XerC
peptidase
ATP-dependent protease
RNA polymerase sigma70
acetoacetate metabolism regulatory protein AtoC
histidine kinase
DNA polymerase III subunit gamma/tau
hypothetical protein
UDP-diphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase
glucose-6-phosphate isomerase
hypothetical protein, partial
endonuclease III
ornithine carbamoyltransferase
phosphoesterase
hypothetical protein
purine NTP phosphatase
ribosomal protein L31
transcription termination factor Rho
hypothetical protein

DNA-binding protein
30S ribosomal protein S20
acyltransferase
hypothetical protein
phosphoribosylformylglycinamidine synthase II
phosphoribosylformylglycinamidine synthase
phosphoribosylaminoimidazole-succinocarboxamide synthase
phosphoribosylaminoimidazole carboxylase, catalytic subunit
amidophosphoribosyltransferase
hypothetical protein BATDEDRAFT_17938
phosphoribosylglycinamide formyltransferase
phosphoribosylaminoimidazolecarboxamide formyltransferase
inosine 5'-monophosphate dehydrogenase
UbiA prenyltransferase
molybdenum-binding protein
molybdopterin-binding protein
molybdenum cofactor biosynthesis protein C
molybdenum cofactor biosynthesis family protein
molybdenum cofactor biosynthesis protein
molybdate ABC transporter substrate-binding protein
molybdate ABC transporter, permease
ABC transporter
GCN5 family acetyltransferase
L-erythro-3,5-diaminohexanoate dehydrogenase
transposase
ABC transporter substrate-binding protein
ABC transporter permease
sugar ABC transporter permease
transporter
adenylate/guanylate cyclase
exoribonuclease II
hypothetical protein
50S ribosomal protein L13
30S ribosomal protein S9
PTS fructose transporter subunit IIA
chromosome segregation protein SMC
threonyl-tRNA synthetase
thymidine kinase
ABC transporter substrate-binding protein
hypothetical protein
peptide chain release factor 2
aldose 1-epimerase
17-beta-hydroxysteroid dehydrogenase
cytidylate kinase
hypothetical protein
UDP-N-acetylmuramate--alanine ligase
alpha-amlyase

acid phosphatase
RluA family pseudouridine synthase
membrane protease HflK
membane protease HflC
MULTISPECIES: hypothetical protein
hypothetical protein
ABC transporter permease
ABC transporter permease
ABC transporter ATP-binding protein
membrane protein
purine nucleoside phosphorylase
tyrosyl-tRNA synthetase
DNA-binding protein
glycyl-tRNA synthetase subunit beta
glutaminyl-tRNA synthetase
glutamyl-tRNA synthetase
histidine triad (HIT) protein
thiamine diphosphokinase
polynucleotide adenylyltransferase
ribonuclease III
acyl carrier protein
pantetheine-phosphate adenylyltransferase
Apolipoprotein N-acyltransferase
radical SAM domain protein
hypothetical protein
glycoside hydrolase
radical SAM protein
hypothetical protein
hypothetical protein
hypothetical protein
integrase
hypothetical protein
hypothetical protein
ABC transporter
hypothetical protein
hypothetical protein DC28_09285
fibronectin-binding protein
preprotein translocase subunit SecA
hypothetical protein
hypothetical protein
CTP pyrophosphohydrolase
exodeoxyribonuclease VII
exodeoxyribonuclease VII large subunit
DEAD/DEAH box helicase
tRNA (guanine-N7)-methyltransferase
tRNA (guanine-N(7)-)-methyltransferase
histidyl-tRNA synthetase

hypothetical protein
membrane protein
MULTISPECIES: hypothetical protein
hypothetical protein JCM21142_52162
RNA helicase, partial
hypothetical protein
2-dehydro-3-deoxy-6-phosphogalactonate aldolase
2-dehydro-3-deoxy-6-phosphogalactonate aldolase
2-dehydro-3-deoxy-6-phosphogalactonate aldolase
2-hydroxyacid dehydrogenase
hypothetical protein
hypothetical protein
sialic acid-binding protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
2-dehydro-3-deoxyphosphogluconate aldolase, partial
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein ING2E5B_1356
polysaccharide biosynthesis protein GtrA
phospholipid/glycerol acyltransferase
site-specific recombinase, phage integrase family
alcohol dehydrogenase
RNase III inhibitor
histidine kinase
Tex-like protein
prevent-host-death protein
DNA-binding protein
hypothetical protein
metal-dependent hydrolase, beta-lactamase superfamily
hypothetical protein
acyltransferase
glycosyl transferase family 2
hypothetical protein
hypothetical protein
dTMP kinase
S-adenosylmethionine tRNA ribosyltransferase
Holliday junction DNA helicase RuvB
ATP-dependent DNA helicase RuvA
crossover junction endodeoxyribonuclease RuvC
transcriptional regulator
3-oxoacyl-
hypothetical protein
hypothetical protein

Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein
High-affinity branched-chain amino acid transport system permease protein LivH
ABC transporter permease
Branched-chain amino acid transport ATP-binding protein LivG
leucine/isoleucine/valine transporter ATP-binding subunit
Putative hydrolase
hypothetical protein, partial
hypothetical protein
MFS transporter
hypothetical protein
SufBD protein
ABC transporter ATP-binding protein
hypothetical protein U27_03640
hypothetical protein U27_03639
dinitrogenase iron-molybdenum cofactor biosynthesis protein
hypothetical protein
4Fe-4S ferredoxin
threonine aldolase
flavin reductase domain protein FMN-binding
hypothetical protein
CrcB-like protein
multidrug ABC transporter ATP-binding protein
ABC transporter related
regulatory protein MarR
AraC family transcriptional regulator
D-xylulokinase
xylose isomerase
multiple sugar-binding periplasmic protein SbpA
ABC transporter ATP-binding protein
ABC transporter permease
oxidoreductase domain protein
MFS transporter
hypothetical protein
DNA mismatch repair protein MutS domain-containing protein
DNA mismatch repair protein MutS domain-containing protein
DNA mismatch repair protein MutS
DNA mismatch repair protein MutS
glutamate-1-semialdehyde 2,1-aminomutase
hypothetical protein
DEAD/DEAH box helicase
6-pyruvoyl-tetrahydropterin synthase
UDP-N-acetylmuramyl peptide synthase
D-alanine--D-alanine ligase
ornithine--oxo-acid aminotransferase
hypothetical protein
Sporulation domain-containing protein
(dimethylallyl)adenosine tRNA methylthiotransferase

GTP cyclohydrolase
bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydr
aminotransferase
CoA-disulfide reductase
Rhodanese-like protein
spermidine/putrescine ABC transporter substrate-binding protein
spermidine/putrescine ABC transporter permease
spermidine/putrescine ABC transporter permease
spermidine/putrescine ABC transporter ATP-binding protein
hypothetical protein
preprotein translocase subunit TatC
hypothetical protein
molybdopterin-guanine dinucleotide biosynthesis protein MobA
xanthine phosphoribosyltransferase
REX family transcriptional regulator
AsnC family transcriptional regulator
Orotidine 5'-phosphate decarboxylase
hypothetical protein
hypothetical protein
metallophosphoesterase
transcriptional regulator
iron ABC transporter
hypothetical protein
adenosine monophosphate-protein transferase
dehydrogenase
glycerol kinase
antitoxin
toxin YoeB
sugar phosphate permease, partial
GlcNAc-PI de-N-acetylase
CMP deaminase
rRNA methyltransferase
pyruvate kinase
hypothetical protein
oxidoreductase
electron transport complex RsxE subunit
NADH:ubiquinone oxidoreductase
FMN-binding domain-containing protein
NQR2 and RnfD family protein
Fur family transcriptional regulator
membrane protein
sulfate ABC transporter ATPase
metal ABC transporter substrate-binding protein
rubrerythrin
aldehyde oxidase
XshC-Cox1-family protein
hypothetical protein, partial

hypothetical protein
amino acid ABC transporter ATPase
hypothetical protein
ABC transporter permease
ABC transporter permease
ABC transporter substrate-binding protein
ABC transporter permease
ABC-type uncharacterized transport system, permease component
mannose-6-phosphate isomerase
ATP-dependent DNA helicase DinG
ROK family protein
exodeoxyribonuclease III
hypothetical protein
2-amino-3-ketobutyrate CoA ligase
hypothetical protein
hypothetical protein
oxidase
cupin
aspartate racemase
amino acid transporter
tagatose-6-phosphate kinase
argininosuccinate synthase
argininosuccinate lyase
butanol dehydrogenase
hypothetical protein
hypothetical protein
hypothetical protein
Pleiotropic regulatory protein
hypothetical protein
UDP-N-acetyl-D-glucosamine dehydrogenase
group 1 glycosyl transferase
UDP-N-acetylglucosamine 2-epimerase
hypothetical protein
hypothetical protein
MULTISPECIES: epimerase
UDP-glucose 4-epimerase
capsular polysaccharide biosynthesis protein Cap8F
UDP-N-acetylglucosamine 2-epimerase
Putative Glycosyl transferase group 1
transposase, partial
hypothetical protein, partial
dTDP-glucose 4,6-dehydratase
hypothetical protein
hypothetical protein
ABC transporter ATP-binding protein
putative lipoprotein
phosphatase GppA

polyphosphate kinase
HAD family hydrolase
alpha amylase catalytic region
hypothetical protein
methionine ABC transporter substrate-binding protein
ABC transporter, permease protein
ABC transporter, ATP-binding protein
positive regulator of sigma(E) RseC/MucC
metallophosphoesterase
cell division protein DedD
peptidylprolyl isomerase
virulence associated protein
MULTISPECIES: hypothetical protein
type VI secretion protein
hypothetical protein
hypothetical protein
DNA (cytosine-5-)-methyltransferase
Diaminopimelate decarboxylase
hypothetical protein
hypothetical protein
magnesium-transporting ATPase
putative PTS IIA-like nitrogen-regulatory protein PtsN
GTP-binding protein
NrdR family transcriptional regulator
MULTISPECIES: hypothetical protein
hypothetical protein
HAD-superfamily hydrolase
phosphomannomutase
DNA polymerase III subunit epsilon family exonuclease
peptidase M23B
Glucokinase
UDP-glucose pyrophosphorylase
molybdopterin oxidoreductase
Lon protease
hypothetical protein
3-oxoacyl-
acetyl-CoA hydrolase
hypothetical protein
PadR family transcriptional regulator
hydrolase, TatD family
hypothetical protein
aminotransferase class I and II
amidohydrolase
hypothetical protein TKV_c21380
hypothetical protein
hypothetical protein
metal dependent phosphohydrolase

Xaa-Pro aminopeptidase
XRE family transcriptional regulator
hypothetical protein
sugar ABC transporter substrate-binding protein
L-ribulose-5-phosphate 4-epimerase
arabinose isomerase
ribulokinase
D-ribose transporter ATP binding protein
sugar ABC transporter permease
LacI family transcriptional regulator
hypothetical protein
hypothetical protein
glycosyl transferase, family 2
acetyltransferase
hypothetical protein, partial
aminotransferase
dTDP-6-deoxy-3,4-keto-hexulose isomerase
bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransfera
hypothetical protein
pyruvate dehydrogenase
glucose-1-phosphate thymidylyltransferase
hypothetical protein
sensor histidine kinase
hypothetical protein ACD_60C00090G0011
DNA topoisomerase IV subunit B
DNA topoisomerase IV subunit A
aminopeptidase
hypothetical protein
glycosyl transferase
diguanylate cyclase (GGDEF) domain-containing protein
diguanylate cyclase (GGDEF) domain-containing protein
carbon starvation protein CstA
hypothetical protein
arsenic ABC transporter ATPase
hypothetical protein
hypothetical protein
chemotaxis protein CheW
chemotaxis protein CheR
MULTISPECIES: chemotaxis protein CheW
hypothetical protein, partial
hypothetical protein ACD_39C01749G0002
hypothetical protein ACD_39C00407G0002
response regulator receiver modulated diguanylate cyclase
AMP-dependent synthetase and ligase
V-type ATP synthase subunit B
ATPase
universal stress protein

peptidase S41
inosine-5-monophosphate dehydrogenase
AMP-binding protein
TatD family hydrolase
hypothetical protein ACD_77C00504G0006
hypothetical protein
fructose-bisphosphate aldolase
translation initiation factor IF-3
50S ribosomal protein L35
50S ribosomal protein L20
hypothetical protein
DNA-directed RNA polymerase subunit omega
tRNA dimethylallyltransferase
ligand-binding protein SH3
ATPase AAA
SAM-dependent methlyltransferase
phosphohydrolase
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
P22 coat protein
hypothetical protein SXAG_00158
tail protein
hypothetical protein
hypothetical protein
hypothetical protein
primosomal protein N'
acetate kinase
hypothetical protein
PTS sugar transporter subunit IIA
50S rRNA methyltransferase
heat shock protein Hsp90
peptidase M23
hypothetical protein
hypothetical protein
cytochrome C biogenesis protein
hypothetical protein
split soret cytochrome c precursor
aspartyl-tRNA synthetase
thiol peroxidase
GntR domain protein
C4-dicarboxylate ABC transporter substrate-binding protein
C4-dicarboxylate ABC transporter permease
C4-dicarboxylate ABC transporter permease
dihydroxy-acid dehydratase
dehydrogenase

histidinol phosphatase
short-chain dehydrogenase
carbohydrate kinase
L-sorbose 1-phosphate reductase
MFS transporter
ABC transporter permease
xylose ABC transporter ATP-binding protein
sugar ABC transporter substrate-binding protein
periplasmic binding protein/LacI transcriptional regulator
AraC family transcriptional regulator
signal transduction histidine kinase, LytS
hypothetical protein
glutamine amidotransferase
2-dehydropantoate 2-reductase
GTP-binding proten HflX
aminotransferase class I/II
diguanylate cyclase
RluA family pseudouridine synthase
molecular chaperone GroEL
ABC transporter
ABC transporter
hypothetical protein
beta-N-acetylhexosaminidase
beta-glucosidase
ABC transporter permease
ABC transporter permease
ABC transporter substrate-binding protein
ROK family protein
beta-mannosidase
multidrug transporter MatE
thioredoxin
hypothetical protein
carbohydrate degradation protein
transketolase
ribose 5-phosphate isomerase B
aldehyde dehydrogenase
succinate--CoA ligase
succinyl-CoA synthetase subunit alpha
MULTISPECIES: anion:sodium symporter
integron integrase
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein
hypothetical protein
hypothetical protein

hypothetical protein
L-erythro-3,5-diaminohexanoate dehydrogenase
glutamate-1-semialdehyde 2,1-aminomutase
3-keto-5-aminohexanoate cleavage protein
lysine 2,3-aminomutase
hypothetical protein
hypothetical protein
dioxygenase
dioxygenase
sodium:proton antiporter
Butyrate-acetoacetate CoA-transferase subunit A
succinyl-CoA:3-ketoacid-CoA transferase
SUF system FeS assembly protein, NifU family
cysteine desulfurase, SufS subfamily
SufBD protein
Fe-S cluster assembly protein SufB
iron ABC transporter ATP-binding protein
hypothetical protein
NAD(P)H dehydrogenase (quinone)
peptidase T
ABC transporter permease
hypothetical protein
chromate transporter
chromate transporter
3-oxoacyl-ACP synthase
3-oxoacyl-ACP synthase
3-hydroxyacyl-ACP dehydratase
trans-2-enoyl-CoA reductase
16S rRNA methyltransferase
oligoendopeptidase F
LacI family transcriptional regulator
uridine kinase
peptide ABC transporter ATP-binding protein
peptide ABC transporter ATP-binding protein
MULTISPECIES: peptide ABC transporter permease
MULTISPECIES: ABC transporter permease
MULTISPECIES: ABC transporter substrate-binding protein
nitrilase
malate dehydrogenase
sugar ABC transporter ATP-binding protein
MFS transporter
galactokinase, partial
carbonic anhydrases/acetyltransferases isoleucine patch superfamily
ABC transporter
iron ABC transporter substrate-binding protein
LuxR family transcriptional regulator
hypothetical protein U27_03227

radical SAM protein
metallophosphoesterase
sucrose phosphorylase
hypothetical protein ACD_38C00012G0010
hypothetical protein
ABC transporter permease
sugar ABC transporter permease
sugar ABC transporter substrate-binding protein
hypothetical protein
hypothetical protein
5'-nucleotidase
hypothetical protein
ABC transporter, ATP-binding protein
ABC transporter permease
ABC transporter substrate-binding protein
hypothetical protein
glycerol-3-phosphate acyltransferase
PIN domain protein
putative two-component system hybrid sensor and regulator
response regulator receiver protein
response regulator receiver protein
lactate utilization protein C
HAD-superfamily hydrolase
hydroxylamine reductase
MULTISPECIES: transcriptional regulator
DNA polymerase III subunit alpha
transposase
transposase
DEAD/DEAH box helicase
restriciton endonuclease subunit S
type I restriction endonuclease
MULTISPECIES: transcriptional regulator
endoribonuclease L-PSP
hypothetical protein
sodium:proton antiporter
D-cysteine desulfhydrase family pyridoxal phosphate-dependent enzyme
aspartate racemase
hypothetical protein
hypothetical protein, partial
conserved domain protein
integrase
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
glutaconyl-CoA decarboxylase subunit beta
beta-lactamase
hypothetical protein JO41_04670
hypothetical protein
hypothetical protein

hypothetical protein
DNA repair protein RadA
conserved domain protein
integrase
hypothetical protein
biopolymer transporter ExbD
flagellar motor protein MotA
adenylosuccinate lyase
single-stranded DNA-binding protein
hypothetical protein
peptidase U32
elongation factor G
hypothetical protein
hypothetical protein
hypothetical protein
ABC transporter
MULTISPECIES: hypothetical protein
GTP-binding protein YchF
hypothetical protein
excinuclease ABC subunit A
excinuclease ABC subunit A
hypothetical protein
phosphate starvation protein PhoH
phosphohydrolase
phosphohydrolase
16S rRNA maturation RNase YbeY
hypothetical protein
2-oxoacid ferredoxin oxidoreductase subunit beta
2-oxoglutarate oxidoreductase, alpha subunit
MULTISPECIES: ferredoxin
carboxylase
hypothetical protein
hypothetical protein
glutamate racemase
membrane protein
esterase
TetR family transcriptional regulator
YbaK/prolyl-tRNA synthetase associated protein
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein, partial
hypothetical protein
hypothetical protein
kinase domain protein
prevent-host-death protein
plasmid stabilization protein
hypothetical protein

ABC transporter substrate binding protein (Ribose)
monosaccharide-transporting ATPase
inner-membrane translocator
hypothetical protein
integral membrane sensor signal transduction histidine kinase
two component, sigma54 specific, transcriptional regulator, Fis family
carbohydrate kinase
mannitol-1-phosphate/altronate dehydrogenases
twitching motility protein PilT
hypothetical protein
alanyl-tRNA synthetase
hypothetical protein, partial
hypothetical protein DC28_12495
hypothetical protein DC28_12490
asparaginase
lytic transglycosylase, partial
TetR family transcriptional regulator
alpha-amylase
hypothetical protein
ATP-dependent exonuclase V beta subunit, helicase and exonuclease domain-containing
XRE family transcriptional regulator
DNA polymerase III subunit delta
conjugal transfer protein TraB
Inorganic diphosphatase
alpha galactosidase
FAD-dependent thymidylate synthase
putative PAS/PAC sensor protein
MULTISPECIES: oxidoreductase
gamma-glutamyl phosphate reductase
glutamate 5-kinase
ABC transporter substrate-binding protein
iron ABC transporter
3-dehydroquinate synthase
chorismate synthase
prephenate dehydratase
prephenate dehydratase
hypothetical protein
hypothetical protein
signal recognition particle protein
hydrolase
penicillin-binding protein
signal peptidase
hypothetical protein
RNA polymerase sigma70 factor
polysaccharide deacetylase family protein
tRNA threonylcarbamoyladenosine modification protein TsaD
peptidase M17

lysyl-tRNA synthetase
peptidase M3
hypothetical protein
hypothetical protein
alpha/beta hydrolase
adenylate kinase
transposase
transposase
DNA replication protein
transposase
transposase
transposase
MULTISPECIES: ArsR family transcriptional regulator
Cadmium, zinc and cobalt-transporting ATPase
hypothetical protein
hypothetical protein
type VI secretion protein
transcriptional regulator AraC family
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
DNA-cytosine methyltransferase
ABC transporter
sugar ABC transporter permease
LacI family transcriptional regulator
beta-phosphoglucomutase
hypothetical protein
hypothetical protein
transposase
helicase domain-containing protein
ATP-dependent DNA helicase RecG
DNA methylase
SMC domain-containing protein
hypothetical protein
hypothetical protein
restriction endonuclease
hypothetical protein
nucleotidyltransferase
DNA polymerase
hypothetical protein
hypothetical protein
replicative DNA helicase
50S ribosomal protein L9
hypothetical protein
30S ribosomal protein S18
single-stranded DNA-binding protein

30S ribosomal protein S6
hypothetical protein, partial
twitching motility protein PilT
AbrB family transcriptional regulator
type III restriction endonuclease
hypothetical conserved protein
type III restriction system endonuclease
type III restriction system methylase
N-acetyltransferase GCN5
diaminopimelate epimerase
peptidase M20
glutamine amidotransferase
diaminopimelate decarboxylase
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein, partial
hypothetical protein
hypothetical protein
transporter
PTS sucrose transporter subunit IIABC
molecular chaperone GroES
cell division protein FtsH
3-oxoacyl-ACP synthase
heme ABC transporter ATP-binding protein
methylated-DNA--protein-cysteine methyltransferase-related protein
glucosamine-6-phosphate deaminase
n-acetylglucosamine-6-phosphate deacetylase
hypothetical protein
hypothetical protein
deoxyguanosine kinase
glycosyl transferase
hypothetical protein
manganese transporter
hypothetical protein
urocanate hydratase
Thioredoxin
lactate dehydrogenase
hypothetical protein
hypothetical protein Q428_11065
MULTISPECIES: hypothetical protein
sortase B cell surface sorting signal
pseudouridine synthase
tRNA pseudouridine synthase A
4'-phosphopantetheinyl transferase
YbbR family protein
hypothetical protein

dihydropteroate synthase
1-deoxy-D-xylulose-5-phosphate synthase
aminotransferase
hypothetical protein
metallophosphoesterase
ribonuclease
RNA-binding protein
ATPase AAA
hypothetical protein
ornithine carbamoyltransferase
cation transporter
ABC transporter, partial
transport system permease protein

olase

se

Gene ID	Length (aa)	Identity	e-value	Annotation
gene_id_1505	54	85.19	5.00E-22	hypothetical protein
gene_id_1506	286	81.47	3.00E-173	hypothetical protein
gene_id_1507	798	50.88	0	hypothetical protein
gene_id_1508	798	59.15	0	hypothetical protein
gene_id_1509	111	72.97	3.00E-54	hypothetical protein
gene_id_1510	268	40.3	5.00E-46	hypothetical protein
gene_id_1511	273	73.99	3.00E-144	hypothetical protein
gene_id_1512	528	44.51	5.00E-144	Aminopeptidase YwaD
gene_id_1513	274	59.85	3.00E-114	hypothetical protein
gene_id_1514	380	79.47	0	hypothetical protein
gene_id_1515	524	83.02	0	hypothetical protein
gene_id_1516	65	66.15	1.00E-14	hypothetical protein
gene_id_1517	309	73.14	3.00E-154	hypothetical protein
gene_id_1518	517	57.06	0	hypothetical protein
gene_id_1519	224	80.36	3.00E-134	hypothetical protein
gene_id_1520	613	81.57	0	hypothetical protein
gene_id_1521	616	71.43	0	hypothetical protein
gene_id_1522	218	60.09	1.00E-90	hypothetical protein
gene_id_1523	220	68.64	6.00E-110	hypothetical protein
gene_id_1524	801	82.15	0	hypothetical protein
gene_id_1525	94	95.74	9.00E-57	hypothetical protein
gene_id_1526	517	85.69	0	hypothetical protein
gene_id_1527	405	47.65	4.00E-129	hypothetical protein
gene_id_1528	540	64.07	0	glycosyl transferase family 39
gene_id_1529	437	78.95	0	Multidrug resistance protein
gene_id_1530	580	73.28	0	hypothetical protein
gene_id_1531	650	67.85	0	Sensor protein
gene_id_1532	223	61.88	3.00E-67	hypothetical protein
gene_id_1533	394	76.9	0	hypothetical protein
gene_id_1534	398	64.32	0	hypothetical protein
gene_id_1535	207	80.68	6.00E-121	Organic radical activating enzyme
gene_id_1536	708	85.03	0	hypothetical protein
gene_id_1537	531	76.27	0	hypothetical protein
gene_id_1538	175	40	7.00E-31	hypothetical protein
gene_id_1539	406	60.84	1.00E-173	hypothetical protein
gene_id_1540	297	60.61	1.00E-98	uncharacterized protein
gene_id_1542	510	34.71	2.00E-74	hypothetical protein
gene_id_1543	628	73.89	0	hypothetical protein
gene_id_1544	785	61.15	0	hypothetical protein
gene_id_1545	988	75.3	0	hypothetical protein
gene_id_1546	281	83.63	5.00E-171	hypothetical protein
gene_id_1547	259	64.86	5.00E-110	3-hydroxybutyryl-CoA dehydratase
gene_id_1548	220	73.18	3.00E-115	hypothetical protein
gene_id_1549	452	62.61	0	Uroporphyrinogen decarboxylase superfamily
gene_id_1550	280	38.21	5.00E-61	hypothetical protein
gene_id_1551	177	38.42	1.00E-30	methionine synthase

gene_id_1552	380	71.32	0	hypothetical protein
gene_id_1553	340	90.29	0	hypothetical protein
gene_id_1554	216	78.24	4.00E-116	hypothetical protein
gene_id_1555	681	80.76	0	hypothetical protein
gene_id_1556	435	78.16	0	hypothetical protein
gene_id_1557	992	61.39	0	hypothetical protein
gene_id_1558	187	59.89	2.00E-67	hypothetical protein
gene_id_1559	326	58.9	4.00E-122	D-cysteine desulfhydrase
gene_id_1560	541	77.82	0	hypothetical protein
gene_id_1561	175	69.14	9.00E-84	hypothetical protein
gene_id_1562	162	40.12	4.00E-31	hypothetical protein
gene_id_1563	272	50	8.00E-77	hypothetical protein
gene_id_1564	359	72.42	0	hypothetical protein BRDCF_p1087
gene_id_1565	253	79.45	3.00E-147	hypothetical protein
gene_id_1566	356	73.6	0	beta-lactamase
gene_id_1567	420	56.19	6.00E-152	hypothetical protein
gene_id_1568	324	81.48	0	hypothetical protein
gene_id_1569	70	80	1.00E-33	hypothetical protein, partial
gene_id_1570	581	60.41	0	Thymidylate kinase
gene_id_1571	613	74.71	0	hypothetical protein
gene_id_1572	517	37.91	3.00E-93	peptidase M28
gene_id_1573	378	66.93	0	Acyltransferase family protein
gene_id_1574	215	77.21	3.00E-96	hypothetical protein
gene_id_1575	128	85.94	1.00E-77	3-aminobutyryl-CoA ammonia lyase
gene_id_1576	274	89.42	5.00E-180	3-keto-5-aminohexanoate cleavage enzyme
gene_id_1577	346	95.95	0	L-erythro-3,5-diaminohexanoate dehydrogenase
gene_id_1578	344	87.21	0	L-erythro-3,5-diaminohexanoate dehydrogenase
gene_id_1579	415	91.57	0	hypothetical protein
gene_id_1580	344	51.16	1.00E-119	hypothetical protein
gene_id_1581	440	51.82	5.00E-150	hypothetical protein
gene_id_1582	517	80.27	0	d-Lysine 5 6-aminomutase alpha subunit
gene_id_1583	259	87.64	5.00E-158	dioxygenase
gene_id_1584	219	83.11	8.00E-132	hypothetical protein
gene_id_1585	401	80.3	0	hypothetical protein
gene_id_1586	482	74.48	0	hypothetical protein
gene_id_1588	577	80.42	0	hypothetical protein
gene_id_1589	424	76.42	0	hypothetical protein
gene_id_1590	274	50	2.00E-84	formate/nitrite transporter
gene_id_1591	146	73.97	5.00E-65	transcriptional regulator, MarR family
gene_id_1592	370	83.24	0	hypothetical protein
gene_id_1594	1074	85.01	0	carbamoyl phosphate synthase large subunit
gene_id_1595	356	87.36	0	hypothetical protein
gene_id_1596	501	73.45	0	peptidase
gene_id_1597	430	60.23	1.00E-152	hypothetical protein
gene_id_1598	450	70.22	0	hypothetical protein
gene_id_1599	203	54.68	1.00E-74	hypothetical protein
gene_id_1600	589	62.48	0	hypothetical protein

gene_id_1601	764	86.78	0	hypothetical protein
gene_id_1602	469	77.83	0	hypothetical protein
gene_id_1603	275	80.36	3.00E-123	hypothetical protein
gene_id_1604	123	75.61	7.00E-63	Thioesterase family protein
gene_id_1605	391	80.82	0	hypothetical protein
gene_id_1606	672	66.67	0	hypothetical protein
gene_id_1607	410	86.83	0	6-phosphofructokinase
gene_id_1608	551	51.72	0	alpha-amylase
gene_id_1609	37	54.05	9.00E-07	SOS mutagenesis and repair protein UmuC
gene_id_1610	139	49.64	1.00E-41	hypothetical protein
gene_id_1611	143	76.22	1.00E-78	Peptidase S24, S26A and S26B
gene_id_1612	393	65.65	0	hypothetical protein
gene_id_1613	424	71.46	1.00E-171	hypothetical protein
gene_id_1614	235	73.62	1.00E-125	hypothetical protein
gene_id_1615	459	51.85	0	hypothetical protein
gene_id_1616	499	65.53	0	hypothetical protein
gene_id_1617	148	79.05	3.00E-75	hypothetical protein
gene_id_1618	221	52.94	1.00E-80	hypothetical protein
gene_id_1619	924	36.9	1.00E-157	hypothetical protein
gene_id_1619	265	25.66	3.00E-06	hypothetical protein
gene_id_1620	211	54.03	3.00E-75	hypothetical protein
gene_id_1621	450	76.67	0	hypothetical protein
gene_id_1622	429	71.56	0	hypothetical protein
gene_id_1623	325	91.08	0	hypothetical protein
gene_id_1624	363	83.75	0	hypothetical protein
gene_id_1625	632	82.59	0	hypothetical protein
gene_id_1626	410	80	0	hypothetical protein
gene_id_1627	393	76.59	0	hypothetical protein
gene_id_1628	467	71.73	0	hypothetical protein
gene_id_1629	214	48.13	1.00E-63	hypothetical protein
gene_id_1630	470	64.26	0	hypothetical protein
gene_id_1631	742	74.8	0	hypothetical protein
gene_id_1632	467	90.79	0	hypothetical protein
gene_id_1633	242	58.68	3.00E-95	hypothetical protein
gene_id_1634	246	74.8	8.00E-138	hypothetical protein
gene_id_1635	641	70.51	0	ATPase component of ABC transporter with duplicated A
gene_id_1636	256	76.17	3.00E-137	hypothetical protein
gene_id_1637	52	90.38	2.00E-10	hypothetical protein
gene_id_1638	134	67.91	2.00E-61	hypothetical protein
gene_id_1639	795	40.25	0	hypothetical protein
gene_id_1640	883	77.01	0	hypothetical protein
gene_id_1641	102	86.27	2.00E-58	hypothetical protein
gene_id_1642	291	83.51	0	hypothetical protein
gene_id_1643	339	82.01	0	hypothetical protein
gene_id_1644	575	84.52	0	hypothetical protein
gene_id_1645	291	58.42	2.00E-99	hypothetical protein
gene_id_1646	424	71.7	0	hypothetical protein

gene_id_1647	453	64.24	0	hypothetical protein
gene_id_1648	270	61.85	3.00E-116	hypothetical protein
gene_id_1649	176	73.86	5.00E-91	3-deoxy-D-manno-octulosonate 8-phosphate phosphata
gene_id_1650	634	69.4	0	hypothetical protein
gene_id_1651	530	87.74	0	hypothetical protein
gene_id_1652	239	64.85	3.00E-107	hypothetical protein
gene_id_1653	542	85.06	0	hypothetical protein
gene_id_1654	267	71.54	3.00E-138	metallo-beta-lactamase superfamily hydrolase
gene_id_1655	204	67.16	3.00E-95	hypothetical protein
gene_id_1656	351	54.13	6.00E-116	hypothetical protein
gene_id_1657	221	72.85	2.00E-122	class II aldolase/adducin family protein
gene_id_1658	273	80.59	8.00E-160	hypothetical protein
gene_id_1659	417	75.3	0	hypothetical protein
gene_id_1660	53	94.34	1.00E-26	Rubredoxin
gene_id_1661	541	47.13	2.00E-174	hypothetical protein
gene_id_1662	684	71.05	0	hypothetical protein
gene_id_1664	73	94.52	6.00E-42	4Fe-4S ferredoxin
gene_id_1665	359	89.14	0	hypothetical protein
gene_id_1666	252	87.3	5.00E-160	2-oxoglutarate oxidoreductase, beta subunit
gene_id_1667	183	84.7	2.00E-107	hypothetical protein
gene_id_1668	97	79.38	2.00E-44	hypothetical protein
gene_id_1669	96	85.42	1.00E-49	hypothetical protein
gene_id_1670	497	91.75	0	hypothetical protein
gene_id_1671	562	49.64	0	hypothetical protein
gene_id_1672	260	50.77	3.00E-94	hypothetical protein
gene_id_1673	607	61.94	0	hypothetical protein
gene_id_1674	451	62.75	0	hypothetical protein
gene_id_1675	696	68.39	0	hypothetical protein
gene_id_1676	515	79.22	0	hypothetical protein
gene_id_1677	362	77.07	0	hypothetical protein
gene_id_1678	519	86.9	0	hypothetical protein
gene_id_1679	998	85.57	0	hypothetical protein
gene_id_1680	445	79.78	0	hypothetical protein
gene_id_1681	251	70.12	2.00E-118	Response regulator of the LytR/AlgR family
gene_id_1682	344	70.35	4.00E-171	hypothetical protein
gene_id_1683	129	73.64	1.00E-45	hypothetical protein
gene_id_1684	891	58.47	0	hypothetical protein
gene_id_1685	389	74.55	0	hypothetical protein
gene_id_1686	332	75.6	0	Asparaginase family protein
gene_id_1687	207	56.52	3.00E-62	hypothetical protein
gene_id_1688	505	68.91	0	Choline-sulfatase
gene_id_1689	350	64.57	1.00E-172	Anaerobic sulfatase-maturating enzyme
gene_id_1690	415	59.76	2.00E-174	hypothetical protein
gene_id_1691	461	51.41	0	hypothetical protein
gene_id_1692	518	76.64	0	hypothetical protein
gene_id_1693	1108	74.82	0	hypothetical protein
gene_id_1694	665	62.71	0	hypothetical protein

gene_id_1695	481	71.73	0	hypothetical protein
gene_id_1696	521	73.7	0	hypothetical protein
gene_id_1697	253	84.19	7.00E-122	hypothetical protein
gene_id_7175	105	80	3.00E-46	TM2 protein
gene_id_7176	241	81.74	2.00E-145	hypothetical protein
gene_id_7177	442	65.61	0	hypothetical protein
gene_id_7178	297	73.06	2.00E-125	hypothetical protein
gene_id_7179	712	78.09	0	hypothetical protein
gene_id_7180	549	76.87	0	hypothetical protein
gene_id_7181	102	82.35	9.00E-53	hypothetical protein
gene_id_7182	576	69.1	0	hypothetical protein
gene_id_7183	592	79.05	0	hypothetical protein
gene_id_7184	450	89.11	0	hypothetical protein
gene_id_7185	402	62.44	6.00E-148	hypothetical protein
gene_id_7186	701	83.45	0	hypothetical protein
gene_id_7187	286	99.3	0	hypothetical protein
gene_id_7188	478	68.41	0	hypothetical protein
gene_id_7189	375	86.4	0	hypothetical protein
gene_id_7190	256	85.55	7.00E-166	hypothetical protein
gene_id_7191	396	65.15	0	hypothetical protein
gene_id_7192	367	56.95	4.00E-133	hypothetical protein
gene_id_7193	356	76.97	0	hypothetical protein
gene_id_7194	300	87	0	hypothetical protein
gene_id_7195	400	87	0	hypothetical protein
gene_id_7196	499	39.28	3.00E-92	Competence protein
gene_id_7197	277	67.51	2.00E-111	hypothetical protein
gene_id_7198	469	79.96	0	hypothetical protein
gene_id_7199	84	96.43	3.00E-51	hypothetical protein
gene_id_7200	706	70.11	0	hypothetical protein
gene_id_7201	366	73.77	3.00E-132	FAD synthase
gene_id_7202	436	69.27	0	hypothetical protein
gene_id_7203	830	87.95	0	hypothetical protein
gene_id_7204	850	83.29	0	hypothetical protein
gene_id_7205	277	49.46	6.00E-83	hypothetical protein
gene_id_7206	219	62.56	9.00E-81	hypothetical protein, partial
gene_id_7207	338	24.85	7.00E-14	hypothetical protein M082_5968
gene_id_7208	337	31.16	1.00E-24	hypothetical protein M082_5968
gene_id_7209	315	34.29	3.00E-42	hypothetical protein
gene_id_7210	554	69.49	0	hypothetical protein
gene_id_7211	142	80.99	1.00E-57	hypothetical protein
gene_id_7212	56	67.86	5.00E-17	hypothetical protein
gene_id_7213	270	50	3.00E-88	protein involved in gliding motility gldl
gene_id_7214	536	67.54	0	Gliding motility-associated protein GldM
gene_id_7215	159	57.86	3.00E-48	hypothetical protein
gene_id_7216	581	56.97	0	hypothetical protein
gene_id_7217	263	68.44	1.00E-133	hypothetical protein
gene_id_7218	158	72.78	7.00E-74	hypothetical protein

gene_id_7220	185	59.46	4.00E-61	hypothetical protein
gene_id_7221	214	76.64	2.00E-120	two-component response regulator
gene_id_7222	382	78.8	0	hypothetical protein
gene_id_7223	84	38.1	2.00E-10	FMN-binding protein
gene_id_7224	383	51.44	1.00E-116	hypothetical protein
gene_id_7225	199	44.72	4.00E-47	hypothetical protein
gene_id_7226	233	44.64	7.00E-62	hypothetical protein
gene_id_7227	251	63.75	2.00E-120	putative NTE family protein ylbK
gene_id_7228	795	67.55	0	aminoacyl peptidase
gene_id_7229	115	44.35	1.00E-23	hypothetical protein, partial
gene_id_7230	224	50.89	9.00E-68	hypothetical protein
gene_id_7231	499	70.94	0	hypothetical protein
gene_id_7232	480	76.67	0	hypothetical protein
gene_id_7233	1000	58	0	hypothetical protein
gene_id_7234	917	64.23	0	hypothetical protein
gene_id_7235	447	74.72	0	hypothetical protein
gene_id_7236	337	80.42	0	hypothetical protein
gene_id_7237	364	72.53	1.00E-178	hypothetical protein
gene_id_7238	151	81.46	7.00E-85	ribonuclease HI
gene_id_7239	353	71.95	1.00E-172	hypothetical protein
gene_id_7240	702	82.34	0	hypothetical protein
gene_id_7241	278	82.01	5.00E-173	hypothetical protein
gene_id_7242	282	77.66	2.00E-165	hypothetical protein
gene_id_7243	455	79.78	0	hypothetical protein
gene_id_7244	556	81.83	0	hypothetical protein
gene_id_7245	286	61.54	2.00E-121	hypothetical protein
gene_id_7246	290	66.21	9.00E-135	hypothetical protein
gene_id_7247	704	64.35	0	hypothetical protein
gene_id_7248	428	75.23	0	hypothetical protein
gene_id_7249	474	65.19	0	Trk system potassium uptake protein trkH
gene_id_7250	256	79.3	4.00E-133	histidine kinase
gene_id_7251	334	91.32	0	glyceraldehyde-3-phosphate dehydrogenase
gene_id_7252	262	80.15	3.00E-155	stationary phase survival protein SurE
gene_id_7253	546	57.88	0	Lipid-A-disaccharide synthase
gene_id_7254	286	74.48	2.00E-159	hypothetical protein
gene_id_7255	157	72.61	5.00E-78	Phosphopantetheine adenylyltransferase
gene_id_7256	511	44.23	7.00E-145	alkyl hydroperoxide reductase/thiol specific antioxidant/
gene_id_7257	942	73.89	0	hypothetical protein
gene_id_7258	572	65.73	0	hypothetical protein
gene_id_7259	80	56.25	4.00E-23	Apolipoprotein N-acyltransferase
gene_id_7260	72	59.72	7.00E-20	Apolipoprotein N-acyltransferase
gene_id_7261	791	40.83	0	hypothetical protein
gene_id_7262	214	68.69	1.00E-78	hypothetical protein
gene_id_7263	646	53.25	0	hypothetical protein
gene_id_7264	279	75.63	4.00E-156	Esterase
gene_id_7265	273	79.49	5.00E-165	hypothetical protein
gene_id_7266	178	45.51	6.00E-48	hypothetical protein

gene_id_7267	433	66.05	0	hypothetical protein
gene_id_7268	1235	70.53	0	Phosphoribosylformylglycinamidine synthase
gene_id_7269	446	81.84	0	hypothetical protein
gene_id_7270	905	88.95	0	hypothetical protein
gene_id_7271	150	62	1.00E-64	hypothetical protein
gene_id_7272	349	80.23	0	hypothetical protein
gene_id_7273	400	72.25	0	hypothetical protein
gene_id_7275	427	54.1	4.00E-155	hypothetical protein
gene_id_7276	429	62.7	0	hypothetical protein
gene_id_7277	330	85.15	0	hypothetical protein
gene_id_7278	174	63.22	7.00E-72	hypothetical protein
gene_id_7279	599	88.98	0	hypothetical protein
gene_id_7280	509	86.05	0	hypothetical protein
gene_id_7282	624	53.53	0	MULTISPECIES: ligand-gated channel protein
gene_id_7283	249	74.7	2.00E-133	hypothetical protein
gene_id_7284	472	81.14	0	hypothetical protein
gene_id_7285	207	65.7	1.00E-96	endonuclease III, partial
gene_id_7286	245	74.29	1.00E-135	hypothetical protein
gene_id_7287	997	67.1	0	hypothetical protein
gene_id_7288	623	50.56	0	TonB-dependent receptor
gene_id_7289	664	85.39	0	DNA gyrase subunit B
gene_id_7290	268	80.97	6.00E-146	peptidase M23
gene_id_7291	415	88.19	0	hypothetical protein
gene_id_7292	267	79.4	1.00E-148	hypothetical protein
gene_id_7293	309	60.84	2.00E-124	hypothetical protein
gene_id_7294	188	79.79	7.00E-106	hypothetical protein
gene_id_7295	238	59.66	2.00E-95	hypothetical protein
gene_id_7296	491	77.39	0	hypothetical protein
gene_id_7297	387	52.2	2.00E-122	hypothetical protein
gene_id_7298	102	64.71	1.00E-40	hypothetical protein
gene_id_7299	185	27.57	7.00E-09	hypothetical protein COPRO5265_0451
gene_id_7300	162	66.67	1.00E-58	GCN5-related N-acetyltransferase
gene_id_7301	132	56.82	3.00E-34	hypothetical protein
gene_id_7302	145	55.86	3.00E-45	hypothetical protein
gene_id_7303	124	86.29	4.00E-70	50S ribosomal protein L19
gene_id_7304	355	78.31	0	hypothetical protein
gene_id_7305	546	35.9	1.00E-105	hypothetical protein, partial
gene_id_7306	389	82.01	0	hypothetical protein
gene_id_7307	156	70.51	1.00E-72	hypothetical protein
gene_id_7308	269	72.12	2.00E-122	hypothetical protein
gene_id_7309	197	64.97	5.00E-91	hypothetical protein
gene_id_7310	225	85.78	1.00E-134	transcriptional regulator
gene_id_7311	188	82.45	5.00E-101	FAD-dependent pyridine nucleotide-disulfide oxidoreduc
gene_id_7312	85	91.76	7.00E-51	SirA-like protein
gene_id_7313	124	83.06	4.00E-75	hypothetical protein
gene_id_7314	431	87.7	0	hypothetical protein
gene_id_7315	577	76.6	0	4Fe-4S ferredoxin iron-sulfur binding protein

gene_id_7316	96	70.83	1.00E-40	hypothetical protein
gene_id_7317	349	75.93	0	4Fe-4S ferredoxin iron-sulfur binding protein
gene_id_7318	413	82.32	0	hypothetical protein
gene_id_7319	103	80.58	1.00E-55	hypothetical protein
gene_id_7320	167	87.43	9.00E-104	hypothetical protein
gene_id_7321	514	61.87	0	MULTISPECIES: sulfatase
gene_id_7322	491	47.86	5.00E-147	hypothetical protein
gene_id_7323	320	94.06	0	hypothetical protein
gene_id_7324	246	76.42	5.00E-127	hypothetical protein
gene_id_7325	183	67.76	1.00E-88	Guanylate kinase
gene_id_7326	190	55.79	5.00E-62	hypothetical protein
gene_id_7327	232	70.69	2.00E-118	hypothetical protein
gene_id_7328	271	86.72	9.00E-174	hypothetical protein
gene_id_7329	644	90.53	0	hypothetical protein
gene_id_7330	133	93.98	7.00E-65	hypothetical protein
gene_id_7331	448	89.29	0	hypothetical protein
gene_id_7332	308	73.7	1.00E-161	hypothetical protein
gene_id_7333	647	61.21	0	hypothetical protein
gene_id_7334	33	72.73	6.00E-10	hypothetical protein HMPREF1078_00799
gene_id_7334	21	61.9	6.00E-10	hypothetical protein HMPREF1078_00799
gene_id_7335	174	40.23	3.00E-31	hypothetical protein CCAN11_2040022
gene_id_7336	470	42.55	4.00E-118	hypothetical protein SapgrDRAFT_0285
gene_id_7337	1922	72.16	0	DNA helicase
gene_id_7338	169	44.38	1.00E-41	uncharacterized protein BN772_03432
gene_id_7339	277	50.9	5.00E-94	exonuclease
gene_id_7340	164	87.2	3.00E-98	isochorismatase
gene_id_7341	338	32.54	5.00E-51	penicillin-binding protein, beta-lactamase class C
gene_id_7342	161	44.72	2.00E-50	hypothetical protein
gene_id_7343	264	50.76	8.00E-95	hypothetical protein
gene_id_7344	123	69.92	2.00E-58	glyoxalase
gene_id_7345	175	54.86	1.00E-65	hypothetical protein
gene_id_7346	121	57.02	2.00E-31	hypothetical protein
gene_id_7347	171	39.77	1.00E-13	hypothetical protein
gene_id_7348	216	77.78	5.00E-123	hypothetical protein
gene_id_7349	358	64.8	2.00E-157	hypothetical protein IW20_21765
gene_id_7350	206	71.84	2.00E-105	hypothetical protein
gene_id_7352	249	70.68	5.00E-136	methyltransferase type 11
gene_id_7353	136	49.26	3.00E-29	hypothetical protein
gene_id_7354	80	65	6.00E-32	hypothetical protein
gene_id_7355	171	66.67	2.00E-80	hypothetical protein
gene_id_7356	331	46.22	9.00E-94	alpha/beta hydrolase
gene_id_7357	394	48.98	2.00E-131	esterase
gene_id_7358	580	36.21	2.00E-128	phospholipase/Carboxylesterase
gene_id_7359	112	66.96	4.00E-49	hypothetical protein
gene_id_7360	329	72.34	1.00E-180	peptidase S9 prolyl oligopeptidase
gene_id_7361	451	71.18	0	hypothetical protein
gene_id_7362	382	27.23	1.00E-18	Transcriptional Regulator, AraC family protein

gene_id_7363	433	64.2	0	hypothetical protein
gene_id_7364	750	37.73	1.00E-140	RND transporter
gene_id_7365	200	61.5	2.00E-87	hypothetical protein
gene_id_7366	90	35.56	5.00E-08	signal transduction histidine kinase
gene_id_7367	487	81.11	0	hypothetical protein
gene_id_7368	199	52.76	4.00E-62	Amidase
gene_id_7369	304	64.47	1.00E-142	hypothetical protein
gene_id_7370	382	62.83	2.00E-126	hypothetical protein
gene_id_7371	253	92.89	1.00E-175	hypothetical protein
gene_id_7372	701	65.34	0	hypothetical protein
gene_id_7373	322	69.88	8.00E-173	extracellular solute-binding protein
gene_id_7374	413	59.32	6.00E-128	hypothetical protein
gene_id_7375	285	59.3	1.00E-119	hypothetical protein
gene_id_7376	290	86.9	5.00E-176	hypothetical protein
gene_id_7377	132	65.91	2.00E-30	hypothetical protein
gene_id_7378	663	80.39	0	hypothetical protein
gene_id_7379	255	77.65	2.00E-122	monofunctional biosynthetic peptidoglycan transglycosy
gene_id_7380	281	65.84	4.00E-141	aminopeptidase
gene_id_7381	248	66.94	4.00E-118	hypothetical protein
gene_id_7382	935	80.21	0	hypothetical protein
gene_id_7383	715	73.85	0	hypothetical protein
gene_id_7384	665	81.65	0	excinuclease ABC subunit B
gene_id_7385	481	65.28	0	hypothetical protein
gene_id_7386	220	73.18	9.00E-107	hypothetical protein
gene_id_7387	423	91.96	0	hypothetical protein
gene_id_7388	752	63.03	0	hypothetical protein
gene_id_7389	565	76.28	0	hypothetical protein
gene_id_7390	282	65.96	7.00E-113	hypothetical protein
gene_id_7391	827	78.48	0	hypothetical protein
gene_id_7392	317	83.6	3.00E-176	cell division protein FtsY
gene_id_7393	59	49.15	1.00E-07	hypothetical protein
gene_id_7394	53	79.25	2.00E-15	hypothetical protein BRDCF_p774
gene_id_7395	60	98.33	8.00E-34	50S ribosomal protein L33
gene_id_7396	80	93.75	5.00E-46	50S ribosomal protein L28
gene_id_7397	449	82.18	0	hypothetical protein
gene_id_7398	114	96.49	4.00E-63	50S ribosomal protein L20
gene_id_7399	64	87.5	6.00E-31	hypothetical protein
gene_id_7400	124	90.32	4.00E-66	translation initiation factor IF-3
gene_id_7401	644	88.66	0	threonyl-tRNA synthetase
gene_id_7402	167	70.66	2.00E-79	hypothetical protein
gene_id_7403	317	82.33	0	hypothetical protein
gene_id_7404	133	87.97	2.00E-80	hypothetical protein
gene_id_7405	462	82.9	0	hypothetical protein
gene_id_7406	1095	81.92	0	preprotein translocase subunit SecA
gene_id_7407	234	43.59	4.00E-60	SAM-dependent methyltransferase
gene_id_7408	262	64.89	3.00E-122	hypothetical protein
gene_id_7409	536	86.38	0	hypothetical protein

gene_id_7410	242	57.44	7.00E-93	acyl-ACP thioesterase
gene_id_7411	258	59.3	4.00E-103	hypothetical protein
gene_id_7412	154	84.42	2.00E-92	hypothetical protein
gene_id_7413	157	77.07	1.00E-84	GCN5-related N-acetyltransferase
gene_id_7414	102	78.43	3.00E-55	hypothetical protein
gene_id_7415	446	69.96	0	histidyl-tRNA synthetase
gene_id_7416	424	85.14	0	dihydropyrimidine dehydrogenase subunit A
gene_id_7417	291	81.44	2.00E-176	hypothetical protein
gene_id_7418	811	74.11	0	hypothetical protein
gene_id_7419	266	69.55	2.00E-138	hypothetical protein
gene_id_7420	98	59.18	4.00E-34	hypothetical protein
gene_id_7421	747	68.94	0	hypothetical protein
gene_id_7422	141	29.79	6.00E-11	hypothetical protein
gene_id_7423	497	78.07	0	hypothetical protein
gene_id_7424	585	65.64	0	Protease 4
gene_id_7425	453	52.98	2.00E-163	hypothetical protein
gene_id_7426	326	70.25	2.00E-130	hypothetical protein
gene_id_7427	232	86.64	1.00E-134	hypothetical protein
gene_id_7428	491	88.8	0	hypothetical protein
gene_id_7429	116	54.31	3.00E-32	hypothetical protein
gene_id_7430	499	45.89	2.00E-131	hypothetical protein
gene_id_7431	198	59.6	1.00E-74	hypothetical protein
gene_id_7432	260	87.69	5.00E-162	hypothetical protein
gene_id_7433	438	79.45	0	hypothetical protein
gene_id_7434	329	77.2	0	hypothetical protein
gene_id_7435	405	75.8	0	hypothetical protein
gene_id_7436	155	65.81	3.00E-50	hypothetical protein
gene_id_7437	412	92.72	0	hypothetical protein
gene_id_7438	797	82.56	0	hypothetical protein
gene_id_7438	117	82.05	7.00E-42	hypothetical protein
gene_id_7439	328	62.8	6.00E-128	hypothetical protein
gene_id_7440	223	73.54	2.00E-115	Thymidylate kinase
gene_id_7441	263	63.5	2.00E-120	hypothetical protein
gene_id_7442	440	71.82	0	hypothetical protein
gene_id_7443	409	64.06	0	hypothetical protein
gene_id_7444	219	75.8	3.00E-122	hypothetical protein
gene_id_7445	305	78.36	1.00E-178	hypothetical protein
gene_id_7446	281	59.43	8.00E-104	hypothetical protein
gene_id_7447	335	51.34	5.00E-125	hypothetical protein
gene_id_7448	123	59.35	1.00E-52	hypothetical protein
gene_id_7449	187	69.52	5.00E-91	hypothetical protein
gene_id_7450	182	68.68	4.00E-84	hypothetical protein
gene_id_7451	391	54.73	4.00E-129	hypothetical protein
gene_id_7452	220	45.91	1.00E-59	hypothetical protein
gene_id_7453	429	44.06	4.00E-98	hypothetical protein
gene_id_7455	707	69.02	0	hypothetical protein
gene_id_7456	441	41.5	3.00E-112	hypothetical protein

gene_id_7457	405	47.9	3.00E-131	tetratricopeptide TPR_2 repeat protein, partial
gene_id_7458	162	31.48	1.00E-06	hypothetical protein
gene_id_7459	1092	67.12	0	hypothetical protein
gene_id_7463	123	49.59	9.00E-35	hypothetical protein
gene_id_7464	197	68.02	3.00E-93	Regulatory protein, partial
gene_id_7465	413	49.88	1.00E-142	transporter
gene_id_7466	304	58.22	9.00E-121	membrane protein
gene_id_7467	306	68.63	6.00E-153	ATPase
gene_id_7468	239	79.08	1.00E-137	electron transfer flavoprotein, beta subunit
gene_id_7469	372	63.44	8.00E-167	hypothetical protein
gene_id_7470	370	60.81	4.00E-141	ABC transporter permease
gene_id_7471	146	56.16	1.00E-56	hypothetical protein
gene_id_7472	157	64.33	7.00E-72	hypothetical protein
gene_id_7473	195	40.51	2.00E-45	hypothetical protein
gene_id_7474	599	75.63	0	hypothetical protein
gene_id_7475	340	70.59	0	pesticidal protein Cry7Aa
gene_id_7476	117	73.5	2.00E-55	hypothetical protein
gene_id_7477	147	74.83	3.00E-77	hypothetical protein
gene_id_7478	52	61.54	3.00E-10	hypothetical protein
gene_id_7479	647	81.76	0	OmpA/MotB protein
gene_id_7480	791	70.54	0	hypothetical protein
gene_id_7480	548	73.72	0	hypothetical protein
gene_id_7481	247	75.71	1.00E-135	hypothetical protein
gene_id_7482	352	74.72	1.00E-130	hypothetical protein
gene_id_7483	125	52.8	8.00E-33	hypothetical protein
gene_id_7484	113	68.14	6.00E-36	hypothetical protein
gene_id_7485	84	77.38	5.00E-19	hypothetical protein
gene_id_7487	141	63.12	1.00E-61	histidine kinase
gene_id_7488	797	62.99	0	hypothetical protein
gene_id_7488	254	48.03	2.00E-53	hypothetical protein
gene_id_7488	232	46.12	3.00E-43	hypothetical protein
gene_id_7489	174	75.29	1.00E-90	AraC family transcriptional regulator
gene_id_7491	254	77.17	2.00E-140	hypothetical protein
gene_id_7492	424	54.25	2.00E-162	hypothetical protein
gene_id_7493	405	48.64	2.00E-121	hypothetical protein
gene_id_7494	230	83.91	6.00E-141	hypothetical protein
gene_id_7495	384	55.47	3.00E-142	hypothetical protein
gene_id_7496	177	36.72	2.00E-35	hypothetical protein
gene_id_7497	139	60.43	5.00E-42	hypothetical protein
gene_id_7498	131	54.96	3.00E-45	hypothetical protein
gene_id_7499	200	40.5	1.00E-52	hypothetical protein
gene_id_7500	375	44.27	2.00E-96	hypothetical protein JCM15093_870
gene_id_7501	360	66.11	6.00E-162	hypothetical protein
gene_id_7502	254	60.24	2.00E-100	short-chain dehydrogenase/reductase SDR
gene_id_7503	721	46.88	0	hypothetical protein
gene_id_7504	380	53.95	2.00E-128	multi-sensor hybrid histidine kinase
gene_id_7505	496	38.31	2.00E-89	PAS:Response regulator receiver:ATP-binding region, AT

gene_id_7506	334	87.13	0	hypothetical protein
gene_id_7507	289	84.08	0	band 7/Mec-2 family protein
gene_id_7509	262	77.1	2.00E-149	hypothetical protein
gene_id_7510	859	59.84	0	hypothetical protein
gene_id_7511	193	48.7	3.00E-51	rubrerythrin
gene_id_7512	486	71.81	0	hypothetical protein
gene_id_7513	236	55.51	2.00E-90	hypothetical protein
gene_id_7514	283	51.94	1.00E-98	hypothetical protein
gene_id_7515	114	47.37	3.00E-22	hypothetical protein
gene_id_7516	425	75.76	0	glycosyl hydrolase family 109
gene_id_7517	282	51.42	3.00E-94	Acid phosphatase
gene_id_7518	529	62.57	0	peptidase U62, modulator of DNA gyrase
gene_id_7519	539	79.96	0	hypothetical protein
gene_id_7522	135	37.78	1.00E-13	hypothetical protein
gene_id_7523	95	63.16	8.00E-32	HipA protein
gene_id_7525	125	50.4	2.00E-34	Hypothetical protein CAP_4415
gene_id_7526	274	24.45	7.00E-10	hypothetical protein
gene_id_7527	211	73.46	2.00E-83	ion transporter
gene_id_7528	122	72.95	2.00E-59	uncharacterized protein
gene_id_7529	667	72.86	0	hypothetical protein
gene_id_7531	447	83.45	0	transporter
gene_id_7532	122	58.2	1.00E-33	hypothetical protein
gene_id_7533	176	76.7	1.00E-83	hypothetical protein
gene_id_7534	434	58.76	0	hypothetical protein
gene_id_7535	533	82.55	0	hypothetical protein
gene_id_7536	534	79.96	0	hypothetical protein
gene_id_7537	598	69.73	0	hypothetical protein
gene_id_7538	161	59.63	4.00E-57	hypothetical protein
gene_id_7539	332	84.34	7.00E-178	hypothetical protein
gene_id_7540	327	81.35	0	aerotolerance regulator BatA
gene_id_7541	278	65.11	1.00E-110	hypothetical protein
gene_id_7542	292	86.3	5.00E-179	hypothetical protein
gene_id_7543	330	89.39	0	ATPase AAA
gene_id_7544	264	71.21	4.00E-140	hypothetical protein
gene_id_7545	118	66.95	2.00E-49	hypothetical protein
gene_id_7546	104	69.23	9.00E-36	lysine exporter protein (LysE/YggA)
gene_id_7548	152	51.32	7.00E-37	hypothetical protein
gene_id_7549	59	76.27	5.00E-26	hypothetical protein
gene_id_7550	188	50.53	9.00E-54	hypothetical protein
gene_id_7551	261	54.41	9.00E-67	hypothetical protein
gene_id_7552	388	52.84	2.00E-87	sodium:proton antiporter
gene_id_7553	273	63	1.00E-130	dioxygenase
gene_id_7554	57	68.42	7.00E-18	nitrite reductase
gene_id_7555	118	80.51	1.00E-69	oxidoreductase DsrE
gene_id_7556	121	41.32	1.00E-22	hypothetical protein, partial
gene_id_7557	191	68.06	2.00E-93	NADPH-quinone reductase
gene_id_7558	71	46.48	9.00E-16	hypothetical protein

gene_id_7559	483	67.08	0	epimerase
gene_id_7560	304	61.18	2.00E-123	hypothetical protein
gene_id_7561	272	68.01	9.00E-130	hypothetical protein
gene_id_7562	387	63.82	0	hypothetical protein
gene_id_7563	331	62.84	2.00E-147	asparagine synthase
gene_id_7564	745	69.66	0	sugar hydrolase
gene_id_7565	172	68.6	9.00E-85	hypothetical protein
gene_id_7566	370	65.41	7.00E-141	chromate transporter
gene_id_7567	616	53.41	1.00E-176	hypothetical protein
gene_id_7568	380	60.26	2.00E-158	Nuclease
gene_id_7569	352	63.92	2.00E-164	hypothetical protein
gene_id_7570	893	69.32	0	hypothetical protein
gene_id_7571	265	58.49	1.00E-100	hypothetical protein
gene_id_7572	194	55.67	4.00E-65	putative nucleoside-diphosphate-sugar epimerase
gene_id_7573	264	52.27	3.00E-87	hypothetical protein
gene_id_7574	177	59.89	2.00E-61	lysine exporter protein LysE/YggA
gene_id_7575	612	56.54	0	hypothetical protein
gene_id_7576	308	53.25	2.00E-107	hypothetical protein OR1_00052
gene_id_7576	145	66.21	2.00E-57	hypothetical protein OR1_00052
gene_id_7577	481	65.7	0	tryptophanase
gene_id_7578	235	87.23	3.00E-137	Outer membrane transport energization protein ExbB
gene_id_7579	137	86.86	2.00E-67	hypothetical protein
gene_id_7580	226	85.4	1.00E-138	hypothetical protein
gene_id_7581	425	84.47	0	hypothetical protein
gene_id_7582	289	74.74	1.00E-144	hypothetical protein
gene_id_7583	302	84.44	3.00E-180	hypothetical protein
gene_id_7584	907	75.3	0	DNA topoisomerase 4 subunit A
gene_id_7585	172	54.07	4.00E-56	Shikimate kinase
gene_id_7586	578	77.85	0	Single-stranded-DNA-specific exonuclease recJ
gene_id_7587	505	84.55	0	Lysyl-tRNA synthetase
gene_id_7588	258	62.79	2.00E-115	SpoU rRNA methylase
gene_id_7589	248	51.61	1.00E-73	hypothetical protein
gene_id_7590	144	72.92	2.00E-70	hypothetical protein
gene_id_7591	421	81.24	0	hypothetical protein
gene_id_7592	473	82.66	0	hypothetical protein
gene_id_7593	432	89.58	0	hypothetical protein
gene_id_7594	624	76.76	0	hypothetical protein
gene_id_7595	453	80.13	0	hypothetical protein
gene_id_7596	42	66.67	6.00E-10	hypothetical protein
gene_id_7597	395	94.68	0	hypothetical protein
gene_id_7598	184	89.13	2.00E-90	Transcription antitermination protein nusG
gene_id_7599	148	96.62	1.00E-97	50S ribosomal protein L11
gene_id_7600	233	89.27	4.00E-150	50S ribosomal protein L1
gene_id_7601	174	83.33	3.00E-98	50S ribosomal protein L10
gene_id_7602	124	92.74	3.00E-52	hypothetical protein
gene_id_7603	1272	94.1	0	hypothetical protein
gene_id_7604	1419	89.29	0	DNA-directed RNA polymerase subunit beta'

gene_id_7605	256	38.28	2.00E-30	hypothetical protein
gene_id_7606	520	52.88	1.00E-175	hypothetical protein
gene_id_7607	1041	58.89	0	susC/RagA family TonB-linked outer membrane protein
gene_id_7608	667	61.17	0	hypothetical protein
gene_id_11392	147	60.54	3.00E-55	hypothetical protein
gene_id_11392	143	52.45	3.00E-31	hypothetical protein
gene_id_11393	434	32.03	3.00E-53	hypothetical protein
gene_id_11394	541	53.23	0	Sensor protein
gene_id_11395	146	89.73	2.00E-88	Response regulator receiver protein
gene_id_11396	500	62	0	hypothetical protein
gene_id_11397	148	44.59	3.00E-31	hypothetical protein
gene_id_11405	220	76.82	5.00E-116	peptidylprolyl isomerase A (peptidyl-prolyl cis-trans isom
gene_id_11406	771	55.38	0	hypothetical protein
gene_id_11407	492	69.92	0	Polysaccharide biosynthesis transmembrane protein
gene_id_11408	128	81.25	4.00E-67	deoxyuridine 5'-triphosphate nucleotidohydrolase
gene_id_11409	434	65.67	0	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine lig
gene_id_11410	340	57.35	1.00E-127	hypothetical protein
gene_id_11411	420	40.24	2.00E-92	hypothetical protein
gene_id_11412	181	69.06	1.00E-74	hypothetical protein
gene_id_11414	522	74.33	0	hypothetical protein
gene_id_11415	373	60.86	7.00E-155	Peptidase M
gene_id_11416	566	79.86	0	hypothetical protein
gene_id_11417	933	75.13	0	hypothetical protein
gene_id_11418	301	75.08	1.00E-163	hypothetical protein
gene_id_11419	214	80.37	6.00E-131	beta-lactamase protein
gene_id_11420	212	78.77	1.00E-125	hypothetical protein
gene_id_11421	204	92.65	2.00E-136	hypothetical protein
gene_id_11422	330	89.7	0	PfkB protein
gene_id_11423	291	70.45	5.00E-144	Pantothenate synthetase
gene_id_11424	116	87.07	9.00E-67	hypothetical protein
gene_id_11425	326	61.66	1.00E-115	hypothetical protein
gene_id_11426	617	57.86	0	hypothetical protein
gene_id_11427	51	84.31	1.00E-21	hypothetical protein BRDCF_p190
gene_id_11428	174	48.85	2.00E-50	hypothetical protein
gene_id_11429	65	49.23	8.00E-13	hypothetical protein
gene_id_11430	290	59.66	2.00E-104	integral membrane protein
gene_id_11431	315	45.4	4.00E-82	hypothetical protein
gene_id_11432	324	46.3	4.00E-92	hypothetical protein
gene_id_11433	655	39.24	2.00E-168	hypothetical protein JCM15093_185
gene_id_11434	393	67.94	2.00E-177	DEAD/DEAH box helicase, partial
gene_id_11435	264	57.2	4.00E-92	hypothetical protein
gene_id_11436	238	78.99	3.00E-137	hypothetical protein
gene_id_11437	497	67.81	0	aminobenzoyl-glutamate transporter
gene_id_11438	501	60.88	0	hypothetical protein
gene_id_11439	462	77.49	0	hypothetical protein
gene_id_11440	324	63.58	3.00E-97	hypothetical protein
gene_id_11441	113	66.37	2.00E-49	hypothetical protein

gene_id_11442	433	80.14	0	hypothetical protein
gene_id_11443	299	47.83	1.00E-81	Bifunctional methyltransferase
gene_id_11444	524	31.68	1.00E-55	hypothetical protein
gene_id_11445	776	52.32	0	hypothetical protein
gene_id_11446	323	78.95	0	hypothetical protein
gene_id_11447	783	77.27	0	hypothetical protein
gene_id_11448	767	71.32	0	hypothetical protein
gene_id_11449	329	48.63	3.00E-114	hypothetical protein
gene_id_11450	165	96.97	1.00E-114	hypothetical protein
gene_id_11451	225	57.78	5.00E-83	hypothetical protein
gene_id_11452	507	72.78	0	hypothetical protein
gene_id_11453	339	95.28	0	hypothetical protein
gene_id_11454	286	60.49	2.00E-106	hypothetical protein
gene_id_11455	171	66.08	1.00E-70	hypothetical protein
gene_id_11456	582	85.05	0	hypothetical protein
gene_id_11457	473	74.42	0	hypothetical protein
gene_id_11458	105	61.9	4.00E-39	hypothetical protein
gene_id_11459	516	86.43	0	methylmalonyl-CoA carboxyltransferase
gene_id_11460	932	86.05	0	hypothetical protein
gene_id_11462	800	75.12	0	MULTISPECIES: PFL2/glycerol dehydratase family glycyl r
gene_id_11463	302	61.92	1.00E-137	hypothetical protein
gene_id_11464	355	73.52	3.00E-180	hypothetical protein
gene_id_11465	430	83.02	0	hypothetical protein
gene_id_11466	363	52.62	1.00E-132	hypothetical protein
gene_id_11467	286	66.78	1.00E-116	tRNA delta(2)-isopentenylpyrophosphate transferase, pa
gene_id_11468	149	87.25	4.00E-92	SsrA-binding protein
gene_id_11469	279	77.78	2.00E-145	Prolipoprotein diacylglyceryl transferase
gene_id_11470	310	80.32	2.00E-170	SAM dependent methyltransferase
gene_id_11471	419	86.4	0	hypothetical protein
gene_id_11472	461	60.09	0	hypothetical protein
gene_id_11473	188	87.77	6.00E-106	Ribosome-recycling factor
gene_id_11474	214	74.3	5.00E-110	hypothetical protein
gene_id_11475	221	76.02	6.00E-92	Succinate dehydrogenase cytochrome B subunit, b558 fa
gene_id_11476	379	55.67	6.00E-131	hypothetical protein
gene_id_11477	288	84.03	8.00E-158	hypothetical protein
gene_id_11478	161	66.46	3.00E-68	hypothetical protein
gene_id_11479	245	71.02	1.00E-123	tRNA (Guanine-N(7)-)-methyltransferase
gene_id_11480	136	42.65	1.00E-24	hypothetical protein
gene_id_11481	368	80.16	0	hypothetical protein
gene_id_11482	373	66.76	4.00E-169	hypothetical protein
gene_id_11483	626	64.38	0	hypothetical protein
gene_id_11484	315	75.56	5.00E-173	hypothetical protein
gene_id_11486	931	72.61	0	hypothetical protein
gene_id_11487	187	73.8	3.00E-93	hypothetical protein
gene_id_11488	306	69.28	6.00E-148	hypothetical protein
gene_id_11489	147	63.27	8.00E-64	hypothetical protein
gene_id_11490	221	63.8	4.00E-87	hypothetical protein

gene_id_11491	105	88.57	5.00E-60	hypothetical protein
gene_id_11492	97	72.16	5.00E-45	hypothetical protein
gene_id_11493	1026	86.55	0	hypothetical protein
gene_id_11494	341	77.13	0	hypothetical protein
gene_id_11495	417	79.86	0	hypothetical protein
gene_id_11496	201	62.69	6.00E-86	hypothetical protein
gene_id_11497	397	90.18	0	hypothetical protein
gene_id_11498	502	68.73	0	phage shock protein C, PspC
gene_id_11499	112	92.86	5.00E-70	Transcriptional regulator, PadR family
gene_id_11500	191	68.59	2.00E-89	Phage Shock Protein C PspC
gene_id_11501	71	91.55	3.00E-38	hypothetical protein
gene_id_11502	267	52.06	5.00E-74	hypothetical protein
gene_id_11503	165	75.76	1.00E-88	hypothetical protein
gene_id_11504	400	79.5	0	hypothetical protein
gene_id_11505	551	76.23	0	hypothetical protein
gene_id_11506	800	53.5	0	hypothetical protein
gene_id_11507	595	90.59	0	elongation factor 4
gene_id_11508	261	77.01	1.00E-150	hypothetical protein
gene_id_11509	318	85.22	0	hypothetical protein
gene_id_11510	180	79.44	4.00E-102	hypothetical protein
gene_id_11511	139	51.08	9.00E-39	hypothetical protein
gene_id_11512	183	55.74	5.00E-64	hypothetical protein
gene_id_11513	284	39.08	1.00E-51	tRNA (adenine-N(6)-)-methyltransferase
gene_id_11514	217	86.18	3.00E-131	hypothetical protein
gene_id_11515	717	87.59	0	hypothetical protein
gene_id_12062	186	73.66	1.00E-97	Ribonuclease HII
gene_id_12063	111	63.96	4.00E-48	hypothetical protein
gene_id_12064	134	79.85	2.00E-73	hypothetical protein
gene_id_12065	112	67.86	2.00E-24	hypothetical protein
gene_id_12066	430	55.58	1.00E-139	hypothetical protein
gene_id_12067	715	75.38	0	hypothetical protein
gene_id_12068	354	83.62	0	hypothetical protein
gene_id_12069	335	71.94	1.00E-155	hypothetical protein
gene_id_12070	308	84.09	0	hypothetical protein
gene_id_12071	587	90.29	0	hypothetical protein
gene_id_12072	476	52.52	6.00E-159	sodium:dicarboxylate symporter
gene_id_12073	510	61.37	0	membrane protein
gene_id_12074	1063	57.29	0	TonB-linked outer membrane protein
gene_id_12075	240	44.17	3.00E-62	hypothetical protein
gene_id_12077	66	51.52	8.00E-11	Nuclease
gene_id_12078	358	25.98	3.00E-20	histidine kinase
gene_id_12079	272	30.88	2.00E-23	MULTISPECIES: hypothetical protein
gene_id_12081	186	24.73	9.00E-10	hypothetical protein
gene_id_12082	359	31.2	1.00E-28	hypothetical protein
gene_id_12083	326	31.6	1.00E-20	uncharacterized protein
gene_id_12084	210	40.48	6.00E-36	hypothetical protein
gene_id_12085	322	30.43	2.00E-23	hypothetical protein

gene_id_12086	426	34.74	1.00E-53	TIR protein
gene_id_12087	470	34.47	4.00E-52	TIR protein
gene_id_12088	428	38.08	7.00E-61	TIR protein
gene_id_12089	171	39.77	6.00E-27	opacity protein
gene_id_12090	337	40.65	4.00E-73	Sensor protein lytS
gene_id_12091	227	55.51	6.00E-83	hypothetical protein
gene_id_12092	344	43.31	6.00E-82	Sensor protein lytS
gene_id_12093	390	46.15	2.00E-124	hypothetical protein
gene_id_12094	242	23.97	2.00E-07	hypothetical protein
gene_id_12096	372	51.34	3.00E-132	putative membrane-spanning protein
gene_id_12096	263	26.62	1.00E-18	putative membrane-spanning protein
gene_id_12096	267	24.72	1.00E-17	putative membrane-spanning protein
gene_id_12097	193	49.22	1.00E-55	hypothetical protein
gene_id_12098	117	44.44	6.00E-23	hypothetical protein
gene_id_12099	259	37.45	8.00E-49	(4Fe-4S)-binding protein
gene_id_12100	243	32.92	1.00E-35	hypothetical protein
gene_id_12101	306	66.01	4.00E-145	hypothetical protein
gene_id_12102	341	54.55	2.00E-134	putative aminopeptidase ybaC
gene_id_12103	134	61.19	9.00E-55	ADP-ribose pyrophosphatase
gene_id_12104	225	50.22	3.00E-71	endonuclease/Exonuclease/phosphatase
gene_id_12105	147	49.66	1.00E-44	hypothetical protein
gene_id_12106	700	74.29	0	hypothetical protein
gene_id_12107	947	83.42	0	hypothetical protein
gene_id_12108	403	79.4	0	hypothetical protein
gene_id_12109	444	80.63	0	hypothetical protein
gene_id_12110	723	70.82	0	hypothetical protein
gene_id_12111	753	59.76	0	hypothetical protein
gene_id_12112	901	79.02	0	hypothetical protein
gene_id_12113	249	77.51	3.00E-144	hypothetical protein
gene_id_12114	60	51.67	6.00E-12	MULTISPECIES: metal-dependent hydrolase
gene_id_12115	754	48.67	0	hypothetical protein
gene_id_12116	547	56.12	0	hypothetical protein
gene_id_12117	143	58.04	4.00E-55	MULTISPECIES: hypothetical protein
gene_id_12119	113	49.56	8.00E-33	hypothetical protein
gene_id_12120	207	54.59	5.00E-59	hypothetical protein
gene_id_12123	264	87.12	3.00E-177	hypothetical protein
gene_id_12124	262	47.33	1.00E-71	hypothetical protein
gene_id_12125	171	63.16	7.00E-71	Dihydrofolate reductase
gene_id_12126	200	74.5	2.00E-107	Superoxide dismutase
gene_id_12128	306	82.68	1.00E-149	hypothetical protein
gene_id_12129	454	69.38	5.00E-155	hypothetical protein
gene_id_12130	160	35.62	2.00E-23	hypothetical protein BRDCF_p33
gene_id_12131	122	34.43	1.00E-09	hypothetical protein
gene_id_12132	175	85.14	9.00E-104	inorganic pyrophosphatase
gene_id_12133	719	63.98	0	Alpha-N-Acetylglucosaminidase
gene_id_12135	830	64.46	0	hypothetical protein
gene_id_12136	444	56.08	6.00E-178	hypothetical protein

gene_id_12137	374	63.9	3.00E-172	hypothetical protein
gene_id_12138	875	75.77	0	hypothetical protein
gene_id_12139	423	73.29	0	hypothetical protein
gene_id_12140	265	66.04	8.00E-116	dimethyladenosine transferase
gene_id_12141	359	48.19	7.00E-103	Endonuclease/Exonuclease/Phosphatase
gene_id_12142	367	86.38	0	GTP-binding protein YchF
gene_id_12143	699	73.25	0	hypothetical protein
gene_id_12144	369	57.72	1.00E-134	hypothetical protein
gene_id_12145	173	73.99	3.00E-92	hypothetical protein
gene_id_12146	402	73.63	0	hypothetical protein
gene_id_12147	434	67.97	0	hypothetical protein
gene_id_12148	239	62.76	2.00E-89	hypothetical protein
gene_id_12149	1104	76	0	hypothetical protein
gene_id_12150	339	89.97	0	hypothetical protein
gene_id_12151	391	66.24	0	hypothetical protein
gene_id_12152	732	70.22	0	hypothetical protein
gene_id_12153	648	89.81	0	hypothetical protein
gene_id_12154	259	91.51	6.00E-152	hypothetical protein
gene_id_12155	171	54.97	1.00E-54	hypothetical protein
gene_id_12156	264	66.67	1.00E-129	hypothetical protein
gene_id_12157	365	80.27	0	hypothetical protein
gene_id_12158	230	90.87	1.00E-112	hypothetical protein
gene_id_12160	313	87.86	1.00E-177	hypothetical protein
gene_id_12161	116	83.62	3.00E-69	Carboxymuconolactone decarboxylase
gene_id_12162	119	62.18	6.00E-43	16S rRNA maturation RNase YbeY
gene_id_12163	692	74.86	0	hypothetical protein
gene_id_12164	311	37.62	7.00E-54	hypothetical protein
gene_id_12165	590	80	0	hypothetical protein
gene_id_12166	340	77.65	0	hypothetical protein
gene_id_12167	108	87.04	3.00E-62	Glycine cleavage system H protein
gene_id_12168	196	72.45	9.00E-96	Holliday junction ATP-dependent DNA helicase ruvA
gene_id_12169	407	70.02	0	hypothetical protein
gene_id_12170	139	84.89	5.00E-83	hypothetical protein
gene_id_12171	100	81	1.00E-51	hypothetical protein
gene_id_12172	160	58.75	6.00E-58	hypothetical protein
gene_id_12173	263	41.06	2.00E-68	transcriptional regulator
gene_id_12174	229	62.01	2.00E-102	hypothetical protein
gene_id_12175	209	71.77	6.00E-110	hypothetical protein
gene_id_12176	667	61.02	0	hypothetical protein
gene_id_12177	512	91.8	0	hypothetical protein
gene_id_12178	325	80	0	hypothetical protein
gene_id_12179	256	46.88	1.00E-78	hypothetical protein
gene_id_12180	108	78.7	2.00E-55	hypothetical protein
gene_id_12182	229	75.98	6.00E-99	hypothetical protein
gene_id_12183	139	35.97	4.00E-18	hypothetical protein
gene_id_12184	377	80.11	0	acyltransferase
gene_id_12185	387	79.59	0	ABC transporter permease

gene_id_12186	317	69.72	4.00E-162	translation factor Sua5
gene_id_12187	254	68.11	4.00E-99	hypothetical protein, partial
gene_id_12188	398	60.3	5.00E-171	ATPase AAA
gene_id_12189	259	45.95	4.00E-66	transglutaminase, partial
gene_id_12190	206	30.1	9.00E-11	hypothetical protein
gene_id_12191	164	34.76	2.00E-12	hypothetical protein
gene_id_12193	60	63.33	1.00E-15	hypothetical protein
gene_id_12195	166	36.14	1.00E-18	hypothetical protein
gene_id_12196	205	72.68	1.00E-87	hypothetical protein
gene_id_12197	615	48.29	4.00E-167	hypothetical protein MYP_341
gene_id_12200	102	63.73	2.00E-44	hypothetical protein
gene_id_12201	206	55.83	6.00E-60	hypothetical protein
gene_id_12202	581	30.98	7.00E-92	hypothetical protein
gene_id_12204	421	49.64	3.00E-133	integrase
gene_id_12205	82	52.44	4.00E-23	hypothetical protein
gene_id_12206	218	40.83	7.00E-43	toxin-antitoxin system, antitoxin component, Xre family
gene_id_12207	68	45.59	2.00E-11	hypothetical protein
gene_id_12208	184	47.83	2.00E-49	MULTISPECIES: transcriptional regulator
gene_id_12210	90	52.22	1.00E-21	hypothetical protein
gene_id_12213	312	65.06	1.00E-148	hypothetical protein
gene_id_12214	236	52.54	1.00E-76	HNH endonuclease
gene_id_12215	102	57.84	4.00E-29	single-stranded DNA-binding protein
gene_id_12216	133	42.11	5.00E-26	hypothetical protein
gene_id_12217	117	52.14	1.00E-31	hypothetical protein
gene_id_12218	220	51.82	4.00E-77	predicted protein
gene_id_12219	66	43.94	6.00E-10	hypothetical protein SALWKB2_1880
gene_id_12220	140	52.14	3.00E-34	MULTISPECIES: endonuclease
gene_id_12221	203	33.99	7.00E-28	hypothetical protein
gene_id_12222	243	34.57	1.00E-42	hypothetical protein
gene_id_12223	91	37.36	5.00E-08	hypothetical protein P12024L_27
gene_id_12224	169	51.48	9.00E-48	hypothetical protein
gene_id_12225	110	41.82	1.00E-23	conserved hypothetical protein
gene_id_12226	500	72.6	0	hypothetical protein
gene_id_12227	455	49.67	3.00E-146	hypothetical protein
gene_id_12228	343	46.36	8.00E-102	hypothetical protein HMPREF1981_02012
gene_id_12230	90	53.33	2.00E-19	hypothetical protein
gene_id_12233	132	46.21	3.00E-31	dnaJ domain protein
gene_id_12234	151	49.01	4.00E-42	DNA repair protein
gene_id_12236	174	28.16	9.00E-06	hypothetical protein BACSTE_02225
gene_id_12237	212	36.32	2.00E-19	hypothetical protein
gene_id_12238	167	30.54	2.00E-10	hypothetical protein
gene_id_12239	361	24.93	1.00E-22	hypothetical protein
gene_id_12240	104	34.62	3.00E-12	hypothetical protein
gene_id_12241	104	38.46	2.00E-12	hypothetical protein
gene_id_12242	144	52.08	3.00E-42	hypothetical protein
gene_id_12243	134	47.01	4.00E-36	uncharacterized protein
gene_id_12244	152	61.84	2.00E-56	hypothetical protein

gene_id_12245	159	49.06	2.00E-33	hypothetical protein
gene_id_12246	69	40.58	1.00E-13	hypothetical protein
gene_id_12247	422	50.71	4.00E-117	phage tape measure protein
gene_id_12247	238	31.93	9.00E-17	phage tape measure protein
gene_id_12248	306	40.85	1.00E-70	hypothetical protein
gene_id_12249	233	46.78	7.00E-14	tail protein
gene_id_12251	196	37.24	7.00E-32	hypothetical protein
gene_id_12252	893	53.42	0	hypothetical protein GV66_19330
gene_id_12253	136	43.38	1.00E-30	hypothetical protein
gene_id_12254	163	53.37	3.00E-63	hypothetical protein
gene_id_12255	202	39.11	2.00E-35	MULTISPECIES: hypothetical protein
gene_id_12256	966	61.18	0	DNA helicase UvrD
gene_id_12257	597	63.48	0	DNA methylase
gene_id_12258	887	61.67	0	hypothetical protein
gene_id_12259	321	96.88	0	hypothetical protein BRDCF_p2220
gene_id_12260	110	56.36	2.00E-28	hypothetical protein
gene_id_12261	595	48.4	0	WD40-like protein beta propeller containing protein
gene_id_12262	1011	84.17	0	hypothetical protein
gene_id_12263	459	86.93	0	L-cysteine desulfhydrase
gene_id_12264	614	75.08	0	glutamine amidotransferase
gene_id_12266	400	66.5	0	hypothetical protein
gene_id_12267	390	70.51	0	hypothetical protein
gene_id_12268	329	71.43	5.00E-134	hypothetical protein
gene_id_12269	475	59.37	0	transporter
gene_id_12270	146	63.01	1.00E-59	MarR Family Transcriptional Regulator
gene_id_12271	674	81.9	0	hypothetical protein
gene_id_12272	505	84.55	0	hypothetical protein
gene_id_12273	1197	78.86	0	hypothetical protein
gene_id_12274	339	65.78	3.00E-148	hypothetical protein
gene_id_12275	477	92.03	0	hypothetical protein
gene_id_12276	217	73.27	2.00E-117	hypothetical protein
gene_id_12277	247	89.07	4.00E-158	transporter
gene_id_12278	346	70.52	0	hypothetical protein
gene_id_12279	147	78.23	7.00E-72	hypothetical protein
gene_id_12280	840	87.38	0	hypothetical protein
gene_id_12281	258	65.5	5.00E-109	hypothetical protein
gene_id_12282	327	75.84	1.00E-159	L-asparaginase
gene_id_12283	390	56.67	6.00E-142	hypothetical protein
gene_id_12284	114	75.44	2.00E-55	hypothetical protein
gene_id_12285	428	83.64	0	Tyrosyl-tRNA synthetase
gene_id_12286	422	77.01	0	hypothetical protein
gene_id_12287	294	69.39	7.00E-146	hypothetical protein
gene_id_12288	293	53.58	6.00E-73	Hemolysin-related protein, containing CBS protein
gene_id_12289	211	78.2	7.00E-114	hypothetical protein
gene_id_12290	148	83.78	7.00E-87	hypothetical protein
gene_id_12291	1064	52.63	0	hypothetical protein BRDCF_p1277
gene_id_12292	528	93.75	0	hypothetical protein

gene_id_12293	89	93.26	1.00E-52	molecular chaperone GroES
gene_id_12294	441	69.16	0	hypothetical protein
gene_id_12295	141	79.43	4.00E-79	cmp/dcmp deaminase zinc-binding protein
gene_id_12296	156	76.92	3.00E-88	hypothetical protein
gene_id_12297	330	46.67	2.00E-101	hypothetical protein
gene_id_12298	346	51.45	2.00E-107	glycosyl transferase, group 1
gene_id_12299	271	66.79	1.00E-130	hypothetical protein BRDCF_p2179
gene_id_12300	543	84.35	0	hypothetical protein
gene_id_12301	944	48.2	0	hypothetical protein
gene_id_12302	600	72.83	0	hypothetical protein
gene_id_12303	596	75.5	0	hypothetical protein
gene_id_12304	132	49.24	3.00E-40	ribonuclease P
gene_id_12305	245	82.45	3.00E-138	hypothetical protein
gene_id_12306	268	60.45	8.00E-86	hypothetical protein
gene_id_12307	116	65.52	4.00E-48	hypothetical protein
gene_id_12308	1020	78.04	0	hypothetical protein
gene_id_12309	336	62.5	2.00E-147	hypothetical protein
gene_id_12310	507	69.82	0	hypothetical protein
gene_id_12311	241	53.94	3.00E-85	hypothetical protein
gene_id_12312	195	70.26	3.00E-90	Nucleoside-triphosphatase
gene_id_12313	538	72.49	0	hypothetical protein
gene_id_12314	208	59.62	5.00E-84	hypothetical protein
gene_id_12315	260	82.31	6.00E-158	protein of unknown function DUF147
gene_id_12316	838	72.43	0	hypothetical protein
gene_id_12317	136	61.03	1.00E-52	hypothetical protein
gene_id_12318	251	59.36	2.00E-99	hypothetical protein
gene_id_12319	128	55.47	5.00E-43	hypothetical protein
gene_id_12320	546	87.73	0	hypothetical protein
gene_id_12321	137	56.2	2.00E-43	hypothetical protein
gene_id_12322	662	85.2	0	hypothetical protein
gene_id_12323	304	63.49	7.00E-126	glutaminase
gene_id_12324	844	61.49	0	hypothetical protein
gene_id_12325	188	88.3	1.00E-117	quinol oxidase
gene_id_12326	496	89.92	0	hypothetical protein
gene_id_12327	361	80.61	0	hypothetical protein
gene_id_12328	257	90.66	9.00E-140	cytochrome c biogenesis protein CcsA
gene_id_12329	280	92.5	0	hypothetical protein
gene_id_12330	425	79.53	0	hypothetical protein
gene_id_12331	537	78.03	0	hypothetical protein
gene_id_12332	198	79.29	1.00E-111	Imidazole glycerol phosphate synthase subunit hisH
gene_id_12333	245	74.29	9.00E-112	hypothetical protein
gene_id_12334	251	85.66	2.00E-138	hypothetical protein
gene_id_12335	200	83.5	3.00E-98	Phosphoribosyl-ATP pyrophosphatase /phosphoribosyl-
gene_id_12336	553	94.21	0	hypothetical protein
gene_id_12337	105	86.67	3.00E-61	hypothetical protein
gene_id_12338	185	61.08	4.00E-59	hypothetical protein
gene_id_12339	429	77.16	0	hypothetical protein

gene_id_12340	345	84.64	0	hypothetical protein
gene_id_12341	153	60.13	7.00E-55	adenylate cyclase
gene_id_12342	124	80.65	4.00E-67	hypothetical protein
gene_id_12343	437	82.38	0	hypothetical protein
gene_id_12344	310	86.45	0	hypothetical protein
gene_id_12345	374	78.34	0	hypothetical protein
gene_id_12346	290	50.34	7.00E-85	hypothetical protein
gene_id_12347	121	90.91	7.00E-73	hypothetical protein
gene_id_12348	391	68.03	1.00E-179	hypothetical protein
gene_id_12349	238	44.12	7.00E-57	hypothetical protein
gene_id_12350	718	57.24	0	hypothetical protein
gene_id_12351	464	51.29	1.00E-147	membrane protein
gene_id_12352	297	53.87	2.00E-101	glycosyl transferase
gene_id_12353	382	53.14	1.00E-119	hypothetical protein
gene_id_12354	373	62.73	2.00E-168	hypothetical protein
gene_id_12355	220	41.36	5.00E-59	transferase
gene_id_12356	281	48.04	5.00E-91	glycosyl transferase family A
gene_id_12357	254	48.03	7.00E-65	hypothetical protein BSIG_1299, partial
gene_id_12358	372	68.01	0	putative uncharacterized protein
gene_id_12359	469	41.58	4.00E-106	transporter
gene_id_12360	395	62.28	3.00E-174	glycosyl transferase
gene_id_12361	371	57.14	4.00E-137	hypothetical protein
gene_id_12362	382	66.49	0	hypothetical protein
gene_id_12363	204	83.82	8.00E-123	hypothetical protein
gene_id_12364	206	41.75	5.00E-36	hypothetical protein
gene_id_12365	785	57.83	0	Outer membrane protein
gene_id_12366	195	60.51	1.00E-84	hypothetical protein
gene_id_12367	318	59.43	2.00E-132	hypothetical protein
gene_id_12368	193	52.33	2.00E-66	hypothetical protein
gene_id_12369	76	64.47	2.00E-29	zinc finger CDGSH-type domain-containing protein
gene_id_12370	184	86.41	2.00E-83	hypothetical protein
gene_id_12371	169	70.41	1.00E-84	Peroxiredoxin
gene_id_12372	501	78.64	0	Long-chain-fatty-acid--CoA ligase
gene_id_12373	371	69.27	2.00E-174	hypothetical protein
gene_id_12374	410	81.71	0	Sodium:dicarboxylate symporter
gene_id_12375	257	39.69	7.00E-47	hypothetical protein
gene_id_12376	484	71.07	0	acyltransferase
gene_id_12377	208	70.19	3.00E-93	hypothetical protein
gene_id_12378	97	82.47	7.00E-52	transcriptional regulator
gene_id_12379	410	79.51	0	hypothetical protein
gene_id_12380	120	81.67	1.00E-59	hypothetical protein
gene_id_12381	212	85.38	4.00E-116	hypothetical protein
gene_id_12383	101	98.02	5.00E-64	hypothetical protein
gene_id_12384	706	90.08	0	hypothetical protein
gene_id_12385	158	96.2	5.00E-108	30S ribosomal protein S7
gene_id_12386	117	95.73	5.00E-75	30S ribosomal protein S12
gene_id_12387	409	86.06	0	hypothetical protein

gene_id_12388	302	70.86	5.00E-153	hypothetical protein
gene_id_12389	653	81.62	0	hypothetical protein
gene_id_12390	1018	55.7	0	hypothetical protein
gene_id_12391	191	72.25	3.00E-99	hypothetical protein
gene_id_12392	430	75.35	0	hypothetical protein
gene_id_12393	273	76.92	5.00E-148	hypothetical protein
gene_id_12394	325	69.23	2.00E-167	hypothetical protein
gene_id_12395	421	81.95	0	hypothetical protein
gene_id_12396	139	66.91	2.00E-67	hypothetical protein
gene_id_12397	416	85.1	0	hypothetical protein
gene_id_12398	1091	82.4	0	hypothetical protein
gene_id_12399	122	50	5.00E-34	hypothetical protein
gene_id_12400	364	75	0	hypothetical protein
gene_id_12401	425	90.12	0	Arginine deiminase
gene_id_12402	1029	71.04	0	hypothetical protein
gene_id_12403	341	87.68	0	hypothetical protein
gene_id_12404	263	45.63	9.00E-74	hypothetical protein
gene_id_12405	192	86.46	7.00E-83	hypothetical protein
gene_id_12407	208	93.27	2.00E-139	50S ribosomal protein L3
gene_id_12408	210	85.71	1.00E-130	50S ribosomal protein L4
gene_id_12409	96	88.54	5.00E-55	50S ribosomal protein L23
gene_id_12410	274	92.7	2.00E-165	50S ribosomal protein L2
gene_id_12411	87	97.7	7.00E-56	30S ribosomal protein S19
gene_id_12412	140	87.86	4.00E-82	50S ribosomal protein L22
gene_id_12413	216	95.83	2.00E-146	30S ribosomal protein S3
gene_id_12414	543	46.04	1.00E-156	Sensor protein gacS
gene_id_12415	209	45.93	8.00E-62	hypothetical protein BRDCF_p2291
gene_id_12416	380	74.21	0	Beta-lactamase (Cephalosporinase)
gene_id_12417	371	67.12	0	hypothetical protein
gene_id_12418	140	62.86	2.00E-56	hypothetical protein
gene_id_12419	665	51.58	0	hypothetical protein
gene_id_12420	340	51.76	2.00E-104	3-dehydroquinate synthase
gene_id_12421	306	60.78	2.00E-123	Competence protein ComM
gene_id_12422	374	45.72	4.00E-88	hypothetical protein
gene_id_12423	212	45.75	2.00E-48	uncharacterized protein BN772_02997
gene_id_12425	72	51.39	5.00E-18	MULTISPECIES: transcriptional regulator
gene_id_12426	439	45.1	6.00E-110	ATPase
gene_id_12427	107	39.25	9.00E-16	MULTISPECIES: uncharacterized protein
gene_id_12428	97	48.45	9.00E-20	XRE family transcriptional regulator
gene_id_12430	96	44.79	2.00E-19	uncharacterized protein
gene_id_12432	262	55.34	2.00E-98	hypothetical protein
gene_id_12433	486	37.45	7.00E-90	hypothetical protein
gene_id_12435	195	67.18	1.00E-87	hypothetical protein
gene_id_12438	125	37.6	1.00E-10	hypothetical protein
gene_id_12440	158	37.34	1.00E-17	hypothetical protein
gene_id_12443	298	57.05	7.00E-112	DNA/RNA non-specific endonuclease
gene_id_12444	83	50.6	5.00E-13	hypothetical protein

gene_id_12445	312	33.01	8.00E-45	hypothetical protein
gene_id_12446	156	51.92	7.00E-28	hypothetical protein
gene_id_12449	224	63.84	3.00E-93	hypothetical protein
gene_id_12451	309	57.28	5.00E-130	hypothetical protein
gene_id_12452	182	53.85	9.00E-56	hypothetical protein
gene_id_12453	43	93.02	1.00E-18	hypothetical protein
gene_id_12454	382	34.29	5.00E-45	hypothetical protein
gene_id_12455	132	43.18	8.00E-23	hypothetical protein GV66_07495
gene_id_12456	200	64.5	3.00E-77	hypothetical protein
gene_id_12457	890	60.9	0	hypothetical protein
gene_id_12458	130	34.62	7.00E-16	hypothetical protein
gene_id_12459	125	33.6	8.00E-14	hypothetical protein
gene_id_12460	215	35.81	7.00E-25	uncharacterized protein
gene_id_12461	121	26.45	1.00E-14	hypothetical protein
gene_id_12461	28	60.71	1.00E-14	hypothetical protein
gene_id_12462	374	31.28	3.00E-44	hypothetical protein
gene_id_12463	224	22.77	7.00E-06	hypothetical protein
gene_id_12464	138	66.67	5.00E-61	hypothetical protein
gene_id_12465	388	81.7	0	hypothetical protein
gene_id_12466	342	69.59	3.00E-174	hypothetical protein
gene_id_12467	118	74.58	1.00E-57	Selenium Metabolism Protein YedF
gene_id_12468	336	68.75	3.00E-170	hypothetical protein
gene_id_12469	454	59.69	0	Putative outer membrane protein
gene_id_12470	799	80.98	0	hypothetical protein
gene_id_12471	163	80.98	2.00E-96	Phosphoesterase, MJ0936 family
gene_id_12472	393	72.52	0	hypothetical protein
gene_id_12473	240	81.25	2.00E-118	hypothetical protein
gene_id_12473	76	46.05	6.00E-12	hypothetical protein
gene_id_12474	189	65.08	4.00E-84	Sua5/YciO/YrdC/YwlC family protein
gene_id_12475	352	69.03	5.00E-164	endonuclease/exonuclease/phosphatase
gene_id_12476	226	83.19	1.00E-130	hypothetical protein
gene_id_12477	601	57.07	0	hypothetical protein
gene_id_12478	116	29.31	2.00E-13	hypothetical protein
gene_id_12479	156	75.64	2.00E-81	hypothetical protein
gene_id_12480	197	50.76	1.00E-61	hypothetical protein
gene_id_12481	352	75	0	hypothetical protein
gene_id_12482	240	81.67	2.00E-137	hypothetical protein BRDCF_p405
gene_id_12483	240	75.83	7.00E-138	nitroreductase
gene_id_12484	846	43.03	0	Metallophosphoesterase domain protein
gene_id_12485	267	54.31	4.00E-99	hypothetical protein
gene_id_12486	711	52.18	0	hypothetical protein, partial
gene_id_12487	531	69.3	0	proline dehydrogenase
gene_id_12488	132	64.39	2.00E-58	hypothetical protein
gene_id_12489	288	50	8.00E-92	hypothetical protein
gene_id_12490	147	80.95	8.00E-74	GNAT family acetyltransferase
gene_id_12491	80	55	8.00E-23	hypothetical protein
gene_id_12492	473	23.89	6.00E-21	hypothetical protein

gene_id_12493	114	75.44	6.00E-57	hypothetical protein
gene_id_12494	409	67.97	0	metallophosphoesterase
gene_id_12495	59	76.27	1.00E-23	hypothetical protein
gene_id_12496	626	41.21	6.00E-121	PAS:Response regulator receiver:ATP-binding region, AT
gene_id_12497	395	49.62	4.00E-133	hypothetical protein N824_18570
gene_id_12498	180	67.78	1.00E-87	hypothetical protein
gene_id_12499	159	52.83	2.00E-59	hypothetical protein
gene_id_12500	196	47.96	4.00E-60	hypothetical protein
gene_id_12502	107	51.4	1.00E-22	hypothetical protein
gene_id_12504	372	37.1	4.00E-77	histidine kinase
gene_id_12505	148	41.22	1.00E-28	hypothetical protein
gene_id_12506	361	68.98	0	radical SAM protein
gene_id_12507	288	79.17	6.00E-168	hypothetical protein
gene_id_12508	287	52.26	4.00E-105	hypothetical protein, partial
gene_id_12509	294	69.05	4.00E-145	LysR family transcriptional regulator
gene_id_12510	279	74.19	1.00E-131	membrane protein
gene_id_12512	190	35.26	1.00E-35	hypothetical protein, partial
gene_id_12513	1055	72.23	0	multidrug transporter AcrB
gene_id_12514	365	36.16	1.00E-70	membrane-fusion protein
gene_id_12515	215	87.91	8.00E-128	transaldolase
gene_id_12516	92	57.61	4.00E-32	membrane protein
gene_id_12517	168	54.17	2.00E-61	acetyltransferase
gene_id_12518	151	51.66	1.00E-45	GNAT family acetyltransferase
gene_id_12519	415	63.86	0	hypothetical protein
gene_id_12520	715	77.62	0	hydroperoxidase
gene_id_12521	289	54.67	1.00E-113	Proline iminopeptidase
gene_id_12522	138	75.36	3.00E-71	glyoxalase
gene_id_12523	105	72.38	2.00E-45	nucleotide pyrophosphohydrolase
gene_id_12524	794	60.58	0	peptidase S24/S26A/S26B conserved region
gene_id_12525	158	74.68	8.00E-83	glutathione peroxidase
gene_id_12526	138	68.84	4.00E-62	MarR family transcriptional regulator
gene_id_12528	166	72.29	6.00E-70	hydrolase
gene_id_12529	323	88.85	0	hypothetical protein
gene_id_12530	625	24.8	2.00E-33	hypothetical protein
gene_id_12531	267	83.9	4.00E-145	hypothetical protein
gene_id_12532	306	41.18	1.00E-70	histidinol phosphatase
gene_id_12534	257	48.64	2.00E-65	hypothetical protein
gene_id_12535	411	56.69	1.00E-157	hypothetical protein
gene_id_12536	371	75.74	0	hypothetical protein
gene_id_12537	123	43.9	5.00E-29	hypothetical protein
gene_id_12538	212	65.09	1.00E-98	hypothetical protein
gene_id_12539	556	91.55	0	glycosyl transferase family 2
gene_id_12540	255	43.92	2.00E-53	hypothetical protein
gene_id_12541	364	45.05	2.00E-103	uncharacterized protein
gene_id_12542	1031	71.97	0	multidrug transporter AcrB
gene_id_12543	531	46.7	2.00E-159	RND transporter MFP subunit
gene_id_12546	181	29.28	2.00E-11	hypothetical protein

gene_id_12547	171	30.41	3.00E-10	hypothetical protein
gene_id_12548	219	59.82	2.00E-97	lipoate-protein ligase B
gene_id_12549	287	72.82	1.00E-136	lipoyl synthase, partial
gene_id_12550	125	40	1.00E-25	hypothetical protein
gene_id_12551	133	54.14	1.00E-39	hypothetical protein
gene_id_12552	143	67.13	2.00E-50	putative DNA polymerase III epsilon chain
gene_id_12553	250	48.4	8.00E-79	dehydrogenase
gene_id_12554	327	49.85	2.00E-109	16S rRNA methyltransferase
gene_id_12555	164	35.37	1.00E-08	hypothetical protein
gene_id_12556	195	31.28	4.00E-27	hypothetical protein
gene_id_12557	547	59.78	0	hypothetical protein
gene_id_12558	282	47.52	1.00E-90	MULTISPECIES: hypothetical protein
gene_id_12559	109	40.37	2.00E-17	thiol-disulfide oxidoreductase
gene_id_12560	345	52.46	4.00E-114	hypothetical protein
gene_id_12561	540	31.85	4.00E-79	PAS/PAC sensor hybrid histidine kinase
gene_id_12562	123	55.28	6.00E-38	hypothetical protein
gene_id_12563	442	55.43	0	regulator
gene_id_12564	868	55.65	0	hypothetical protein
gene_id_12565	318	57.86	9.00E-134	hypothetical protein
gene_id_12565	188	33.51	2.00E-23	hypothetical protein
gene_id_12566	112	45.54	5.00E-18	hypothetical protein
gene_id_12567	222	54.05	1.00E-80	Pyridoxine/pyridoxamine 5'-phosphate oxidase
gene_id_12568	134	42.54	6.00E-24	hypothetical protein
gene_id_12569	179	51.96	2.00E-56	dithiol-disulfide isomerase
gene_id_12570	310	53.87	7.00E-127	hypothetical protein
gene_id_12571	176	40.34	5.00E-43	hypothetical protein
gene_id_12572	330	41.21	2.00E-79	hypothetical protein
gene_id_12573	465	71.18	0	hypothetical protein
gene_id_12574	275	54.91	3.00E-82	hypothetical protein
gene_id_12575	187	71.12	3.00E-97	hypothetical protein
gene_id_12576	491	64.36	0	MULTISPECIES: hypothetical protein
gene_id_12577	359	54.04	8.00E-119	hypothetical protein
gene_id_12578	289	32.87	9.00E-58	hypothetical protein
gene_id_12579	949	62.07	0	putative Zn-dependent peptidase
gene_id_12580	644	79.66	0	4Fe-4S ferredoxin iron-sulfur binding protein
gene_id_12581	927	67.53	0	hypothetical protein
gene_id_12582	412	75.97	0	hypothetical protein
gene_id_12583	534	64.23	0	hypothetical protein
gene_id_12584	724	75.41	0	Peptidase S46
gene_id_12585	701	79.74	0	hypothetical protein
gene_id_12586	272	84.93	1.00E-165	hypothetical protein
gene_id_12587	115	46.09	1.00E-18	hypothetical protein
gene_id_12588	205	69.27	3.00E-98	Phosphoglycerate mutase
gene_id_12589	107	90.65	4.00E-66	hypothetical protein
gene_id_12590	490	80.41	0	hypothetical protein
gene_id_12591	381	79.53	0	hypothetical protein
gene_id_12592	261	45.59	3.00E-66	hypothetical protein

gene_id_12593	1145	59.13	0	hypothetical protein
gene_id_12594	1151	50.91	0	hypothetical protein
gene_id_12595	931	64.02	0	hypothetical protein
gene_id_12596	688	82.85	0	hypothetical protein
gene_id_12598	527	64.52	0	TIR protein
gene_id_12599	248	41.13	5.00E-58	hypothetical protein
gene_id_12600	509	35.76	1.00E-90	ABC-type multidrug transport system, ATPase and perme
gene_id_12601	304	68.09	1.00E-153	hypothetical protein
gene_id_12602	138	67.39	1.00E-57	hypothetical protein
gene_id_12603	88	75	5.00E-39	hypothetical protein
gene_id_12604	700	68.14	0	hypothetical protein
gene_id_12605	358	54.47	5.00E-141	hypothetical protein
gene_id_12606	171	64.91	8.00E-69	Nitroreductase family protein
gene_id_12607	828	56.04	0	hypothetical protein
gene_id_12608	188	66.49	5.00E-86	Phosphoribosylglycinamide formyltransferase
gene_id_12609	78	96.15	3.00E-43	Acyl carrier protein
gene_id_12610	415	84.58	0	hypothetical protein
gene_id_12611	455	43.52	2.00E-129	hypothetical protein
gene_id_12612	278	83.09	7.00E-174	hypothetical protein
gene_id_12613	292	62.33	2.00E-110	hypothetical protein
gene_id_12614	81	69.14	2.00E-32	hypothetical protein
gene_id_12615	262	72.14	3.00E-116	hypothetical protein
gene_id_12616	250	66.8	1.00E-124	hypothetical protein
gene_id_12617	202	70.3	1.00E-102	hypothetical protein
gene_id_12618	357	63.03	6.00E-145	putative membrane-bound dipeptidase
gene_id_12620	139	97.12	2.00E-91	50S ribosomal protein L16
gene_id_12621	66	86.36	2.00E-32	hypothetical protein
gene_id_12622	84	95.24	3.00E-40	30S ribosomal protein S17
gene_id_12623	121	97.52	1.00E-77	50S ribosomal protein L14
gene_id_12624	107	88.79	1.00E-61	50S ribosomal protein L24
gene_id_12625	188	91.49	1.00E-118	50S ribosomal protein L5
gene_id_12626	89	95.51	8.00E-56	30S ribosomal protein S14
gene_id_12627	131	91.6	4.00E-72	30S ribosomal protein S8
gene_id_12628	186	85.48	1.00E-111	50S ribosomal protein L6
gene_id_12629	120	92.5	7.00E-73	50S ribosomal protein L18
gene_id_12630	172	96.51	3.00E-103	30S ribosomal protein S5
gene_id_12631	60	76.67	3.00E-22	hypothetical protein
gene_id_12632	148	85.81	2.00E-64	hypothetical protein
gene_id_12633	440	89.77	0	preprotein translocase subunit SecY
gene_id_12634	254	85.83	1.00E-152	hypothetical protein
gene_id_12635	72	95.83	1.00E-42	translation initiation factor IF-1
gene_id_12636	110	89.09	7.00E-66	hypothetical protein
gene_id_12637	114	99.12	2.00E-77	30S ribosomal protein S11
gene_id_12638	201	91.54	7.00E-136	30S ribosomal protein S4
gene_id_12639	337	96.14	0	hypothetical protein
gene_id_12640	139	86.33	5.00E-82	50S ribosomal protein L17
gene_id_12641	207	54.11	2.00E-69	Copper homeostasis protein CutC

gene_id_12642	410	79.51	0	hypothetical protein
gene_id_12643	376	84.84	0	hypothetical protein
gene_id_12644	363	79.34	0	hypothetical protein
gene_id_12645	314	81.85	0	hypothetical protein
gene_id_12646	305	57.7	3.00E-118	iron-sulfur cluster binding protein
gene_id_12647	288	61.46	8.00E-124	hypothetical protein
gene_id_12648	90	95.56	2.00E-29	hypothetical protein
gene_id_12649	204	59.8	2.00E-88	Thiamine pyrophosphokinase
gene_id_12650	320	55.94	5.00E-125	methionyl-tRNA formyltransferase
gene_id_12651	481	77.13	0	hypothetical protein
gene_id_12652	870	73.22	0	alanyl-tRNA synthetase
gene_id_12653	320	79.38	7.00E-180	hypothetical protein
gene_id_12654	317	74.13	3.00E-152	Membrane protein
gene_id_12655	99	83.84	2.00E-54	transcriptional regulator
gene_id_12656	246	60.57	4.00E-101	hypothetical protein
gene_id_12657	270	83.33	9.00E-159	hypothetical protein
gene_id_12658	338	77.22	0	hypothetical protein
gene_id_12659	492	72.76	0	Replicative DNA helicase
gene_id_12660	276	59.78	2.00E-117	hypothetical protein
gene_id_12661	137	70.07	3.00E-44	hypothetical protein
gene_id_12662	286	84.62	2.00E-133	hypothetical protein
gene_id_12663	168	83.33	4.00E-91	hypothetical protein
gene_id_12875	459	56.21	1.00E-168	hypothetical protein
gene_id_12876	1040	61.54	0	hypothetical protein
gene_id_12877	445	87.64	0	glutamate dehydrogenase
gene_id_12878	338	86.98	0	2-oxoacid:ferredoxin oxidoreductase subunit beta
gene_id_12879	611	85.76	0	hypothetical protein
gene_id_12880	173	86.13	2.00E-103	acetyltransferase
gene_id_12881	370	79.73	0	hypothetical protein
gene_id_12882	712	87.64	0	hypothetical protein
gene_id_12883	260	54.62	4.00E-95	Glutamate racemase
gene_id_12884	176	78.98	8.00E-85	Outer membrane protein
gene_id_12885	170	52.94	9.00E-57	hypothetical protein
gene_id_12886	817	86.54	0	hypothetical protein
gene_id_12887	245	73.47	1.00E-131	hypothetical protein
gene_id_12888	293	66.55	9.00E-144	NAD(+) kinase
gene_id_12889	239	74.9	3.00E-135	hypothetical protein
gene_id_12890	201	77.61	9.00E-79	hypothetical protein
gene_id_12891	372	72.85	0	hypothetical protein
gene_id_12892	316	86.39	0	hypothetical protein
gene_id_12893	557	39.86	8.00E-132	hypothetical protein
gene_id_12895	192	93.23	7.00E-117	rubrerythrin
gene_id_12896	304	65.46	3.00E-135	hypothetical protein
gene_id_12897	311	88.42	0	hypothetical protein
gene_id_12898	263	79.85	1.00E-147	putative lipoprotein
gene_id_12899	104	90.38	3.00E-60	hypothetical protein
gene_id_12900	401	67.08	0	hypothetical protein

gene_id_12901	553	64.74	0	hypothetical protein
gene_id_12902	270	87.78	1.00E-170	hypothetical protein
gene_id_12903	359	59.05	2.00E-138	hypothetical protein
gene_id_12904	283	71.73	4.00E-150	hypothetical protein
gene_id_12905	159	79.87	2.00E-88	Glutathione peroxidase
gene_id_12906	703	72.12	0	hypothetical protein
gene_id_12907	131	67.94	2.00E-60	transcriptional regulator, badm/rrf2 family
gene_id_12908	198	60.61	2.00E-82	YceI family protein
gene_id_12909	306	77.78	5.00E-175	hypothetical protein
gene_id_12910	181	46.96	3.00E-48	YceI family protein
gene_id_12911	246	80.89	3.00E-151	Glycoside hydrolase family 16
gene_id_12912	798	61.78	0	NB-Dependent Receptor
gene_id_12913	808	65.22	0	NB-Dependent Receptor
gene_id_12914	188	89.36	3.00E-124	hypothetical protein
gene_id_12915	470	60.64	0	Transglutaminase Domain-Containing Protein
gene_id_12916	209	58.85	4.00E-84	hypothetical protein
gene_id_12917	406	59.11	2.00E-170	hypothetical protein
gene_id_12918	284	61.97	2.00E-128	hypothetical protein
gene_id_12919	593	70.99	0	hypothetical protein
gene_id_12920	293	86.01	1.00E-173	hypothetical protein
gene_id_12921	154	64.29	5.00E-55	hypothetical protein
gene_id_12922	620	79.68	0	hypothetical protein
gene_id_12923	708	93.22	0	hypothetical protein
gene_id_12924	274	53.28	1.00E-84	hypothetical protein
gene_id_12925	269	77.32	6.00E-151	hypothetical protein
gene_id_12926	399	73.93	0	hypothetical protein
gene_id_12927	573	74.69	0	hypothetical protein
gene_id_12928	474	66.88	0	hypothetical protein
gene_id_12930	433	77.14	0	hypothetical protein
gene_id_12931	339	74.04	0	hypothetical protein
gene_id_12932	809	69.47	0	hypothetical protein
gene_id_12933	338	69.82	2.00E-173	hypothetical protein
gene_id_12934	610	81.15	0	hypothetical protein
gene_id_12935	131	40.46	6.00E-20	AraC Family Transcriptional Regulator
gene_id_12936	368	40.22	2.00E-60	hypothetical protein
gene_id_12937	300	81	8.00E-152	hypothetical protein
gene_id_12938	296	82.77	1.00E-148	hypothetical protein
gene_id_12939	261	73.18	1.00E-138	Phenazine biosynthesis protein PhzF family
gene_id_12940	896	80.47	0	leucyl-tRNA synthetase
gene_id_14087	593	89.88	0	hypothetical protein
gene_id_14088	229	36.68	1.00E-37	hypothetical protein
gene_id_14089	291	83.16	1.00E-165	hypothetical protein
gene_id_14090	228	50.44	2.00E-65	hypothetical protein
gene_id_14092	1174	87.31	0	hypothetical protein
gene_id_14093	564	77.84	0	Methenyltetrahydrofolate cyclohydrolase
gene_id_14094	214	57.48	2.00E-90	hypothetical protein
gene_id_14095	427	68.15	0	hypothetical protein

gene_id_14096	484	75	0	hypothetical protein
gene_id_14097	157	43.31	7.00E-35	hypothetical protein
gene_id_14098	495	68.89	0	hypothetical protein
gene_id_14099	1036	79.34	0	hypothetical protein
gene_id_14100	703	88.9	0	hypothetical protein
gene_id_14101	89	93.26	5.00E-41	30S ribosomal protein S15
gene_id_14102	396	59.85	4.00E-156	hypothetical protein
gene_id_14103	232	49.57	2.00E-72	hypothetical protein BRDCF_p336
gene_id_14104	90	66.67	1.00E-30	hypothetical protein
gene_id_14105	380	83.16	0	hypothetical protein
gene_id_14106	398	66.33	0	hypothetical protein
gene_id_14107	311	72.99	2.00E-165	hypothetical protein
gene_id_14108	148	72.3	2.00E-76	hypothetical protein
gene_id_14109	306	71.24	2.00E-156	hypothetical protein
gene_id_14110	676	70.12	0	hypothetical protein BRDCF_p330
gene_id_14111	489	87.53	0	hypothetical protein
gene_id_14112	270	71.85	4.00E-140	hypothetical protein
gene_id_14113	454	80.4	0	hypothetical protein
gene_id_14114	336	50	4.00E-104	hypothetical protein
gene_id_14114	211	47.87	3.00E-50	hypothetical protein
gene_id_14115	426	90.61	0	serine hydroxymethyltransferase
gene_id_14116	552	47.46	1.00E-112	Peptidase
gene_id_14117	125	72.8	2.00E-49	Transcriptional regulator, BlaI/MecI/CopY family
gene_id_14118	318	69.5	3.00E-140	hypothetical protein
gene_id_14119	389	75.58	0	OmpA family protein
gene_id_14120	150	84.67	1.00E-87	50S ribosomal protein L9
gene_id_14121	85	100	2.00E-53	30S ribosomal protein S18
gene_id_14122	114	87.72	6.00E-60	30S ribosomal protein S6
gene_id_14123	485	83.3	0	hypothetical protein
gene_id_14124	357	67.51	5.00E-156	hypothetical protein
gene_id_14125	516	71.51	0	MULTISPECIES: symporter
gene_id_14126	227	77.53	1.00E-116	hypothetical protein
gene_id_14127	188	82.45	2.00E-111	hypothetical protein
gene_id_14128	316	68.35	4.00E-139	hypothetical protein
gene_id_14129	125	76	6.00E-58	molybdenum-binding protein
gene_id_14130	351	66.38	2.00E-168	molybdopterin oxidoreductase/precorrin-4 methylase
gene_id_14131	351	78.92	0	hypothetical protein
gene_id_14132	67	68.66	2.00E-23	hypothetical protein
gene_id_14133	195	77.95	1.00E-96	hypothetical protein
gene_id_14134	720	64.03	0	tungsten-containing aldehyde ferredoxin oxidoreductase
gene_id_14135	235	70.21	2.00E-117	hypothetical protein
gene_id_14136	370	64.86	8.00E-178	hypothetical protein
gene_id_14137	108	81.48	1.00E-61	30S ribosomal protein S16
gene_id_14138	181	52.49	5.00E-49	hypothetical protein
gene_id_14139	213	59.62	4.00E-85	hypothetical protein
gene_id_14140	285	35.44	7.00E-45	hypothetical protein
gene_id_14141	164	59.76	4.00E-48	hypothetical protein

gene_id_14142	199	48.24	9.00E-52	hypothetical protein
gene_id_14143	163	75.46	4.00E-87	hypothetical protein
gene_id_14144	395	80	0	hypothetical protein
gene_id_14145	371	77.63	1.00E-168	protein of unknown function DUF819
gene_id_14146	914	43	0	hypothetical protein
gene_id_14147	476	59.24	6.00E-165	hypothetical protein
gene_id_14148	306	51.63	1.00E-105	hypothetical protein BRDCF_p300
gene_id_14149	447	77.4	0	hypothetical protein
gene_id_14150	183	70.49	1.00E-85	hypothetical protein
gene_id_14151	135	89.63	5.00E-83	hypothetical protein
gene_id_14152	127	63.78	1.00E-59	hypothetical protein
gene_id_14153	287	79.79	9.00E-159	hypothetical protein
gene_id_14154	385	74.55	0	hypothetical protein
gene_id_14155	441	78	0	hypothetical protein
gene_id_14156	312	75.96	1.00E-179	hypothetical protein
gene_id_14157	83	92.77	5.00E-46	hypothetical protein
gene_id_14158	229	73.8	5.00E-110	hypothetical protein
gene_id_14159	217	89.4	1.00E-142	hypothetical protein
gene_id_14160	541	78.19	0	hypothetical protein
gene_id_14161	449	88.42	0	hypothetical protein
gene_id_14162	279	70.25	6.00E-148	hypothetical protein
gene_id_14163	314	82.8	0	hypothetical protein
gene_id_14164	158	65.82	3.00E-68	hypothetical protein
gene_id_14165	154	68.18	2.00E-65	hypothetical protein
gene_id_14166	457	77.24	0	hypothetical protein
gene_id_14167	136	83.09	1.00E-78	hypothetical protein
gene_id_14168	360	50.83	1.00E-99	hypothetical protein
gene_id_14169	646	51.39	0	hypothetical protein
gene_id_14170	936	77.24	0	hypothetical protein
gene_id_14171	517	41.01	1.00E-121	hypothetical protein HMPREF1079_04133
gene_id_14172	133	50.38	1.00E-39	site-specific recombinase
gene_id_14176	159	25.16	8.00E-06	virE domain-containing protein
gene_id_14180	558	53.05	0	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arab
gene_id_14181	204	68.14	1.00E-91	hypothetical protein
gene_id_14182	243	78.19	5.00E-141	hypothetical protein
gene_id_14183	391	74.68	0	hypothetical protein
gene_id_14184	105	72.38	8.00E-49	hypothetical protein
gene_id_14185	425	64.94	0	hemerythrin
gene_id_14186	158	50	6.00E-47	hypothetical protein
gene_id_14187	769	56.44	0	copper-translocating P-type ATPase
gene_id_14188	595	39.33	3.00E-120	hypothetical protein
gene_id_14189	321	81	0	hypothetical protein
gene_id_14190	173	47.98	2.00E-54	hypothetical protein
gene_id_14191	130	73.08	2.00E-65	hypothetical protein
gene_id_14192	356	84.83	0	hypothetical protein
gene_id_14193	306	61.76	3.00E-126	hypothetical protein
gene_id_14194	188	69.68	3.00E-96	hypothetical protein

gene_id_14195	288	83.68	9.00E-180	hypothetical protein
gene_id_14196	354	59.04	2.00E-139	Patatin family protein
gene_id_14197	171	77.19	1.00E-96	hypothetical protein
gene_id_14199	284	83.8	1.00E-156	hypothetical protein
gene_id_14200	376	80.85	0	hypothetical protein
gene_id_14201	339	45.72	2.00E-88	udp-glucose 4-epimerase
gene_id_14202	411	68.13	0	hypothetical protein
gene_id_14203	88	38.64	3.00E-12	uncharacterized protein
gene_id_14204	241	30.71	5.00E-12	TIR protein
gene_id_14205	419	57.04	1.00E-132	rOK family protein
gene_id_14207	1150	57.39	0	hypothetical protein
gene_id_14615	407	91.4	0	hypothetical protein
gene_id_14616	200	78.5	5.00E-105	TetR family transcriptional regulator protein
gene_id_14617	382	79.06	0	hypothetical protein
gene_id_14618	342	91.52	0	hypothetical protein
gene_id_14619	135	65.93	1.00E-44	hypothetical protein
gene_id_14620	171	69.59	1.00E-78	RNA polymerase sigma factor
gene_id_14622	492	60.77	0	hypothetical protein
gene_id_14623	382	53.66	2.00E-142	hypothetical protein
gene_id_14624	96	48.96	2.00E-26	hypothetical protein
gene_id_14625	362	70.44	1.00E-176	DNA replication and repair protein recF
gene_id_14626	220	79.09	7.00E-125	tetratricopeptide protein
gene_id_14627	238	87.82	1.00E-147	hypothetical protein
gene_id_14628	139	84.89	4.00E-81	methylmalonyL-CoA epimerase
gene_id_14629	517	93.81	0	hypothetical protein
gene_id_14630	302	69.54	4.00E-154	hypothetical protein
gene_id_14631	146	73.97	2.00E-62	Biotin carboxyl carrier protein
gene_id_14632	384	87.24	0	glutaconyl-CoA decarboxylase subunit beta
gene_id_14633	203	68.47	3.00E-88	hypothetical protein
gene_id_14634	209	61.24	1.00E-94	hypothetical protein
gene_id_14635	582	86.94	0	hypothetical protein
gene_id_14636	438	88.13	0	ATP synthase subunit B
gene_id_14637	199	77.39	3.00E-108	hypothetical protein
gene_id_14638	598	63.88	0	hypothetical protein
gene_id_14639	138	89.13	5.00E-81	hypothetical protein
gene_id_14640	420	76.9	0	hypothetical protein
gene_id_14641	408	75	0	hypothetical protein
gene_id_14642	248	79.84	3.00E-129	hypothetical protein
gene_id_14643	433	36.03	9.00E-87	hypothetical protein
gene_id_14644	124	79.84	3.00E-66	hypothetical protein
gene_id_14645	95	49.47	2.00E-23	ferric siderophore transport system
gene_id_14646	119	32.77	1.00E-16	hypothetical protein
gene_id_14647	232	64.66	3.00E-109	hypothetical protein
gene_id_14648	190	81.05	1.00E-111	zeta toxin
gene_id_14649	51	86.27	9.00E-22	hypothetical protein BRDCF_p1225
gene_id_14650	517	51.84	0	hypothetical protein
gene_id_14652	85	89.41	2.00E-45	hypothetical protein

gene_id_14653	421	69.36	0	hypothetical protein
gene_id_14654	253	73.91	2.00E-131	hypothetical protein
gene_id_14655	337	80.12	0	hypothetical protein
gene_id_14656	133	59.4	9.00E-53	hypothetical protein
gene_id_14657	379	74.67	0	hypothetical protein
gene_id_14658	310	62.9	1.00E-120	dialkylrecorsinol condensing enzyme DarA
gene_id_14659	195	53.33	2.00E-61	hypothetical protein
gene_id_14660	431	77.96	0	hypothetical protein
gene_id_14661	538	62.83	0	hypothetical protein
gene_id_14662	488	52.25	5.00E-171	hypothetical protein
gene_id_14663	1286	58.09	0	hypothetical protein
gene_id_14664	374	63.37	5.00E-172	hypothetical protein
gene_id_14665	115	40	5.00E-23	Dehydratase
gene_id_14666	176	54.55	3.00E-60	hypothetical protein
gene_id_14667	185	43.78	1.00E-44	Outer membrane lipoprotein carrier protein
gene_id_14668	202	54.95	4.00E-77	Polysaccharide deacetylase
gene_id_14669	306	55.23	2.00E-102	hypothetical protein
gene_id_14670	394	72.84	0	hypothetical protein
gene_id_14671	574	58.71	0	hypothetical protein
gene_id_14672	149	77.18	2.00E-81	hypothetical protein
gene_id_14673	145	57.93	3.00E-46	hypothetical protein
gene_id_14674	455	76.48	0	radical SAM protein
gene_id_14675	300	61.67	3.00E-119	Lipid A biosynthesis (KDO)2-(Lauroyl)-lipid IVA acyltransf
gene_id_14676	83	83.13	9.00E-28	hypothetical protein
gene_id_14677	405	87.16	0	hypothetical protein
gene_id_14678	242	73.55	3.00E-116	hypothetical protein
gene_id_14679	491	70.06	0	hypothetical protein
gene_id_14680	312	67.95	1.00E-155	putative transcriptional regulator
gene_id_14681	473	73.36	0	hypothetical protein
gene_id_14682	446	64.57	0	hypothetical protein
gene_id_14683	414	79.47	0	hypothetical protein
gene_id_14684	160	85	1.00E-92	Peptidyl-prolyl cis-trans isomerase
gene_id_14685	511	46.77	3.00E-145	carbohydrate-binding protein SusD
gene_id_14686	1091	45.28	0	hypothetical protein
gene_id_14687	340	76.18	0	tRNA threonylcarbamoyladenosine modification protein
gene_id_14688	1487	49.7	0	hypothetical protein
gene_id_14689	429	76.69	0	hypothetical protein
gene_id_14690	123	72.36	5.00E-63	hypothetical protein
gene_id_14691	231	70.13	7.00E-120	hypothetical protein
gene_id_14692	268	72.39	8.00E-143	Phosphonate metabolism protein PhnP
gene_id_14693	282	47.52	7.00E-87	hypothetical protein
gene_id_14694	697	57.39	0	lysine 2 3-aminomutase
gene_id_14695	50	82	8.00E-21	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltra
gene_id_14696	120	82.5	7.00E-69	hypothetical protein
gene_id_14697	160	82.5	6.00E-92	hypothetical protein
gene_id_14698	312	63.14	1.00E-140	glycoside hydrolase family protein
gene_id_14699	338	62.43	2.00E-156	hypothetical protein

gene_id_14700	504	66.87	0	hypothetical protein
gene_id_14701	307	65.8	3.00E-140	hypothetical protein
gene_id_14702	606	91.58	0	hypothetical protein
gene_id_14703	424	73.58	0	hypothetical protein
gene_id_14704	287	82.93	0	hypothetical protein
gene_id_14705	255	69.02	5.00E-125	hypothetical protein
gene_id_14706	191	63.87	3.00E-61	hypothetical protein
gene_id_14707	496	82.06	0	hypothetical protein
gene_id_14708	205	67.8	1.00E-103	hypothetical protein
gene_id_14709	270	82.59	2.00E-162	hypothetical protein
gene_id_14710	278	83.81	3.00E-174	hypothetical protein
gene_id_14711	170	48.82	7.00E-39	hypothetical protein
gene_id_14712	741	68.02	0	hypothetical protein
gene_id_14713	299	40.47	2.00E-78	hypothetical protein
gene_id_14714	263	71.86	1.00E-118	D-aminopeptidase
gene_id_14715	248	91.13	4.00E-164	hypothetical protein
gene_id_14716	440	74.77	0	hypothetical protein
gene_id_14717	122	73.77	3.00E-62	hypothetical protein
gene_id_14718	243	76.13	2.00E-111	hypothetical protein
gene_id_14719	197	66.5	6.00E-88	hypothetical protein
gene_id_14720	329	52.58	2.00E-95	hypothetical protein
gene_id_14721	107	83.18	2.00E-39	hypothetical protein
gene_id_14722	315	70.16	2.00E-144	hypothetical protein
gene_id_14723	116	81.9	5.00E-61	hypothetical protein
gene_id_14724	272	52.21	4.00E-83	hypothetical protein
gene_id_14725	821	52.01	0	putative aminopeptidase 2
gene_id_14726	159	64.78	4.00E-72	hypothetical protein
gene_id_14727	399	68.17	2.00E-180	hypothetical protein
gene_id_14728	194	75.77	4.00E-105	hypothetical protein
gene_id_14729	480	50.83	6.00E-163	hypothetical protein
gene_id_14730	395	72.15	0	hypothetical protein
gene_id_14731	729	78.46	0	hypothetical protein
gene_id_14732	487	63.86	0	hypothetical protein
gene_id_14733	398	84.92	0	hypothetical protein
gene_id_14734	337	34.12	9.00E-61	hypothetical protein
gene_id_14735	272	35.66	2.00E-41	hypothetical protein
gene_id_14736	427	66.74	0	hypothetical protein
gene_id_14737	203	84.73	4.00E-129	hypothetical protein
gene_id_14738	191	51.31	1.00E-58	hypothetical protein
gene_id_14739	219	65.3	4.00E-97	Amidohydrolase 1
gene_id_14862	329	64.74	8.00E-157	hypothetical protein
gene_id_14863	285	23.51	8.00E-15	AraC family transcriptional regulator
gene_id_14864	440	63.86	0	hypothetical protein
gene_id_14865	275	26.18	7.00E-15	hypothetical protein
gene_id_14866	378	29.89	2.00E-29	hypothetical protein
gene_id_14867	969	58.1	0	hypothetical protein
gene_id_14868	162	87.65	2.00E-100	hypothetical protein

gene_id_14869	205	71.71	5.00E-96	hypothetical protein
gene_id_14870	135	94.07	2.00E-86	hypothetical protein
gene_id_14871	156	71.15	3.00E-78	CMP/dCMP deaminase zinc-binding
gene_id_14872	1145	80.96	0	hypothetical protein
gene_id_14873	142	64.08	3.00E-40	hypothetical protein
gene_id_14874	690	43.77	0	hypothetical protein
gene_id_14875	63	79.37	5.00E-26	hypothetical protein
gene_id_14876	69	57.97	1.00E-15	hypothetical protein
gene_id_14877	367	73.84	0	hypothetical protein
gene_id_14878	404	79.95	0	hypothetical protein
gene_id_14879	232	71.98	2.00E-115	putative glycoprotease
gene_id_14880	382	66.23	0	Thiol:disulfide interchange protein
gene_id_14881	132	79.55	7.00E-71	hypothetical protein
gene_id_14882	157	87.26	3.00E-83	Transcription elongation factor
gene_id_14884	304	74.34	3.00E-170	Riboflavin biosynthesis protein RibF
gene_id_14885	1413	70.77	0	hypothetical protein
gene_id_14886	394	73.35	0	hypothetical protein
gene_id_14887	426	87.32	0	hypothetical protein
gene_id_14888	641	73.79	0	hypothetical protein
gene_id_14889	660	68.94	0	hypothetical protein
gene_id_14890	68	55.88	3.00E-15	hypothetical protein
gene_id_14891	390	66.92	0	hypothetical protein
gene_id_14892	197	75.13	3.00E-106	putative GTP-binding protein engB, partial
gene_id_14893	316	89.56	0	hypothetical protein
gene_id_14894	280	71.43	1.00E-135	hypothetical protein
gene_id_14895	53	77.36	4.00E-22	hypothetical protein
gene_id_14896	436	79.36	0	ribosome-associated GTPase EngA
gene_id_14897	1202	59.65	0	hypothetical protein
gene_id_14898	157	72.61	1.00E-73	Ribosomal RNA large subunit methyltransferase H
gene_id_14899	132	84.09	2.00E-77	hypothetical protein
gene_id_14900	387	89.41	0	hypothetical protein
gene_id_14901	307	63.19	7.00E-139	Ppx/GppA phosphatase
gene_id_14902	238	72.69	9.00E-111	Cytidylate kinase
gene_id_14903	291	73.54	6.00E-156	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
gene_id_14904	669	50.67	0	Primosomal protein N'
gene_id_14905	317	61.51	8.00E-136	hypothetical protein
gene_id_14906	256	87.89	4.00E-165	hypothetical protein
gene_id_14907	298	76.17	6.00E-165	hypothetical protein
gene_id_14908	292	76.71	3.00E-143	hypothetical protein
gene_id_14909	551	62.79	0	Membrane-bound lytic murein transglycosylase D
gene_id_14910	656	43.6	2.00E-163	hypothetical protein
gene_id_14911	162	85.8	8.00E-78	hypothetical protein
gene_id_14912	180	78.33	9.00E-100	hypothetical protein
gene_id_14913	190	65.26	8.00E-84	hypothetical protein
gene_id_14914	329	87.23	0	hypothetical protein
gene_id_14915	197	51.78	2.00E-60	PAP2 family protein
gene_id_14916	330	72.73	0	hypothetical protein

gene_id_14917	97	83.51	2.00E-50	Sigma-54 modulation protein
gene_id_14918	296	71.96	1.00E-158	hypothetical protein
gene_id_14919	63	90.48	3.00E-30	30S ribosomal protein S21
gene_id_14920	677	79.91	0	urocanate hydratase
gene_id_14921	172	70.93	3.00E-86	hypothetical protein
gene_id_14922	306	74.18	1.00E-161	hypothetical protein
gene_id_14923	114	59.65	5.00E-34	hypothetical protein
gene_id_14924	130	58.46	2.00E-49	hypothetical protein
gene_id_14925	117	68.38	7.00E-50	hypothetical protein
gene_id_14926	162	64.2	2.00E-61	thioredoxin
gene_id_14927	115	64.35	1.00E-46	hypothetical protein
gene_id_14928	186	76.34	2.00E-100	hypothetical protein
gene_id_14929	587	71.04	0	hypothetical protein
gene_id_14930	255	74.12	3.00E-131	hypothetical protein
gene_id_14931	243	67.49	8.00E-104	hypothetical protein
gene_id_14932	450	68.22	0	hypothetical protein
gene_id_14933	301	83.72	0	hypothetical protein
gene_id_14934	338	42.9	4.00E-75	hypothetical protein
gene_id_14935	224	80.8	3.00E-131	hypothetical protein
gene_id_14936	261	55.17	8.00E-81	hypothetical protein
gene_id_14937	187	86.63	1.00E-117	thymidine kinase
gene_id_14938	153	80.39	1.00E-69	hypothetical protein
gene_id_14939	360	66.94	1.00E-179	hypothetical protein
gene_id_14940	353	56.66	1.00E-131	hypothetical protein
gene_id_14941	135	68.89	6.00E-61	Type I restriction enzyme R protein
gene_id_14942	468	82.26	0	hypothetical protein
gene_id_14943	364	42.03	5.00E-79	putative sensor-like histidine kinase
gene_id_14944	484	73.35	0	hypothetical protein
gene_id_14945	933	73.2	0	hypothetical protein
gene_id_14946	247	71.66	2.00E-108	hypothetical protein
gene_id_14947	470	60.21	0	Sensor protein
gene_id_14948	197	88.32	9.00E-129	hypothetical protein
gene_id_14949	225	81.78	1.00E-124	hypothetical protein
gene_id_14950	284	58.1	1.00E-110	hypothetical protein
gene_id_14951	232	80.6	2.00E-126	macrolide ABC transporter ATP-binding protein
gene_id_14952	181	83.43	4.00E-109	ATP/cobalamin adenosyltransferase
gene_id_14953	73	100	1.00E-42	hypothetical protein
gene_id_14954	449	92.87	0	hypothetical protein
gene_id_14955	476	79.2	0	hypothetical protein
gene_id_14956	637	67.97	0	hypothetical protein
gene_id_14957	558	92.65	0	hypothetical protein
gene_id_14958	403	74.69	0	hypothetical protein
gene_id_14959	148	83.78	2.00E-86	Protein mraZ
gene_id_14960	298	69.8	8.00E-152	hypothetical protein
gene_id_14961	106	73.58	1.00E-40	hypothetical protein
gene_id_14962	704	78.84	0	hypothetical protein
gene_id_14963	460	80.22	0	hypothetical protein

gene_id_14964	426	87.32	0	hypothetical protein
gene_id_14965	423	85.58	0	hypothetical protein
gene_id_14966	407	77.15	0	hypothetical protein
gene_id_14967	307	78.18	2.00E-165	hypothetical protein
gene_id_14968	454	65.2	0	hypothetical protein
gene_id_14969	266	51.5	4.00E-84	hypothetical protein
gene_id_14970	453	73.29	0	hypothetical protein
gene_id_14971	460	79.35	0	hypothetical protein
gene_id_14972	533	64.92	0	glutamate--tRNA ligase
gene_id_14973	347	76.08	0	hypothetical protein
gene_id_14974	375	68.8	5.00E-173	hypothetical protein
gene_id_14975	142	75.35	6.00E-75	hypothetical protein
gene_id_14976	227	72.25	1.00E-112	tRNA pseudouridine synthase B
gene_id_14977	349	91.12	0	hypothetical protein
gene_id_14978	367	58.04	7.00E-150	hypothetical protein
gene_id_14979	258	58.91	1.00E-109	hypothetical protein
gene_id_14980	344	81.1	0	hypothetical protein
gene_id_14981	247	89.07	1.00E-129	hypothetical protein
gene_id_14982	136	66.18	5.00E-53	hypothetical protein
gene_id_14983	192	94.27	2.00E-129	hypothetical protein
gene_id_14984	157	89.17	6.00E-99	Biopolymer transport protein ExbD/TolR
gene_id_14985	384	62.24	5.00E-157	hypothetical protein
gene_id_14986	485	77.32	0	hypothetical protein
gene_id_14987	464	87.72	0	hypothetical protein
gene_id_14988	205	87.8	3.00E-115	hypothetical protein
gene_id_14989	235	68.51	8.00E-82	hypothetical protein
gene_id_14990	527	72.49	0	hypothetical protein
gene_id_14991	139	89.21	2.00E-87	hypothetical protein
gene_id_14992	553	82.46	0	hypothetical protein
gene_id_14993	608	81.25	0	hypothetical protein
gene_id_14994	84	55.95	2.00E-29	hypothetical protein
gene_id_14995	773	54.33	0	Ribonuclease HII
gene_id_14996	500	80.8	0	hypothetical protein
gene_id_14997	733	86.49	0	hypothetical protein
gene_id_14998	342	74.27	0	hypothetical protein
gene_id_14999	309	78.32	4.00E-161	hypothetical protein
gene_id_15000	237	78.06	4.00E-129	Peptidyl-prolyl cis-trans isomerase
gene_id_15001	122	64.75	2.00E-48	hypothetical protein
gene_id_15002	280	67.14	1.00E-141	hypothetical protein
gene_id_15003	159	73.58	2.00E-83	hypothetical protein
gene_id_15004	343	51.6	6.00E-127	acyl-CoA reductase
gene_id_15005	200	68.5	7.00E-98	hypothetical protein
gene_id_15006	303	84.49	0	hypothetical protein
gene_id_15007	154	81.82	9.00E-75	hypothetical protein
gene_id_15008	357	89.36	0	hypothetical protein
gene_id_15009	306	79.74	3.00E-165	hypothetical protein
gene_id_15010	413	85.71	0	hypothetical protein

gene_id_15011	376	58.78	5.00E-163	hypothetical protein
gene_id_15012	82	91.46	9.00E-46	hypothetical protein
gene_id_15013	201	73.13	8.00E-94	hypothetical protein
gene_id_15014	248	60.89	1.00E-103	hypothetical protein
gene_id_15015	211	45.5	2.00E-41	membrane protein
gene_id_15016	120	48.33	2.00E-26	hypothetical protein
gene_id_15017	150	68	6.00E-74	GCN5-related N-acetyltransferase
gene_id_15018	526	69.2	0	peptidase M28
gene_id_15019	304	70.72	1.00E-161	Phosphate-selective porin O and P family protein
gene_id_15020	553	55.88	0	hypothetical protein
gene_id_15021	383	41.25	2.00E-94	hypothetical protein
gene_id_15022	890	72.58	0	hypothetical protein
gene_id_15023	214	47.66	2.00E-58	hypothetical protein
gene_id_15024	428	81.07	0	hypothetical protein
gene_id_15025	319	85.58	0	hypothetical protein
gene_id_15027	294	70.41	2.00E-153	hypothetical protein
gene_id_15383	447	87.25	0	hypothetical protein
gene_id_15384	198	72.22	4.00E-100	hypothetical protein
gene_id_15385	156	73.08	4.00E-77	hypothetical protein
gene_id_15386	448	61.16	0	MULTISPECIES: UDP-N-acetyl-D-galactosamine dehydrog
gene_id_15388	254	43.7	2.00E-63	transposase
gene_id_15389	92	85.87	1.00E-38	50S ribosomal protein L27
gene_id_15390	102	88.24	2.00E-58	50S ribosomal protein L21
gene_id_15391	367	67.57	7.00E-165	Archaeal ATPase
gene_id_15392	127	75.59	2.00E-60	hypothetical protein
gene_id_15393	672	61.01	0	hypothetical protein
gene_id_15394	630	78.1	0	hypothetical protein
gene_id_15395	792	72.85	0	hypothetical protein
gene_id_15396	392	70.41	6.00E-152	lipopolysaccharide biosynthesis protein
gene_id_15397	179	87.15	2.00E-110	transcriptional regulator, PaaX family
gene_id_15398	321	81.93	0	nAD dependent epimerase/dehydratase family protein
gene_id_15399	378	74.6	0	aminotransferase DegT
gene_id_15400	212	62.26	1.00E-84	hypothetical protein
gene_id_15401	334	66.17	4.00E-163	hypothetical protein
gene_id_15402	363	55.1	5.00E-138	UDP-N-acetylglucosamine 2-epimerase
gene_id_15403	339	52.21	2.00E-120	nucleotidyltransferase
gene_id_15404	227	56.39	3.00E-77	CMP-N-acetylneuraminic acid synthetase
gene_id_15405	316	36.71	8.00E-57	hypothetical protein
gene_id_15406	315	53.97	8.00E-110	hypothetical protein
gene_id_15407	209	37.8	6.00E-36	hypothetical protein
gene_id_15408	491	37.88	1.00E-78	polysaccharide biosynthesis protein
gene_id_15409	360	36.39	9.00E-59	lipooligosaccharide sialyltransferase
gene_id_15410	293	41.3	5.00E-60	hypothetical protein
gene_id_15411	355	35.21	4.00E-48	hypothetical protein
gene_id_15412	169	44.38	1.00E-45	hypothetical protein
gene_id_15413	318	45.28	4.00E-86	MULTISPECIES: hypothetical protein, partial
gene_id_15414	408	32.6	2.00E-66	MULTISPECIES: hypothetical protein

gene_id_15415	262	30.92	3.00E-10	hypothetical protein
gene_id_15416	403	38.71	1.00E-75	glycosyl transferase family 1
gene_id_15417	111	62.16	4.00E-25	hypothetical protein
gene_id_15418	350	46.57	6.00E-114	glycoside hydrolase family protein
gene_id_15419	403	57.32	1.00E-150	group 1 glycosyl transferase
gene_id_15420	375	69.07	0	LPS biosynthesis protein
gene_id_15421	204	62.75	4.00E-86	imidazole glycerol phosphate synthase
gene_id_15422	256	69.92	2.00E-111	imidazole glycerol phosphate synthase
gene_id_15423	326	82.82	0	UDP-glucose 4-epimerase
gene_id_15424	373	69.97	0	epimerase
gene_id_15425	377	85.41	0	UDP-N-acetylglucosamine 2-epimerase
gene_id_15426	413	60.29	2.00E-165	glycosyl transferase family 1
gene_id_15427	317	65.93	2.00E-147	hypothetical protein
gene_id_15428	298	73.15	2.00E-132	hypothetical protein
gene_id_15429	318	73.9	2.00E-176	transcriptional regulator
gene_id_15430	104	37.5	2.00E-14	protein of unknown function DUF323
gene_id_15431	652	54.6	0	Vitamin B12 transporter BtuB
gene_id_16883	170	52.94	2.00E-50	hypothetical protein BRDCF_p270
gene_id_16885	314	26.11	1.00E-19	hypothetical protein
gene_id_16886	152	67.76	4.00E-73	Cell division inhibitor
gene_id_16887	634	32.49	1.00E-96	hypothetical protein
gene_id_16888	634	35.96	2.00E-131	hypothetical protein
gene_id_16889	304	41.78	7.00E-68	PAS/PAC sensor hybrid histidine kinase
gene_id_16890	372	38.98	2.00E-82	histidine kinase
gene_id_16891	346	74.28	3.00E-175	hypothetical protein
gene_id_16892	210	45.24	5.00E-46	MULTISPECIES: hypothetical protein, partial
gene_id_16894	397	80.86	0	hypothetical protein
gene_id_16895	314	83.76	1.00E-153	permease
gene_id_16896	113	53.98	2.00E-35	rhodanese family protein
gene_id_16897	186	65.59	4.00E-83	hypothetical protein ING2E5B_2195
gene_id_16898	135	47.41	2.00E-37	hypothetical protein
gene_id_16899	110	35.45	5.00E-17	Rhodanese-like protein
gene_id_16900	263	34.98	3.00E-36	rhodanese-like protein
gene_id_16901	367	36.51	3.00E-61	hypothetical protein
gene_id_16902	303	38.61	4.00E-61	hypothetical protein
gene_id_16903	118	37.29	2.00E-14	MULTISPECIES: sulfurtransferase
gene_id_16904	408	34.8	3.00E-56	hypothetical protein
gene_id_16905	59	49.15	1.00E-11	preprotein translocase subunit TatC
gene_id_16906	193	35.75	3.00E-35	hypothetical protein
gene_id_16908	155	73.55	5.00E-75	acetyltransferase
gene_id_16909	462	62.99	0	Potassium uptake protein KtrB
gene_id_16910	356	73.03	0	hypothetical protein
gene_id_16911	642	68.07	0	CoA-disulfide reductase
gene_id_16912	136	71.32	1.00E-70	hypothetical protein
gene_id_16913	91	63.74	3.00E-37	hypothetical protein
gene_id_16914	270	41.11	3.00E-61	hypothetical protein
gene_id_16915	125	73.6	1.00E-47	hypothetical protein

gene_id_16916	711	68.64	0	protease
gene_id_16917	467	70.24	0	Beta-lactamase
gene_id_16918	463	82.07	0	hypothetical protein
gene_id_16919	657	57.08	0	hypothetical protein
gene_id_16920	1032	61.53	0	membrane protein
gene_id_16921	168	75	2.00E-80	hypothetical protein
gene_id_16922	149	29.53	2.00E-13	lipoprotein
gene_id_16923	592	81.25	0	hypothetical protein
gene_id_16924	1016	55.22	0	TonB-linked outer membrane protein, SusC/RagA family
gene_id_16925	610	80.66	0	hypothetical protein
gene_id_16926	1111	75.52	0	hypothetical protein
gene_id_16927	334	65.27	2.00E-163	tetraacyldisaccharide 4'-kinase
gene_id_16928	324	83.33	0	hypothetical protein
gene_id_16929	150	86	6.00E-93	50S ribosomal protein L13
gene_id_16930	129	93.02	1.00E-80	30S ribosomal protein S9
gene_id_16931	259	86.49	2.00E-160	30S ribosomal protein S2
gene_id_16932	274	82.85	4.00E-168	hypothetical protein
gene_id_16933	249	46.59	1.00E-70	hypothetical protein
gene_id_16934	801	67.17	0	hypothetical protein
gene_id_16935	246	86.59	2.00E-135	hypothetical protein
gene_id_16936	251	85.66	2.00E-155	hypothetical protein
gene_id_17470	178	83.15	2.00E-93	RNA polymerase ECF-type sigma factor
gene_id_17471	381	73.49	0	FecR protein
gene_id_17472	987	93.82	0	hypothetical protein
gene_id_17473	406	87.93	0	hypothetical protein
gene_id_17474	504	33.53	2.00E-92	hypothetical protein
gene_id_17475	496	83.06	0	hypothetical protein
gene_id_17476	758	80.08	0	hypothetical protein
gene_id_17477	717	82.98	0	hypothetical protein
gene_id_17478	221	47.51	5.00E-67	hypothetical protein
gene_id_17479	916	64.63	0	TonB-dependent receptor
gene_id_17480	387	42.64	5.00E-94	hypothetical protein
gene_id_17481	551	43.92	4.00E-156	hypothetical protein
gene_id_17482	47	51.06	8.00E-06	hypothetical protein
gene_id_17877	295	84.07	6.00E-176	hypothetical protein
gene_id_17878	333	85.89	0	hypothetical protein
gene_id_17879	200	76.5	7.00E-106	transporter
gene_id_17880	193	83.42	5.00E-108	Electron transport complex, RnfABCDGE type, E subunit
gene_id_17881	199	85.93	4.00E-116	Na(+)-translocating NADH-quinone reductase subunit e
gene_id_17882	89	80.9	4.00E-45	hypothetical protein
gene_id_17883	212	60.85	4.00E-86	tungstate/molybdate transport system ATP-binding prot
gene_id_17884	261	75.48	3.00E-111	Anion transport system permease protein
gene_id_17885	324	52.47	7.00E-110	(Fe-S)-binding protein
gene_id_17886	310	71.94	1.00E-145	molybdenum cofactor synthesis protein
gene_id_17887	153	74.51	3.00E-73	molybdenum cofactor biosynthesis protein C
gene_id_17888	239	64.85	3.00E-95	hypothetical protein
gene_id_17889	178	69.1	1.00E-85	hypothetical protein

gene_id_17890	363	72.45	0	RND family efflux transporter, MFP subunit
gene_id_17891	1012	88.34	0	hypothetical protein
gene_id_17892	408	75.25	0	outer membrane efflux protein
gene_id_17893	775	53.68	0	hypothetical protein
gene_id_17894	435	69.43	0	Beta-lactamase
gene_id_17895	407	68.55	4.00E-178	hypothetical protein
gene_id_17896	212	48.11	8.00E-65	hypothetical protein
gene_id_17897	402	34.08	3.00E-66	hypothetical protein
gene_id_17898	1091	82.58	0	hypothetical protein
gene_id_17899	529	73.16	0	hypothetical protein
gene_id_17900	149	73.83	4.00E-74	RNA polymerase ECF-type sigma factor
gene_id_17901	280	47.86	5.00E-79	hypothetical protein
gene_id_17902	805	49.57	0	hypothetical protein
gene_id_17903	131	64.12	6.00E-50	hypothetical protein
gene_id_17904	217	54.84	1.00E-74	hypothetical protein
gene_id_17905	359	83.29	0	beta-lactamase
gene_id_17906	198	35.86	1.00E-16	hypothetical protein
gene_id_17907	218	41.74	6.00E-52	hypothetical protein
gene_id_17908	143	65.03	5.00E-63	osmotically inducible protein C
gene_id_17909	243	62.14	7.00E-77	cation transporter
gene_id_17910	380	66.84	1.00E-175	hypothetical protein
gene_id_17911	486	52.26	0	hypothetical protein
gene_id_17912	273	52.38	1.00E-96	anti-sigma factor
gene_id_17913	182	67.58	4.00E-81	RNA polymerase ECF-type sigma factor
gene_id_17914	418	64.35	0	hypothetical protein
gene_id_17915	152	88.16	1.00E-94	hypothetical protein
gene_id_17916	394	90.36	0	hypothetical protein
gene_id_17917	596	88.09	0	hypothetical protein
gene_id_17919	178	82.02	7.00E-109	
gene_id_17920	1054	84.82	0	hypothetical protein
gene_id_17921	590	82.03	0	hypothetical protein
gene_id_17922	715	63.78	0	Sensor protein
gene_id_17923	678	84.96	0	hypothetical protein
gene_id_17924	652	83.28	0	hypothetical protein
gene_id_17925	329	87.23	0	hypothetical protein
gene_id_17926	344	89.83	0	hypothetical protein
gene_id_17927	334	74.55	0	hypothetical protein
gene_id_17928	958	74.95	0	hypothetical protein
gene_id_17929	399	73.93	0	alkyl hydroperoxide reductase/thiol specific antioxidant/
gene_id_17930	138	56.52	2.00E-40	hypothetical protein
gene_id_17931	311	85.85	0	hypothetical protein
gene_id_17932	537	89.76	0	hypothetical protein
gene_id_17933	330	57.58	3.00E-145	hypothetical protein
gene_id_17934	290	62.41	2.00E-126	cation transporter
gene_id_17935	374	64.17	2.00E-177	hypothetical protein
gene_id_17937	143	72.03	8.00E-71	hypothetical protein
gene_id_17938	198	87.37	1.00E-109	hypothetical protein

gene_id_17939	323	59.13	2.00E-135	hypothetical protein
gene_id_17940	334	66.47	2.00E-160	hypothetical protein
gene_id_17941	537	59.59	0	N-acyl-D-glutamate deacylase
gene_id_17942	315	81.27	8.00E-175	hypothetical protein
gene_id_17943	335	66.27	5.00E-161	hypothetical protein
gene_id_17944	443	68.17	0	hypothetical protein
gene_id_17945	200	48.5	6.00E-51	hypothetical protein
gene_id_17946	367	90.19	0	hypothetical protein
gene_id_17947	110	66.36	3.00E-48	hypothetical protein
gene_id_17948	123	86.99	1.00E-74	hypothetical protein
gene_id_17949	423	60.52	1.00E-176	peptidase M28
gene_id_18262	394	54.82	4.00E-138	hypothetical protein
gene_id_18263	416	90.87	0	hypothetical protein
gene_id_18264	205	82.93	2.00E-105	hypothetical protein
gene_id_18265	206	86.89	2.00E-98	hypothetical protein
gene_id_18266	216	73.15	9.00E-99	hypothetical protein
gene_id_18267	387	83.72	0	hypothetical protein
gene_id_18268	460	78.04	0	hypothetical protein
gene_id_18269	738	66.94	0	hypothetical protein
gene_id_18269	64	60.94	2.00E-14	hypothetical protein
gene_id_18270	1082	79.85	0	hypothetical protein
gene_id_18271	348	54.31	2.00E-133	hypothetical protein
gene_id_18272	192	78.65	1.00E-107	hypothetical protein
gene_id_18273	118	84.75	1.00E-70	thioredoxin
gene_id_18274	203	59.11	2.00E-86	methyltransferase type 12
gene_id_18275	60	36.67	8.00E-06	hypothetical protein
gene_id_18276	72	79.17	4.00E-14	hypothetical protein
gene_id_18277	288	90.97	0	hypothetical protein
gene_id_18278	75	72	3.00E-21	redox-active disulfide protein 2
gene_id_18279	232	72.41	3.00E-117	cytochrome C biogenesis protein
gene_id_18280	129	44.19	4.00E-28	hypothetical protein
gene_id_18281	344	86.92	0	Arsenite resistance protein ArsB
gene_id_18282	141	78.01	1.00E-77	protein tyrosine phosphatase
gene_id_18283	108	68.52	2.00E-50	ArsR family transcriptional regulator
gene_id_18284	225	54.22	7.00E-81	hypothetical protein
gene_id_19303	51	49.02	2.00E-07	hypothetical protein
gene_id_19304	541	64.33	0	hypothetical protein
gene_id_19305	138	58.7	5.00E-55	hypothetical protein
gene_id_19306	212	79.72	4.00E-123	Orotate phosphoribosyltransferase
gene_id_19307	201	66.67	8.00E-88	hypothetical protein
gene_id_19308	139	62.59	4.00E-59	hypothetical protein
gene_id_19309	536	80.41	0	hypothetical protein
gene_id_19309	195	67.69	1.00E-67	hypothetical protein
gene_id_19616	248	60.48	3.00E-76	hypothetical protein
gene_id_19617	259	39.77	2.00E-62	metal-dependent hydrolase
gene_id_19618	845	73.73	0	hypothetical protein
gene_id_19619	138	81.88	2.00E-75	hypothetical protein

gene_id_19620	178	81.46	4.00E-103	methyltransferase
gene_id_19621	270	60.37	7.00E-124	hypothetical protein
gene_id_19622	201	81.59	1.00E-119	hypothetical protein
gene_id_19623	347	60.23	1.00E-149	hypothetical protein
gene_id_19624	320	70.62	1.00E-163	70 kDa peptidylprolyl isomerase
gene_id_19625	434	87.79	0	4-hydroxybutyrate CoA transferase
gene_id_19626	256	54.69	3.00E-103	hypothetical protein BRDCF_p1409
gene_id_19627	266	76.69	2.00E-142	hypothetical protein
gene_id_19628	241	78.42	7.00E-103	Dinucleotide-utilizing enzyme involved in molybdopterin
gene_id_19629	371	57.95	5.00E-173	hypothetical protein
gene_id_19630	114	66.67	7.00E-50	hypothetical protein
gene_id_19631	137	77.37	4.00E-70	hypothetical protein
gene_id_19632	442	76.7	0	hypothetical protein
gene_id_19633	110	79.09	3.00E-58	hypothetical protein
gene_id_19634	241	62.24	7.00E-107	Phosphoesterase PHP
gene_id_19635	180	64.44	1.00E-80	histidine kinase
gene_id_19636	225	60.44	4.00E-84	hypothetical protein
gene_id_19637	133	89.47	7.00E-81	hypothetical protein
gene_id_19638	597	91.62	0	hypothetical protein
gene_id_19639	587	86.03	0	Iron hydrogenase 1
gene_id_19640	159	87.42	2.00E-95	NADH-ubiquinone oxidoreductase subunit
gene_id_19641	234	78.63	8.00E-138	peroxiredoxin
gene_id_19642	228	67.98	4.00E-109	cAMP-binding protein
gene_id_19643	553	81.19	0	hypothetical protein
gene_id_19644	135	71.11	3.00E-67	hypothetical protein HMPREF9449_00887
gene_id_19645	361	86.43	0	peptide chain release factor 1
gene_id_19646	259	69.5	3.00E-125	Orotidine 5'-phosphate decarboxylase
gene_id_19647	218	70.18	5.00E-110	Phosphatidylserine decarboxylase proenzyme
gene_id_19648	275	66.91	1.00E-118	Phosphatidate cytidylyltransferase
gene_id_19649	636	88.99	0	hypothetical protein
gene_id_19650	111	78.38	1.00E-59	hypothetical protein
gene_id_19651	247	48.58	2.00E-80	hypothetical protein
gene_id_19652	216	70.83	2.00E-111	Ribulose-phosphate 3-epimerase
gene_id_19653	467	65.74	0	hypothetical protein
gene_id_19654	469	89.98	0	hypothetical protein
gene_id_19655	288	69.79	2.00E-135	hypothetical protein
gene_id_19656	396	60.86	8.00E-160	hypothetical protein
gene_id_19657	666	80.78	0	hypothetical protein
gene_id_19658	126	82.54	2.00E-63	Endoribonuclease L-PSP family protein
gene_id_19659	521	79.85	0	hypothetical protein
gene_id_19659	52	78.85	8.00E-13	hypothetical protein
gene_id_19660	416	67.07	2.00E-155	hypothetical protein
gene_id_19661	354	81.36	0	Putative GTPase
gene_id_19662	365	60.27	6.00E-160	hypothetical protein
gene_id_19663	53	94.34	2.00E-26	4Fe-4S ferredoxin
gene_id_19664	263	30.04	5.00E-20	uncharacterized protein
gene_id_19665	422	82.23	0	hypothetical protein

gene_id_19666	184	73.91	5.00E-96	Holliday junction resolvase
gene_id_19667	926	58.53	0	hypothetical protein
gene_id_19668	323	77.71	0	hypothetical protein
gene_id_19669	271	69.37	4.00E-124	hypothetical protein
gene_id_19670	350	74.86	0	hypothetical protein
gene_id_19671	50	94	3.00E-11	50S ribosomal protein L34
gene_id_19672	214	67.29	9.00E-102	Ribosomal RNA small subunit methyltransferase G
gene_id_19673	198	64.14	6.00E-75	hypothetical protein
gene_id_19674	886	65.35	0	hypothetical protein
gene_id_19675	146	78.77	2.00E-81	hypothetical protein
gene_id_19676	395	77.22	0	hypothetical protein
gene_id_19677	251	70.52	5.00E-124	hypothetical protein
gene_id_19678	307	87.3	0	Transport system permease protein
gene_id_19679	252	79.37	8.00E-153	Triosephosphate isomerase
gene_id_19680	286	62.59	4.00E-130	hypothetical protein
gene_id_19681	424	78.07	0	hypothetical protein
gene_id_19682	224	92.86	2.00E-148	hypothetical protein
gene_id_19683	413	84.75	0	hypothetical protein
gene_id_19685	341	44.87	1.00E-90	MULTISPECIES: hypothetical protein
gene_id_19686	204	32.35	1.00E-31	putative tetratricopeptide TPR_2
gene_id_19687	100	49	5.00E-23	hypothetical protein
gene_id_19688	139	44.6	1.00E-34	hypothetical protein
gene_id_19689	339	62.24	3.00E-136	hypothetical protein
gene_id_19690	348	36.78	8.00E-59	MULTISPECIES: hypothetical protein
gene_id_19691	242	57.44	7.00E-98	hypothetical protein
gene_id_19692	244	62.7	4.00E-111	hypothetical protein
gene_id_19693	450	85.11	0	peptidase M20
gene_id_19694	151	39.07	6.00E-25	hypothetical protein
gene_id_19695	277	63.54	2.00E-121	Deoxyribose-phosphate aldolase
gene_id_19696	148	72.97	3.00E-69	hypothetical protein
gene_id_19697	258	68.22	2.00E-127	hypothetical protein
gene_id_19698	172	63.95	5.00E-76	Amidohydrolase 1
gene_id_20521	93	60.22	9.00E-31	hypothetical protein BRDCF_p1227
gene_id_20522	541	29.57	2.00E-45	hypothetical protein
gene_id_20523	219	62.1	9.00E-97	hypothetical protein
gene_id_20524	159	81.13	7.00E-61	hypothetical protein
gene_id_20525	178	64.61	2.00E-68	hypothetical protein
gene_id_20974	104	43.27	1.00E-24	dNA-binding helix-turn-helix protein
gene_id_20975	240	35.42	3.00E-42	transcriptional regulator
gene_id_20976	173	44.51	6.00E-43	hypothetical protein
gene_id_20977	137	86.86	1.00E-81	Fur family transcriptional regulator
gene_id_20978	48	77.08	5.00E-18	hypothetical protein
gene_id_20979	1421	79.52	0	multidrug transporter AcrB
gene_id_20980	409	71.64	0	RND transporter
gene_id_20981	108	76.85	3.00E-53	nitrogen regulatory protein P-II
gene_id_20982	128	67.97	1.00E-58	hypothetical protein
gene_id_20983	264	89.77	3.00E-167	cobalt-zinc-cadmium resistance protein

gene_id_20984	109	80.73	3.00E-55	membrane protein
gene_id_20985	295	95.59	0	cobalt transporter
gene_id_20986	43	74.42	5.00E-15	hypothetical protein
gene_id_20989	334	50.9	8.00E-100	transposase
gene_id_20991	118	35.59	2.00E-12	hypothetical protein
gene_id_20993	167	63.47	2.00E-51	resolvase domain
gene_id_20994	263	50.95	1.00E-88	hypothetical protein
gene_id_22522	533	62.48	0	FAD-dependent oxidoreductase
gene_id_22523	338	68.34	6.00E-168	hypothetical protein
gene_id_22524	100	36	7.00E-10	hypothetical protein
gene_id_22525	384	76.82	0	hypothetical protein
gene_id_22526	104	81.73	5.00E-53	hypothetical protein
gene_id_22527	411	79.08	0	hypothetical protein
gene_id_22528	266	73.68	7.00E-123	hypothetical protein
gene_id_22529	665	91.43	0	hypothetical protein
gene_id_22530	193	88.08	2.00E-128	hypothetical protein
gene_id_22531	395	84.05	0	hypothetical protein
gene_id_22532	324	70.99	1.00E-160	hypothetical protein
gene_id_22533	377	79.31	0	hypothetical protein
gene_id_22534	317	80.44	2.00E-180	hypothetical protein
gene_id_22535	258	75.58	5.00E-143	hypothetical protein
gene_id_22536	349	63.04	3.00E-160	hypothetical protein
gene_id_22537	427	64.64	0	hypothetical protein
gene_id_22538	410	67.56	5.00E-173	hypothetical protein
gene_id_22539	543	76.98	0	hypothetical protein
gene_id_22875	848	64.39	0	ATPase
gene_id_22876	514	70.82	0	cation transporter
gene_id_22877	486	55.97	1.00E-174	transporter
gene_id_22878	1281	79.78	0	cation transporter
gene_id_22879	154	37.01	3.00E-22	hypothetical protein
gene_id_22880	154	33.12	3.00E-06	hypothetical protein
gene_id_23043	567	62.26	0	Metallophosphoesterase
gene_id_23044	386	79.02	0	N-acylglucosamine 2-epimerase
gene_id_23045	311	84.57	0	MULTISPECIES: hypothetical protein
gene_id_23046	226	52.65	8.00E-73	MULTISPECIES: GDSL family lipase
gene_id_23047	438	74.2	0	hypothetical protein
gene_id_23048	539	69.57	0	hypothetical protein
gene_id_23049	557	72.35	0	RagB/SusD Domain-Containing Protein
gene_id_23050	1057	70.96	0	hypothetical protein BRDCF_p372
gene_id_23051	430	67.44	0	S-layer protein
gene_id_23052	612	80.07	0	hypothetical protein
gene_id_23053	402	75.87	0	hypothetical protein
gene_id_23054	380	83.68	0	hypothetical protein
gene_id_23055	622	76.21	0	AmpG permease
gene_id_23056	437	75.97	0	hypothetical protein
gene_id_23057	317	66.25	4.00E-152	hypothetical protein
gene_id_23058	486	84.16	0	hypothetical protein

gene_id_23059	524	73.85	0	hypothetical protein
gene_id_23060	278	79.86	2.00E-158	hypothetical protein
gene_id_23061	308	77.6	0	hypothetical protein
gene_id_23063	420	35	8.00E-62	hypothetical protein
gene_id_23064	399	36.59	1.00E-60	hypothetical protein

and thiamine biosynthesis family 1

Gene ID	Length (aa)	Identity	e-value	Annotation
gene_id_261	203	53.69	2.00E-71	HD domain protein
gene_id_262	434	67.97	4.00E-175	branched-chain amino acid transport system carri
gene_id_263	162	71.6	3.00E-75	citrulline cluster-linked protein
gene_id_264	641	59.13	0	nADH:flavin oxidoreductase/NADH oxidase
gene_id_265	397	79.85	0	alanine racemase
gene_id_266	118	71.19	5.00E-56	hypothetical protein
gene_id_267	812	78.33	0	CoA-disulfide reductase
gene_id_268	374	82.89	0	radical SAM protein
gene_id_269	282	64.89	1.00E-126	chemotaxis protein CheY
gene_id_270	153	50.98	4.00E-40	hypothetical protein
gene_id_271	40	70	3.00E-10	ferredoxin
gene_id_272	111	71.17	5.00E-53	cupin domain protein
gene_id_273	614	84.36	0	hydroxylamine reductase
gene_id_274	188	51.6	1.00E-60	hypothetical protein
gene_id_275	185	61.62	1.00E-76	conserved hypothetical protein
gene_id_276	220	67.73	1.00E-110	Crp/Fnr family transcriptional regulator
gene_id_277	231	56.71	1.00E-94	beta-lactamase domain protein
gene_id_278	468	54.91	3.00E-135	amino acid carrier protein
gene_id_279	304	30.26	7.00E-34	hypothetical protein
gene_id_280	501	43.91	3.00E-121	hypothetical protein, partial
gene_id_281	307	43.97	3.00E-74	diguanylate cyclase (GGDEF) domain protein
gene_id_282	123	47.97	8.00E-36	hypothetical protein
gene_id_283	94	61.7	1.00E-32	ferredoxin
gene_id_284	82	79.27	3.00E-38	MULTISPECIES: XRE family transcriptional regulato
gene_id_286	347	60.81	2.00E-140	oxidoreductase
gene_id_287	103	60.19	1.00E-31	hypothetical protein, partial
gene_id_288	255	74.51	1.00E-142	hAD hydrolase family
gene_id_289	792	84.09	0	ribonucleoside triphosphate reductase
gene_id_290	230	62.17	5.00E-108	ribonucleoside-triphosphate reductase activating
gene_id_291	297	64.31	1.00E-134	eDD domain protein DegV family
gene_id_292	146	47.95	4.00E-36	hypothetical protein
gene_id_293	362	76.24	2.00E-174	pilT protein domain protein
gene_id_294	228	67.11	5.00E-101	2-C-methyl-D-erythritol 4-phosphate cytidylyltran
gene_id_295	155	80.65	5.00E-84	ribonuclease H
gene_id_296	66	96.97	2.00E-26	cold-shock protein
gene_id_298	161	78.88	6.00E-92	hD domain protein
gene_id_299	860	88.37	0	hypothetical protein
gene_id_300	344	47.09	3.00E-93	diguanylate cyclase domain protein
gene_id_301	57	66.67	1.00E-08	hypothetical protein
gene_id_303	217	76.5	2.00E-84	hypothetical protein
gene_id_304	206	59.22	1.00E-85	hypothetical protein
gene_id_305	270	74.44	1.00E-135	AraC family transcriptional regulator
gene_id_306	293	74.4	5.00E-126	membrane protein
gene_id_307	140	65.71	6.00E-63	hypothetical protein
gene_id_308	142	57.04	1.00E-52	hypothetical protein
gene_id_309	301	63.12	4.00E-137	transcriptional regulator

gene_id_310	151	67.55	7.00E-70	transcriptional regulator
gene_id_311	294	72.45	1.00E-164	radical SAM protein
gene_id_312	504	65.28	0	glutamate synthase
gene_id_313	417	71.7	1.00E-176	hydroxypyruvate reductase
gene_id_314	162	55.56	4.00E-64	ybaK/prolyl-tRNA synthetase associated region
gene_id_315	466	80.04	0	(Dimethylallyl)adenosine tRNA methylthiotransfer
gene_id_316	117	67.52	1.00E-43	hypothetical protein
gene_id_317	873	83.28	0	dNA mismatch repair protein MutS
gene_id_318	664	63.86	0	dNA mismatch repair protein MutL
gene_id_319	313	75.4	0	tRNA dimethylallyltransferase
gene_id_320	286	54.55	2.00E-89	uncharacterized protein
gene_id_321	435	61.15	9.00E-177	serine-type D-Ala-D-Ala carboxypeptidase
gene_id_322	292	65.07	1.00E-124	degV family protein
gene_id_324	715	69.23	0	DNA topoisomerase III
gene_id_325	422	84.83	0	aluminum resistance protein
gene_id_326	72	54.17	3.00E-18	restriction endonuclease DpnI
gene_id_327	507	68.44	0	polysaccharide biosynthesis protein
gene_id_329	440	80.68	0	amino acid permease
gene_id_331	145	53.79	2.00E-52	hypothetical protein
gene_id_332	106	70.75	5.00E-41	putative transporter
gene_id_333	101	63.37	1.00E-28	hypothetical protein
gene_id_334	83	81.93	3.00E-41	hypothetical protein
gene_id_335	301	71.1	4.00E-115	hypothetical protein
gene_id_336	124	87.1	8.00E-72	na(+)/H(+) antiporter subunit C
gene_id_337	482	73.44	0	hypothetical protein
gene_id_338	488	71.72	0	sodium/proton antiporter ShaA
gene_id_339	492	73.37	0	putative transporter
gene_id_340	651	65.59	0	formate hydrogenlyase subunit 3/Multisubunit Na
gene_id_341	359	63.23	2.00E-163	apbE family protein
gene_id_342	62	40.32	5.00E-08	hypothetical protein
gene_id_343	207	28.99	4.00E-18	transcriptional regulator, TetR family
gene_id_344	384	23.96	2.00E-22	hypothetical protein IYC_06876
gene_id_345	480	59.58	0	hypothetical protein
gene_id_346	492	65.04	0	glycosyl transferase family 1
gene_id_347	136	75.74	2.00E-72	GCN5 family acetyltransferase
gene_id_348	274	78.83	6.00E-145	UDP pyrophosphate phosphatase
gene_id_349	156	72.44	1.00E-79	MULTISPECIES: PadR family transcriptional regulat
gene_id_350	208	65.38	5.00E-101	hypothetical protein, partial
gene_id_351	157	71.97	1.00E-78	flavodoxin
gene_id_352	81	72.84	2.00E-33	uncharacterized protein
gene_id_354	52	57.69	2.00E-14	hypothetical protein
gene_id_355	39	48.72	1.00E-05	hypothetical protein
gene_id_356	227	34.8	8.00E-39	transcriptional regulator
gene_id_357	128	49.22	3.00E-22	membrane protein
gene_id_358	130	38.46	6.00E-19	membrane protein
gene_id_359	131	61.83	2.00E-55	hypothetical protein, partial
gene_id_360	54	72.22	4.00E-20	uncharacterized protein

gene_id_361	512	93.55	0	gMP synthase
gene_id_362	429	81.82	0	hypothetical protein
gene_id_363	407	75.43	0	6-phosphofructokinase
gene_id_364	177	50.28	3.00E-47	hypothetical protein
gene_id_366	668	58.83	0	hypothetical protein
gene_id_367	215	60.47	4.00E-87	rNA pseudouridylate synthase
gene_id_368	815	74.11	0	aTPase AAA-2 domain protein
gene_id_369	137	73.72	1.00E-67	hypothetical protein
gene_id_370	466	73.61	0	dNA repair protein radA
gene_id_371	1153	86.04	0	pyruvate carboxylase
gene_id_372	191	66.49	1.00E-90	hypothetical protein
gene_id_373	174	49.43	4.00E-53	sporulation protein YunB
gene_id_374	785	68.41	0	glycosyltransferase Family 51 candidate bifunctio
gene_id_375	328	64.94	3.00E-156	lipoyltransferase and lipoate-protein ligase
gene_id_376	258	69.77	3.00E-129	putative polysaccharide deacetylase PdaB
gene_id_377	308	54.87	8.00E-118	hypothetical protein
gene_id_378	304	70.72	3.00E-143	pseudouridine-5'-phosphate glycosidase
gene_id_379	384	75.78	0	hypothetical oxygen-independent coproporphyrin
gene_id_381	232	79.31	2.00E-111	hypothetical protein
gene_id_382	290	68.62	5.00E-106	cBS domain-containing protein
gene_id_383	170	75.29	3.00E-91	ferritin-like protein
gene_id_384	263	42.21	3.00E-70	hypothetical protein
gene_id_385	397	87.66	0	hypothetical protein
gene_id_386	353	58.92	4.00E-155	twitching motility protein
gene_id_387	395	36.96	4.00E-96	hypothetical protein
gene_id_388	640	47.66	7.00E-165	hypothetical protein, partial
gene_id_389	203	54.19	3.00E-76	phosphohydrolase
gene_id_390	404	76.24	2.00E-177	TRAP transporter, DctM subunit
gene_id_391	126	73.02	5.00E-56	C4-dicarboxylate ABC transporter permease
gene_id_392	348	70.11	3.00E-178	C4-dicarboxylate ABC transporter substrate-bindi
gene_id_393	340	72.35	3.00E-162	alcohol dehydrogenase
gene_id_394	211	52.13	1.00E-69	hypothetical protein
gene_id_395	472	67.58	0	altronate oxidoreductase
gene_id_396	497	61.97	0	Altronate dehydratase
gene_id_397	361	81.44	0	sugar kinase
gene_id_398	210	60	9.00E-85	2-dehydro-3-deoxyphosphogluconate aldolase
gene_id_399	756	46.03	0	putative Signal transduction protein containing di
gene_id_400	571	58.49	9.00E-157	methyl-accepting chemotaxis protein
gene_id_401	535	54.02	6.00E-169	diguanylate cyclase and metal dependent phosph
gene_id_402	332	54.82	8.00E-123	phospholipase, patatin family
gene_id_403	81	72.84	1.00E-35	competence protein TfoX
gene_id_404	133	74.44	3.00E-70	ArsC family transcriptional regulator
gene_id_405	303	68.98	1.00E-145	methyltransferase
gene_id_406	327	68.5	2.00E-169	beta-lactamase
gene_id_407	625	58.24	0	MULTISPECIES: heavy metal transporter
gene_id_408	168	60.71	2.00E-68	membrane protein, partial
gene_id_409	118	73.73	2.00E-49	HxlR family transcriptional regulator

gene_id_1698	84	63.1	2.00E-14	hypothetical protein
gene_id_1699	62	87.1	1.00E-30	MULTISPECIES: hypothetical protein
gene_id_1700	425	88.24	0	hypothetical protein
gene_id_1702	80	75	3.00E-31	hypothetical protein
gene_id_1703	256	82.42	6.00E-134	hypothetical protein
gene_id_1705	454	64.98	0	hypothetical protein
gene_id_1706	209	40.19	3.00E-41	Cyclic nucleotide-binding domain-containing prot
gene_id_1708	106	83.96	4.00E-58	hypothetical protein
gene_id_1709	200	91	5.00E-134	hypothetical protein, partial
gene_id_1710	174	83.91	3.00E-97	hypothetical protein
gene_id_1712	546	79.67	0	serine recombinase
gene_id_1713	36	52.78	8.00E-07	conjugative transposon protein
gene_id_1714	179	41.34	7.00E-39	CHC2 zinc finger domain protein
gene_id_1715	376	48.94	7.00E-117	plasmid recombination protein
gene_id_1716	295	41.36	8.00E-72	hypothetical protein, partial
gene_id_1717	58	43.1	5.00E-10	excisionase
gene_id_1718	233	37.34	2.00E-41	XRE family transcriptional regulator
gene_id_1719	151	58.94	2.00E-54	hypothetical protein
gene_id_1720	72	44.44	2.00E-11	hypothetical protein
gene_id_1721	303	49.17	3.00E-91	histidine kinase
gene_id_1722	972	75.72	0	MULTISPECIES: DEAD/DEAH box helicase
gene_id_1723	140	47.86	3.00E-23	hypothetical protein POTG_02230
gene_id_1724	194	72.16	1.00E-102	hypothetical protein
gene_id_1725	428	50.47	5.00E-127	MULTISPECIES: restriction endonuclease
gene_id_1726	604	75.33	0	N-6 DNA methylase
gene_id_1727	68	58.82	2.00E-24	MULTISPECIES: hypothetical protein
gene_id_1728	452	69.69	0	23S rRNA (Uracil-5-)-methyltransferase RumA
gene_id_1729	172	60.47	1.00E-66	cRISPR-associated protein Cas4
gene_id_1730	75	70.67	1.00E-28	hypothetical protein
gene_id_1731	314	83.12	0	metal dependent phosphohydrolase
gene_id_1732	376	42.82	1.00E-87	copper amine oxidase N-domain superfamily
gene_id_1733	102	78.43	3.00E-55	XRE family transcriptional regulator
gene_id_1734	68	51.47	2.00E-15	Sporulation initiation factor Spo0A C terminal
gene_id_1735	102	68.63	4.00E-43	XRE family transcriptional regulator
gene_id_1736	570	67.37	0	ammonium transporter
gene_id_1737	258	84.5	3.00E-161	rNA polymerase sigma factor
gene_id_1738	180	68.89	6.00E-85	hypothetical protein
gene_id_1739	185	74.05	2.00E-95	hypothetical protein
gene_id_1740	348	66.38	2.00E-170	tRNA (5-methylaminomethyl-2-thiouridylate)-met
gene_id_1741	561	72.73	0	hypothetical protein
gene_id_1742	436	52.06	8.00E-161	aspartokinase
gene_id_1743	376	78.99	0	carboxynorspermidine decarboxylase
gene_id_1744	400	87.75	0	saccharopine dehydrogenase
gene_id_1745	280	77.5	1.00E-163	agmatinase
gene_id_1746	283	76.33	8.00E-160	spermidine synthase
gene_id_1747	473	83.72	0	arginine decarboxylase
gene_id_1748	256	92.58	5.00E-175	S-adenosylmethionine decarboxylase

gene_id_1750	295	30.17	2.00E-35	hypothetical protein
gene_id_1751	350	50.86	1.00E-120	L-threonine 3-dehydrogenase
gene_id_1752	735	62.99	0	integral membrane sensor signal transduction hist
gene_id_1753	230	93.91	9.00E-155	two component transcriptional regulator winged l
gene_id_1754	407	57.99	4.00E-135	chloride transporter ClC family
gene_id_1755	213	70.42	1.00E-90	yheO-like protein
gene_id_1756	182	68.68	1.00E-64	hypothetical protein
gene_id_1758	245	79.59	1.00E-144	tRNA (guanine-N(1)-)-methyltransferase
gene_id_1759	169	82.25	8.00E-97	ribosome maturation factor RimM
gene_id_1760	76	80.26	5.00E-35	uPF0109 protein CKR_1299
gene_id_1761	82	96.34	2.00E-48	30S ribosomal protein S16
gene_id_1762	446	89.01	0	signal recognition particle protein
gene_id_1763	116	68.97	4.00E-36	uPF0122 protein Desor_4692
gene_id_1765	197	58.38	1.00E-82	alpha-ribazole phosphatase
gene_id_1766	185	78.38	1.00E-93	hDIG domain protein
gene_id_1767	159	84.28	3.00E-98	s-ribosylhomocysteine lyase
gene_id_1768	61	85.25	5.00E-30	transposase IS200/IS605 family
gene_id_2194	643	68.27	0	hypothetical protein
gene_id_2195	287	76.66	4.00E-137	membrane protein
gene_id_2196	444	56.76	0	FAD-linked oxidase
gene_id_2197	117	58.97	2.00E-45	hypothetical protein
gene_id_2198	277	62.82	1.00E-121	ATPase
gene_id_2199	280	65	8.00E-117	ATPase
gene_id_2200	117	70.09	6.00E-54	dinitrogenase iron-molybdenum cofactor
gene_id_2201	306	78.76	6.00E-173	peptidase family T4
gene_id_2202	416	67.79	0	uDP-N-acetylglucosamine 1-carboxyvinyltransfera
gene_id_2203	262	54.2	8.00E-100	polypeptide-transport-associated domain protein
gene_id_2204	233	57.51	1.00E-84	uncharacterized protein
gene_id_2205	96	61.46	3.00E-34	hypothetical protein
gene_id_2206	362	99.17	0	cell division protein
gene_id_2207	278	69.78	1.00E-134	hypothetical protein
gene_id_2208	278	80.94	2.00E-145	phosphate ABC transporter permease PstC
gene_id_2209	289	74.74	5.00E-136	phosphate ABC transporter permease PstA
gene_id_2210	248	89.11	2.00E-166	phosphate ABC transporter ATP-binding protein P
gene_id_2211	213	71.36	1.00E-103	phosphate transport system regulatory protein Ph
gene_id_2212	219	79.45	6.00E-129	MULTISPECIES: HDIG domain protein
gene_id_2213	224	76.34	1.00E-108	response regulators consisting of a CheY-like recei
gene_id_2214	522	58.43	0	sensor histidine kinase
gene_id_2216	489	73.01	0	hydrogenase large subunit domain protein
gene_id_2217	170	46.47	3.00E-34	hypothetical protein
gene_id_2218	286	58.74	2.00E-121	quinolinate synthetase complex A subunit
gene_id_2219	421	58.91	0	L-aspartate oxidase
gene_id_2220	276	69.93	6.00E-138	nicotinate-nucleotide pyrophosphorylase
gene_id_2221	85	62.35	8.00E-32	hypothetical protein
gene_id_2222	702	82.34	0	hypothetical protein
gene_id_2223	215	74.88	4.00E-109	hypothetical protein
gene_id_2224	71	83.1	7.00E-34	hypothetical protein

gene_id_2225	352	84.94	0	hypothetical protein
gene_id_2226	250	93.2	7.00E-173	hypothetical protein
gene_id_2227	182	62.64	6.00E-82	hypothetical protein
gene_id_2228	96	60.42	4.00E-33	hypothetical protein
gene_id_2229	809	68.11	0	peptidase U32
gene_id_2230	447	77.18	0	hypothetical protein
gene_id_2231	441	71.66	0	cell division protein FtsI/penicillin-binding protein
gene_id_2234	259	98.46	1.00E-172	RecName: Full=Activator of lactoyl-CoA dehydrata
gene_id_2235	411	99.27	0	RecName: Full=Lactoyl-CoA dehydratase subunit a
gene_id_2236	374	99.2	0	RecName: Full=Lactoyl-CoA dehydratase subunit b
gene_id_2237	524	99.24	0	propionate CoA-transferase
gene_id_2238	359	59.89	2.00E-160	chemotaxis protein CheY
gene_id_2239	982	37.47	0	multi-sensor hybrid histidine kinase
gene_id_2241	516	46.51	7.00E-159	copper amine oxidase domain-containing protein
gene_id_2242	68	75	2.00E-28	hypothetical protein
gene_id_2243	101	64.36	8.00E-36	hypothetical protein
gene_id_2244	526	59.32	0	aBC-type multidrug transport system ATPase and
gene_id_2245	574	58.36	0	aBC transporter permease/ATP-binding protein
gene_id_2246	281	27.76	9.00E-24	DtxR family iron (metal) dependent repressor
gene_id_2248	524	34.92	3.00E-82	hypothetical protein
gene_id_2249	358	55.87	2.00E-127	hypothetical protein
gene_id_2250	256	71.09	7.00E-133	hypothetical protein
gene_id_2251	327	73.7	2.00E-156	hypothetical protein
gene_id_2252	252	61.51	9.00E-105	aBC-type cobalamin/Fe3+-siderophores transport
gene_id_2253	201	84.58	3.00E-130	integrase
gene_id_2254	97	87.63	6.00E-44	transposase
gene_id_2255	434	67.05	0	antifreeze protein type I
gene_id_2256	203	31.53	8.00E-14	hypothetical protein
gene_id_2257	181	42.54	2.00E-30	hypothetical protein
gene_id_2258	217	31.34	1.00E-28	hypothetical protein
gene_id_2259	136	37.5	4.00E-22	hypothetical protein
gene_id_2260	144	40.97	1.00E-29	hypothetical protein
gene_id_2261	47	51.06	9.00E-07	hypothetical protein
gene_id_2262	434	65.67	0	hypothetical protein
gene_id_2263	152	71.05	4.00E-78	phage-like element PBSX protein xkdM
gene_id_2264	140	63.57	3.00E-58	MULTISPECIES: Phage XkdN-like protein
gene_id_2265	490	35.31	4.00E-67	tape measure domain-containing protein
gene_id_2266	228	47.81	3.00E-52	peptidoglycan-binding protein
gene_id_2267	316	54.75	1.00E-113	hydrolase
gene_id_2268	128	45.31	2.00E-23	hypothetical protein
gene_id_2269	128	52.34	3.00E-40	hypothetical protein
gene_id_2270	353	60.06	4.00E-154	putative phage Mu protein gp47-like protein
gene_id_2271	180	53.33	2.00E-60	hypothetical protein
gene_id_2272	48	70.83	4.00E-17	possible tail fiber protein
gene_id_2273	564	61.52	0	hypothetical protein
gene_id_2274	57	66.67	5.00E-18	hypothetical protein
gene_id_2275	55	61.82	8.00E-10	hypothetical protein

gene_id_2276	121	58.68	2.00E-44	hypothetical protein
gene_id_2279	309	69.26	4.00E-155	hypothetical protein
gene_id_2280	82	48.78	2.00E-13	hypothetical protein
gene_id_2281	373	42.9	1.00E-88	hypothetical protein
gene_id_2282	129	65.89	4.00E-55	hypothetical protein
gene_id_2283	135	57.78	5.00E-40	hypothetical protein
gene_id_2284	73	54.79	4.00E-23	hypothetical protein
gene_id_2285	153	57.52	9.00E-57	hypothetical protein
gene_id_2286	83	74.7	1.00E-36	MULTISPECIES: hypothetical protein
gene_id_2287	756	47.75	0	hydrogenase maturation protein HypF
gene_id_2288	74	45.95	8.00E-17	hydrogenase assembly protein HypC
gene_id_2289	332	53.01	9.00E-118	MULTISPECIES: hydrogenase assembly protein Hu
gene_id_2290	331	56.19	6.00E-125	MULTISPECIES: hydrogenase expression protein H
gene_id_2291	157	38.85	5.00E-31	cytochrome b5
gene_id_2292	299	75.25	3.00E-172	hydrogenase (NiFe) small subunit HydA
gene_id_2293	429	75.29	0	Ni/Fe hydrogenase
gene_id_2294	332	88.86	0	isocitrate dehydrogenase (NAD(+))
gene_id_2295	642	89.88	0	aconitate hydratase
gene_id_2296	459	83.22	0	pyruvate carboxyltransferase
gene_id_2297	332	71.69	4.00E-160	hypothetical protein
gene_id_2298	885	73.11	0	dNA polymerase
gene_id_2299	149	59.73	4.00E-60	dephospho-CoA kinase
gene_id_2300	179	56.42	2.00E-58	lytic transglycosylase catalytic
gene_id_2301	536	52.8	0	aBC-type transporter periplasmic subunit
gene_id_2302	317	56.78	7.00E-130	galactose-1-phosphate uridylyltransferase
gene_id_2303	134	50.75	4.00E-43	hypothetical protein
gene_id_2304	274	48.91	1.00E-73	hypothetical protein
gene_id_2305	513	56.14	0	hypothetical protein
gene_id_2306	119	84.03	4.00E-68	BlaI family transcriptional regulator
gene_id_2307	173	82.66	4.00E-87	peptidyl-prolyl cis-trans isomerase
gene_id_2309	254	65.75	7.00E-121	metallophosphoesterase
gene_id_2310	407	71.74	0	dNA polymerase IV 1
gene_id_2311	99	43.43	5.00E-19	hypothetical protein
gene_id_2312	123	66.67	8.00E-55	NUDIX hydrolase
gene_id_2313	94	52.13	8.00E-26	antibiotic biosynthesis monooxygenase
gene_id_2314	152	65.79	6.00E-67	hypothetical protein
gene_id_2315	228	50.88	5.00E-78	dNA repair protein RadC
gene_id_2316	72	61.11	2.00E-26	phage shock protein C PspC
gene_id_2317	332	84.34	0	tryptophan--tRNA ligase
gene_id_2634	816	81.99	0	phosphorylase
gene_id_2636	169	68.05	2.00E-72	chromate transport protein
gene_id_2637	181	69.06	1.00E-78	chromate transport protein
gene_id_2638	353	86.4	0	peptide chain release factor 1
gene_id_2639	282	58.87	6.00E-115	release factor glutamine methyltransferase
gene_id_2640	303	80.53	1.00E-163	uncharacterized protein
gene_id_2641	67	94.03	6.00E-39	50S ribosomal protein L31
gene_id_2642	472	75.42	0	transcription termination factor Rho

gene_id_2643	377	55.44	9.00E-96	hypothetical protein
gene_id_2644	536	72.57	0	hypothetical protein
gene_id_2645	215	61.86	2.00E-90	adapter protein MecA
gene_id_2646	226	50.88	8.00E-77	hypothetical protein
gene_id_2647	659	91.5	0	putative K(+)-stimulated pyrophosphate-energize
gene_id_2649	309	79.61	3.00E-176	auxin efflux carrier family protein
gene_id_2650	172	56.98	6.00E-52	pAP2 family protein
gene_id_2651	188	70.74	9.00E-63	putative manganese efflux pump MntP
gene_id_2652	167	71.86	4.00E-73	hypothetical protein
gene_id_2653	31	80.65	5.00E-09	hypothetical protein
gene_id_2654	159	59.12	2.00E-27	spore cortex protein YabQ (Spore_YabQ)
gene_id_2655	92	68.48	2.00E-39	sporulation protein YabP
gene_id_2657	79	78.48	3.00E-28	hypothetical protein
gene_id_2658	91	96.7	4.00E-53	hypothetical protein
gene_id_2659	256	71.09	7.00E-123	mazG family protein
gene_id_2660	283	89.4	4.00E-177	hypothetical protein
gene_id_2661	463	89.2	0	hypothetical protein
gene_id_2662	202	68.81	7.00E-98	metallo-beta-lactamase domain protein
gene_id_2663	492	77.03	0	glycerol kinase
gene_id_2664	705	92.48	0	anaerobic ribonucleoside-triphosphate reductase
gene_id_2665	164	74.39	2.00E-90	anaerobic ribonucleoside-triphosphate reductase-
gene_id_2666	143	89.51	5.00E-92	deoxyuridine 5'-triphosphate nucleotidohydrolas
gene_id_2667	207	58.45	1.00E-89	VanW family protein
gene_id_2668	279	65.23	2.00E-101	lipoprotein
gene_id_2669	219	74.43	5.00E-84	aBC-type transporter integral membrane subunit
gene_id_2670	331	75.53	2.00E-176	aBC transporter ATP-binding protein
gene_id_2671	309	68.61	1.00E-153	cell envelope-like function transcriptional attenua
gene_id_2673	271	85.61	4.00E-167	phosphomethylpyrimidine kinase
gene_id_2674	161	78.88	2.00E-85	thiW protein
gene_id_2676	394	55.08	7.00E-152	uncharacterized protein
gene_id_2677	77	79.22	5.00E-18	hypothetical protein
gene_id_2678	380	72.89	0	aTP-dependent RNA helicase DEAD/DEAH box fan
gene_id_2679	196	66.84	6.00E-92	n-acetylmuramoyl-L-alanine amidase CwlD
gene_id_2680	361	87.26	0	phosphoserine aminotransferase
gene_id_2681	392	74.74	0	hypothetical protein
gene_id_2682	416	77.16	0	uncharacterized conserved protein
gene_id_2683	56	51.79	9.00E-14	hypothetical protein
gene_id_2684	535	75.33	0	uDP-N-acetylglucosamine 2-epimerase
gene_id_2685	292	74.66	4.00E-152	ureidoglycolate lyase
gene_id_2686	404	88.86	0	argininosuccinate synthase
gene_id_2687	457	87.53	0	argininosuccinate lyase
gene_id_2688	49	73.47	8.00E-17	toxin-antitoxin system protein
gene_id_2689	216	69.44	9.00E-104	hypothetical protein
gene_id_2691	318	58.81	6.00E-126	hypothetical protein
gene_id_2692	374	77.27	0	hypothetical protein
gene_id_2693	394	80.71	0	putative amino acid aminotransferase
gene_id_2695	177	83.05	6.00E-94	hypothetical protein

gene_id_2696	520	85.38	0	spermidine/putrescine ABC transporter ATP-bindi
gene_id_2697	273	79.85	1.00E-156	aBC transporter permease protein
gene_id_2698	260	79.23	3.00E-121	spermidine/putrescine ABC transporter spermidin
gene_id_2699	330	80.61	0	hypothetical protein
gene_id_2701	389	57.33	4.00E-148	hypothetical protein
gene_id_2702	456	71.49	0	uncharacterized protein conserved in bacteria
gene_id_2703	512	74.8	0	aTPase family protein
gene_id_2704	164	54.27	3.00E-62	acetyltransferase family protein
gene_id_2705	252	64.68	6.00E-76	sulfite exporter TauE/SafE
gene_id_2706	443	54.18	7.00E-166	amino acid decarboxylase
gene_id_2707	457	74.18	0	arylsulfatase regulator (Fe-S oxidoreductase)
gene_id_2708	204	49.02	2.00E-60	hypothetical protein
gene_id_2709	374	71.93	0	glycine/betaine ABC transporter ATPase
gene_id_2710	207	63.77	7.00E-65	choline ABC transporter permease
gene_id_2711	194	51.03	2.00E-57	glycine/betaine ABC transporter permease
gene_id_2712	292	61.3	1.00E-115	glycine/betaine ABC transporter substrate-bindin
gene_id_2713	226	65.49	1.00E-110	methyltransferase
gene_id_2714	252	72.22	2.00E-124	ZIP family zinc transporter
gene_id_2715	202	48.02	1.00E-65	putative transcription regulator
gene_id_2716	270	58.89	1.00E-109	transcriptional regulator, LysR family
gene_id_2717	307	77.52	2.00E-145	membrane protein
gene_id_2718	132	82.58	6.00E-71	endoribonuclease, L-PSP family
gene_id_2719	449	82.41	0	phosphoglucosamine mutase
gene_id_2720	423	45.63	7.00E-128	ybbR-like protein
gene_id_2721	286	81.12	3.00E-132	disA bacterial checkpoint controller nucleotide-bi
gene_id_2722	501	87.62	0	lysine--tRNA ligase
gene_id_2723	158	74.68	2.00E-70	transcription elongation factor GreA
gene_id_2724	309	47.25	8.00E-67	shikimate/quinate 5-dehydrogenase
gene_id_2725	1176	86.99	0	pyruvate-flavodoxin oxidoreductase
gene_id_2726	346	32.08	6.00E-39	hypothetical protein
gene_id_2727	218	43.58	3.00E-45	hypothetical protein
gene_id_2728	130	68.46	6.00E-63	cupin
gene_id_2729	270	70.37	2.00E-129	pyrroline-5-carboxylate reductase
gene_id_2730	117	68.38	2.00E-54	hypothetical protein
gene_id_2731	232	68.53	3.00E-117	short-chain dehydrogenase
gene_id_2732	183	42.08	1.00E-39	flavodoxin
gene_id_2733	190	72.63	6.00E-95	uracil-DNA glycosylase superfamily
gene_id_2734	312	49.68	1.00E-90	putative membrane protein
gene_id_3381	103	51.46	8.00E-24	hypothetical protein
gene_id_3382	141	37.59	1.00E-20	hypothetical protein HMPREF0372_02458
gene_id_3384	552	34.96	2.00E-97	hypothetical protein
gene_id_3385	120	50	1.00E-38	hypothetical protein
gene_id_3386	870	52.76	0	hypothetical protein
gene_id_3387	157	38.85	3.00E-19	hypothetical protein
gene_id_3388	188	42.02	2.00E-44	protein GP15
gene_id_3389	139	48.92	5.00E-40	hypothetical protein
gene_id_3391	158	67.09	2.00E-65	hypothetical protein

gene_id_3392	128	50.78	1.00E-37	hypothetical protein
gene_id_3393	130	62.31	1.00E-52	hypothetical protein
gene_id_3394	130	32.31	6.00E-13	hypothetical protein
gene_id_3395	127	41.73	3.00E-20	hypothetical protein
gene_id_3396	391	76.21	0	hypothetical protein
gene_id_3397	176	38.64	3.00E-24	hypothetical protein
gene_id_3399	376	66.22	5.00E-173	minor capsid 2 protein
gene_id_3400	449	65.7	0	hypothetical protein
gene_id_3401	408	55.88	2.00E-152	phage terminase large subunit PBSX family
gene_id_3402	166	60.84	2.00E-47	terminase
gene_id_3403	670	34.33	8.00E-122	hypothetical protein
gene_id_3405	123	46.34	1.00E-30	hypothetical protein
gene_id_3407	68	80.88	9.00E-33	MULTISPECIES: cold-shock protein
gene_id_3408	100	42	7.00E-09	uncharacterized protein
gene_id_3409	122	48.36	4.00E-34	MULTISPECIES: hypothetical protein
gene_id_3410	460	72.39	0	DEAD/DEAH box helicase
gene_id_3411	95	61.05	5.00E-32	VRR-NUC domain protein
gene_id_3412	781	68.37	0	virulence-associated protein E
gene_id_3413	672	66.22	0	XRE family transcriptional regulator
gene_id_3414	173	75.72	4.00E-94	hypothetical protein, partial
gene_id_3415	367	49.32	2.00E-124	hypothetical protein
gene_id_3416	56	62.5	7.00E-16	hypothetical protein, partial
gene_id_3417	73	60.27	9.00E-20	seryl-tRNA synthetase
gene_id_3418	67	38.81	9.00E-08	hypothetical protein
gene_id_3419	41	90.24	2.00E-14	hypothetical protein M670_00487
gene_id_3421	136	65.44	6.00E-58	phage protein, partial
gene_id_3422	62	45.16	2.00E-10	excisionase family DNA binding domain-containin
gene_id_3423	341	33.14	3.00E-45	transcriptional regulator
gene_id_3424	391	51.66	2.00E-138	integrase
gene_id_3425	601	84.53	0	aspartyl-tRNA synthetase
gene_id_3426	197	74.11	4.00E-88	hypothetical protein
gene_id_3427	325	69.54	3.00E-169	ketol-acid reductoisomerase
gene_id_3428	161	55.9	1.00E-59	acetolactate synthase small subunit
gene_id_3429	553	56.96	0	acetolactate synthase catalytic subunit
gene_id_3432	750	52.53	0	spoIID/LytB domain protein
gene_id_3433	873	38.03	0	hypothetical protein
gene_id_3434	124	70.97	9.00E-56	hypothetical protein
gene_id_3435	335	85.07	0	aspartate--ammonia ligase 1
gene_id_3436	252	63.49	1.00E-109	alpha/beta hydrolase
gene_id_3437	120	40.83	2.00E-14	glycosyltransferases involved in cell wall biogenes
gene_id_3438	399	84.46	0	aminotransferase class I and II
gene_id_3439	197	92.89	7.00E-105	ATP synthase subunit D
gene_id_3440	458	96.07	0	ATP synthase subunit B
gene_id_3441	591	92.39	0	ATP synthase subunit A
gene_id_3442	105	93.33	2.00E-61	ATP synthase subunit F
gene_id_3443	309	87.06	0	ATP synthase subunit C
gene_id_3444	186	82.8	1.00E-71	hypothetical protein

gene_id_3445	161	94.41	2.00E-69	permease
gene_id_3446	658	82.83	0	hypothetical protein
gene_id_3447	107	82.24	7.00E-24	hypothetical protein
gene_id_3448	144	65.97	8.00E-62	a/G-specific adenine glycosylase
gene_id_3449	280	82.14	6.00E-171	33 kDa chaperonin
gene_id_3450	249	57.43	5.00E-101	methyltransferase domain protein
gene_id_3451	44	75	6.00E-14	small acid-soluble spore protein beta
gene_id_3453	330	87.88	0	aspartate-semialdehyde dehydrogenase
gene_id_3454	293	83.62	0	dihydrodipicolinate synthase
gene_id_3455	250	79.2	1.00E-132	dihydrodipicolinate reductase
gene_id_3457	166	66.87	3.00E-72	aTP:corrinoid adenosyltransferase BtuR/CobO/Co
gene_id_3458	208	78.37	3.00E-118	hypothetical protein
gene_id_3459	102	68.63	8.00E-46	hypothetical protein
gene_id_3460	941	87.57	0	uvrABC system protein A
gene_id_3461	655	88.24	0	excinuclease ABC subunit B
gene_id_3462	219	71.69	3.00E-106	4Fe-4S ferredoxin
gene_id_3463	216	55.56	5.00E-84	Crp/Fnr family transcriptional regulator
gene_id_3464	73	84.93	3.00E-38	hypothetical protein
gene_id_3465	193	66.32	6.00E-88	amino acid transporter LysE
gene_id_3466	332	29.82	9.00E-46	hypothetical protein
gene_id_3467	368	76.36	0	hypothetical protein
gene_id_3468	214	62.15	2.00E-93	sugar fermentation stimulation protein homolog
gene_id_3469	177	59.89	2.00E-75	rubrerythrin
gene_id_3471	87	66.67	4.00E-25	hypothetical protein
gene_id_3472	333	85.89	0	holliday junction ATP-dependent DNA helicase Ru
gene_id_3473	202	68.81	2.00E-89	holliday junction ATP-dependent DNA helicase Ru
gene_id_3475	146	89.04	8.00E-92	cMP/dCMP deaminase zinc-binding
gene_id_3476	435	80.92	0	4-hydroxybutyrate coenzyme A transferase
gene_id_3477	137	80.29	3.00E-72	hypothetical protein
gene_id_3478	322	60.56	1.00E-111	hypothetical protein
gene_id_3479	172	61.05	2.00E-68	hypothetical protein
gene_id_3480	676	37.72	1.00E-130	ferrous iron transport protein B
gene_id_3481	75	40	1.00E-11	MULTISPECIES: iron transporter FeoA
gene_id_3482	402	51.99	7.00E-132	copper amine oxidase domain protein
gene_id_3483	158	82.91	7.00E-93	hypothetical protein
gene_id_3484	281	46.26	2.00E-80	N-glycosylase
gene_id_3485	415	50.84	3.00E-136	hypothetical protein
gene_id_3486	138	57.25	3.00E-48	hypothetical protein
gene_id_3489	214	85.98	4.00E-135	endonuclease III
gene_id_3490	261	31.8	4.00E-33	uncharacterized protein
gene_id_3491	144	97.22	5.00E-101	Chain A, Beta-alanyl-coa:ammonia Lyase From Clc
gene_id_3492	397	98.99	0	beta-alanine CoA-transferase
gene_id_3493	284	67.61	5.00E-126	hypothetical protein
gene_id_3494	459	43.57	1.00E-116	amino acid permease
gene_id_3495	448	56.92	7.00E-172	cytochrome C biogenesis protein
gene_id_3496	1037	89.97	0	isoleucyl-tRNA synthetase
gene_id_3498	482	83.2	0	nicotinate phosphoribosyltransferase

gene_id_3499	180	57.78	5.00E-70	phosphinothricin acetyltransferase
gene_id_3500	392	82.4	0	phosphopentomutase
gene_id_3501	436	74.08	0	pyrimidine-nucleoside phosphorylase
gene_id_3503	137	71.53	3.00E-66	hypothetical protein
gene_id_3504	86	88.37	5.00E-42	30S ribosomal protein S20
gene_id_3506	333	72.67	5.00E-155	germination protease
gene_id_3508	169	66.86	3.00E-79	hypothetical protein
gene_id_3509	528	66.48	0	hypothetical protein
gene_id_3510	87	58.62	2.00E-33	phage phi LC3 family holin
gene_id_3511	536	53.73	1.00E-163	acetyl-CoA carboxylase carboxyl transferase beta
gene_id_3512	439	81.78	0	acetyl-CoA carboxylase biotin carboxylase
gene_id_3513	137	83.21	5.00E-78	3-hydroxyacyl-
gene_id_3514	151	61.59	3.00E-39	acetyl-CoA carboxylase biotin carboxyl carrier pro
gene_id_3515	410	75.12	0	3-oxoacyl-
gene_id_3516	244	77.87	1.00E-135	3-oxoacyl-
gene_id_3517	301	69.77	5.00E-151	malonyl CoA-acyl carrier protein transacylase
gene_id_3518	308	87.66	2.00E-156	enoyl-
gene_id_3519	72	81.94	4.00E-17	acyl carrier protein 1
gene_id_3520	317	82.33	5.00E-175	3-oxoacyl-
gene_id_3521	107	41.12	1.00E-15	hypothetical protein
gene_id_3522	171	74.85	3.00E-86	rNA polymerase sigma-24 subunit ECF subfamily
gene_id_3523	219	73.97	5.00E-97	b3/4 domain protein
gene_id_3524	301	44.85	5.00E-97	hypothetical protein
gene_id_3525	391	79.54	0	cys/Met metabolism lyase (PLP-dependent)
gene_id_3526	137	60.58	4.00E-47	hypothetical protein
gene_id_3527	214	59.81	5.00E-87	hydrolase
gene_id_3528	227	33.48	5.00E-28	MULTISPECIES: hypothetical protein
gene_id_3529	235	66.38	6.00E-110	ATPase AAA
gene_id_3530	140	45	1.00E-35	hypothetical protein
gene_id_3531	366	34.43	3.00E-66	copper amine oxidase family protein
gene_id_3532	231	77.92	5.00E-122	MULTISPECIES: XRE family transcriptional regulatc
gene_id_3533	452	56.19	3.00E-165	MULTISPECIES: histidine kinase
gene_id_3535	206	76.21	6.00E-114	MULTISPECIES: potassium transporter TrkA
gene_id_3536	445	63.37	6.00E-171	TrkH family potassium uptake protein
gene_id_3538	91	67.03	1.00E-30	hypothetical protein
gene_id_3540	39	58.97	2.00E-07	hypothetical protein C810_01391
gene_id_3541	69	79.71	8.00E-33	cold-shock protein
gene_id_3543	78	64.1	4.00E-26	single-stranded DNA-binding protein
gene_id_3544	144	65.28	2.00E-65	MarR family transcriptional regulator
gene_id_3545	181	69.61	3.00E-91	glutathione peroxidase
gene_id_3546	273	52.75	3.00E-95	putative histidinol-phosphatase
gene_id_3547	216	76.85	5.00E-119	phosphoribosyl-AMP pyrophosphatase/phosphori
gene_id_3548	251	80.88	3.00E-145	imidazole glycerol phosphate synthase subunit His
gene_id_3549	237	77.22	4.00E-124	1-(5-phosphoribosyl)-5-
gene_id_3551	205	72.2	4.00E-104	imidazole glycerol phosphate synthase subunit His
gene_id_3552	195	78.97	4.00E-108	imidazoleglycerol-phosphate dehydratase
gene_id_3553	354	74.01	0	histidinol-phosphate aminotransferase

gene_id_3554	423	71.63	0	histidinol dehydrogenase
gene_id_3555	203	81.77	4.00E-116	aTP phosphoribosyltransferase
gene_id_3556	375	69.07	1.00E-179	aTP phosphoribosyltransferase regulatory subunit
gene_id_3557	115	53.04	2.00E-21	hypothetical protein
gene_id_3558	209	63.16	3.00E-89	rNA polymerase ECF-type sigma factor
gene_id_3560	528	89.02	0	peptide chain release factor 3
gene_id_3561	124	79.84	1.00E-68	putative endoribonuclease L-PSP
gene_id_3562	151	50.33	2.00E-38	lipoprotein signal peptidase
gene_id_3563	314	88.22	0	fructose-bisphosphate aldolase
gene_id_3564	291	74.91	1.00E-164	beta-lactamase domain protein
gene_id_3565	452	67.92	0	hypothetical protein
gene_id_3566	391	74.42	0	peptidase M20
gene_id_3567	290	77.59	1.00E-139	aBC-type metal ion transport system periplasmic
gene_id_3568	225	80.44	6.00E-96	MULTISPECIES: ABC transporter permease
gene_id_3569	342	75.44	3.00E-155	aBC-type metal ion transport system ATPase com
gene_id_3570	98	60.2	6.00E-26	hypothetical protein
gene_id_3571	150	78	6.00E-80	rNA binding S1 domain protein
gene_id_3572	456	79.17	0	rNA methyltransferase TrmA family
gene_id_3573	232	84.05	6.00E-145	transglutaminase
gene_id_3574	195	81.03	2.00E-116	AraC family transcriptional regulator
gene_id_3575	41	82.93	6.00E-17	hypothetical protein, partial
gene_id_3576	44	84.09	6.00E-18	hypothetical protein
gene_id_3577	206	60.68	3.00E-79	hypothetical protein
gene_id_3578	58	77.59	1.00E-23	hypothetical protein
gene_id_3579	334	61.08	4.00E-148	alpha/beta hydrolase family
gene_id_3580	200	52.5	1.00E-67	hypothetical protein
gene_id_3581	269	57.25	5.00E-107	MerR family transcriptional regulator
gene_id_3582	296	24.32	1.00E-10	hypothetical protein
gene_id_3583	572	40.91	2.00E-129	chemotaxis protein
gene_id_3584	519	68.4	0	hypothetical protein
gene_id_3585	1500	74.13	0	glutamate synthase
gene_id_3586	111	75.68	2.00E-55	hypothetical protein
gene_id_3587	410	79.02	0	probable nicotinate-nucleotide adenylyltransferas
gene_id_3588	360	44.44	2.00E-108	hypothetical protein
gene_id_3589	87	85.06	1.00E-41	hypothetical protein
gene_id_3590	183	69.95	2.00E-89	putative Xre family DNA-binding protein
gene_id_3591	323	65.63	7.00E-164	hypothetical protein
gene_id_3592	404	69.55	0	hypothetical protein
gene_id_3594	130	94.62	1.00E-83	30S ribosomal protein S9
gene_id_3595	145	87.59	2.00E-91	50S ribosomal protein L13
gene_id_3596	247	76.92	9.00E-139	tRNA pseudouridine synthase A 1
gene_id_3597	273	75.82	3.00E-128	hypothetical protein
gene_id_3598	284	84.51	6.00E-178	polyamine-transporting ATPase
gene_id_3599	290	82.07	3.00E-177	cobalt import ATP-binding protein CbiO 3
gene_id_3602	180	91.11	1.00E-103	50S ribosomal protein L17
gene_id_3603	319	97.81	0	DNA-directed RNA polymerase subunit alpha
gene_id_3604	200	96	6.00E-139	30S ribosomal protein S4

gene_id_3605	111	97.3	2.00E-61	30S ribosomal protein S11
gene_id_3606	122	93.44	2.00E-73	30S ribosomal protein S13
gene_id_3607	72	95.83	3.00E-43	translation initiation factor IF-1
gene_id_3608	76	68.42	3.00E-22	hypothetical protein
gene_id_3609	248	67.34	6.00E-123	methionine aminopeptidase, type I
gene_id_3610	208	87.5	3.00E-130	adenylate kinase
gene_id_3611	399	84.96	0	preprotein translocase subunit SecY
gene_id_3612	146	86.3	4.00E-87	50S ribosomal protein L15
gene_id_3613	59	94.92	5.00E-31	50S ribosomal protein L30
gene_id_3614	167	91.02	2.00E-103	30S ribosomal protein S5
gene_id_3615	83	85.54	1.00E-33	50S ribosomal protein L18
gene_id_3616	180	91.67	4.00E-112	50S ribosomal protein L6
gene_id_3617	133	90.98	9.00E-82	30S ribosomal protein S8
gene_id_3618	179	90.5	8.00E-116	50S ribosomal protein L5
gene_id_3619	78	88.46	1.00E-41	50S ribosomal protein L24
gene_id_3620	122	97.54	7.00E-60	50S ribosomal protein L14
gene_id_3621	85	97.65	2.00E-51	30S ribosomal protein S17
gene_id_3622	66	90.91	2.00E-34	50S ribosomal protein L29
gene_id_3623	145	93.1	4.00E-84	50S ribosomal protein L16
gene_id_3624	209	90.91	1.00E-136	30S ribosomal protein S3
gene_id_3625	129	96.12	1.00E-84	50S ribosomal protein L22
gene_id_3626	94	96.81	2.00E-60	30S ribosomal protein S19
gene_id_3627	261	92.34	4.00E-177	50S ribosomal protein L2
gene_id_3628	99	85.86	4.00E-54	50S ribosomal protein L23
gene_id_3629	206	91.75	2.00E-136	50S ribosomal protein L4
gene_id_3630	199	87.44	6.00E-122	50S ribosomal protein L3
gene_id_3631	104	99.04	6.00E-66	30S ribosomal protein S10
gene_id_3633	452	91.81	0	uPF0210 protein FVAG_02149
gene_id_3634	90	75.56	2.00E-40	uPF0237 protein CLONEX_01555
gene_id_3635	181	62.98	6.00E-79	2'-5' RNA ligase
gene_id_3636	660	84.24	0	transketolase
gene_id_3637	215	93.49	4.00E-144	probable transaldolase 1
gene_id_3639	481	80.46	0	threonine synthase
gene_id_3640	445	70.79	0	rNA methylase NOL1/NOP2/sun family
gene_id_3641	183	79.78	8.00E-108	flavin reductase domain protein FMN-binding
gene_id_3642	77	58.44	2.00E-17	hypothetical protein
gene_id_3644	229	65.94	1.00E-115	hypothetical protein
gene_id_3645	263	79.85	2.00E-142	relA/SpoT domain protein
gene_id_3646	171	54.97	5.00E-62	hypothetical protein
gene_id_3647	75	89.33	2.00E-42	hypothetical protein
gene_id_3648	192	57.81	7.00E-73	hypothetical protein
gene_id_3649	137	72.26	2.00E-67	flavodoxin
gene_id_3650	687	50.22	0	methyl-accepting chemotaxis sensory transducer
gene_id_3651	719	75.1	0	iron transporter FeoB
gene_id_3652	73	79.45	4.00E-34	feoA domain protein
gene_id_3653	69	75.36	4.00E-27	iron transporter FeoA
gene_id_3654	146	30.82	3.00E-10	hypothetical protein

gene_id_3655	241	41.91	5.00E-45	uncharacterized protein
gene_id_3656	112	72.32	5.00E-52	putative transcriptional regulator
gene_id_3659	305	41.64	5.00E-58	hypothetical protein
gene_id_3661	270	37.41	8.00E-52	RpiR family transcriptional regulator
gene_id_3662	313	51.12	6.00E-100	carbohydrate kinase
gene_id_3663	319	69.59	1.00E-135	periplasmic-binding protein domain protein
gene_id_3664	496	71.98	0	putative ribose transport, ATP-binding protein Rb
gene_id_3665	322	75.47	7.00E-130	hypothetical protein
gene_id_3666	316	65.82	4.00E-155	hypothetical protein
gene_id_3667	283	77.03	1.00E-152	MULTISPECIES: fructose-bisphosphate aldolase
gene_id_3668	318	68.24	1.00E-156	hypothetical protein
gene_id_3669	418	56.94	1.00E-170	tagatose-bisphosphate aldolase
gene_id_3670	219	81.28	1.00E-100	hypothetical protein
gene_id_3671	224	83.48	3.00E-132	hypothetical protein
gene_id_3672	245	79.59	3.00E-140	hypothetical protein
gene_id_3673	294	77.89	2.00E-167	amino acid ABC transporter substrate-binding pro
gene_id_3674	309	79.29	3.00E-161	cysteine synthase
gene_id_3675	301	53.49	1.00E-106	methyltransferase
gene_id_3676	151	74.83	2.00E-80	hypothetical protein
gene_id_3677	380	73.95	0	cystathionine beta-lyase
gene_id_3678	303	75.25	1.00E-148	cysteine synthase
gene_id_3679	300	74.67	1.00E-168	LysR family transcriptional regulator
gene_id_3680	239	58.58	1.00E-96	methionine ABC transporter ATPase
gene_id_3681	333	56.76	5.00E-122	methionine ABC transporter ATP-binding protein
gene_id_3682	180	62.78	2.00E-48	methionine ABC transporter permease
gene_id_3683	178	61.8	1.00E-62	pyruvate/ketoisovalerate oxidoreductase gamma
gene_id_3684	96	72.92	7.00E-44	pyruvate:ferredoxin oxidoreductase
gene_id_3685	387	79.59	0	pyruvate ferredoxin oxidoreductase alpha subuni
gene_id_3686	296	82.77	4.00E-177	pyruvate synthase
gene_id_3687	433	85.68	0	phenylacetate-coenzyme A ligase family protein
gene_id_3688	389	84.32	0	aminotransferase
gene_id_3689	143	69.23	1.00E-64	MULTISPECIES: Rrf2 family transcriptional regulat
gene_id_3690	310	85.81	2.00E-161	cysteine synthase
gene_id_3691	269	54.65	4.00E-101	hypothetical protein
gene_id_3693	339	74.63	0	tRNA (5-methylaminomethyl-2-thiouridylate)-met
gene_id_3694	254	79.53	6.00E-139	dinucleotide-utilizing enzyme possibly involved in
gene_id_3695	372	69.35	0	aminotransferase V
gene_id_3696	279	82.8	2.00E-177	potassium ABC transporter ATPase
gene_id_3697	428	78.04	0	homoserine dehydrogenase
gene_id_3698	284	49.65	1.00E-73	hypothetical protein
gene_id_3699	240	87.08	1.00E-144	RNA polymerase sigma-E factor
gene_id_3701	142	76.76	2.00E-55	hypothetical protein, partial
gene_id_3702	137	77.37	2.00E-58	hypothetical protein HMPREF0322_03104, partial
gene_id_3703	42	80.95	9.00E-14	transposase IS200/IS605 family
gene_id_3743	408	78.68	0	hypothetical protein
gene_id_3744	292	80.14	9.00E-131	hypothetical protein
gene_id_3745	220	76.36	4.00E-98	hypothetical protein

gene_id_3746	532	90.98	0	60 kDa chaperonin
gene_id_3747	95	87.37	2.00E-52	10 kDa chaperonin
gene_id_3749	286	79.02	2.00E-148	thioredoxin-disulfide reductase
gene_id_3750	690	86.96	0	translation elongation factor EF-G
gene_id_3751	145	88.28	3.00E-88	hypothetical protein
gene_id_3752	391	80.05	0	cysteine desulfurase
gene_id_3753	136	52.94	1.00E-39	transcriptional regulator XRE family
gene_id_3754	554	64.8	0	dNA replication and repair protein RecN
gene_id_3755	151	95.36	1.00E-100	arginine repressor
gene_id_3756	283	74.2	4.00E-144	probable inorganic polyphosphate/ATP-NAD kinas
gene_id_3757	267	82.02	1.00E-157	hemolysin A
gene_id_3758	624	74.36	0	1-deoxy-D-xylulose-5-phosphate synthase
gene_id_3759	140	67.86	9.00E-65	acid phosphatase/vanadium-dependent haloper
gene_id_3760	295	76.95	2.00E-168	polyprenyl synthetase
gene_id_3761	78	70.51	2.00E-18	exodeoxyribonuclease 7 small subunit
gene_id_3762	409	66.75	0	exodeoxyribonuclease 7 large subunit
gene_id_3764	131	70.99	1.00E-53	n utilization substance protein B homolog
gene_id_3765	122	72.13	8.00E-40	hypothetical protein
gene_id_3766	212	71.7	1.00E-94	hypothetical protein
gene_id_3767	185	51.35	2.00E-43	hypothetical protein
gene_id_3768	174	35.63	1.00E-18	stage III sporulation protein AF
gene_id_3769	351	65.81	6.00E-121	stage III sporulation protein AE
gene_id_3770	127	74.02	2.00E-57	sporulation stage III protein AD
gene_id_3771	64	92.19	1.00E-31	stage III sporulation protein AC
gene_id_3772	143	53.15	4.00E-43	hypothetical protein
gene_id_3773	310	51.29	6.00E-102	stage III sporulation protein AA
gene_id_3774	241	36.93	3.00E-49	accessory gene regulator protein A
gene_id_3775	205	54.63	2.00E-54	esterase
gene_id_3776	181	56.35	1.00E-72	putative N-acetylmuramoyl-L-alanine amidase
gene_id_3777	367	67.85	0	iron-containing alcohol dehydrogenase
gene_id_3778	82	63.41	3.00E-13	hypothetical protein
gene_id_3779	255	60.78	2.00E-102	exonuclease superfamily protein
gene_id_3780	424	77.59	0	adenylosuccinate synthetase
gene_id_3781	188	42.55	1.00E-41	response regulator receiver
gene_id_3782	185	69.19	8.00E-94	MULTISPECIES: cyclase
gene_id_3783	331	62.84	3.00E-135	hypothetical protein
gene_id_3784	727	47.46	0	dNA internalization-related competence protein
gene_id_3785	298	50.67	3.00E-102	hypothetical protein
gene_id_3786	496	68.95	0	integral membrane sensor signal transduction his
gene_id_3787	229	91.27	4.00E-151	dNA-binding response regulator VicR
gene_id_3788	61	57.38	2.00E-13	competence protein ComEA
gene_id_3789	392	64.8	5.00E-170	serine-type D-Ala-D-Ala carboxypeptidase
gene_id_3790	378	58.2	4.00E-154	bacterial SH3 domain family protein
gene_id_3791	576	75.17	0	ABC transporter, permease/ATP-binding protein
gene_id_3792	591	73.27	0	ABC transporter ATP-binding protein
gene_id_3793	317	59.62	2.00E-138	MULTISPECIES: hypothetical protein, partial
gene_id_3794	670	67.01	0	hypothetical protein

gene_id_3795	96	62.5	2.00E-30	uncharacterized protein
gene_id_3796	145	46.21	9.00E-42	Fur family transcriptional regulator
gene_id_3797	147	42.86	1.00E-33	hypothetical protein
gene_id_3798	109	40.37	2.00E-12	hypothetical protein
gene_id_3799	164	71.34	3.00E-82	MULTISPECIES: cysteine methyltransferase
gene_id_3800	486	73.46	0	AraC family transcriptional regulator
gene_id_3802	215	56.28	8.00E-62	hypothetical protein
gene_id_3803	418	49.04	2.00E-141	hypothetical protein
gene_id_3804	478	80.13	0	glycogen synthase 1
gene_id_3805	598	77.42	0	oligoendopeptidase F
gene_id_3806	208	67.31	1.00E-106	dihydroorotate dehydrogenase
gene_id_3807	136	67.65	2.00E-62	hypothetical protein
gene_id_3808	152	68.42	8.00E-76	5-nitroimidazole antibiotic resistance protein
gene_id_3809	463	47.08	8.00E-134	cell division protein FtsW
gene_id_3810	90	71.11	3.00E-39	PadR family transcriptional regulator
gene_id_3811	159	67.92	1.00E-72	predicted phosphoesterase
gene_id_3812	185	88.65	2.00E-115	non-canonical purine NTP pyrophosphatase
gene_id_3813	242	73.55	2.00E-132	ribonuclease PH
gene_id_3814	135	45.93	1.00E-32	hypothetical protein
gene_id_3815	703	51.92	0	cell wall hydrolase/autolysin
gene_id_3817	792	78.79	0	putative ATP-dependent protease
gene_id_3818	154	72.73	1.00E-78	ribosomal-protein-alanine acetyltransferase
gene_id_3819	222	70.27	6.00E-95	hypothetical protein
gene_id_3820	141	69.5	5.00E-66	hypothetical protein
gene_id_3821	567	38.8	1.00E-110	hypothetical protein
gene_id_3824	358	52.51	7.00E-116	peptidase M23
gene_id_3825	214	91.12	4.00E-139	transcriptional regulator, TetR family
gene_id_3826	122	88.52	3.00E-67	hypothetical protein
gene_id_3827	270	52.59	2.00E-90	hypothetical protein
gene_id_3828	1226	60.52	0	aTP-dependent helicase/nuclease subunit A
gene_id_3829	184	61.96	3.00E-77	hypothetical protein
gene_id_3831	86	48.84	1.00E-17	hypothetical protein
gene_id_3832	141	84.4	3.00E-81	transcriptional repressor NrdR
gene_id_3833	87	80.46	1.00E-40	hypothetical protein
gene_id_3834	781	82.46	0	anaerobic ribonucleoside-triphosphate reductase
gene_id_3835	164	64.63	7.00E-72	anaerobic ribonucleoside-triphosphate reductase-
gene_id_3836	631	54.2	0	histidine kinase A domain protein
gene_id_3837	232	93.97	2.00E-158	dNA-binding response regulator
gene_id_3838	400	49	1.00E-128	putative glycosyl transferase group 2 family prote
gene_id_3839	385	22.6	2.00E-14	hypothetical protein
gene_id_3840	141	78.01	4.00E-75	fe2+/Zn2+ uptake regulation proteins
gene_id_3841	162	85.19	2.00E-100	putative tRNA (cytidine(34)-2'-O)-methyltransfera
gene_id_3842	343	51.02	5.00E-122	hypothetical protein
gene_id_3843	89	48.31	9.00E-21	hypothetical protein
gene_id_3844	370	72.43	2.00E-166	putative 8-amino-7-oxononanoate synthase/2-am
gene_id_3845	872	65.48	0	calcium-translocating P-type ATPase, PMCA-type
gene_id_3846	165	50.3	2.00E-29	putative sporulation protein YtaF

gene_id_3847	74	41.89	7.00E-14	hypothetical protein
gene_id_3848	254	57.48	7.00E-98	hypothetical protein
gene_id_3849	628	69.11	0	C4-dicarboxylate ABC transporter
gene_id_3850	124	57.26	2.00E-39	hypothetical protein
gene_id_3851	271	66.79	5.00E-120	TAXI family TRAP transporter solute receptor
gene_id_3852	235	62.98	3.00E-101	hypothetical protein
gene_id_3853	140	52.14	1.00E-23	flagellar export protein FliJ
gene_id_3854	433	73.9	0	flagellar protein export ATPase FliI
gene_id_3855	173	45.09	6.00E-48	hypothetical protein
gene_id_3856	333	62.46	7.00E-153	flagellar motor switch protein FliG
gene_id_3857	555	48.11	5.00E-154	hypothetical protein
gene_id_3858	76	57.89	4.00E-24	flagellar hook-basal body protein FliE
gene_id_3859	142	62.68	3.00E-59	flagellar basal body rod protein FlgC
gene_id_3860	116	53.45	3.00E-34	flagellar basal-body rod protein FlgB
gene_id_3862	480	77.5	0	fumarate reductase
gene_id_3863	132	46.21	1.00E-34	hypothetical protein
gene_id_3864	704	64.35	0	ferredoxin
gene_id_3865	268	47.39	3.00E-76	MerR family transcriptional regulator
gene_id_3866	868	89.29	0	pyruvate phosphate dikinase
gene_id_3867	216	79.63	3.00E-130	chloramphenicol acetyltransferase
gene_id_3868	462	88.53	0	glycyl-tRNA synthetase subunit beta
gene_id_3869	242	55.79	7.00E-83	dNA repair protein RecO
gene_id_3871	300	84	0	gTPase Era
gene_id_3872	132	70.45	1.00E-64	hypothetical protein
gene_id_3873	186	81.72	3.00E-111	hypothetical protein
gene_id_3874	130	76.92	2.00E-66	cytidine deaminase
gene_id_3875	155	78.71	8.00E-72	16S rRNA maturation RNase YbeY
gene_id_3876	705	62.27	0	7TM receptor with intracellular metal dependent
gene_id_3877	324	84.88	0	phosphate starvation-inducible protein PhoH prec
gene_id_3878	368	54.62	2.00E-132	sporulation protein YqfD
gene_id_3879	86	59.3	3.00E-28	sporulation protein YqfC
gene_id_3881	264	85.61	8.00E-153	aBC transporter ATP-binding protein
gene_id_3882	288	78.82	1.00E-134	hypothetical protein
gene_id_3883	330	70.3	4.00E-147	aBC-type uncharacterized transport system peripl
gene_id_3884	148	80.41	8.00E-81	gatB/YqeY domain protein
gene_id_3885	43	100	2.00E-21	30S ribosomal protein S21
gene_id_3886	729	70.37	0	1 4-alpha-glucan branching enzyme GlgB
gene_id_3887	540	79.63	0	predicted exonuclease of the beta-lactamase fold
gene_id_3889	85	89.41	1.00E-46	hypothetical protein
gene_id_3890	89	74.16	5.00E-32	hypothetical protein
gene_id_3891	447	61.07	0	peptidase U62 modulator of DNA gyrase
gene_id_3892	460	75.87	0	peptidase U62 modulator of DNA gyrase
gene_id_3893	173	75.72	9.00E-94	holliday junction resolvase RecU
gene_id_3894	260	58.46	4.00E-103	hypothetical protein
gene_id_3895	452	63.27	0	putative efflux protein MATE family
gene_id_3896	163	47.24	5.00E-36	hypothetical protein
gene_id_3897	60	46.67	5.00E-07	hypothetical protein

gene_id_3899	191	88.48	2.00E-108	xanthine phosphoribosyltransferase
gene_id_3900	359	53.76	9.00E-131	MULTISPECIES: ABC transporter substrate-binding
gene_id_3901	493	72.41	0	ABC transporter ATP-binding protein
gene_id_3902	346	64.16	1.00E-140	branched-chain amino acid ABC transporter perm
gene_id_3903	308	63.64	2.00E-123	ABC transporter permease
gene_id_3904	543	85.64	0	sulfate transporter family/STAS domain protein
gene_id_3905	169	49.7	1.00E-49	CDP-alcohol phosphatidyltransferase
gene_id_3906	458	84.5	0	pyridoxal-phosphate dependent TrpB-like enzyme
gene_id_3907	641	52.42	0	chemotaxis protein, partial
gene_id_3908	117	70.94	2.00E-43	hypothetical protein
gene_id_3909	185	84.86	8.00E-115	elongation factor P
gene_id_3910	167	70.66	3.00E-82	hAD superfamily (Subfamily IIIA) phosphatase TIG
gene_id_3911	113	61.06	3.00E-43	dinitrogenase iron-molybdenum cofactor
gene_id_3912	357	84.59	0	aminopeptidase
gene_id_3913	665	85.26	0	methionine--tRNA ligase
gene_id_3914	251	79.28	5.00E-137	hydrolase TatD family
gene_id_3916	264	69.32	1.00E-120	g5 domain protein
gene_id_3917	79	73.42	1.00E-34	Cro/Cl family transcriptional regulator
gene_id_3918	70	55.71	2.00E-18	hypothetical protein
gene_id_3919	391	79.28	0	probable tRNA sulfurtransferase
gene_id_3920	382	81.94	0	cysteine sulfinate desulfinase/cysteine desulfuras
gene_id_3921	241	74.27	5.00E-114	ribosomal RNA small subunit methyltransferase E
gene_id_3922	325	85.23	0	ribosomal protein L11 methyltransferase
gene_id_3923	243	80.66	5.00E-145	nucleotidyl transferase
gene_id_3924	324	70.06	4.00E-169	pseudouridine synthase
gene_id_3925	318	90.57	0	peptide chain release factor 2
gene_id_3926	109	55.96	2.00E-28	acetyltransferase N-acetylglutamate synthase
gene_id_3927	90	52.22	6.00E-22	hypothetical protein
gene_id_3928	857	89.26	0	preprotein translocase subunit SecA
gene_id_3929	213	64.79	3.00E-98	hypothetical protein
gene_id_3930	443	58.69	7.00E-157	hypothetical protein
gene_id_3931	173	66.47	2.00E-82	hD domain protein
gene_id_3932	196	74.49	1.00E-104	thymidine kinase
gene_id_3933	181	83.98	2.00E-108	sigma 54 modulation protein/ribosomal protein S
gene_id_3934	171	75.44	6.00E-91	appr-1-p processing domain protein
gene_id_3935	235	45.11	6.00E-53	hypothetical protein
gene_id_3936	285	65.96	7.00E-125	stage II sporulation protein D
gene_id_3937	267	57.68	7.00E-94	hypothetical protein
gene_id_3938	256	83.98	2.00E-155	fe-S oxidoreductase
gene_id_3940	934	43.36	0	s-layer y domain-containing protein
gene_id_3941	127	40.16	3.00E-17	hypothetical protein
gene_id_3942	50	48	3.00E-06	hypothetical protein
gene_id_3943	365	87.95	0	GTP-binding protein YchF
gene_id_3944	101	55.45	6.00E-31	hypothetical protein
gene_id_3945	389	77.38	0	alcohol dehydrogenase iron-dependent
gene_id_3946	293	53.58	6.00E-97	hypothetical protein
gene_id_3947	608	85.03	0	asparagine synthetase

gene_id_3948	525	60.57	0	4-alpha-glucanotransferase
gene_id_3949	109	37.61	3.00E-06	hypothetical protein
gene_id_3950	115	79.13	1.00E-39	hypothetical protein
gene_id_3951	158	56.96	6.00E-42	hypothetical protein C820_02387
gene_id_3952	100	44	1.00E-25	hypothetical protein
gene_id_3953	194	51.03	2.00E-62	integral membrane protein
gene_id_3954	336	33.04	4.00E-30	putative TolA domain protein
gene_id_3955	118	72.88	7.00E-41	hypothetical protein
gene_id_3956	399	65.66	0	hypothetical protein
gene_id_3957	199	75.88	2.00E-112	putative transcriptional regulator (TetR/AcrR fami
gene_id_3958	500	70.4	0	sodium/proline symporter
gene_id_3959	557	77.02	0	phosphoglucomutase/phosphomannomutase alpl
gene_id_3960	491	47.86	1.00E-137	pEGA domain protein
gene_id_3961	305	56.39	2.00E-112	spore coat protein CotS
gene_id_3962	389	61.7	1.00E-167	uncharacterized domain HDIG
gene_id_3963	162	69.14	3.00E-67	dihydrofolate reductase
gene_id_3964	276	87.68	0	thymidylate synthase
gene_id_3965	371	67.65	6.00E-162	extracellular ligand-binding receptor
gene_id_3966	290	78.62	3.00E-137	branched-chain amino acid ABC-type transport sy
gene_id_3967	337	66.77	1.00E-117	aBC-type branched-chain amino acid transport sys
gene_id_3968	278	75.54	2.00E-141	ABC transporter
gene_id_3969	239	79.08	4.00E-132	branched-chain amino acid ABC transporter ATP-k
gene_id_3970	272	71.32	2.00E-142	MerR family transcriptional regulator
gene_id_3971	445	69.21	0	mATE efflux family protein
gene_id_3972	192	64.06	7.00E-79	lysine exporter protein (LYSE/YGGA)
gene_id_3973	226	92.48	3.00E-139	redox-sensing transcriptional repressor rex
gene_id_3974	637	79.28	0	hypothetical protein
gene_id_3975	186	26.88	2.00E-17	uncharacterized protein
gene_id_3976	66	84.85	1.00E-33	hydrid cluster protein-associated redox disulfide c
gene_id_3977	65	61.54	4.00E-19	hypothetical protein
gene_id_3978	116	37.07	3.00E-16	uncharacterized protein
gene_id_3979	174	73.56	6.00E-90	signal peptidase I
gene_id_3980	307	81.43	0	sufB/sufD domain protein
gene_id_3981	235	85.96	5.00E-148	aBC transporter related
gene_id_3982	190	59.47	7.00E-70	hypothetical protein
gene_id_3983	163	53.37	2.00E-39	hypothetical protein
gene_id_3984	151	58.94	1.00E-55	MULTISPECIES: methylated-DNA--protein-cysteine
gene_id_3985	277	76.53	4.00E-144	probable endonuclease 4
gene_id_3986	130	66.15	4.00E-58	hemerythrin
gene_id_3987	540	77.96	0	na+/H+ antiporter NhaC
gene_id_3989	238	74.37	9.00E-117	purine nucleoside phosphorylase
gene_id_3990	400	81.75	0	putative RNA methylase
gene_id_3991	480	85.21	0	glutamate--tRNA ligase
gene_id_3992	447	74.5	0	carbon starvation protein CstA
gene_id_3994	255	47.84	3.00E-83	histidine kinase
gene_id_3995	575	48.87	1.00E-169	hypothetical protein HMPREF9473_03954
gene_id_3996	389	56.81	9.00E-119	putative membrane protein

gene_id_3997	246	61.79	3.00E-93	n-acetylmuramoyl-L-alanine amidase
gene_id_3998	229	58.52	4.00E-96	putative metal dependent hydrolase
gene_id_3999	172	40.7	1.00E-35	hypothetical protein
gene_id_4000	183	70.49	1.00E-97	carbonic anhydrase
gene_id_4002	321	42.99	3.00E-75	copper amine oxidase-like domain-containing pro
gene_id_4005	553	65.64	0	phosphoribulokinase/uridine kinase
gene_id_4006	372	65.32	1.00E-172	hypothetical protein
gene_id_4007	227	60.35	4.00E-74	predicted SAM-dependent methyltransferase
gene_id_4008	357	95.24	0	rNA polymerase sigma factor
gene_id_4009	592	74.32	0	DNA primase
gene_id_4010	337	78.93	0	deoxyguanosinetriphosphate triphosphohydrolas
gene_id_4011	262	77.86	4.00E-140	bis(5'-nucleosyl)-tetraphosphatase PrpE
gene_id_4014	156	34.62	3.00E-21	hypothetical protein
gene_id_4016	51	82.35	3.00E-22	hypothetical protein
gene_id_4017	428	84.58	0	tRAP transporter DctM subunit
gene_id_4018	162	78.4	8.00E-90	tRAP transporter DctQ-like membrane protein
gene_id_4019	374	74.06	0	tRAP transporter solute receptor DctP family
gene_id_4020	232	68.97	2.00E-119	hypothetical protein
gene_id_4021	199	67.34	3.00E-89	thiamine-phosphate synthase
gene_id_4022	275	65.82	7.00E-126	hydroxyethylthiazole kinase
gene_id_4023	303	67	3.00E-147	resolvase N-terminal domain protein
gene_id_4024	86	48.84	7.00E-24	hypothetical protein
gene_id_4025	232	62.07	8.00E-97	peptidase S8 and S53 subtilisin kexin sedolisin
gene_id_4026	120	51.67	9.00E-36	hypothetical protein
gene_id_4027	239	64.02	2.00E-103	transcriptional regulator XRE family
gene_id_4028	429	77.62	0	branched-chain amino acid transport system carri
gene_id_4029	460	78.48	0	hypothetical protein
gene_id_4030	879	80.89	0	alanyl-tRNA synthetase
gene_id_4031	66	43.94	5.00E-07	putative membrane protein
gene_id_4032	474	72.78	0	transcriptional regulator GntR family with aminot
gene_id_4033	454	61.23	0	hypothetical protein
gene_id_4034	432	93.29	0	electron transport complex RnfABCDGE type C su
gene_id_4035	321	83.8	0	electron transport complex RnfABCDGE type D su
gene_id_4036	175	73.71	8.00E-78	rnfG/nqrC
gene_id_4037	199	91.46	2.00E-116	electron transport complex RnfABCDGE type E su
gene_id_4038	192	90.62	8.00E-105	rnfA
gene_id_4039	261	84.67	2.00E-118	hypothetical protein
gene_id_4040	78	66.67	1.00E-26	hypothetical protein
gene_id_4041	342	92.98	0	cell shape determining protein MreB/Mrl family
gene_id_4042	249	71.08	5.00E-125	cell shape-determining protein MreC
gene_id_4043	155	64.52	3.00E-58	rod shape-determining protein MreD
gene_id_4044	947	66.21	0	penicillin-binding protein dimerization domain pr
gene_id_4045	210	77.62	3.00E-101	probable septum site-determining protein MinC
gene_id_4046	265	90.19	5.00E-157	site-determining protein
gene_id_4047	92	93.48	7.00E-56	cell division topological specificity factor
gene_id_4048	382	72.51	0	rod shape-determining protein RodA
gene_id_4049	131	90.08	4.00E-83	methylglyoxal synthase

gene_id_4050	96	61.46	2.00E-24	putative membrane protein
gene_id_4051	206	74.27	2.00E-104	sporulation stage II protein R
gene_id_4052	340	44.12	2.00E-77	germination protein Ger(X)C family
gene_id_4053	367	42.51	2.00E-70	spore germination protein
gene_id_4054	487	69.61	0	bacillus/Clostridium GerA spore germination prot
gene_id_4055	391	41.94	3.00E-89	hypothetical protein
gene_id_4056	680	48.09	2.00E-164	copper amine oxidase-like domain-containing pro
gene_id_4056	112	53.57	2.00E-13	copper amine oxidase-like domain-containing pro
gene_id_4057	821	47.14	0	copper amine oxidase domain protein/surface-lay
gene_id_4059	270	52.22	6.00E-81	putative ribonuclease
gene_id_4060	248	62.5	1.00E-116	hypothetical protein
gene_id_4061	340	72.65	2.00E-177	hydroxymethylpyrimidine-binding protein
gene_id_4062	247	85.02	2.00E-132	aBC-type transporter integral membrane subunit
gene_id_4063	251	75.3	1.00E-133	taurine-transporting ATPase
gene_id_4064	215	74.88	7.00E-116	putative transcription activator
gene_id_4066	230	50	7.00E-65	putative membrane protein
gene_id_4067	151	54.97	2.00E-37	hypothetical protein
gene_id_4068	198	86.87	2.00E-123	recombination protein RecR
gene_id_4069	98	86.73	2.00E-32	nucleoid-associated protein Clo1313_2801
gene_id_4070	532	71.8	0	DNA polymerase III subunit gamma/tau
gene_id_4073	150	80	3.00E-86	hypothetical protein
gene_id_4074	443	50.56	2.00E-137	hypothetical protein
gene_id_4075	175	74.86	8.00E-88	hypothetical protein
gene_id_4076	188	75.53	7.00E-97	nucleoside recognition domain protein
gene_id_4077	86	90.7	3.00E-47	transcriptional regulator AbrB family
gene_id_4078	270	87.04	2.00E-171	aAA family ATPase
gene_id_4079	399	80.2	0	hypothetical protein
gene_id_4080	312	77.88	2.00E-155	l-lactate dehydrogenase 1
gene_id_4081	433	60.74	4.00E-169	putative transporter
gene_id_4541	409	73.59	0	peptidase T
gene_id_4542	411	87.35	0	tyrosyl-tRNA synthetase
gene_id_4543	192	90.62	4.00E-117	intracellular protease PfpI family
gene_id_4544	294	74.15	8.00E-162	tyrosine recombinase XerD
gene_id_4545	188	55.32	4.00E-45	stage II sporulation protein M
gene_id_4546	174	66.67	3.00E-73	nUDIX hydrolase
gene_id_4547	397	79.09	0	aminotransferase class I and II
gene_id_4548	306	51.31	2.00E-97	zn-dependent dipeptidase microsomal dipeptidas
gene_id_4550	271	67.53	3.00E-129	spo0A protein (CheY-like receiver domain and HT
gene_id_4551	406	57.14	3.00E-156	stage IV sporulation protein B
gene_id_4552	209	54.55	3.00E-73	gntR family transcriptional regulator
gene_id_4553	437	89.7	0	enolase
gene_id_4554	515	81.75	0	2 3-bisphosphoglycerate-independent phosphogl
gene_id_4555	247	79.76	2.00E-147	triosephosphate isomerase
gene_id_4556	308	48.38	2.00E-85	polysaccharide deacetylase
gene_id_4557	397	86.9	0	phosphoglycerate kinase
gene_id_4558	338	72.78	6.00E-173	transcriptional regulator DeoR family
gene_id_4560	154	94.81	5.00E-104	hypothetical protein

gene_id_4561	218	66.97	2.00E-99	hypothetical protein
gene_id_4562	443	66.37	0	hypothetical protein
gene_id_4563	685	62.63	0	hypothetical protein
gene_id_4564	219	85.39	7.00E-136	phosphonate-transporting ATPase
gene_id_4565	50	60	9.00E-10	hypothetical protein CLOSTHATH_00089
gene_id_4566	423	81.56	0	gTPase HflX
gene_id_4567	277	69.68	3.00E-143	diaminopimelate epimerase
gene_id_4568	70	74.29	3.00E-28	uncharacterized protein
gene_id_4569	406	70.2	0	putative Zn-dependent peptidase
gene_id_4570	704	88.35	0	polyribonucleotide nucleotidyltransferase
gene_id_4571	87	93.1	3.00E-41	30S ribosomal protein S15
gene_id_4572	299	54.85	5.00E-91	dMT superfamily drug/metabolite transporter
gene_id_4573	318	78.3	2.00E-178	riboflavin biosynthesis protein RibF
gene_id_4574	309	66.02	4.00E-142	tRNA pseudouridine synthase B
gene_id_4575	320	61.88	1.00E-131	exopolyphosphatase-related proteins
gene_id_4576	127	70.87	2.00E-63	ribosome-binding factor A
gene_id_4577	583	89.71	0	translation initiation factor IF-2
gene_id_4577	96	43.75	2.00E-11	translation initiation factor IF-2
gene_id_4578	89	62.92	1.00E-23	50S ribosomal protein L7ae
gene_id_4579	90	85.56	1.00E-48	hypothetical protein
gene_id_4580	370	86.49	0	transcription termination factor NusA
gene_id_4581	155	78.06	2.00E-80	ribosome maturation factor RimP
gene_id_4582	201	62.19	2.00E-82	membrane protein
gene_id_4584	118	56.78	4.00E-29	hypothetical protein
gene_id_4585	242	86.36	6.00E-150	glutamate transport ATP-binding protein
gene_id_4586	216	74.07	8.00E-104	glutamine ABC superfamily ATP binding cassette t
gene_id_4587	266	72.93	3.00E-132	aBC transporter substrate-binding protein family 3
gene_id_4588	214	72.43	1.00E-91	deoxyribose-phosphate aldolase
gene_id_4590	269	55.39	5.00E-95	aBC transporter substrate-binding protein family 3
gene_id_4591	638	79.15	0	4-hydroxy-3-methylbut-2-enyl diphosphate reduc
gene_id_4592	186	63.44	2.00E-83	1-acyl-sn-glycerol-3-phosphate acyltransferase
gene_id_4593	221	58.37	3.00E-85	cytidylate kinase
gene_id_4594	389	75.06	0	hI0933 family protein
gene_id_4595	214	61.21	6.00E-96	fructose-2 6-bisphosphatase
gene_id_4596	238	80.67	5.00E-121	pseudouridine synthase
gene_id_4597	361	62.6	5.00E-163	serine-type D-Ala-D-Ala carboxypeptidase
gene_id_4598	109	48.62	1.00E-24	hypothetical protein
gene_id_4599	169	84.02	2.00E-93	segregation and condensation protein B
gene_id_4600	253	75.49	3.00E-111	segregation and condensation protein A
gene_id_4601	168	70.24	6.00E-82	peptidase M50
gene_id_4602	66	77.27	3.00E-27	hypothetical protein
gene_id_4603	81	38.27	1.00E-08	hypothetical protein HOLDEFILI_04216
gene_id_4604	273	50.55	1.00E-94	2-dehydropantoate 2-reductase
gene_id_4605	308	59.42	3.00E-120	hypothetical protein
gene_id_4606	415	82.17	0	gamma-glutamyl phosphate reductase
gene_id_4607	182	46.15	2.00E-28	uPF0291 protein HMPREF0988_00246
gene_id_4608	203	42.36	6.00E-57	putative membrane protein

gene_id_4609	145	55.17	9.00E-22	hypothetical protein
gene_id_4610	260	76.92	4.00E-142	glutamate 5-kinase
gene_id_4611	899	45.72	0	diguanylate cyclase
gene_id_4612	558	91.04	0	glutamine--tRNA ligase
gene_id_4613	151	54.97	6.00E-52	hypothetical protein
gene_id_4614	676	74.41	0	heat shock protein Hsp90
gene_id_4615	165	35.76	7.00E-34	hypothetical protein
gene_id_4616	533	69.79	0	carbon starvation protein A
gene_id_4617	249	82.33	2.00E-157	exodeoxyribonuclease III Xth
gene_id_4618	110	81.82	1.00E-60	arsenate reductase and related proteins glutared
gene_id_4619	259	53.28	4.00E-101	nitrilase/cyanide hydratase and apolipoprotein N-
gene_id_4620	137	68.61	4.00E-62	protein tyrosine phosphatase
gene_id_4621	254	67.32	2.00E-118	tryptophan synthase alpha chain
gene_id_4622	383	85.12	0	tryptophan synthase beta chain
gene_id_4623	200	58	3.00E-70	hypothetical protein
gene_id_4624	257	61.48	2.00E-111	indole-3-glycerol phosphate synthase
gene_id_4625	335	60.9	4.00E-143	anthranilate phosphoribosyltransferase
gene_id_4626	188	62.77	2.00E-77	glutamine amidotransferase of anthranilate synth
gene_id_4627	491	63.14	0	anthranilate synthase subunit I
gene_id_4629	261	67.43	6.00E-125	putative epimerase
gene_id_4630	472	53.18	0	GntR family transcriptional regulator
gene_id_4631	287	70.73	1.00E-125	cation diffusion facilitator family transporter
gene_id_4633	389	74.04	0	chaperone protein DnaJ
gene_id_4634	611	91.98	0	chaperone protein DnaK
gene_id_4635	154	83.12	7.00E-88	co-chaperone GrpE
gene_id_4636	342	77.49	0	heat-inducible transcription repressor hrcA
gene_id_4637	377	58.62	9.00E-143	putative oxygen-independent coproporphyrinoge
gene_id_4638	627	53.27	0	hypothetical protein
gene_id_4639	396	71.21	0	diaminopropionate ammonia-lyase
gene_id_4640	291	67.7	1.00E-144	hypothetical protein
gene_id_4641	412	75.73	0	hypothetical protein
gene_id_4642	109	50.46	2.00E-33	putative membrane protein TIGR04086 family/int
gene_id_4643	284	58.1	6.00E-116	putative metal-dependent phosphoesterase PHP
gene_id_4644	514	39.11	8.00E-123	hypothetical protein
gene_id_4645	495	56.57	1.00E-177	sensory transduction histidine kinase
gene_id_4646	227	84.14	2.00E-122	response regulator receiver
gene_id_4647	314	53.18	1.00E-118	redoxin
gene_id_4648	425	51.29	9.00E-156	glycoside hydrolase
gene_id_4649	414	73.67	1.00E-175	putative transporter
gene_id_4650	633	77.09	0	aBC transporter related protein
gene_id_4651	300	65.67	3.00E-119	prolipoprotein diacylglyceryl transferase
gene_id_4652	417	43.88	5.00E-123	hypothetical protein
gene_id_4653	408	47.79	1.00E-100	hypothetical protein
gene_id_4654	525	27.81	6.00E-51	hypothetical protein
gene_id_4656	425	86.12	0	GTPase CgtA
gene_id_4658	96	97.92	2.00E-61	50S ribosomal protein L27
gene_id_4659	110	69.09	4.00E-49	hypothetical protein

gene_id_4660	101	90.1	3.00E-39	50S ribosomal protein L21
gene_id_4661	927	38.83	0	tetratricopeptide repeat protein
gene_id_4662	206	58.25	2.00E-76	regulatory protein RecX
gene_id_4663	345	83.77	0	recombinase RecA
gene_id_4664	294	63.95	1.00E-111	permease of the drug/metabolite transporter sup
gene_id_4665	412	75	0	competence/damage-inducible domain protein Ci
gene_id_4666	177	83.05	4.00E-88	hypothetical protein
gene_id_4667	452	80.53	0	ribosomal protein S12 methylthiotransferase Rim
gene_id_4668	284	83.8	1.00E-153	bifunctional protein FolD
gene_id_4669	556	89.75	0	formate--tetrahydrofolate ligase
gene_id_4670	481	84.41	0	cell division protein FtsK/SpoIIIE
gene_id_4670	234	52.56	7.00E-37	cell division protein FtsK/SpoIIIE
gene_id_4671	175	48.57	2.00E-52	ferredoxin
gene_id_4672	298	63.76	4.00E-109	hypothetical protein
gene_id_4673	396	75.51	0	hypothetical protein
gene_id_4674	426	88.26	0	aTP-dependent Clp protease ATP-binding subunit
gene_id_4675	199	90.95	4.00E-132	aTP-dependent Clp protease proteolytic subunit
gene_id_4676	429	76.46	0	trigger factor
gene_id_4677	92	72.83	5.00E-43	hypothetical protein
gene_id_4678	248	51.61	2.00E-86	radical SAM protein
gene_id_4679	227	80.18	1.00E-130	MULTISPECIES: hypothetical protein
gene_id_4681	120	70	5.00E-48	hypothetical protein
gene_id_4682	190	82.63	1.00E-98	hydrolase
gene_id_4683	183	77.05	7.00E-102	MULTISPECIES: DNA-binding protein
gene_id_4685	667	80.06	0	hypothetical protein
gene_id_4686	73	83.56	6.00E-34	feoA family protein
gene_id_4687	243	57.2	3.00E-96	aBC transporter related
gene_id_4688	514	28.4	3.00E-41	hypothetical protein
gene_id_4689	215	44.19	2.00E-31	hypothetical protein
gene_id_4690	127	55.91	9.00E-43	transcriptional regulator GntR family
gene_id_4691	607	78.25	0	glucosamine--fructose-6-phosphate aminotransfe
gene_id_4692	303	44.22	1.00E-77	hypothetical protein
gene_id_4693	156	80.13	4.00E-86	GNAT family acetyltransferase
gene_id_4694	528	72.73	0	fAD dependent oxidoreductase
gene_id_4695	245	66.53	4.00E-119	tRNA pseudouridine synthase A 1
gene_id_4696	547	74.41	0	inorganic diphosphatase
gene_id_4697	199	53.27	8.00E-58	hypothetical protein
gene_id_4698	91	64.84	1.00E-35	toxin-antitoxin system antitoxin component ArsR
gene_id_4699	43	72.09	6.00E-13	chloramphenicol acetyltransferase
gene_id_4700	62	61.29	9.00E-20	chloramphenicol acetyltransferase
gene_id_4701	37	64.86	2.00E-09	chloramphenicol acetyltransferase
gene_id_4702	191	74.35	7.00E-105	hypothetical protein
gene_id_4704	206	63.11	3.00E-73	membrane protein
gene_id_5599	620	42.42	3.00E-145	hypothetical protein
gene_id_5600	111	59.46	2.00E-28	hypothetical protein
gene_id_5602	43	60.47	3.00E-21	hypothetical protein, partial
gene_id_5602	42	61.9	3.00E-21	hypothetical protein, partial

gene_id_5603	286	53.85	2.00E-94	hypothetical protein
gene_id_5604	297	65.32	1.00E-129	AraC family transcriptional regulator
gene_id_5605	339	75.52	0	iron ABC transporter substrate-binding protein
gene_id_5606	327	81.35	1.00E-120	iron ABC transporter
gene_id_5607	331	79.15	9.00E-146	MULTISPECIES: iron ABC transporter permease
gene_id_5608	279	79.21	3.00E-163	ABC transporter ATP-binding protein
gene_id_5609	114	68.42	8.00E-39	hypothetical protein
gene_id_5610	586	76.96	0	MULTISPECIES: hypothetical protein
gene_id_5611	577	78.16	0	MULTISPECIES: hypothetical protein
gene_id_5612	60	63.33	9.00E-20	Nickel ABC transporter, ATP-binding protein
gene_id_5613	48	58.33	1.00E-12	ABC transporter related protein
gene_id_5614	189	46.03	3.00E-54	TetR family transcriptional regulator
gene_id_5615	443	60.5	3.00E-165	multidrug transporter MatE
gene_id_5616	573	53.75	0	ABC transporter ATP-binding protein
gene_id_5617	565	61.24	0	ABC transporter, ATP-binding protein
gene_id_5618	494	53.85	0	ABC transporter, ATP-binding protein
gene_id_5619	130	51.54	2.00E-32	cell wall binding repeat-containing protein
gene_id_5621	112	49.11	2.00E-28	RNA polymerase subunit sigma-24
gene_id_5688	211	68.72	8.00E-108	NADPH-dependent FMN reductase
gene_id_5689	157	78.98	1.00E-67	2-C-methyl-D-erythritol 2 4-cyclodiphosphate syn
gene_id_5690	188	81.91	1.00E-105	serine acetyltransferase
gene_id_5691	470	89.57	0	cysteinyl-tRNA synthetase
gene_id_5692	141	71.63	2.00E-68	mini-ribonuclease 3
gene_id_5693	247	88.26	4.00E-160	rRNA methylase putative group 3
gene_id_5694	172	79.65	5.00E-95	hypothetical protein
gene_id_5695	214	70.09	3.00E-106	rNA polymerase sigma-24 subunit ECF subfamily
gene_id_5696	124	51.61	2.00E-33	hypothetical protein, partial
gene_id_5697	64	56.25	6.00E-19	hypothetical protein
gene_id_5698	346	24.86	2.00E-12	hypothetical protein
gene_id_5699	97	63.92	2.00E-19	hypothetical protein
gene_id_5700	54	64.81	1.00E-15	hypothetical protein
gene_id_5701	208	65.38	8.00E-82	putative resolvase
gene_id_5702	438	53.65	4.00E-168	hypothetical protein
gene_id_5703	707	54.88	0	hypothetical protein
gene_id_5704	1049	44.04	0	hypothetical protein
gene_id_5705	265	59.25	2.00E-106	MerR family transcriptional regulator
gene_id_5706	392	64.03	0	cystathionine gamma-synthase
gene_id_5707	475	78.95	0	hypothetical protein
gene_id_5708	382	39.79	2.00E-81	alanine racemase
gene_id_5709	139	64.03	2.00E-46	hypothetical protein
gene_id_5710	341	44.28	2.00E-95	hypothetical protein, partial
gene_id_5711	65	60	3.00E-22	hypothetical protein
gene_id_5712	302	58.28	7.00E-135	hypothetical protein
gene_id_5713	790	80.89	0	hypothetical protein
gene_id_5714	164	55.49	2.00E-64	DNA-binding protein
gene_id_5715	177	48.59	1.00E-49	hypothetical protein, partial
gene_id_5716	131	73.28	9.00E-68	pyridoxamine 5'-phosphate oxidase-like protein

gene_id_5717	108	71.3	2.00E-46	transcriptional regulator
gene_id_5718	282	88.3	3.00E-180	phenazine biosynthesis protein PhzF family
gene_id_5719	97	70.1	2.00E-43	hypothetical protein
gene_id_5720	73	56.16	4.00E-19	MULTISPECIES: hypothetical protein
gene_id_5721	322	72.67	0	MULTISPECIES: AraC family transcriptional regulat
gene_id_5722	272	75.74	1.00E-136	Fe3+-hydroxamate ABC transporter substrate-bin
gene_id_5723	307	62.87	1.00E-140	ABC-type Fe3+-hydroxamate transport system, pe
gene_id_5724	313	87.86	0	MULTISPECIES: ferrichrome ABC transporter perm
gene_id_5725	336	79.76	9.00E-172	sugar ABC transporter substrate-binding protein
gene_id_5726	273	87.18	1.00E-177	MULTISPECIES: iron-dicitrate transporter ATP-bin
gene_id_5727	574	85.54	0	ABC transporter permease
gene_id_5728	275	68.36	2.00E-118	hypothetical protein
gene_id_5729	79	45.57	4.00E-15	ParB-like partition protein
gene_id_5730	42	69.05	5.00E-11	hypothetical protein
gene_id_5731	121	46.28	1.00E-29	amino acid-binding protein
gene_id_5732	146	59.59	6.00E-56	signal peptidase I
gene_id_5733	520	47.12	2.00E-173	lysM domain-containing protein
gene_id_5734	280	75	1.00E-145	putative amino acid ABC transporter amino acid-b
gene_id_5735	237	66.24	1.00E-96	polar amino acid transport system substrate-bindi
gene_id_5736	252	87.3	5.00E-161	amino acid ABC transporter ATP-binding protein P
gene_id_5737	272	51.47	7.00E-95	hypothetical protein
gene_id_5739	144	40.28	9.00E-38	hypothetical protein
gene_id_5740	196	55.61	4.00E-73	hypothetical protein
gene_id_5741	333	48.95	2.00E-97	hypothetical protein
gene_id_5742	541	46.21	5.00E-148	hypothetical protein
gene_id_5743	109	40.37	1.00E-18	hypothetical protein
gene_id_5744	103	36.89	4.00E-11	hypothetical protein
gene_id_5745	346	63.58	4.00E-157	chemotaxis protein
gene_id_5746	269	60.59	2.00E-121	chemotaxis protein CheR
gene_id_5747	137	50.36	2.00E-36	CheW-like protein
gene_id_5748	716	58.8	0	chemotaxis protein CheA
gene_id_5749	474	45.57	6.00E-135	hypothetical protein
gene_id_5750	88	73.86	1.00E-40	FlhB domain-containing protein
gene_id_5751	159	26.42	1.00E-14	hypothetical protein
gene_id_5752	769	46.55	0	hypothetical protein
gene_id_5752	1085	30.78	2.00E-131	hypothetical protein
gene_id_5902	165	61.21	8.00E-58	degV family protein
gene_id_5903	138	43.48	1.00E-35	hypothetical protein, partial
gene_id_5904	193	84.46	4.00E-118	probable GTP-binding protein EngB
gene_id_5905	775	74.71	0	lon protease
gene_id_5907	551	66.61	0	sigma 54 interacting domain protein
gene_id_5908	397	92.19	0	elongation factor Tu
gene_id_5909	694	92.65	0	elongation factor G
gene_id_5910	156	93.59	5.00E-104	30S ribosomal protein S7
gene_id_5911	139	97.84	7.00E-92	30S ribosomal protein S12
gene_id_5912	240	76.25	2.00E-122	ABC transporter ATP-binding protein
gene_id_5913	773	75.16	0	ABC transporter permease

gene_id_5914	208	86.06	4.00E-130	TetR family transcriptional regulator
gene_id_5915	284	66.9	1.00E-125	MerR family transcriptional regulator
gene_id_5917	1197	89.39	0	DNA-directed RNA polymerase subunit beta'
gene_id_5918	1251	90.81	0	DNA-directed RNA polymerase subunit beta
gene_id_5919	207	69.57	6.00E-102	hypothetical protein
gene_id_5920	294	67.69	6.00E-122	putative membrane protein
gene_id_5921	124	82.26	8.00E-24	50S ribosomal protein L7/L12
gene_id_5922	164	87.2	2.00E-86	50S ribosomal protein L10
gene_id_5923	231	93.51	1.00E-134	50S ribosomal protein L1
gene_id_5924	141	85.11	2.00E-73	50S ribosomal protein L11
gene_id_5925	186	85.48	3.00E-108	transcription termination/antitermination factor
gene_id_5926	89	66.29	5.00E-29	preprotein translocase subunit SecE
gene_id_5927	61	73.77	2.00E-24	hypothetical protein HMPREF0491_00002
gene_id_5928	83	75.9	9.00E-42	hypothetical protein
gene_id_5929	56	82.14	1.00E-08	4Fe-4S ferredoxin iron-sulfur binding domain-con
gene_id_5930	449	88.86	0	glutamate dehydrogenase (NADP+)
gene_id_5932	352	88.35	0	cell shape determining protein MreB/Mrl family
gene_id_5933	397	57.93	3.00E-161	c-processing peptidase
gene_id_5934	299	71.57	6.00E-135	hypothetical protein
gene_id_5935	228	90.79	5.00E-149	cell division ATP-binding protein FtsE
gene_id_5936	363	96.14	0	carbohydrate diacid regulator
gene_id_5937	286	45.1	4.00E-54	yitT family protein
gene_id_5938	242	79.34	1.00E-131	glycosyl transferase WecB/TagA/CpsF family
gene_id_5939	739	79.03	0	polysaccharide pyruvyl transferase CsaB
gene_id_5940	156	59.62	4.00E-49	hypothetical protein
gene_id_5941	118	71.19	2.00E-50	hypothetical protein
gene_id_5942	370	62.43	7.00E-158	glycosyl transferase group 1
gene_id_5943	1049	66.44	0	integral membrane protein MviN
gene_id_5944	756	65.74	0	copper amine oxidase domain protein
gene_id_5945	186	65.05	3.00E-88	hypothetical protein
gene_id_5946	114	85.96	2.00E-65	transcriptional modulator of MazE/toxin MazF
gene_id_5947	60	43.33	1.00E-09	hypothetical protein
gene_id_5948	204	79.41	7.00E-116	uridine kinase
gene_id_5949	453	59.38	2.00E-172	cell envelope-related transcriptional attenuator
gene_id_5950	303	63.37	1.00E-136	cell envelope-related transcriptional attenuator
gene_id_5951	602	53.49	0	phosphoglycerol transferase family protein alkali
gene_id_5952	464	74.57	0	transporter
gene_id_5953	450	80.22	0	mg2+ transporter MgtE
gene_id_5954	447	89.71	0	replicative DNA helicase
gene_id_5955	147	84.35	2.00E-68	50S ribosomal protein L9
gene_id_5956	629	68.68	0	putative signaling protein consisting of a modified
gene_id_5957	95	52.63	4.00E-26	hypothetical protein
gene_id_5958	285	54.74	4.00E-105	hypothetical protein
gene_id_5959	319	71.47	8.00E-171	aTPase associated with various cellular activities
gene_id_5961	405	57.04	3.00E-151	hypothetical protein
gene_id_5962	297	44.44	8.00E-63	cAAX amino terminal protease
gene_id_5963	61	67.21	8.00E-21	hypothetical protein

gene_id_5964	181	88.4	8.00E-115	spoVT
gene_id_5965	329	74.16	9.00E-180	glycerol-3-phosphate dehydrogenase
gene_id_5966	184	66.3	6.00E-62	glycerol-3-phosphate acyltransferase
gene_id_5967	441	91.38	0	ribosome-associated GTPase EngA
gene_id_5968	267	68.16	1.00E-136	hypothetical protein
gene_id_5969	378	65.87	1.00E-166	ribonuclease HII
gene_id_5970	102	62.75	5.00E-39	hypothetical protein
gene_id_5971	540	86.67	0	ribocuclease J
gene_id_5972	100	81	2.00E-47	hypothetical protein
gene_id_5973	142	74.65	1.00E-68	putative Holliday junction resolvase
gene_id_5974	86	86.05	7.00E-39	uPF0297 protein Toce_1354
gene_id_5975	429	81.59	0	rNA modification enzyme MiaB family
gene_id_5976	263	61.6	2.00E-116	hAD hydrolase
gene_id_5977	180	52.22	5.00E-57	uncharacterized protein
gene_id_5978	150	90.67	4.00E-97	hypothetical protein
gene_id_5979	235	74.04	2.00E-106	mTA/SAH nucleosidase
gene_id_5980	228	59.21	4.00E-87	peptidase C26
gene_id_5981	274	69.71	2.00E-140	mscS Mechanosensitive ion channel
gene_id_5982	49	91.84	8.00E-25	hypothetical protein
gene_id_5983	170	53.53	6.00E-65	hypothetical protein, partial
gene_id_5985	724	62.57	0	cadmium-exporting ATPase
gene_id_5986	100	76	2.00E-50	transcriptional regulator ArsR family
gene_id_5987	298	84.9	4.00E-173	transcriptional regulator LysR family
gene_id_5988	256	69.53	3.00E-109	4Fe-4S ferredoxin iron-sulfur binding domain prot
gene_id_5990	296	52.36	8.00E-97	foldase protein PrsA
gene_id_5991	1168	75.77	0	transcription-repair coupling factor
gene_id_5992	195	78.46	1.00E-109	peptidyl-tRNA hydrolase
gene_id_5994	326	84.05	0	d-isomer specific 2-hydroxyacid dehydrogenase N
gene_id_5995	319	88.09	0	ribose-phosphate pyrophosphokinase
gene_id_5996	449	78.62	0	bifunctional protein GlmU
gene_id_5997	372	75.27	0	glucose-1-phosphate adenylyltransferase GlgD sul
gene_id_5998	423	83.92	0	glucose-1-phosphate adenylyltransferase
gene_id_6000	451	72.06	0	uDP-N-acetylmuramate--L-alanine ligase
gene_id_6001	159	82.39	2.00E-85	ribosomal RNA large subunit methyltransferase H
gene_id_6002	264	69.7	3.00E-129	beta-lactamase domain protein
gene_id_6003	416	81.25	0	uDP-N-acetylglucosamine 1-carboxyvinyltransfera
gene_id_6005	283	48.06	5.00E-80	hypothetical protein
gene_id_6006	471	62.42	0	hypothetical protein
gene_id_6007	138	43.48	3.00E-31	hypothetical protein
gene_id_6008	570	78.25	0	multi-sensor signal transduction histidine kinase
gene_id_6009	231	82.68	7.00E-121	response regulator with CheY-like receiver domai
gene_id_6010	545	43.12	6.00E-111	hypothetical protein
gene_id_6010	243	25.1	6.00E-08	hypothetical protein
gene_id_6011	1428	82.63	0	coA-substrate-specific enzyme activase
gene_id_6012	116	50	8.00E-32	hypothetical protein
gene_id_6013	276	78.26	1.00E-140	ribosomal RNA small subunit methyltransferase I
gene_id_6014	251	73.71	5.00E-131	methyltransferase type 11

gene_id_6015	265	86.04	4.00E-164	pSP1 domain protein
gene_id_6016	328	59.45	3.00E-124	hypothetical protein
gene_id_6017	108	85.19	3.00E-61	hypothetical protein
gene_id_6018	206	65.53	9.00E-97	dTMP kinase
gene_id_6019	332	58.73	6.00E-129	istB domain protein ATP-binding protein
gene_id_6020	314	54.78	2.00E-115	hypothetical protein
gene_id_6021	345	83.77	1.00E-174	glycosyl transferase family 4
gene_id_6023	208	88.46	8.00E-130	uracil phosphoribosyltransferase
gene_id_6024	142	90.85	7.00E-89	ribose 5-phosphate isomerase B
gene_id_6025	351	74.64	0	hypothetical protein
gene_id_6026	149	73.83	3.00E-77	hypothetical protein
gene_id_6027	134	44.03	3.00E-26	hypothetical protein
gene_id_6028	526	74.14	0	CTP synthase
gene_id_6029	127	40.94	3.00E-28	uncharacterized protein
gene_id_6030	260	60.77	2.00E-103	peptidyl-prolyl cis-trans isomerase
gene_id_6031	348	74.71	0	uDP-N-acetylglucosamine--N-acetylmuramyl-(pen
gene_id_6033	141	48.23	9.00E-31	hypothetical protein
gene_id_6034	136	82.35	1.00E-77	histidine triad domain protein
gene_id_6036	248	58.87	1.00E-103	acyl-ACP thioesterase
gene_id_6037	487	75.15	0	cardiolipin synthase
gene_id_6038	122	78.69	5.00E-55	hypothetical protein
gene_id_6039	153	56.86	2.00E-33	TspO and MBR
gene_id_6040	330	58.18	5.00E-140	adenosine deaminase
gene_id_6041	493	82.76	0	hypothetical protein
gene_id_6042	211	46.45	2.00E-56	putative amidophosphoribosyltransferase
gene_id_6043	744	74.87	0	helicase RecD/TraA family
gene_id_6044	392	87.24	0	s-adenosylmethionine synthase
gene_id_6045	163	65.03	9.00E-71	hypothetical protein
gene_id_6046	232	58.19	7.00E-92	predicted DNA alkylation repair enzyme
gene_id_6048	111	65.77	8.00E-50	hypothetical protein
gene_id_6049	190	84.21	2.00E-113	nitroreductase
gene_id_6050	281	84.34	4.00E-174	pirin
gene_id_6051	143	83.92	3.00E-86	MarR family transcriptional regulator
gene_id_6052	497	45.27	2.00E-135	hypothetical protein
gene_id_6053	255	52.16	1.00E-100	4Fe-4S binding domain protein
gene_id_6054	131	58.78	2.00E-48	hypothetical protein
gene_id_6055	150	49.33	3.00E-40	pyridoxamine 5'-phosphate oxidase
gene_id_6056	417	77.22	0	uracil transporter
gene_id_6058	321	82.87	0	tRNA-dihydrouridine synthase
gene_id_6059	255	84.71	2.00E-144	type III pantothenate kinase
gene_id_6060	258	76.74	1.00E-136	type III pantothenate kinase
gene_id_6061	204	57.35	2.00E-70	hypothetical protein
gene_id_6062	112	71.43	1.00E-53	hypothetical protein
gene_id_6063	321	64.49	1.00E-141	biotin/acetyl-CoA-carboxylase ligase
gene_id_6064	132	84.09	3.00E-71	thioesterase family protein
gene_id_6065	623	79.61	0	aTP-dependent zinc metalloprotease FtsH 1
gene_id_6066	176	77.27	1.00E-97	hypoxanthine phosphoribosyltransferase

gene_id_6067	457	49.23	5.00E-131	tRNA(Ile)-lysidine synthetase
gene_id_6068	805	52.55	0	stage II sporulation protein E protein serine/threo
gene_id_6069	754	44.96	9.00E-174	s-layer domain protein
gene_id_6070	402	58.46	4.00E-162	amidohydrolase
gene_id_6071	269	63.94	2.00E-111	metallo-beta-lactamase family protein
gene_id_6072	442	75.79	0	glucose-6-phosphate isomerase 1
gene_id_6073	365	50.68	2.00E-107	peptidase M23
gene_id_6074	224	75.89	2.00E-115	hypothetical protein
gene_id_6075	305	67.54	7.00E-150	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
gene_id_6076	39	79.49	6.00E-11	hypothetical protein
gene_id_6077	354	57.06	1.00E-149	diaminohydroxyphosphoribosylaminopyrimidine
gene_id_6078	215	57.21	1.00E-81	riboflavin synthase subunit alpha
gene_id_6079	401	83.04	0	riboflavin biosynthesis protein ribBA
gene_id_6080	153	71.9	3.00E-74	6,7-dimethyl-8-ribityllumazine synthase
gene_id_6081	353	57.22	9.00E-119	sporulation integral membrane protein YtvI
gene_id_6082	198	52.02	2.00E-53	traX family protein
gene_id_6083	305	77.38	2.00E-160	cysteine synthase
gene_id_6084	289	81.31	2.00E-175	methionine aminopeptidase
gene_id_6085	375	48.8	1.00E-93	major Facilitator Superfamily
gene_id_6086	410	52.93	4.00E-152	hypothetical protein
gene_id_6087	505	36.04	1.00E-83	methyl-accepting chemotaxis protein
gene_id_6089	247	69.64	7.00E-114	hypothetical protein
gene_id_6090	176	68.75	8.00E-82	putative surface protein
gene_id_6091	76	73.68	3.00E-31	hypothetical protein
gene_id_6092	342	77.78	5.00E-172	l-allo-threonine aldolase
gene_id_6093	539	89.61	0	aTPase component of ABC transporters with dupli
gene_id_6094	290	39.31	1.00E-48	hypothetical protein
gene_id_6095	234	75.64	3.00E-124	uBA/THIF-type NAD/FAD binding protein
gene_id_6096	445	65.84	0	hypothetical protein
gene_id_6098	364	77.2	0	glycerol dehydrogenase
gene_id_6099	58	84.48	2.00E-25	electron transfer flavoprotein alpha subunit
gene_id_6101	150	43.33	2.00E-24	hypothetical protein
gene_id_6102	1454	35.21	0	hypothetical protein
gene_id_6103	169	26.63	3.00E-12	hypothetical protein
gene_id_6104	238	84.03	3.00E-128	hypothetical protein
gene_id_6105	258	67.05	1.00E-124	hypothetical protein
gene_id_6106	302	54.97	8.00E-103	plasmid stablization protein ParB
gene_id_6107	404	41.58	3.00E-85	hypothetical protein
gene_id_6108	1308	54.74	0	S-layer protein
gene_id_6109	92	68.48	1.00E-37	hypothetical protein
gene_id_6110	176	65.34	1.00E-78	hypothetical protein
gene_id_6111	597	76.72	0	hypothetical protein
gene_id_6112	401	86.53	0	TRAG family protein
gene_id_6113	71	91.55	2.00E-36	hypothetical protein
gene_id_6114	289	67.47	6.00E-146	hypothetical protein EAL2_c06520
gene_id_6116	233	41.63	1.00E-56	hypothetical protein
gene_id_6117	132	57.58	2.00E-47	conjugal transfer protein

gene_id_6118	790	66.08	0	conjugal transfer protein TraE
gene_id_6119	581	49.74	4.00E-168	hypothetical protein
gene_id_6120	281	49.82	9.00E-96	hypothetical protein
gene_id_6121	68	41.18	9.00E-12	hypothetical protein
gene_id_6122	187	40.64	8.00E-27	cell surface protein
gene_id_6123	703	59.03	0	DNA topoisomerase III
gene_id_6124	119	39.5	5.00E-22	hypothetical protein C807_01175
gene_id_6125	118	66.1	2.00E-48	toxin RelE
gene_id_6126	96	73.96	3.00E-44	XRE family transcriptional regulator
gene_id_6127	66	78.79	2.00E-27	hypothetical protein
gene_id_6128	51	52.94	3.00E-10	MULTISPECIES: hypothetical protein
gene_id_6129	1819	59.92	0	hypothetical protein
gene_id_6129	928	34.48	4.00E-122	hypothetical protein
gene_id_6131	90	62.22	9.00E-30	hypothetical protein
gene_id_6132	443	56.88	5.00E-174	relaxase
gene_id_6134	886	27.2	2.00E-61	hypothetical protein
gene_id_6136	83	49.4	3.00E-16	hypothetical protein
gene_id_6137	148	39.19	1.00E-25	MULTISPECIES: hypothetical protein, partial
gene_id_6138	60	60	2.00E-18	Transcriptional regulator
gene_id_6139	46	69.57	1.00E-12	integrase, catalytic region
gene_id_6140	200	71	2.00E-98	integrase, catalytic region
gene_id_6142	39	69.23	3.00E-09	transposase IS3/IS911
gene_id_6143	283	71.02	1.00E-141	aldo/keto reductase
gene_id_6144	216	48.61	8.00E-61	hypothetical protein
gene_id_6145	314	62.74	9.00E-141	hypothetical protein
gene_id_6146	424	63.21	0	aminotransferase
gene_id_6147	448	46.21	2.00E-120	sodium:dicarboxylate symporter
gene_id_6148	321	84.74	0	hypothetical protein
gene_id_6149	355	38.59	3.00E-65	hypothetical protein
gene_id_6150	477	56.18	5.00E-179	pyruvate kinase
gene_id_6151	376	58.24	2.00E-139	glycerate kinase
gene_id_6152	418	67.46	0	enolase
gene_id_6153	126	40.48	1.00E-17	hypothetical protein
gene_id_6154	80	58.75	1.00E-27	hypothetical protein
gene_id_6155	538	61.71	0	recombinase
gene_id_6156	560	46.96	4.00E-167	site-specific recombinase, resolvase family
gene_id_6157	520	44.04	5.00E-143	resolvase, N terminal domain protein
gene_id_6158	271	94.83	2.00E-166	serine recombinase
gene_id_6159	114	97.37	1.00E-76	hypothetical protein
gene_id_6160	154	91.56	3.00E-96	hypothetical protein
gene_id_6161	679	96.61	0	hypothetical protein
gene_id_6162	196	97.45	9.00E-139	XRE family transcriptional regulator
gene_id_6163	405	100	0	MULTISPECIES: major facilitator transporter
gene_id_6164	284	100	0	MULTISPECIES: DNA polymerase
gene_id_6165	246	99.59	8.00E-173	MULTISPECIES: SAM-dependent methyltransferas
gene_id_6166	164	100	7.00E-98	MULTISPECIES: phosphohydrolase
gene_id_6167	113	100	1.00E-77	MULTISPECIES: hypothetical protein, partial

gene_id_6168	152	100	4.00E-107	MULTISPECIES: ATP/GTP-binding protein
gene_id_6169	39	97.44	3.00E-17	hypothetical protein
gene_id_6170	221	80.54	4.00E-132	hypothetical protein
gene_id_6171	158	74.05	4.00E-69	transposase
gene_id_6203	87	51.72	2.00E-08	hypothetical protein
gene_id_6204	110	32.73	3.00E-06	hypothetical protein
gene_id_6206	349	79.37	0	16S rRNA methyltransferase
gene_id_6207	77	35.06	4.00E-07	hypothetical protein
gene_id_6208	846	74.35	0	ABC transporter permease
gene_id_6209	226	90.71	9.00E-146	peptide ABC transporter ATP-binding protein
gene_id_6210	329	79.33	0	histidine kinase
gene_id_6211	228	83.33	3.00E-131	transcriptional regulator
gene_id_6212	203	57.64	4.00E-73	hypothetical protein
gene_id_6213	320	74.69	0	putative Zn-dependent hydrolase
gene_id_6214	229	64.63	4.00E-98	hypothetical protein
gene_id_6216	171	63.74	3.00E-56	hypothetical protein
gene_id_6217	473	55.39	8.00E-108	SPFH domain/band 7 family protein, partial
gene_id_6219	242	90.08	1.00E-113	probable transcriptional regulatory protein Closa_
gene_id_6220	114	80.7	1.00E-56	stage V sporulation protein AE
gene_id_6221	342	76.61	0	stage V sporulation protein AD
gene_id_6222	147	74.15	6.00E-71	sporulation stage V protein AC
gene_id_6223	141	65.25	4.00E-28	hypothetical protein
gene_id_6224	200	60.5	5.00E-79	hypothetical protein
gene_id_6225	215	62.33	1.00E-62	hypothetical protein
gene_id_6226	271	52.77	6.00E-86	UDP pyrophosphate phosphatase
gene_id_6228	537	86.22	0	rNA helicase
gene_id_6229	875	76.91	0	acetaldehyde dehydrogenase
gene_id_6230	311	72.67	6.00E-164	LysR family transcriptional regulator
gene_id_6231	455	67.47	0	MULTISPECIES: putative membrane protein
gene_id_6232	616	70.62	0	asparagine synthetase
gene_id_6233	206	55.34	4.00E-78	superoxide dismutase
gene_id_6234	339	66.08	6.00E-168	hypothetical protein
gene_id_6235	532	75.94	0	membrane-bound O-acyltransferase family protei
gene_id_6236	75	86.67	1.00E-37	hypothetical protein
gene_id_6237	260	46.54	1.00E-71	gCN5-related N-acetyltransferase
gene_id_6238	500	75.4	0	amino acid adenylation domain-containing protei
gene_id_6239	158	86.08	5.00E-99	ybaK/EbsC protein
gene_id_6240	136	75.74	2.00E-72	transcriptional regulator BadM/Rrf2 family
gene_id_6241	257	86.38	6.00E-162	aBC transporter ATP-binding protein
gene_id_6242	292	76.37	5.00E-137	putative ABC transporter permease protein
gene_id_6243	291	81.79	2.00E-159	putative ABC transporter substrate-binding protei
gene_id_6245	586	48.46	2.00E-149	hypothetical protein, partial
gene_id_6247	462	69.05	0	acetoin dehydrogenase E3 component
gene_id_6248	540	45.93	6.00E-137	hypothetical protein
gene_id_6249	322	71.74	8.00E-156	hypothetical protein
gene_id_6250	317	62.78	9.00E-139	hypothetical protein
gene_id_6251	449	46.77	2.00E-123	hypothetical protein

gene_id_6252	55	49.09	8.00E-09	hypothetical protein
gene_id_6709	388	63.14	9.00E-163	hypothetical protein
gene_id_6711	1618	64.28	0	hypothetical protein
gene_id_6712	379	70.18	0	hypothetical protein
gene_id_6713	354	65.82	3.00E-172	hypothetical protein
gene_id_6714	512	74.41	0	asparagine synthetase
gene_id_6716	694	68.88	0	glutamine synthetase
gene_id_6718	554	27.8	7.00E-51	hypothetical protein
gene_id_6719	285	54.74	2.00E-103	6-phosphogluconate dehydrogenase
gene_id_6720	275	81.45	3.00E-163	3-methyl-2-oxobutanoate hydroxymethyltransfera
gene_id_6721	253	69.17	2.00E-128	pantothenate synthetase PanC
gene_id_6722	62	59.68	9.00E-20	transcription initiation factor TFIIIB
gene_id_6723	167	29.94	6.00E-12	hypothetical protein HMPREF1216_00089
gene_id_6724	353	63.74	7.00E-110	hypothetical protein, partial
gene_id_6725	195	39.49	2.00E-37	hypothetical protein
gene_id_6726	118	47.46	5.00E-26	DNA-binding protein
gene_id_6727	68	41.18	3.00E-10	phage repressor protein
gene_id_6728	133	43.61	1.00E-29	hypothetical protein
gene_id_6729	525	61.33	0	potassium transporter
gene_id_6730	355	66.76	2.00E-166	3-isopropylmalate dehydrogenase
gene_id_6731	163	81.6	6.00E-95	3-isopropylmalate dehydratase, small subunit
gene_id_6732	398	84.42	0	3-isopropylmalate dehydratase large subunit
gene_id_6733	553	73.78	0	2-isopropylmalate synthase
gene_id_6735	221	36.65	7.00E-39	MULTISPECIES: hypothetical protein
gene_id_6736	553	67.63	0	dihydroxy-acid dehydratase
gene_id_6737	360	63.89	1.00E-151	tripartite ATP-independent periplasmic transporte
gene_id_6738	160	52.5	2.00E-52	tripartite ATP-independent periplasmic transporte
gene_id_6739	419	71.84	6.00E-149	TRAP transporter, DctM subunit
gene_id_6740	292	49.32	2.00E-97	hypothetical protein
gene_id_6741	187	59.36	3.00E-70	cell wall hydrolase
gene_id_6742	864	36.11	3.00E-173	hypothetical protein
gene_id_6743	187	57.75	2.00E-66	hypothetical protein
gene_id_6744	325	64.92	4.00E-117	secretion protein HlyD family protein
gene_id_6745	402	61.44	2.00E-163	aBC-2 type transporter
gene_id_6746	355	67.04	1.00E-169	aBC-2 type transporter
gene_id_6747	445	59.1	9.00E-133	outer membrane protein-like protein
gene_id_6748	474	74.89	0	transcriptional regulator containing PAS AAA-type
gene_id_6749	425	71.53	0	uPF0597 protein Desor_5047
gene_id_6750	371	36.93	1.00E-72	hypothetical protein
gene_id_6751	739	76.73	0	dNA gyrase/topoisomerase IV subunit A
gene_id_6752	647	87.48	0	dNA gyrase subunit B domain protein
gene_id_6753	117	77.78	7.00E-62	steroid delta-isomerase
gene_id_6754	129	57.36	3.00E-30	hypothetical protein
gene_id_6755	133	57.89	7.00E-48	hypothetical protein
gene_id_6756	305	56.72	6.00E-128	lysophospholipase
gene_id_6757	153	59.48	4.00E-61	phosphatidylethanolamine-binding protein
gene_id_6758	242	78.51	1.00E-139	LytTR family transcriptional regulator

gene_id_6759	428	82.48	0	ATP-binding protein
gene_id_6760	138	50.72	2.00E-37	MarR family transcriptional regulator
gene_id_6761	226	50	1.00E-78	metal-dependent hydrolase
gene_id_6762	83	62.65	4.00E-29	hypothetical protein
gene_id_6763	62	75.81	4.00E-15	hypothetical protein
gene_id_6764	143	63.64	3.00E-52	hypothetical protein
gene_id_6765	116	81.9	2.00E-65	4-carboxymuconolactone decarboxylase
gene_id_6766	564	73.23	0	hypothetical protein
gene_id_6767	291	61.51	4.00E-123	hypothetical protein, partial
gene_id_6768	71	78.87	2.00E-34	hypothetical protein
gene_id_6769	115	70.43	7.00E-53	lactoylglutathione lyase
gene_id_6770	223	82.06	8.00E-137	flavin reductase
gene_id_6772	688	63.23	0	putative ATP-dependent DNA helicase replicase
gene_id_6773	279	69.53	4.00E-142	AraC family transcriptional regulator
gene_id_6774	150	68	6.00E-72	hypothetical protein
gene_id_6775	149	69.8	1.00E-69	MULTISPECIES: acetyltransferase
gene_id_6776	178	71.91	2.00E-90	hypothetical protein
gene_id_6777	289	79.24	9.00E-168	transcriptional regulator
gene_id_6778	147	68.03	2.00E-64	SufBD protein
gene_id_6779	165	57.58	2.00E-54	hypothetical protein
gene_id_6780	106	62.26	5.00E-44	hypothetical protein
gene_id_6781	276	63.04	9.00E-127	MULTISPECIES: methyltransferase
gene_id_6782	344	85.47	0	Chloramphenicol acetyltransferase
gene_id_6783	285	84.56	0	AraC family transcriptional regulator
gene_id_6784	175	77.71	1.00E-94	hypothetical protein
gene_id_6785	122	69.67	4.00E-53	hypothetical protein
gene_id_6785	57	57.89	2.00E-10	hypothetical protein
gene_id_6786	214	69.63	7.00E-107	flavodoxin
gene_id_6787	211	61.61	4.00E-91	hypothetical protein
gene_id_6788	217	85.25	3.00E-135	two component transcriptional regulator, winged
gene_id_6789	464	79.09	0	histidine kinase
gene_id_6790	297	60.61	1.00E-122	hypothetical protein
gene_id_6791	147	55.1	7.00E-57	hypothetical protein
gene_id_6792	569	72.41	0	hypothetical protein
gene_id_6793	596	78.02	0	aBC transporter ATP-binding protein
gene_id_6794	224	72.77	5.00E-115	2-haloalkanoic acid dehalogenase
gene_id_6795	206	64.08	5.00E-54	membrane protein
gene_id_6796	205	72.2	2.00E-104	Crp/Fnr family transcriptional regulator
gene_id_6797	184	86.41	2.00E-102	LemA family protein
gene_id_6798	538	71.93	0	hypothetical protein
gene_id_6799	221	61.99	2.00E-90	PhoB family transcriptional regulator
gene_id_6800	352	45.45	3.00E-96	membrane protein
gene_id_6801	256	75.39	1.00E-137	ABC transporter ATP-binding protein
gene_id_6802	661	44.93	4.00E-167	hypothetical protein
gene_id_6803	233	86.7	4.00E-147	transcriptional regulator
gene_id_6804	366	73.22	0	hypothetical protein
gene_id_6805	190	61.58	2.00E-81	MULTISPECIES: peptidase M15

gene_id_6806	88	70.45	3.00E-37	hisitidine kinase
gene_id_6807	239	83.26	2.00E-146	methyltransferase
gene_id_6809	361	68.42	4.00E-180	aminomethyltransferase
gene_id_6810	125	68	4.00E-53	glycine cleavage system H protein
gene_id_6811	437	68.19	0	glycine dehydrogenase
gene_id_6812	475	72	0	glycine dehydrogenase subunit 2
gene_id_6813	468	57.26	0	dihydrolipoamide dehydrogenase
gene_id_6814	292	50.34	1.00E-96	hypothetical protein
gene_id_6815	427	64.64	0	electron transporter RnfC
gene_id_6816	592	81.25	0	proline reductase
gene_id_6817	144	57.64	6.00E-57	hypothetical protein
gene_id_6818	241	92.12	1.00E-166	proline reductase
gene_id_6819	416	55.77	7.00E-175	hypothetical protein
gene_id_6820	332	71.08	8.00E-179	proline racemase
gene_id_6821	269	73.98	1.00E-130	permease
gene_id_6822	82	73.17	3.00E-39	transcriptional regulator
gene_id_6823	107	62.62	1.00E-35	hypothetical protein
gene_id_6824	65	80	6.00E-26	XRE family transcriptional regulator, partial
gene_id_6825	112	35.71	5.00E-11	hypothetical protein
gene_id_6826	1077	76.79	0	restriction endonuclease subunit R, partial
gene_id_6827	314	37.26	4.00E-54	Protein of unknown function (DUF2971)
gene_id_6828	296	51.69	6.00E-100	MULTISPECIES: hypothetical protein
gene_id_6829	481	83.37	0	type I restriction-modification system methyltrans
gene_id_6830	352	72.16	0	cell division protein Fic
gene_id_6831	451	82.26	0	nickel ABC transporter substrate-binding protein
gene_id_6832	236	77.54	3.00E-127	MULTISPECIES: iron ABC transporter ATPase
gene_id_6833	249	73.49	9.00E-129	hypothetical protein
gene_id_6834	177	90.4	9.00E-110	peptide ABC transporter ATP-binding protein
gene_id_6835	277	84.84	1.00E-161	nickel ABC transporter permease
gene_id_6836	323	89.47	0	AraC family transcriptional regulator
gene_id_6837	382	92.41	0	MFS transporter
gene_id_6838	256	96.09	0	hypothetical protein
gene_id_6839	343	95.04	0	iron ABC transporter permease
gene_id_6840	355	94.37	0	ABC transporter substrate-binding protein
gene_id_6841	150	96.67	5.00E-92	MarR family transcriptional regulator
gene_id_6842	331	91.24	0	hypothetical protein, partial
gene_id_6843	296	54.73	5.00E-103	plasmid stablization protein ParB
gene_id_6844	255	66.67	3.00E-126	hypothetical protein
gene_id_6846	64	45.31	5.00E-12	hypothetical protein CLOSTHATH_02416
gene_id_6911	152	67.76	3.00E-68	nimA protein
gene_id_6912	333	80.18	0	putative spore photoproduct lyase
gene_id_6913	213	81.69	1.00E-127	peroxiredoxin
gene_id_6914	192	40.1	1.00E-38	transcriptional regulator, TetR family
gene_id_6915	436	43.58	3.00E-92	efflux transporter, RND family, MFP subunit
gene_id_6916	1027	58.13	0	hypothetical protein
gene_id_6917	217	70.05	6.00E-107	GntR family transcriptional regulator
gene_id_6918	1167	76.86	0	pyruvate-ferredoxin (flavodoxin) oxidoreductase

gene_id_6919	489	82.62	0	4-hydroxybutyryl-CoA dehydratase
gene_id_6920	384	77.34	0	aspartate aminotransferase
gene_id_6921	253	77.08	9.00E-148	hypothetical protein
gene_id_6922	353	61.19	5.00E-139	hypothetical protein
gene_id_6923	211	54.03	7.00E-75	hypothetical protein
gene_id_6924	594	64.31	0	indolepyruvate oxidoreductase subunit IorA
gene_id_6925	189	67.2	1.00E-85	MULTISPECIES: indolepyruvate oxidoreductase
gene_id_6926	442	76.24	0	coA-transferase
gene_id_6927	392	60.71	2.00E-175	aspartate aminotransferase
gene_id_6928	426	48.83	4.00E-97	branched-chain amino acid transport system carri
gene_id_6930	471	59.02	2.00E-154	hypothetical protein, partial
gene_id_6931	250	68.4	1.00E-120	2-deoxy-D-gluconate 3-dehydrogenase
gene_id_6932	228	55.26	6.00E-88	hypothetical protein
gene_id_6933	337	70.03	2.00E-163	dehydrogenase
gene_id_6934	382	80.1	0	galactonate dehydratase
gene_id_6935	467	56.75	0	hypothetical protein
gene_id_6936	352	56.25	3.00E-133	TRAP transporter solute receptor, DctP family
gene_id_6937	165	51.52	2.00E-58	TRAP transporter, DctQ-like membrane protein
gene_id_6938	424	78.77	0	TRAP transporter, DctM subunit
gene_id_6939	332	45.18	1.00E-83	hypothetical protein
gene_id_6940	205	51.22	5.00E-60	2-dehydro-3-deoxyphosphogluconate aldolase
gene_id_6941	315	53.97	1.00E-112	hypothetical protein
gene_id_6942	207	64.73	2.00E-86	2-dehydro-3-deoxyphosphogluconate aldolase
gene_id_6943	456	50.88	1.00E-159	6-phosphogluconate dehydrogenase
gene_id_6944	47	61.7	9.00E-11	phosphoglycerate dehydrogenase
gene_id_6945	311	59.49	7.00E-120	predicted permeases
gene_id_6946	137	57.66	1.00E-53	hypothetical protein
gene_id_6947	566	73.32	0	hypothetical protein
gene_id_6948	418	86.84	0	hypothetical protein
gene_id_6949	449	79.29	0	hypothetical protein
gene_id_6952	45	55.56	9.00E-09	putative N-acetyltransferase
gene_id_6953	341	58.06	5.00E-128	hypothetical protein
gene_id_6954	211	66.82	3.00E-87	hypothetical protein
gene_id_6955	290	58.28	4.00E-99	phosphatidylserine decarboxylase
gene_id_6956	366	24.59	3.00E-21	methyl-accepting chemotaxis sensory transducer
gene_id_6957	152	47.37	3.00E-18	methyl-accepting chemotaxis (MCP) signaling dom
gene_id_6958	404	67.33	0	peptidoglycan-binding protein
gene_id_6959	513	54.78	0	hypothetical protein, partial
gene_id_6960	534	56.93	0	hypothetical protein, partial
gene_id_6961	196	68.37	5.00E-93	metal dependent phosphohydrolase
gene_id_6962	703	49.64	4.00E-160	hypothetical protein, partial
gene_id_6963	217	56.68	8.00E-73	predicted membrane protein
gene_id_6964	510	77.25	0	mg chelatase subunit ChlI
gene_id_6965	362	66.3	6.00E-176	transcriptional regulator MarR family
gene_id_6966	682	81.09	0	dNA topoisomerase
gene_id_6967	222	91.89	3.00E-151	30S ribosomal protein S2
gene_id_6968	308	87.66	0	elongation factor Ts

gene_id_6970	234	83.76	1.00E-140	uridylate kinase
gene_id_6971	139	86.33	2.00E-81	ribosome recycling factor
gene_id_6972	230	73.04	1.00E-124	isoprenyl transferase
gene_id_6973	271	76.01	1.00E-114	phosphatidate cytidylyltransferase
gene_id_6974	377	81.17	0	1-deoxy-D-xylulose 5-phosphate reductoisomeras
gene_id_6975	338	63.02	4.00E-147	rIP metalloprotease RseP
gene_id_6976	349	81.95	0	4-hydroxy-3-methylbut-2-en-1-yl diphosphate syn
gene_id_6977	1443	76.58	0	dNA polymerase III polC-type
gene_id_6978	193	61.66	1.00E-70	uncharacterized protein
gene_id_6979	211	66.82	1.00E-91	channel protein hemolysin III family
gene_id_6980	140	38.57	2.00E-20	MarR family transcriptional regulator
gene_id_6981	571	69.53	0	aBC transporter related protein
gene_id_6982	583	73.93	0	aBC transporter related protein
gene_id_6983	803	84.93	0	leucyl-tRNA synthetase
gene_id_6984	221	31.22	4.00E-30	4'-phosphopantetheinyl transferase
gene_id_6985	387	64.86	4.00E-160	peptidase M23 family
gene_id_6986	151	41.72	2.00E-39	gCN5-related N-acetyltransferase
gene_id_6987	969	54.9	0	peptidase M16C associated domain protein
gene_id_6988	180	91.11	1.00E-102	Reverse rubrerythrin-1
gene_id_6989	250	60.4	5.00E-101	macrolide transporter
gene_id_6990	311	71.06	3.00E-155	inosine-uridine preferring nucleoside hydrolase
gene_id_6991	310	86.45	0	inosine-uridine preferring nucleoside hydrolase
gene_id_6992	314	78.34	3.00E-124	amino acid or sugar ABC transport system permea
gene_id_6993	370	77.57	0	amino acid or sugar ABC transport system permea
gene_id_6994	520	87.5	0	aBC transporter ATP-binding protein
gene_id_6995	336	77.38	5.00E-173	basic membrane protein
gene_id_6996	127	55.91	6.00E-43	preprotein translocase YajC subunit
gene_id_6997	375	88.8	0	queuine tRNA-ribosyltransferase
gene_id_6998	376	90.16	0	rRNA (Guanine-N(2)-)-methyltransferase
gene_id_6999	65	81.54	1.00E-29	phosphotransferase system HPr (HPr) family prote
gene_id_7000	321	68.54	8.00E-159	putative sporulation transcription regulator WhiA
gene_id_7001	282	80.85	1.00E-170	uPF0042 nucleotide-binding protein CcarbDRAFT_
gene_id_7002	301	68.77	2.00E-146	uDP-N-acetylenolpyruvoylglucosamine reductase
gene_id_7003	310	78.06	3.00E-176	hPr kinase/phosphorylase
gene_id_7004	620	79.68	0	uvrABC system protein C
gene_id_7005	485	57.11	2.00E-175	hypothetical protein, partial
gene_id_7006	543	66.48	0	polysaccharide biosynthesis protein
gene_id_7007	609	86.86	0	hypothetical protein
gene_id_7008	880	39.43	0	hypothetical protein
gene_id_7009	516	64.73	0	flagellin
gene_id_7011	799	78.72	0	phenylalanyl-tRNA synthetase subunit beta
gene_id_7012	339	85.84	0	phenylalanyl-tRNA synthetase subunit alpha
gene_id_7013	397	31.99	1.00E-63	hypothetical protein
gene_id_7014	103	67.96	3.00E-35	PadR family transcriptional regulator
gene_id_7015	373	26.54	6.00E-24	hypothetical protein
gene_id_7016	439	79.04	0	aTPase
gene_id_7017	343	84.84	0	s-adenosylmethionine:tRNA ribosyltransferase-isc

gene_id_7018	76	47.37	2.00E-17	hypothetical protein
gene_id_7019	527	59.96	0	spoIID/LytB domain protein
gene_id_7020	32	71.88	6.00E-07	conjugal transfer protein TraX, partial
gene_id_7021	72	38.89	4.00E-08	hypothetical protein
gene_id_7022	94	80.85	4.00E-46	hypothetical protein
gene_id_7023	308	75	4.00E-173	homoserine O-succinyltransferase
gene_id_7025	427	83.37	0	o-acetylhomoserine/O-acetylserine sulfhydrylase
gene_id_7026	188	73.94	1.00E-96	dipicolinate synthase subunit B
gene_id_7027	238	49.58	7.00E-61	dipicolinate synthase
gene_id_7028	1047	42.5	0	sMC domain-containing protein
gene_id_7029	374	55.61	3.00E-147	exonuclease SbcD
gene_id_7030	352	84.94	0	hypothetical protein
gene_id_7031	177	72.88	8.00E-93	putative oxidoreductase
gene_id_7032	305	68.2	3.00E-136	putative ribokinase
gene_id_7033	149	63.09	5.00E-63	pF04657 family protein
gene_id_7034	139	68.35	5.00E-60	uncharacterized protein
gene_id_7035	244	79.1	2.00E-128	purine nucleoside phosphorylase DeoD-type
gene_id_7036	220	36.82	9.00E-37	hypothetical protein
gene_id_7037	449	67.93	0	4-aminobutyrate aminotransferase
gene_id_7038	362	79.56	0	hypothetical protein
gene_id_7039	185	83.78	7.00E-109	cupin 2 conserved barrel domain protein
gene_id_7040	305	65.9	3.00E-139	auxin Efflux Carrier
gene_id_7041	117	94.87	3.00E-72	50S ribosomal protein L20
gene_id_7042	66	92.42	6.00E-26	50S ribosomal protein L35
gene_id_7043	163	92.02	4.00E-92	translation initiation factor IF-3
gene_id_7044	635	87.24	0	threonyl-tRNA synthetase
gene_id_7046	286	70.28	2.00E-135	mg2+ transporter protein CorA2
gene_id_7047	103	68.93	6.00E-45	hypothetical protein
gene_id_7048	248	89.11	2.00E-160	hypothetical protein
gene_id_7049	239	76.15	9.00E-124	amino acid ABC transporter permease/substrate-
gene_id_7050	269	72.49	1.00E-125	aBC transporter substrate-binding protein family
gene_id_7051	418	62.2	2.00E-161	chloride transporter ClC family
gene_id_7052	373	79.62	0	peptidase M29 aminopeptidase II
gene_id_7053	172	65.7	3.00E-78	amidase
gene_id_7054	478	87.66	0	prolyl-tRNA synthetase
gene_id_7055	81	38.27	1.00E-09	hypothetical protein
gene_id_7056	92	57.61	6.00E-30	hypothetical protein
gene_id_7057	388	68.81	0	carbohydrate hydrolase
gene_id_7058	155	63.23	2.00E-68	MULTISPECIES: glyoxalase
gene_id_7059	558	46.42	7.00E-116	methyl-accepting chemotaxis protein
gene_id_7060	149	46.31	1.00E-34	transcriptional regulator, partial
gene_id_7061	141	65.25	3.00E-39	permease
gene_id_7062	181	58.56	6.00E-71	permease
gene_id_7063	412	64.81	2.00E-178	shikimate kinase
gene_id_7064	546	64.47	0	hypothetical protein
gene_id_7065	178	73.03	2.00E-91	PadR family transcripitonal regulator
gene_id_7066	215	74.88	9.00E-110	methyltransferase

gene_id_7067	141	64.54	2.00E-57	DNA-binding protein
gene_id_7068	69	82.61	1.00E-34	ferrous iron transporter A
gene_id_7069	438	72.15	0	iron transporter FeoB
gene_id_7071	143	80.42	2.00E-81	glyoxalase
gene_id_7073	165	69.7	2.00E-85	amidase
gene_id_7074	177	49.15	2.00E-50	hypothetical protein
gene_id_7078	389	83.29	0	malate dehydrogenase
gene_id_7079	141	64.54	1.00E-57	uPF0178 protein Cpap_0299
gene_id_7080	212	73.58	9.00E-118	uncharacterized protein
gene_id_7081	260	63.08	6.00E-124	rNA methyltransferase TrmH family group 3
gene_id_7082	101	65.35	2.00E-43	hypothetical protein
gene_id_7083	337	83.38	0	3-deoxy-D-arabinoheptulosonate-7-phosphate sy
gene_id_7084	282	79.08	3.00E-163	putative dehydrogenase
gene_id_7085	350	70	6.00E-161	3-dehydroquinate synthase
gene_id_7086	422	59.72	5.00E-169	3-phosphoshikimate 1-carboxyvinyltransferase
gene_id_7087	359	70.75	6.00E-174	chorismate synthase
gene_id_7088	379	74.93	0	prephenate dehydratase
gene_id_7089	143	78.32	1.00E-75	3-dehydroquinate dehydratase
gene_id_7090	395	70.63	0	aminotransferase class I/II
gene_id_7091	143	86.01	2.00E-88	protein MraZ
gene_id_7092	310	80.32	9.00E-177	16S rRNA methyltransferase
gene_id_7093	179	53.63	2.00E-54	hypothetical protein
gene_id_7094	735	65.85	0	penicillin-binding protein 2B
gene_id_7095	647	75.58	0	peptidoglycan glycosyltransferase
gene_id_7097	484	67.56	0	uDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2 6
gene_id_7098	460	66.3	0	uDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-ala
gene_id_7099	305	80	4.00E-162	phospho-N-acetylmuramoyl-pentapeptide-transf
gene_id_7100	450	76.89	0	uDP-N-acetylmuramoylalanine--D-glutamate ligas
gene_id_7101	347	73.49	1.00E-152	hypothetical protein
gene_id_7102	260	38.46	2.00E-60	hypothetical protein
gene_id_7103	876	86.76	0	valyl-tRNA synthetase
gene_id_7104	317	54.26	3.00E-81	predicted membrane protein
gene_id_7105	411	82.73	0	serine hydroxymethyltransferase
gene_id_7106	239	65.69	6.00E-117	hypothetical protein
gene_id_7107	102	90.2	3.00E-59	trpR like protein YerC/YecD
gene_id_7109	758	76.12	0	aTP-dependent DNA helicase PcrA
gene_id_7110	646	74.92	0	NAD-dependent DNA ligase LigA
gene_id_7111	600	31.83	2.00E-75	hypothetical protein
gene_id_7112	82	58.54	2.00E-26	hypothetical protein
gene_id_7113	54	51.85	3.00E-10	hypothetical protein
gene_id_7114	71	47.89	2.00E-18	XRE family transcriptional regulator
gene_id_7115	192	51.04	7.00E-50	hypothetical protein
gene_id_7116	568	66.02	0	putative terminase large subunit
gene_id_7117	184	66.85	3.00E-89	integrase family protein
gene_id_7119	592	64.53	0	hypothetical protein
gene_id_7121	213	36.15	2.00E-22	hypothetical protein
gene_id_7122	121	57.85	2.00E-33	hypothetical protein

gene_id_7123	77	84.42	5.00E-40	hypothetical protein
gene_id_7124	324	61.42	1.00E-138	hypothetical protein
gene_id_7125	213	39.44	6.00E-39	hypothetical protein
gene_id_7126	644	68.32	0	hypothetical protein
gene_id_7127	239	50.63	1.00E-67	hypothetical protein
gene_id_7130	46	52.17	8.00E-10	hypothetical protein
gene_id_7131	123	58.54	2.00E-36	putative holin
gene_id_7132	249	54.22	1.00E-87	cell wall hydrolase/autolysin
gene_id_7133	313	45.37	3.00E-60	hypothetical protein
gene_id_7133	225	51.11	6.00E-33	hypothetical protein
gene_id_7133	75	46.67	3.00E-06	hypothetical protein
gene_id_7134	954	43.29	0	hypothetical protein
gene_id_7134	279	27.24	2.00E-13	hypothetical protein
gene_id_7136	104	50	3.00E-23	hypothetical protein
gene_id_7137	142	35.92	6.00E-17	hypothetical protein
gene_id_7138	130	46.15	5.00E-26	hypothetical protein
gene_id_7139	73	63.01	3.00E-22	Ig-like domain-containing surface protein
gene_id_7140	316	25.32	1.00E-12	hypothetical protein
gene_id_7142	118	44.92	1.00E-24	transcriptional regulator
gene_id_7145	100	62	8.00E-35	hypothetical protein
gene_id_7146	115	50.43	5.00E-31	replication terminator protein phage associated
gene_id_7147	237	49.37	2.00E-72	hypothetical protein
gene_id_7149	64	51.56	3.00E-10	XRE family transcriptional regulator
gene_id_7150	293	36.18	2.00E-51	dnaD domain protein
gene_id_7151	467	42.18	1.00E-111	replicative DNA helicase
gene_id_7154	68	47.06	1.00E-11	hypothetical protein
gene_id_7155	515	46.02	6.00E-136	hypothetical protein
gene_id_7156	38	92.11	3.00E-14	binding-protein-dependent transport systems inn
gene_id_7157	98	75.51	4.00E-35	binding-protein-dependent transport systems inn
gene_id_7158	248	77.02	4.00E-140	aBC-type nitrate/sulfonate/bicarbonate transport
gene_id_7161	120	40.83	4.00E-19	hypothetical protein HMPREF1006_00176
gene_id_7162	834	46.76	0	hypothetical protein
gene_id_7163	195	50.26	7.00E-55	accessory protein regulator protein B
gene_id_7164	420	48.33	3.00E-133	hypothetical protein
gene_id_7165	229	63.32	2.00E-100	lytTr DNA-binding domain-containing protein
gene_id_7609	170	65.29	3.00E-70	hypothetical protein
gene_id_7610	267	59.55	2.00E-106	cof-like hydrolase
gene_id_7611	419	90.21	0	seryl-tRNA synthetase
gene_id_7612	106	81.13	4.00E-42	multidrug transporter
gene_id_7613	216	48.15	1.00E-52	hypothetical protein
gene_id_7614	309	67.31	6.00E-151	pfkB domain protein
gene_id_7615	357	75.35	9.00E-149	pfoR protein
gene_id_7617	69	94.2	2.00E-39	sporulation transcriptional regulator SpoIIID
gene_id_7618	213	56.81	7.00E-85	hypothetical protein
gene_id_7619	124	79.84	1.00E-55	desulfoferrodoxin
gene_id_7620	842	68.53	0	fAD-dependent pyridine nucleotide-disulphide oxi
gene_id_7621	179	78.77	1.00E-101	rubrerythrin

gene_id_7622	1350	66.07	0	carbamoyl-phosphate synthase large subunit
gene_id_7623	350	61.43	9.00E-159	carbamoyl-phosphate synthase, small subunit
gene_id_7624	301	86.05	0	ornithine carbamoyltransferase catabolic
gene_id_7625	390	73.08	0	acetylornithine aminotransferase
gene_id_7626	280	80.36	1.00E-121	acetylglutamate kinase
gene_id_7627	405	80.74	0	arginine biosynthesis bifunctional protein ArgJ
gene_id_7628	309	73.14	1.00E-169	n-acetyl-gamma-glutamyl-phosphate reductase
gene_id_7629	297	59.26	2.00E-129	MULTISPECIES: aldo/keto reductase
gene_id_7630	337	71.51	2.00E-168	hypothetical protein
gene_id_7631	283	58.3	7.00E-116	abortive infection protein
gene_id_7632	464	89.01	0	asparagine--tRNA ligase
gene_id_7633	322	68.32	8.00E-167	peptide-methionine (S)-S-oxide reductase MsrA /
gene_id_7635	271	61.99	3.00E-118	hypothetical protein
gene_id_7636	204	41.18	1.00E-42	abortive infection protein
gene_id_7637	457	76.37	0	transporter
gene_id_7638	417	65.71	4.00E-169	uPF0597 protein CBO1815/CLC_1757
gene_id_7639	515	80	0	amino acid carrier protein
gene_id_7640	92	60.87	7.00E-31	hypothetical protein
gene_id_7641	162	75.31	4.00E-75	heptaprenyl diphosphate synthase component I
gene_id_7642	501	90.42	0	inosine-5'-monophosphate dehydrogenase
gene_id_7643	61	59.02	2.00E-14	4Fe-4S ferredoxin
gene_id_7644	138	40.58	9.00E-27	membrane protein
gene_id_7645	75	58.67	7.00E-23	hypothetical protein
gene_id_7646	844	76.18	0	cation-transporting ATPase
gene_id_7647	715	79.58	0	tex-like protein-like protein
gene_id_7648	346	65.03	1.00E-149	uncharacterized protein
gene_id_7649	64	85.94	8.00E-34	Cro/Cl family transcriptional regulator
gene_id_7650	70	38.57	3.00E-09	hypothetical protein CB17B2517
gene_id_7651	148	45.27	5.00E-22	MULTISPECIES: hypothetical protein
gene_id_7652	95	91.58	4.00E-45	30S ribosomal protein S6
gene_id_7653	147	87.07	2.00E-83	single-stranded DNA-binding protein
gene_id_7654	76	94.74	5.00E-38	30S ribosomal protein S18
gene_id_7656	182	75.27	1.00E-87	hypothetical protein
gene_id_7657	358	70.39	0	d-alanine--D-alanine ligase
gene_id_7658	267	76.78	6.00E-150	glutamate racemase
gene_id_7659	354	56.5	1.00E-140	MULTISPECIES: Response regulator containing a C
gene_id_7660	92	46.74	2.00E-08	MULTISPECIES: putative Hpt domain protein
gene_id_7661	55	69.09	2.00E-19	hypothetical protein CBFG_02774
gene_id_7662	104	78.85	9.00E-54	thioredoxin
gene_id_7664	74	55.41	2.00E-13	hypothetical protein
gene_id_7761	313	58.47	7.00E-113	transporter auxin efflux carrier family protein
gene_id_7762	251	42.23	3.00E-69	hypothetical protein
gene_id_7763	154	71.43	3.00E-71	uncharacterized protein
gene_id_7764	292	73.29	7.00E-154	phosphogluconate dehydrogenase NAD binding d
gene_id_7765	573	82.72	0	acetoin dehydrogenase E3 component
gene_id_7766	412	78.16	0	tPP-dependent acetoin dehydrogenase complex E
gene_id_7767	326	93.56	0	acetoin dehydrogenase E1 component beta subu

gene_id_7768	329	82.98	0	acetoin dehydrogenase E1 component alpha subu
gene_id_7769	411	68.13	3.00E-143	hypothetical protein
gene_id_7770	149	55.03	2.00E-50	c4-dicarboxylate transport system permease smal
gene_id_7772	330	49.7	8.00E-97	c4-dicarboxylate transport system substrate-bindi
gene_id_7773	227	51.1	2.00E-53	MULTISPECIES: hypothetical protein
gene_id_7774	1229	78.93	0	phosphoribosylformylglycinamidine synthase
gene_id_7775	420	83.81	0	phosphoribosylamine--glycine ligase
gene_id_7776	394	85.28	0	hypothetical protein
gene_id_7777	478	83.47	0	adenylosuccinate lyase
gene_id_7778	239	81.59	1.00E-144	hypothetical protein
gene_id_7779	199	85.43	2.00E-120	phosphoribosylglycinamide formyltransferase
gene_id_7780	332	90.06	0	phosphoribosylformylglycinamidine cyclo-ligase
gene_id_7781	481	78.59	0	amidophosphoribosyltransferase
gene_id_7782	230	79.57	2.00E-132	phosphoribosylaminoimidazole-succinocarboxami
gene_id_7784	164	73.17	2.00E-55	N5-carboxyaminoimidazole ribonucleotide mutas
gene_id_7785	420	72.14	0	dihydroorotase
gene_id_7786	1057	88.46	0	carbamoyl-phosphate synthase large chain
gene_id_7787	224	80.8	2.00E-123	dihydroorotate dehydrogenase B (NAD(+)) electr
gene_id_7788	304	88.82	0	dihydroorotate dehydrogenase
gene_id_7789	235	80	6.00E-136	orotidine 5'-phosphate decarboxylase
gene_id_7790	208	86.54	3.00E-130	orotate phosphoribosyltransferase
gene_id_7791	303	82.18	0	aspartate carbamoyltransferase
gene_id_7792	138	66.67	7.00E-57	aspartate carbamoyltransferase regulatory chain
gene_id_7793	187	57.22	2.00E-77	esterase
gene_id_7794	320	60	7.00E-141	hypothetical protein
gene_id_7794	78	46.15	5.00E-10	hypothetical protein
gene_id_7795	116	56.03	1.00E-36	c_GCAxxG_C_C family protein
gene_id_7796	139	61.15	3.00E-45	positive regulator of sigma(E) RseC/MucC
gene_id_7798	379	57.26	2.00E-130	hypothetical protein
gene_id_7799	483	60.46	0	aminoacyl-histidine dipeptidase (Peptidase D)
gene_id_7800	230	83.48	3.00E-136	ribonuclease III
gene_id_7801	76	69.74	8.00E-30	phosphate acyltransferase
gene_id_7804	347	78.96	0	chemotaxis protein histidine kinase-like protein
gene_id_7805	331	89.43	0	phosphate acetyltransferase
gene_id_7806	398	89.2	0	acetate kinase
gene_id_7807	168	72.02	2.00E-81	cOG1399 protein clustered with ribosomal protei
gene_id_7808	330	82.42	0	phosphate acyltransferase
gene_id_7809	408	67.16	0	uPF0348 protein Cther_2657
gene_id_7810	341	52.79	4.00E-102	sporulation integral membrane protein YlbJ
gene_id_7811	167	89.82	3.00E-93	hypothetical protein
gene_id_7812	159	81.13	4.00E-92	phosphopantetheine adenylyltransferase
gene_id_7813	183	71.04	2.00E-84	rsmD family RNA methyltransferase
gene_id_7814	586	73.21	0	pyruvate kinase
gene_id_7815	326	88.65	0	6-phosphofructokinase 1
gene_id_7816	72	80.56	6.00E-33	tryptophan RNA-binding attenuator protein
gene_id_7817	1159	79.81	0	hypothetical protein
gene_id_7818	390	63.59	2.00E-124	hypothetical protein

gene_id_7819	229	81.22	1.00E-133	aBC transporter related
gene_id_7820	375	56.8	8.00E-132	efflux transporter RND family MFP subunit
gene_id_7821	1176	88.18	0	pyruvate-flavodoxin oxidoreductase
gene_id_7822	298	34.23	2.00E-49	copper amine oxidase N-domain superfamily
gene_id_7823	157	87.26	1.00E-96	single-stranded DNA-binding protein
gene_id_7825	113	38.94	2.00E-15	hypothetical protein
gene_id_7826	446	46.19	5.00E-129	recombinase
gene_id_7827	54	68.52	2.00E-16	recombinase, partial
gene_id_7828	95	45.26	2.00E-15	hypothetical protein
gene_id_7829	81	53.09	1.00E-18	Mor transcription activator family
gene_id_7832	171	42.69	7.00E-37	MULTISPECIES: hypothetical protein
gene_id_7833	321	47.98	2.00E-96	hypothetical protein
gene_id_7834	317	71.92	9.00E-169	hypothetical protein X276_26200
gene_id_7835	105	57.14	9.00E-32	hypothetical protein
gene_id_7837	85	42.35	6.00E-13	hypothetical protein
gene_id_7840	79	43.04	1.00E-14	hypothetical protein
gene_id_7844	211	31.75	1.00E-22	hypothetical protein
gene_id_7845	134	49.25	4.00E-39	putative regulatory protein
gene_id_7846	492	39.02	2.00E-77	hypothetical protein
gene_id_7846	226	36.73	4.00E-09	hypothetical protein
gene_id_7847	223	68.61	1.00E-108	PhoB family transcriptional regulator
gene_id_7848	460	46.52	1.00E-125	sensor histidine kinase
gene_id_7849	50	78	3.00E-22	rubredoxin
gene_id_7850	271	54.98	3.00E-107	hypothetical protein
gene_id_7851	400	66	0	hypothetical protein
gene_id_7853	244	26.64	5.00E-10	hypothetical protein
gene_id_7854	387	37.21	4.00E-79	hypothetical protein
gene_id_7855	291	74.23	9.00E-144	putative membrane protein
gene_id_8103	372	59.41	1.00E-70	peptidoglycan-binding lysin domain-containing pr
gene_id_8103	183	59.56	3.00E-51	peptidoglycan-binding lysin domain-containing pr
gene_id_8103	79	78.48	3.00E-22	peptidoglycan-binding lysin domain-containing pr
gene_id_8104	421	84.8	0	ATP-binding region ATPase domain-containing pro
gene_id_8105	244	84.84	4.00E-151	LytTR family transcriptional regulator
gene_id_8107	75	73.33	1.00E-16	hypothetical protein
gene_id_8108	326	72.39	8.00E-170	VanZ family protein
gene_id_8109	38	68.42	7.00E-09	transcriptional regulator
gene_id_8110	555	27.75	3.00E-39	hypothetical protein
gene_id_8111	2428	32.37	0	RHS repeat-associated core domain protein
gene_id_8113	61	72.13	2.00E-20	integrase core domain protein
gene_id_8114	270	82.59	1.00E-141	hypothetical protein
gene_id_8115	226	92.48	3.00E-122	hypothetical protein
gene_id_8116	307	95.44	1.00E-178	bacitracin ABC transporter ATP-binding protein
gene_id_8117	307	81.76	0	histidine kinase
gene_id_8118	231	90.48	1.00E-149	PhoP family transcriptional regulator
gene_id_8119	53	64.15	2.00E-17	mutator mutT protein
gene_id_8120	273	62.64	1.00E-119	hypothetical protein
gene_id_8121	771	80.42	0	DNA or RNA helicases of superfamily II

gene_id_8122	92	85.87	1.00E-37	transposase IS116
gene_id_8123	283	82.69	2.00E-173	transposase, IS116/IS110/IS902 family
gene_id_8125	74	47.3	1.00E-17	hypothetical protein
gene_id_8127	287	21.6	6.00E-13	hypothetical protein
gene_id_8132	221	36.2	4.00E-33	hypothetical protein
gene_id_8133	135	40.74	1.00E-30	hypothetical protein
gene_id_8134	48	43.75	1.00E-08	hypothetical protein
gene_id_8135	72	55.56	4.00E-20	hypothetical protein CINTURNW_2244
gene_id_8136	358	25.14	4.00E-13	hypothetical protein
gene_id_8137	140	76.43	2.00E-73	integrase
gene_id_8138	124	59.68	4.00E-46	rutC family protein PYRAB12510
gene_id_8139	172	67.44	4.00E-82	pyruvate/2-ketoisovalerate family 2-oxoacid:acce
gene_id_8140	242	75.62	4.00E-136	hypothetical protein
gene_id_8141	349	72.21	0	hypothetical protein
gene_id_8142	70	71.43	3.00E-30	hypothetical protein
gene_id_8143	257	51.75	2.00E-87	transcriptional regulator IclR family
gene_id_8144	394	57.61	4.00E-169	amidohydrolase
gene_id_8145	288	43.4	7.00E-66	transporter
gene_id_8146	325	80	0	pyridoxal-5'-phosphate-dependent protein beta s
gene_id_8147	344	69.19	3.00E-159	tRAP dicarboxylate transporter DctP subunit
gene_id_8148	396	81.57	0	amidohydrolase
gene_id_8149	406	77.59	0	tRAP dicarboxylate transporter DctM subunit
gene_id_8150	173	63.01	3.00E-71	tRAP dicarboxylate transporter DctQ subunit
gene_id_8151	391	85.17	0	xaa-Pro aminopeptidase
gene_id_8153	257	43.19	3.00E-65	transcriptional regulator IclR family
gene_id_8154	152	87.5	5.00E-94	hypothetical protein C820_00165
gene_id_8155	65	86.15	3.00E-33	diacylglycerol kinase
gene_id_8156	193	84.46	4.00E-119	nitroreductase
gene_id_8159	92	61.96	9.00E-27	copper amine oxidase
gene_id_8161	263	38.78	2.00E-60	hypothetical protein
gene_id_8163	141	84.4	6.00E-87	hypothetical protein
gene_id_8165	205	75.61	4.00E-110	TetR family transcriptional regulator
gene_id_8166	430	46.74	7.00E-128	hypothetical protein
gene_id_8167	222	80.63	5.00E-129	PhoB family transcriptional regulator
gene_id_8168	330	48.18	1.00E-96	hypothetical protein
gene_id_8169	529	63.89	0	hypothetical protein
gene_id_8170	75	62.67	5.00E-26	hypothetical protein
gene_id_8171	392	60.97	1.00E-174	hypothetical protein
gene_id_8172	500	57.8	0	AMP-dependent synthetase
gene_id_8175	314	54.46	4.00E-117	resolvase
gene_id_8176	144	72.22	1.00E-68	resolvase
gene_id_8177	290	75.52	7.00E-150	resolvase
gene_id_8178	517	44.49	1.00E-142	resolvase, N terminal domain protein
gene_id_8179	560	47.68	0	site-specific recombinase, resolvase family
gene_id_8180	538	60.97	0	recombinase
gene_id_8181	80	60	4.00E-28	hypothetical protein
gene_id_8182	58	48.28	9.00E-10	hypothetical protein

gene_id_8183	186	55.38	1.00E-73	hypothetical protein
gene_id_8184	321	40.5	7.00E-74	hypothetical protein
gene_id_8185	88	54.55	1.00E-17	hypothetical protein
gene_id_8186	63	73.02	2.00E-25	hypothetical protein
gene_id_8188	135	37.04	9.00E-17	hypothetical protein
gene_id_8190	256	71.09	3.00E-120	hypothetical protein
gene_id_8191	73	57.53	2.00E-18	hypothetical protein
gene_id_8192	253	45.45	7.00E-59	hypothetical protein
gene_id_8193	380	33.95	3.00E-43	hypothetical protein T479_18610
gene_id_8194	283	39.93	5.00E-66	hypothetical protein
gene_id_8195	517	46.62	7.00E-138	hypothetical protein
gene_id_8649	278	53.24	7.00E-117	penicillin amidase
gene_id_8650	299	41.14	7.00E-55	diguanylate cyclase
gene_id_8651	339	73.16	0	glyceraldehyde-3-phosphate dehydrogenase
gene_id_8652	334	88.62	0	hypothetical protein
gene_id_8654	122	63.11	5.00E-53	hypothetical protein
gene_id_8655	235	65.11	1.00E-89	rNA polymerase sigma factor
gene_id_8656	142	73.94	2.00E-69	anti-sigma F factor
gene_id_8657	116	54.31	8.00E-39	anti-sigma F factor antagonist
gene_id_8658	516	39.15	6.00E-112	hypothetical protein
gene_id_8659	320	46.25	1.00E-97	hypothetical protein, partial
gene_id_8660	523	48.37	4.00E-166	recombinase
gene_id_8661	77	55.84	3.00E-22	hypothetical protein
gene_id_8662	417	86.33	0	dihydropyrimidine dehydrogenase
gene_id_8663	425	73.18	0	dihydropyrimidine dehydrogenase
gene_id_8665	418	76.79	0	allantoate amidohydrolase
gene_id_8666	528	53.41	9.00E-168	hypothetical protein
gene_id_8667	450	77.78	0	hydantoinase
gene_id_8813	624	84.46	0	tRNA uridine 5-carboxymethylaminomethyl modi
gene_id_8814	141	43.26	7.00E-31	hypothetical protein
gene_id_8815	239	74.48	4.00E-127	ribosomal RNA small subunit methyltransferase G
gene_id_8817	281	81.49	6.00E-155	parB-like partition protein
gene_id_8818	151	50.99	3.00E-52	thioesterase family protein
gene_id_8819	153	44.44	2.00E-45	hypothetical protein
gene_id_8820	315	51.75	3.00E-114	hypothetical protein
gene_id_8821	232	56.47	4.00E-85	molecular chaperone
gene_id_8822	225	55.56	7.00E-68	cell division protein FtsZ
gene_id_8823	367	54.22	1.00E-117	lipoprotein
gene_id_8823	128	39.84	5.00E-14	lipoprotein
gene_id_8824	221	72.4	1.00E-112	transcriptional regulator
gene_id_8825	426	42.02	9.00E-100	hypothetical protein
gene_id_8827	210	54.76	5.00E-79	Crp/Fnr family transcriptional regulator
gene_id_8828	185	70.81	2.00E-70	membrane protein, partial
gene_id_8829	63	60.32	1.00E-18	hypothetical protein
gene_id_8830	58	63.79	1.00E-15	4Fe-4S ferredoxin
gene_id_8831	154	66.23	1.00E-67	c_GCAxxG_C_C family protein
gene_id_8832	345	44.06	2.00E-91	copper amine oxidase domain protein

gene_id_8833	240	51.25	1.00E-78	metallo-beta-lactamase domain protein
gene_id_8834	998	66.43	0	acriflavin resistance protein
gene_id_8835	348	57.18	9.00E-137	efflux transporter RND family MFP subunit
gene_id_8836	156	40.38	8.00E-25	transcriptional regulator MarR family
gene_id_8837	373	64.08	2.00E-164	peptidase M20 family protein
gene_id_8838	236	80.08	1.00E-99	2 3 4 5-tetrahydropyridine-2 6-dicarboxylate N-ac
gene_id_8839	142	45.77	1.00E-29	hypothetical protein
gene_id_8840	60	60	2.00E-17	hypothetical protein
gene_id_8841	79	53.16	6.00E-12	pro-sigmaK processing inhibitor BofA
gene_id_8842	179	67.04	3.00E-82	hypothetical protein, partial
gene_id_8843	195	85.64	2.00E-119	hypothetical protein
gene_id_8844	273	55.31	7.00E-100	hypothetical protein
gene_id_8845	234	75.64	7.00E-127	lantibiotic ABC transporter ATP-binding protein
gene_id_8846	240	53.75	7.00E-88	hypothetical protein
gene_id_8847	248	47.58	1.00E-46	hypothetical protein
gene_id_8848	219	67.58	7.00E-107	multidrug ABC transporter
gene_id_8849	453	44.15	1.00E-128	hypothetical protein
gene_id_8851	457	54.92	6.00E-167	hypothetical protein
gene_id_8852	50	80	2.00E-22	MULTISPECIES: hypothetical protein
gene_id_8853	441	73.7	0	peptidase
gene_id_8854	88	79.55	6.00E-41	MULTISPECIES: iron-only hydrogenase system reg
gene_id_8855	342	73.68	4.00E-179	biotin synthase
gene_id_8856	472	84.75	0	thiamine biosynthesis protein ThiH
gene_id_8857	398	69.6	0	ATP-binding protein
gene_id_8858	879	57.68	0	putative surface layer protein
gene_id_8859	366	43.17	7.00E-107	hypothetical protein
gene_id_8860	590	47.97	0	hypothetical protein
gene_id_8861	329	71.73	6.00E-169	glucose sorbosone dehydrogenase
gene_id_8864	531	48.96	1.00E-138	methyl-accepting chemotaxis protein
gene_id_8865	538	67.66	0	hypothetical protein
gene_id_8866	67	67.16	2.00E-18	iron transporter FeoB
gene_id_8867	179	81.56	1.00E-97	iron transporter FeoB
gene_id_8868	743	86.81	0	formate acetyltransferase 1
gene_id_8869	237	67.93	5.00E-117	pyruvate formate-lyase 1-activating enzyme
gene_id_8871	294	90.14	0	lysR substrate-binding protein
gene_id_8872	541	85.95	0	hydroxylamine reductase
gene_id_8874	264	67.42	4.00E-124	ferredoxin
gene_id_8875	427	54.1	2.00E-164	diguanylate cyclase/phosphodiesterase
gene_id_8876	103	65.05	4.00E-44	transcriptional regulator
gene_id_8877	49	83.67	8.00E-20	hypothetical protein K413DRAFT_4481
gene_id_8878	359	63.23	4.00E-125	hypothetical protein
gene_id_8879	143	51.75	1.00E-46	Fur family transcriptional regulator
gene_id_8880	273	72.16	2.00E-92	Zinc ABC transporter, inner membrane permease
gene_id_8881	250	59.6	2.00E-102	Zinc ABC transporter, ATP-binding protein ZnuC
gene_id_8882	298	65.44	1.00E-134	ABC transporter substrate-binding protein
gene_id_8884	639	61.5	0	hypothetical protein, partial
gene_id_8885	213	79.81	2.00E-123	membrane protein

gene_id_8886	107	75.7	9.00E-53	hypothetical protein
gene_id_9132	197	62.94	7.00E-79	hypothetical protein
gene_id_9133	467	44.11	7.00E-131	hypothetical protein
gene_id_9134	212	49.06	3.00E-63	hypothetical protein
gene_id_9135	98	53.06	2.00E-28	hypothetical protein
gene_id_9136	353	64.02	1.00E-162	hypothetical protein
gene_id_9137	33	51.52	3.00E-06	hypothetical protein
gene_id_9138	233	79.83	3.00E-126	metal-dependent hydrolase
gene_id_9139	200	53.5	3.00E-58	hypothetical protein
gene_id_9140	228	46.05	4.00E-60	hypothetical protein
gene_id_9141	78	55.13	2.00E-25	hypothetical protein
gene_id_9142	166	66.27	2.00E-74	hypothetical protein
gene_id_9143	369	34.96	1.00E-71	Antirestriction protein (ArdA)
gene_id_9144	81	66.67	1.00E-27	hypothetical protein
gene_id_9145	235	50.21	8.00E-65	putative phage antirepressor protein
gene_id_9146	315	66.03	1.00E-139	DNA adenine methylase
gene_id_9147	142	37.32	6.00E-24	hypothetical protein
gene_id_9148	172	66.86	5.00E-71	hypothetical protein
gene_id_9149	111	77.48	2.00E-57	SpoVG family protein
gene_id_9150	70	67.14	4.00E-11	hypothetical protein
gene_id_9151	1283	59.94	0	S-layer protein
gene_id_9152	609	61.58	0	rNA-directed DNA polymerase (Reverse transcript
gene_id_9153	76	65.79	6.00E-11	hypothetical protein
gene_id_9154	146	45.89	1.00E-34	hypothetical protein
gene_id_9156	262	71.37	2.00E-133	Flp pilus assembly protein CpaB
gene_id_9157	269	80.3	1.00E-143	ATPase AAA
gene_id_9158	468	85.47	0	type II secretion system protein E
gene_id_9159	300	75.33	1.00E-170	membrane protein
gene_id_9160	266	75.56	1.00E-141	secretion protein F
gene_id_9161	129	78.29	1.00E-68	hypothetical protein
gene_id_9162	169	73.96	3.00E-90	hypothetical protein
gene_id_9163	185	56.76	5.00E-47	hypothetical protein
gene_id_9164	564	71.81	0	hypothetical protein
gene_id_9165	113	78.76	2.00E-55	MULTISPECIES: hypothetical protein
gene_id_9166	115	100	3.00E-70	MULTISPECIES: hypothetical protein
gene_id_9168	108	100	7.00E-62	permease, partial
gene_id_9169	97	100	1.00E-65	cupin
gene_id_9170	845	100	0	HAD family hydrolase
gene_id_9171	291	100	0	MULTISPECIES: methionine aminopeptidase
gene_id_9172	113	100	2.00E-78	AraC family transcriptional regulator
gene_id_9173	135	100	2.00E-95	MULTISPECIES: ArsC family transcriptional regulat
gene_id_9174	348	100	0	MULTISPECIES: arsenic transporter
gene_id_9175	147	100	4.00E-66	MULTISPECIES: hypothetical protein
gene_id_9176	80	98.75	3.00E-35	MULTISPECIES: hypothetical protein
gene_id_9177	257	99.61	0	MULTISPECIES: hypothetical protein
gene_id_9178	337	100	0	permease
gene_id_9179	104	99.04	1.00E-69	MULTISPECIES: ArsR family transcriptional regulat

gene_id_9180	240	100	3.00E-176	hypothetical protein
gene_id_9181	67	98.51	4.00E-41	hypothetical protein
gene_id_9182	156	98.72	2.00E-109	glyoxalase
gene_id_9183	273	99.63	0	AraC family transcriptional regulator
gene_id_9184	293	73.38	4.00E-163	LysR family transcriptional regulator
gene_id_9185	169	65.09	1.00E-75	flavodoxin
gene_id_9187	69	63.77	2.00E-21	hypothetical protein
gene_id_9188	107	82.24	4.00E-60	hypothetical protein
gene_id_9189	138	69.57	1.00E-64	hypothetical protein
gene_id_9190	324	76.23	2.00E-168	alpha/beta hydrolase
gene_id_9191	180	59.44	1.00E-75	NADPH-dependent FMN reductase
gene_id_9192	213	87.32	6.00E-135	transcriptional regulator
gene_id_9193	148	92.57	6.00E-62	permease
gene_id_9194	237	81.86	1.00E-143	permease
gene_id_9195	102	80.39	6.00E-56	hypothetical protein
gene_id_9196	54	83.33	3.00E-24	rubredoxin
gene_id_9197	539	85.71	0	hydroxylamine reductase
gene_id_9198	320	39.38	2.00E-56	hypothetical protein
gene_id_9199	74	91.89	6.00E-40	XRE family transcriptional regulator
gene_id_9200	255	39.61	5.00E-48	hypothetical protein
gene_id_9201	68	61.76	1.00E-19	hypothetical protein
gene_id_9202	310	64.52	2.00E-136	hypothetical protein, partial
gene_id_9203	119	81.51	8.00E-67	CopY family transcriptional regulator
gene_id_9204	395	29.87	1.00E-45	hypothetical protein SAMD00020551_0296
gene_id_9205	98	51.02	1.00E-28	transcriptional regulator PadR family
gene_id_9206	212	84.91	7.00E-129	glutamine amidotransferase
gene_id_9207	310	79.03	1.00E-177	transcriptional regulator
gene_id_9208	118	65.25	3.00E-53	hypothetical protein C820_02834
gene_id_9209	653	44.26	3.00E-164	hypothetical protein
gene_id_9211	97	87.63	8.00E-55	4-oxalocrotonate tautomerase
gene_id_9212	91	34.07	1.00E-12	hypothetical protein
gene_id_9213	300	82	3.00E-169	hypothetical protein
gene_id_9214	218	74.31	9.00E-114	DNA-cytosine methyltransferase
gene_id_9215	397	51.64	1.00E-130	DNA-cytosine methyltransferase
gene_id_9216	81	81.48	3.00E-40	hypothetical protein
gene_id_9217	197	77.66	1.00E-99	hypothetical protein
gene_id_9218	212	60.38	1.00E-89	hypothetical protein
gene_id_9219	614	84.04	0	type VI secretion protein
gene_id_9220	142	71.83	2.00E-70	hypothetical protein
gene_id_9221	314	72.93	2.00E-176	hypothetical protein
gene_id_9222	329	56.23	2.00E-133	hypothetical protein
gene_id_9223	124	62.1	6.00E-53	hypothetical protein
gene_id_9224	80	62.5	1.00E-23	hypothetical protein
gene_id_9225	140	70.71	4.00E-66	hypothetical protein
gene_id_9226	908	55.51	0	Sel1 domain-containing protein repeat-containing
gene_id_9228	299	68.9	4.00E-151	hypothetical protein
gene_id_9229	271	83.03	2.00E-169	metallo-beta-lactamase

gene_id_9230	567	85.19	0	conjugal transfer protein TraG
gene_id_9231	84	75	2.00E-41	transcriptional regulator
gene_id_9232	318	32.08	9.00E-58	hypothetical protein
gene_id_9233	191	52.88	3.00E-53	hypothetical protein
gene_id_9234	282	43.97	2.00E-73	hypothetical protein
gene_id_9235	59	54.24	1.00E-12	Predicted Zn peptidase
gene_id_9236	126	53.97	1.00E-40	XRE family transcriptional regulator
gene_id_9237	175	49.71	2.00E-52	hypothetical protein
gene_id_9238	153	47.06	1.00E-33	dNA-directed RNA polymerase specialized sigma s
gene_id_9239	67	68.66	1.00E-22	hypothetical protein
gene_id_9240	532	71.43	0	resolvase
gene_id_9241	319	47.96	8.00E-100	recombinase
gene_id_9242	550	82	0	resolvase
gene_id_9637	229	47.6	3.00E-62	uncharacterized protein
gene_id_9638	308	91.56	0	uPF0365 protein Desku_2652
gene_id_9639	151	59.6	3.00E-37	hypothetical protein
gene_id_9640	91	54.95	2.00E-29	hypothetical protein
gene_id_9641	203	88.67	3.00E-116	lexA repressor
gene_id_9642	646	74.77	0	nAD+ synthetase
gene_id_9643	469	62.9	0	integral membrane sensor signal transduction hist
gene_id_9644	113	36.28	3.00E-14	hypothetical protein
gene_id_9645	225	83.56	8.00E-137	response regulator receiver domain protein
gene_id_9646	790	82.28	0	mutS2 protein
gene_id_9647	658	87.99	0	fructose-1 6-bisphosphatase class 3
gene_id_9648	279	32.62	8.00E-35	uncharacterized protein
gene_id_9649	241	69.71	4.00E-119	dehydrogenases with different specificities (Relate
gene_id_9650	225	51.56	5.00E-76	2-haloacid dehalogenase
gene_id_9651	173	57.8	3.00E-64	GCN5-related N-acetyltransferase
gene_id_9652	339	88.79	0	tRNA threonylcarbamoyladenosine modification p
gene_id_9653	305	76.07	9.00E-165	ribonuclease Z
gene_id_9654	212	66.98	3.00E-96	thiamine pyrophosphokinase
gene_id_9655	221	81.45	5.00E-127	ribulose-phosphate 3-epimerase
gene_id_9656	281	83.63	2.00E-163	putative ribosome biogenesis GTPase RsgA
gene_id_9657	835	58.92	0	serine/threonine protein kinase
gene_id_9658	243	67.49	7.00E-116	protein serine/threonine phosphatase
gene_id_9659	343	77.55	0	ribosomal RNA large subunit methyltransferase N
gene_id_9660	447	68.01	0	sun protein
gene_id_9661	224	67.41	2.00E-89	hypothetical protein
gene_id_9662	309	69.9	1.00E-156	methionyl-tRNA formyltransferase
gene_id_9663	149	83.22	6.00E-84	peptide deformylase
gene_id_9664	817	58.51	0	primosome assembly protein PriA
gene_id_9665	73	87.67	8.00E-38	dNA-directed RNA polymerase subunit omega
gene_id_9666	202	81.19	5.00E-121	guanylate kinase
gene_id_9667	85	87.06	1.00E-49	uncharacterized protein
gene_id_9668	295	79.66	1.00E-169	hypothetical protein
gene_id_9669	588	73.3	0	fibronectin-binding protein
gene_id_9670	441	62.36	2.00E-169	mATE efflux family protein

gene_id_9671	495	91.31	0	ribonuclease Y
gene_id_9672	474	62.24	0	rNAse G
gene_id_9673	243	31.69	9.00E-13	hypothetical protein
gene_id_9674	147	72.11	1.00E-72	peptidase M23
gene_id_9675	100	48	3.00E-21	hypothetical protein
gene_id_9676	336	61.31	5.00E-150	ribosome biogenesis GTPase RsgA
gene_id_9677	138	58.7	2.00E-52	hypothetical protein
gene_id_9678	137	54.01	4.00E-43	hypothetical protein
gene_id_9679	1127	63.53	0	aTP-dependent helicase/deoxyribonuclease subur
gene_id_9680	577	67.59	0	thiamine ABC transporter permease
gene_id_9681	475	69.05	0	hypothetical protein
gene_id_9682	119	79.83	2.00E-66	glyoxalase/Bleomycin resistance protein/Dioxyger
gene_id_9683	207	63.29	6.00E-90	hypothetical protein
gene_id_9684	115	52.17	9.00E-35	hypothetical protein
gene_id_9685	82	57.32	1.00E-26	hypothetical protein
gene_id_9686	370	58.38	5.00E-145	phage endopeptidase
gene_id_9687	42	66.67	1.00E-10	hypothetical protein
gene_id_9689	206	50	6.00E-61	hypothetical protein
gene_id_9690	216	57.41	4.00E-88	putative phage tail component
gene_id_9691	346	33.82	1.00E-52	tail tape measure protein, TIGR01760 family
gene_id_9692	191	51.31	4.00E-63	bacteriophage Gp15 family protein
gene_id_9694	142	69.01	5.00E-55	hypothetical protein
gene_id_9695	138	49.28	4.00E-40	uncharacterized protein
gene_id_9696	128	42.19	1.00E-25	Minor capsid
gene_id_9697	109	33.03	4.00E-10	hypothetical protein HMPREF1143_1754
gene_id_9698	115	40	2.00E-12	hypothetical protein
gene_id_9700	286	74.83	2.00E-156	hypothetical protein
gene_id_9701	153	39.87	2.00E-17	hypothetical protein
gene_id_9702	374	27.54	1.00E-28	hypothetical protein
gene_id_9703	407	53.32	1.00E-138	phage portal protein
gene_id_9704	143	50.35	7.00E-42	hypothetical protein
gene_id_9706	50	80	7.00E-18	conserved hypothetical protein
gene_id_10255	60	85	2.00E-26	hypothetical protein
gene_id_10256	263	92.4	2.00E-172	electron transfer flavoprotein domain-containing
gene_id_10257	379	89.45	0	hypothetical protein
gene_id_10259	152	36.84	1.00E-14	hypothetical protein
gene_id_10260	172	61.63	1.00E-32	bioY family protein
gene_id_10262	89	46.07	5.00E-21	hypothetical protein
gene_id_10263	93	72.04	9.00E-46	cotJB protein
gene_id_10264	62	61.29	3.00E-16	catalase
gene_id_10265	234	63.68	1.00E-105	isochorismatase hydrolase
gene_id_10268	38	73.68	7.00E-09	hypothetical protein
gene_id_10269	55	65.45	5.00E-18	hypothetical protein
gene_id_10270	56	41.07	1.00E-07	hypothetical protein
gene_id_10271	183	37.7	5.00E-23	hypothetical protein
gene_id_10272	444	59.23	0	hypothetical protein
gene_id_10274	90	42.22	2.00E-15	hypothetical protein

gene_id_10275	162	29.01	6.00E-17	hypothetical protein
gene_id_10276	181	63.54	8.00E-61	YcfA-like protein
gene_id_10277	127	50.39	6.00E-16	MULTISPECIES: cell agglutination protein Mam3
gene_id_10278	294	42.86	1.00E-57	hypothetical protein
gene_id_10279	177	55.37	3.00E-63	rNA polymerase sigma factor sigma-70 family
gene_id_10280	412	61.65	0	DNA polymerase IV
gene_id_10281	75	64	4.00E-27	hypothetical protein
gene_id_10282	479	26.3	1.00E-34	funZ protein
gene_id_10283	103	47.57	5.00E-27	transcriptional regulator
gene_id_10284	171	43.27	4.00E-35	hypothetical protein LR68_02835
gene_id_10285	179	55.31	1.00E-61	hypothetical protein C804_01109
gene_id_10286	65	75.38	2.00E-26	uncharacterized protein
gene_id_10287	55	63.64	7.00E-10	hypothetical protein
gene_id_10288	113	46.02	7.00E-26	MULTISPECIES: hypothetical protein
gene_id_10289	39	69.23	1.00E-08	hypothetical protein C820_02008
gene_id_10290	99	49.49	2.00E-20	hypothetical protein
gene_id_10292	47	55.32	5.00E-06	hypothetical protein
gene_id_10293	178	44.94	3.00E-47	hypothetical protein
gene_id_10294	343	42.27	9.00E-73	hypothetical protein
gene_id_10295	138	49.28	3.00E-39	XkdS-like protein
gene_id_10296	131	24.43	4.00E-08	hypothetical protein
gene_id_10297	314	42.36	3.00E-79	hypothetical protein
gene_id_10298	202	38.12	1.00E-36	peptidoglycan-binding protein
gene_id_10299	464	31.25	1.00E-45	tail protein
gene_id_10300	270	31.11	2.00E-31	hypothetical protein
gene_id_10302	110	40	3.00E-17	hypothetical protein
gene_id_10303	138	48.55	2.00E-39	phage portal protein
gene_id_10304	362	51.1	9.00E-115	terminase
gene_id_10307	123	41.46	8.00E-22	head-tail adaptor protein
gene_id_10308	97	40.21	5.00E-18	hypothetical protein
gene_id_10310	372	41.13	3.00E-84	hypothetical protein
gene_id_10311	169	52.07	3.00E-52	phage head maturation protease
gene_id_10312	416	50.48	1.00E-147	phage portal protein, HK97 family
gene_id_10314	567	67.02	0	terminase
gene_id_10315	185	51.89	2.00E-45	hypothetical protein
gene_id_10316	128	53.91	2.00E-37	hypothetical protein
gene_id_10317	154	46.75	4.00E-26	hypothetical protein
gene_id_10318	281	58.01	3.00E-107	hypothetical protein
gene_id_10321	67	55.22	3.00E-15	seryl-tRNA synthetase
gene_id_10323	50	50	3.00E-07	hypothetical protein
gene_id_10324	64	60.94	7.00E-22	hypothetical protein, partial
gene_id_10325	64	65.62	9.00E-19	hypothetical protein
gene_id_10326	525	54.86	0	recombinase
gene_id_10327	124	83.87	1.00E-70	hypothetical protein
gene_id_10328	408	89.71	0	aspartokinase
gene_id_10329	300	74.67	2.00E-168	homoserine kinase
gene_id_10331	176	80.68	6.00E-93	uPF0735 ACT domain-containing protein Mahau_

gene_id_10333	530	47.92	3.00E-168	hypothetical protein
gene_id_10334	361	75.35	0	hypothetical protein
gene_id_10335	130	54.62	6.00E-39	hypothetical protein
gene_id_10336	300	67.33	3.00E-148	conserved hypothetical radical SAM protein
gene_id_10337	185	75.68	3.00E-93	hypothetical protein
gene_id_10338	208	82.21	4.00E-127	tRNA (guanine-N(7)-)-methyltransferase
gene_id_10339	166	57.83	6.00E-49	hypothetical protein
gene_id_10339	245	31.43	6.00E-23	hypothetical protein
gene_id_10341	129	61.24	6.00E-35	adenylate cyclase
gene_id_10342	182	56.04	7.00E-70	dJ-1 family protein
gene_id_10343	173	83.24	1.00E-92	hypothetical protein
gene_id_10344	287	88.85	0	hypothetical protein
gene_id_10345	155	77.42	6.00E-63	putative small multi-drug export protein
gene_id_10346	287	83.28	1.00E-175	dimethyladenosine transferase
gene_id_10347	264	84.47	8.00E-161	sporulation transcriptional activator Spo0A
gene_id_10348	601	92.85	0	elongation factor 4
gene_id_10350	483	68.53	0	trk system potassium uptake protein TrkH
gene_id_10351	452	71.02	0	hypothetical protein
gene_id_10352	415	86.51	0	histidyl-tRNA synthetase
gene_id_10353	481	78.38	0	coproporphyrinogen dehydrogenase
gene_id_10354	150	89.33	8.00E-92	d-tyrosyl-tRNA(Tyr) deacylase
gene_id_10355	743	83.71	0	hypothetical protein
gene_id_10356	384	58.07	4.00E-151	glycoside hydrolase family 3 domain protein
gene_id_10357	591	66.16	0	single-stranded-DNA-specific exonuclease RecJ
gene_id_10358	170	74.12	2.00E-89	adenine phosphoribosyltransferase
gene_id_10850	113	41.59	8.00E-21	degV family protein
gene_id_10851	355	58.31	8.00E-150	threonine/alanine tRNA ligase second additional c
gene_id_10852	411	72.51	0	xaa-pro aminopeptidase
gene_id_10853	229	65.94	2.00E-97	hypothetical protein
gene_id_10854	120	67.5	2.00E-50	hypothetical protein
gene_id_10855	105	79.05	4.00E-51	hypothetical protein
gene_id_10856	146	52.05	1.00E-43	hypothetical protein
gene_id_10857	68	85.29	8.00E-35	Cro/Cl family transcriptional regulator
gene_id_10858	427	57.38	2.00E-177	hypothetical protein
gene_id_10859	240	88.75	5.00E-156	pP-loop domain protein
gene_id_10860	353	77.9	0	site-specific recombinase phage integrase family
gene_id_10861	206	58.25	1.00E-87	phosphohydrolase
gene_id_10862	310	78.71	0	ribosome biogenesis GTPase A
gene_id_10863	154	68.18	1.00E-65	signal peptidase I
gene_id_10864	114	95.61	7.00E-70	50S ribosomal protein L19
gene_id_10865	305	45.57	2.00E-82	hypothetical protein
gene_id_10866	182	52.75	2.00E-58	transcriptional regulator TetR family
gene_id_10867	174	42.53	4.00E-28	putative uncharacterized protein
gene_id_10868	472	73.52	0	putative uncharacterized protein
gene_id_11062	259	57.14	4.00E-97	MerR family transcriptional regulator
gene_id_11063	177	66.67	1.00E-84	nitroreductase
gene_id_11064	122	86.07	2.00E-71	acyl-CoA hydrolase

gene_id_11065	152	88.16	4.00E-95	beta-alanyl-CoA:ammonia lyase
gene_id_11066	393	80.66	0	bile acid-inducible operon protein F
gene_id_11067	367	97	0	RecName: Full=Acryloyl-CoA reductase electron tr
gene_id_11068	267	97	0	RecName: Full=Acryloyl-CoA reductase electron tr
gene_id_11069	394	98.73	0	RecName: Full=Acryloyl-CoA reductase (NADH); A
gene_id_11070	184	30.98	1.00E-14	hypothetical protein
gene_id_11071	193	36.27	1.00E-24	hypothetical protein
gene_id_11072	316	38.61	8.00E-80	type IV pilus assembly protein PilM
gene_id_11073	257	48.64	5.00E-63	peptidase, A24 type IV prepilin peptidase family p
gene_id_11074	66	66.67	4.00E-07	prepilin-type cleavage/methylation N-terminal do
gene_id_11075	400	48.5	4.00E-126	type II secretion system protein F
gene_id_11076	347	67.15	9.00E-153	twitching motility protein PilT
gene_id_11077	565	66.19	0	type II secretion system protein E
gene_id_11078	193	28.5	1.00E-12	hypothetical protein
gene_id_11080	83	38.55	8.00E-12	hypothetical protein
gene_id_11081	807	29.86	2.00E-44	prepilin-type cleavage/methylation N-terminal do
gene_id_11081	652	27.91	8.00E-25	prepilin-type cleavage/methylation N-terminal do
gene_id_11082	140	86.43	2.00E-85	hypothetical protein
gene_id_11083	416	80.05	0	peptidase U32
gene_id_11084	230	85.22	5.00E-138	putative acyl-CoA O-methyltransferase
gene_id_11085	334	64.07	6.00E-154	predicted periplasmic solute-binding protein
gene_id_11086	427	61.12	0	folC bifunctional protein
gene_id_11087	50	66	4.00E-15	hypothetical protein
gene_id_11088	469	62.9	0	tetratricopeptide repeat
gene_id_11089	174	41.38	7.00E-41	cytochrome O ubiquinol oxidase
gene_id_11090	308	68.51	4.00E-156	hypothetical protein
gene_id_11091	361	49.58	7.00E-116	hypothetical protein
gene_id_11092	152	50	4.00E-49	NUDIX hydrolase
gene_id_11093	338	63.61	5.00E-156	a/G-specific adenine glycosylase
gene_id_11094	206	67.48	9.00E-100	putative membrane protein
gene_id_11095	443	82.62	0	probable D-serine dehydratase
gene_id_11096	418	84.21	0	diaminopimelate decarboxylase
gene_id_11097	496	58.06	0	sensor histidine kinase
gene_id_11098	232	74.57	5.00E-109	two component transcriptional regulator winged l
gene_id_11099	74	59.46	2.00E-24	hypothetical protein
gene_id_11100	296	70.61	4.00E-156	radical SAM domain protein
gene_id_11101	116	77.59	3.00E-63	mannose-6-phosphate isomerase
gene_id_11102	115	66.09	2.00E-33	hypothetical protein
gene_id_11103	237	60.34	1.00E-104	hypothetical protein
gene_id_11104	501	65.87	0	cell division protein FtsY
gene_id_11105	1184	64.7	0	chromosome partition protein Smc
gene_id_11106	422	69.43	0	dihydroorotase
gene_id_11107	309	78.96	0	aspartate carbamoyltransferase
gene_id_11108	304	82.57	0	hypothetical protein
gene_id_11109	149	71.14	1.00E-49	lipoprotein signal peptidase
gene_id_11110	152	71.05	1.00E-50	cell division initiation protein DivIVA
gene_id_11111	263	59.32	1.00E-95	hypothetical protein

gene_id_11112	85	70.59	6.00E-35	hypothetical protein
gene_id_11113	174	77.01	1.00E-82	uncharacterized protein
gene_id_11114	231	77.06	1.00E-118	hypothetical protein
gene_id_11115	474	59.49	0	hypothetical protein
gene_id_11116	582	75.77	0	dihydrolipoamide dehydrogenase
gene_id_11117	461	63.12	0	hypothetical protein
gene_id_11118	337	55.19	4.00E-122	hypothetical protein
gene_id_11119	320	75.31	3.00E-164	acetoin dehydrogenase
gene_id_11120	328	75.3	1.00E-175	acetoin:2,6-dichlorophenolindophenol oxidoredu
gene_id_11121	117	67.52	8.00E-43	hypothetical protein
gene_id_11122	641	46.8	0	hypothetical protein
gene_id_11123	492	81.91	0	stage IV sporulation protein A
gene_id_11124	74	55.41	9.00E-22	MULTISPECIES: hypothetical protein
gene_id_11398	585	50.94	0	n-terminal double-transmembrane domain-contai
gene_id_11399	899	52.5	0	uncharacterized membrane protein
gene_id_11400	450	58.22	1.00E-172	hypothetical protein
gene_id_11401	330	66.06	4.00E-156	hydrogenase maturation factor
gene_id_11402	386	77.46	0	hypothetical protein
gene_id_11403	421	63.66	0	hypothetical protein
gene_id_11404	242	74.79	7.00E-135	nAD-dependent protein deacetylases SIR2 family
gene_id_11517	58	82.76	8.00E-25	electron transfer flavoprotein alpha subunit
gene_id_11519	221	71.04	2.00E-109	hypothetical protein
gene_id_11521	371	56.06	5.00E-142	hypothetical protein
gene_id_11522	80	78.75	1.00E-18	preprotein translocase subunit SecG
gene_id_11523	715	74.97	0	ribonuclease R
gene_id_11525	452	74.56	0	amino acid transporter
gene_id_11527	128	66.41	4.00E-51	putative DNA-binding protein
gene_id_11528	248	85.08	3.00E-136	hypothetical protein
gene_id_11529	454	77.31	0	amino acid carrier protein
gene_id_11530	452	75	0	amino acid carrier protein
gene_id_11531	454	77.31	0	amino acid carrier protein
gene_id_11532	437	63.62	0	glycosyl transferase group 1
gene_id_11533	618	61.65	0	uvrD/REP helicase
gene_id_11534	860	33.14	3.00E-130	hypothetical protein
gene_id_11535	306	74.18	2.00E-167	aBC-type multidrug transport system ATPase com
gene_id_11536	289	52.94	6.00E-92	hypothetical protein
gene_id_11537	491	42.36	1.00E-86	hypothetical protein
gene_id_14360	60	86.67	1.00E-26	hypothetical protein
gene_id_14361	263	90.11	2.00E-169	electron transfer flavoprotein domain-containing
gene_id_14362	380	88.68	0	butyryl-CoA dehydrogenase
gene_id_14363	467	77.73	0	putative sigma54 specific transcriptional regulato
gene_id_14364	407	51.11	2.00E-134	beta-lactamase domain-containing protein
gene_id_14365	621	76.49	0	aTP-dependent zinc metalloprotease FtsH 3
gene_id_14366	145	43.45	9.00E-32	transcriptional regulator MarR family
gene_id_14367	420	73.1	0	uDP-N-acetylglucosamine 1-carboxyvinyltransfera
gene_id_14369	129	64.34	5.00E-33	hypothetical protein
gene_id_14370	226	48.67	3.00E-74	cell division protein FtsE

gene_id_14371	167	53.29	4.00E-56	hypothetical protein, partial
gene_id_14372	134	29.1	2.00E-07	hypothetical protein
gene_id_14373	128	53.91	1.00E-44	flagellar protein FliS
gene_id_14374	830	37.83	3.00E-147	hypothetical protein
gene_id_14375	246	65.85	9.00E-103	chromosome partitioning protein ParA
gene_id_14376	237	30.8	2.00E-24	Late competence development protein ComFB
gene_id_14377	301	68.44	4.00E-143	two-component system, chemotaxis family, respo
gene_id_14378	161	59.63	3.00E-63	chemotaxis protein CheD
gene_id_14379	208	55.77	3.00E-79	chemotaxis protein CheC
gene_id_14380	257	43.19	4.00E-57	MULTISPECIES: hypothetical protein
gene_id_14381	249	49.4	3.00E-59	hypothetical protein
gene_id_14382	244	57.38	4.00E-92	FliA/WhiG family RNA polymerase sigma factor
gene_id_14383	204	71.57	6.00E-102	flagellar biosynthesis protein FlhA
gene_id_15077	90	72.22	6.00E-22	hypothetical protein
gene_id_15080	501	37.92	5.00E-88	hypothetical protein
gene_id_15081	207	66.67	4.00E-90	hypothetical protein
gene_id_15082	112	60.71	9.00E-33	uncharacterized protein
gene_id_15083	79	67.09	3.00E-31	hypothetical protein
gene_id_15084	91	54.95	3.00E-22	hypothetical protein
gene_id_15182	122	53.28	4.00E-36	glyoxalase
gene_id_15183	545	86.61	0	hydroxylamine reductase
gene_id_15184	424	61.08	1.00E-172	citrate transporter
gene_id_15185	267	62.92	2.00E-108	crotonase
gene_id_15186	506	68.58	0	3-oxoacid CoA-transferase
gene_id_15187	465	64.52	0	ATPase AAA
gene_id_15188	458	56.11	4.00E-165	histidine kinase
gene_id_15189	229	71.18	3.00E-118	transcriptional regulator
gene_id_15190	68	64.71	5.00E-25	copper-binding protein
gene_id_15191	214	63.55	3.00E-91	MULTISPECIES: hypothetical protein
gene_id_15192	822	82.36	0	ATPase
gene_id_20700	131	48.85	2.00E-35	Fe-S oxidoreductase
gene_id_20702	69	78.26	3.00E-33	putative cold shock protein
gene_id_20703	680	68.97	0	aTP-dependent DNA helicase RecG
gene_id_20704	560	73.04	0	hypothetical protein
gene_id_20705	118	89.83	1.00E-68	hypothetical protein
gene_id_20706	404	75.74	2.00E-168	hypothetical protein
gene_id_20707	164	69.51	1.00E-80	tRAP-type C4-dicarboxylate transport system sma
gene_id_20708	298	73.49	8.00E-166	hypothetical protein
gene_id_20709	248	75.4	8.00E-134	putative acetoacetyl-CoA reductase PhaB

lpha; AltName: Full=(R)-lactyl-CoA dehydratase component E II; AltName: Full=2-hydroxybutyroyl-CoA dehydrat
eta; AltName: Full=(R)-lactyl-CoA dehydratase component E II; AltName: Full=2-hydroxybutyroyl-CoA dehydrata

ansfer subunit beta; AltName: Full=Electron transfer flavoprotein large subunit; Short=ETFLS; AltName: Full=Ele

ansfer subunit gamma; AltName: Full=Electron transfer flavoprotein small subunit; Short=ETFSS; AltName: Full=

ctron transfer flavoprotein subunit beta; Short=Beta-ETF
Electron transfer flavoprotein subunit gamma; Short=Gamma-ETF

Contig	Gene_ID	Bin_genome	RPKM HiTCEB12_T1	RPKM HiTCE_T1
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31	gene_id_2803	Bin_1	78.4627	70.9091
31	gene_id_2804	Bin_1	152.097	89.8774
31	gene_id_2805	Bin_1	175.368	138.983
31	gene_id_2806	Bin_1	42.1663	47.8859
31	gene_id_2807	Bin_1	57.0711	46.6131
31	gene_id_2808	Bin_1	61.1549	53.9499
31	gene_id_2809	Bin_1	110.763	109.477
31	gene_id_2810	Bin_1	32.8516	61.5526
31	gene_id_2811	Bin_1	75.6411	65.886
31	gene_id_2812	Bin_1	41.8714	62.9005
31	gene_id_2813	Bin_1	66	84.3872
31	gene_id_2815	Bin_1	51.1852	42.7491
31	gene_id_2816	Bin_1	12.1298	33.4327
31	gene_id_2818	Bin_1	32.8274	26.6737
31	gene_id_2819	Bin_1	53.3894	51.2916
31	gene_id_2820	Bin_1	124.928	122.807
31	gene_id_2821	Bin_1	12.4443	19.6991
31	gene_id_2822	Bin_1	7.79542	17.5526
31	gene_id_2823	Bin_1	4.24532	28.0477
31	gene_id_2824	Bin_1	4.11595	19.1847
31	gene_id_2825	Bin_1	6.81555	15.249
31	gene_id_2826	Bin_1	9.25368	21.463
31	gene_id_2827	Bin_1	171.888	157.038
31	gene_id_2828	Bin_1	41837.1	28526.9
31	gene_id_2829	Bin_1	17698.5	12338.1
31	gene_id_2830	Bin_1	126.38	133.491
31	gene_id_2831	Bin_1	103.297	87.5725
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31	gene_id_2833	Bin_1	67.2683	262.274
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31	gene_id_2838	Bin_1	33.7012	48.2818
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31	gene_id_2844	Bin_1	54.3121	643.756
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31	gene_id_2847	Bin_1	8.18387	12.1006
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31	gene_id_2858	Bin_1	1.42916	17.359
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31	gene_id_3216	Bin_1	73.7634	59.329
31	gene_id_3217	Bin_1	14.0851	21.2665
31	gene_id_3218	Bin_1	80.2859	169.376
31	gene_id_3219	Bin_1	68.5712	100.589
31	gene_id_3220	Bin_1	279.869	223.189
31	gene_id_3221	Bin_1	54.7929	55.0888
31	gene_id_3222	Bin_1	128.536	82.9001
31	gene_id_3223	Bin_1	238.558	213.875
31	gene_id_3224	Bin_1	390.074	306.737
31	gene_id_3225	Bin_1	18.5584	38.0592
31	gene_id_3226	Bin_1	84.1313	43.0299

31	gene_id_3227	Bin_1	84.1234	95.0971
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31	gene_id_3229	Bin_1	444.827	263.496
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31	gene_id_3232	Bin_1	102.15	107.75
31	gene_id_3243	Bin_1	423.227	271.209
31	gene_id_3244	Bin_1	176.015	134.406
31	gene_id_3245	Bin_1	186.283	145.958
31	gene_id_3246	Bin_1	135.235	113.353
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31	gene_id_3249	Bin_1	118.286	95.1752
31	gene_id_3250	Bin_1	387.732	334.262
31	gene_id_3251	Bin_1	284.556	229.504
31	gene_id_3252	Bin_1	195.275	307.89
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31	gene_id_3256	Bin_1	165.371	182.684
31	gene_id_3257	Bin_1	94.245	112.82
31	gene_id_3258	Bin_1	656.416	417.717
31	gene_id_3259	Bin_1	45.7518	81.9976
31	gene_id_3260	Bin_1	536.029	607.953
31	gene_id_3261	Bin_1	168.71	125.739
31	gene_id_3262	Bin_1	1962.28	2162.39
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31	gene_id_3264	Bin_1	987.803	777.218
31	gene_id_3265	Bin_1	1074.86	939.963
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31	gene_id_3275	Bin_1	153.174	105.62
31	gene_id_3276	Bin_1	423.115	332.346
31	gene_id_3277	Bin_1	6666.73	3736.98
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31	gene_id_3314	Bin_1	262.617	307.331
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40	gene_id_4112	Bin_1	266.202	303.783
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43	gene_id_4492	Bin_1	119.825	78.105
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43	gene_id_4502	Bin_1	55.2177	71.5233
43	gene_id_4503	Bin_1	204.193	249.636
43	gene_id_4504	Bin_1	150.996	165.602
43	gene_id_4505	Bin_1	189.5	176.617
43	gene_id_4506	Bin_1	610.757	409.675
43	gene_id_4507	Bin_1	331.087	169.834

43	gene_id_4508	Bin_1	1401.57	1559.37
43	gene_id_4509	Bin_1	223.932	271.759
43	gene_id_4510	Bin_1	15.5344	17.1066
43	gene_id_4511	Bin_1	22.8722	20.9913
43	gene_id_4512	Bin_1	36.4873	24.8587
43	gene_id_4513	Bin_1	26.7699	24.1363
43	gene_id_4514	Bin_1	21.7569	18.1644
43	gene_id_4515	Bin_1	40.9962	32.8977
43	gene_id_4516	Bin_1	21.3619	39.3421
43	gene_id_4517	Bin_1	84.1313	17.212
43	gene_id_4519	Bin_1	313.822	360.295
43	gene_id_4520	Bin_1	249.354	336.015
43	gene_id_4521	Bin_1	7.19717	21.7253
43	gene_id_4523	Bin_1	53.113	271.882
43	gene_id_4524	Bin_1	0.989935	18.1645
43	gene_id_4528	Bin_1	1.90023	11.6301
43	gene_id_4530	Bin_1	1.62561	10.9686
43	gene_id_4536	Bin_1	216.076	253.148
43	gene_id_4537	Bin_1	101.928	174.482
43	gene_id_4538	Bin_1	99.0091	79.6516
43	gene_id_4539	Bin_1	48.8836	50.1864
43	gene_id_4540	Bin_1	107.481	62.1264
47	gene_id_4859	Bin_1	1430.45	1477.87
47	gene_id_4860	Bin_1	1115.28	871.998
47	gene_id_4861	Bin_1	1007.1	1194.32
47	gene_id_4862	Bin_1	800.091	545.678
47	gene_id_4863	Bin_1	433.794	397.478
47	gene_id_4864	Bin_1	581.985	528.476
47	gene_id_4865	Bin_1	759.691	720.088
47	gene_id_4866	Bin_1	40.968	51.6226
47	gene_id_4867	Bin_1	119.897	76.4047
47	gene_id_4868	Bin_1	155.674	144.245
47	gene_id_4869	Bin_1	649.967	380.75
47	gene_id_4870	Bin_1	31.3644	242.026
47	gene_id_4871	Bin_1	30.8701	44.8811
47	gene_id_4872	Bin_1	124.399	84.4898
47	gene_id_4873	Bin_1	52.1759	61.6122
47	gene_id_4874	Bin_1	292.316	297.987
47	gene_id_4875	Bin_1	762.99	529.843
47	gene_id_4876	Bin_1	16023.4	16164.5
47	gene_id_4877	Bin_1	872.788	459.638
47	gene_id_4878	Bin_1	281.807	309.846
47	gene_id_4879	Bin_1	68.5345	84.4649
47	gene_id_4884	Bin_1	62.8216	69.4145
47	gene_id_4885	Bin_1	174.19	110.236
47	gene_id_4886	Bin_1	613.435	515.815
47	gene_id_4887	Bin_1	564.928	307.389
47	gene_id_4889	Bin_1	55.761	64.2763
47	gene_id_4890	Bin_1	219.088	176.407
47	gene_id_4891	Bin_1	180.771	132.9

47	gene_id_4892	Bin_1	94.5238	84.9714
47	gene_id_4893	Bin_1	100.046	78.2712
47	gene_id_4894	Bin_1	479.215	330.043
47	gene_id_4895	Bin_1	114.567	75.385
47	gene_id_4896	Bin_1	48.3842	41.2841
47	gene_id_4897	Bin_1	142.942	135.289
47	gene_id_4898	Bin_1	25.5502	31.5471
47	gene_id_4898	Bin_1	12.203	23.7401
47	gene_id_4899	Bin_1	128.018	168.206
47	gene_id_4900	Bin_1	465.658	526.522
47	gene_id_4901	Bin_1	3464.83	2514.16
47	gene_id_4902	Bin_1	5453.35	5245.2
47	gene_id_4903	Bin_1	355.542	355.94
47	gene_id_4904	Bin_1	45.0757	66.0215
47	gene_id_4905	Bin_1	204.588	173.531
47	gene_id_4906	Bin_1	16.7756	18.5145
47	gene_id_4907	Bin_1	72.81	69.8142
47	gene_id_4908	Bin_1	73.1988	66.716
47	gene_id_4909	Bin_1	46.5649	48.8267
47	gene_id_4910	Bin_1	159.721	152.584
47	gene_id_4911	Bin_1	862.433	872.128
47	gene_id_4912	Bin_1	8185.2	9480.89
47	gene_id_4913	Bin_1	1004.81	1348.14
47	gene_id_4914	Bin_1	525.866	581.83
47	gene_id_4915	Bin_1	535.869	605.503
47	gene_id_4916	Bin_1	723.203	665.693
47	gene_id_4917	Bin_1	191.337	218.118
47	gene_id_4918	Bin_1	729.38	832.283
47	gene_id_4919	Bin_1	511.881	400.192
47	gene_id_4920	Bin_1	428.635	432.958
47	gene_id_4921	Bin_1	295.163	247.248
47	gene_id_4922	Bin_1	122.725	90.3578
47	gene_id_4923	Bin_1	228.076	217.983
47	gene_id_4924	Bin_1	488.582	288.126
47	gene_id_4925	Bin_1	138.919	117.03
47	gene_id_4926	Bin_1	158.061	207.968
47	gene_id_4927	Bin_1	33.8902	47.3963
47	gene_id_4928	Bin_1	26808.7	15029.4
47	gene_id_4929	Bin_1	1133.86	1007.1
47	gene_id_4930	Bin_1	233.352	277.784
47	gene_id_4931	Bin_1	246.349	304.001
47	gene_id_4932	Bin_1	210.791	321.488
47	gene_id_4933	Bin_1	78.5904	127.621
47	gene_id_4934	Bin_1	110.308	123.747
47	gene_id_4935	Bin_1	196.997	175.59
47	gene_id_4936	Bin_1	212.019	204.005
47	gene_id_4937	Bin_1	203.984	230.847
47	gene_id_4938	Bin_1	362.255	305.859
47	gene_id_4939	Bin_1	4101.23	3910.1
47	gene_id_4940	Bin_1	204.78	177.669

47	gene_id_4941	Bin_1	35.8873	31.5159
47	gene_id_4942	Bin_1	119.883	137.719
47	gene_id_4943	Bin_1	200.772	174.133
47	gene_id_4944	Bin_1	68.6754	97.9838
47	gene_id_4945	Bin_1	145.765	184.087
47	gene_id_4946	Bin_1	38.0041	45.0946
47	gene_id_4947	Bin_1	85.0518	107.328
47	gene_id_4948	Bin_1	24.4003	31.2243
47	gene_id_4949	Bin_1	697.783	650.604
47	gene_id_4950	Bin_1	336.91	188.701
47	gene_id_4951	Bin_1	110.548	101.931
47	gene_id_4952	Bin_1	420.921	147.107
47	gene_id_4953	Bin_1	169.362	129.942
47	gene_id_4954	Bin_1	2570.07	1275.78
47	gene_id_4955	Bin_1	907.781	710.087
47	gene_id_4956	Bin_1	3888.7	2705.49
47	gene_id_4957	Bin_1	432.758	417.531
47	gene_id_4958	Bin_1	177.659	204.341
47	gene_id_4959	Bin_1	133.183	125.047
47	gene_id_4960	Bin_1	45.3887	51.635
47	gene_id_4961	Bin_1	86.2184	82.151
47	gene_id_4962	Bin_1	38.2457	57.9002
47	gene_id_4963	Bin_1	86.3535	108.599
47	gene_id_4964	Bin_1	181.646	186.626
47	gene_id_4965	Bin_1	155.595	174.367
47	gene_id_4966	Bin_1	100.705	133.258
47	gene_id_4967	Bin_1	502.344	650.277
47	gene_id_4968	Bin_1	176.927	210.624
47	gene_id_4969	Bin_1	385.463	291.864
47	gene_id_4970	Bin_1	178.634	110.083
47	gene_id_4971	Bin_1	135.023	128.27
47	gene_id_4972	Bin_1	194.04	172.713
47	gene_id_4973	Bin_1	287.47	296.955
47	gene_id_4974	Bin_1	206.267	198.006
47	gene_id_4975	Bin_1	435.167	420.558
47	gene_id_4976	Bin_1	756.033	751.122
47	gene_id_4977	Bin_1	622.621	585.483
47	gene_id_4978	Bin_1	350.239	339.122
47	gene_id_4979	Bin_1	403.867	413.312
47	gene_id_4980	Bin_1	391.301	429.976
47	gene_id_4981	Bin_1	520.725	528.868
47	gene_id_4982	Bin_1	509.161	479.624
47	gene_id_4983	Bin_1	1262.11	1584.7
47	gene_id_4984	Bin_1	144.063	120.113
47	gene_id_4985	Bin_1	287.801	238.126
47	gene_id_4986	Bin_1	216.452	239.118
47	gene_id_4987	Bin_1	72.8871	71.1717
47	gene_id_4988	Bin_1	890.971	947.853
47	gene_id_4989	Bin_1	667.915	704.211
47	gene_id_4990	Bin_1	80.6991	101.125

47	gene_id_4991	Bin_1	47.1763	47.4647
47	gene_id_4992	Bin_1	216.259	250.082
47	gene_id_4993	Bin_1	392.174	306.153
47	gene_id_4994	Bin_1	107.871	78.351
47	gene_id_4995	Bin_1	15.0464	25.2681
47	gene_id_4996	Bin_1	13.4662	24.3871
47	gene_id_4997	Bin_1	476.835	416.535
47	gene_id_4998	Bin_1	440.977	339.605
47	gene_id_4999	Bin_1	42.0946	47.6643
47	gene_id_5000	Bin_1	26.616	37.6101
47	gene_id_5001	Bin_1	580.026	735.033
47	gene_id_5002	Bin_1	86.9088	122.9
47	gene_id_5003	Bin_1	74.595	188.769
47	gene_id_5004	Bin_1	33.8631	124.681
47	gene_id_5005	Bin_1	32.3487	134.701
47	gene_id_5006	Bin_1	38.1321	161.317
47	gene_id_5007	Bin_1	30.5124	83.9039
47	gene_id_5008	Bin_1	29.5404	81.6954
47	gene_id_5009	Bin_1	27.5557	62.8175
47	gene_id_5010	Bin_1	31.9282	100.126
47	gene_id_5011	Bin_1	35.595	101.263
47	gene_id_5012	Bin_1	67.8042	96.4958
47	gene_id_5013	Bin_1	57.1693	64.8245
47	gene_id_5014	Bin_1	41.461	58.5686
47	gene_id_5015	Bin_1	154.932	142.027
47	gene_id_5016	Bin_1	396.403	421.03
47	gene_id_5017	Bin_1	2730.02	2630.99
47	gene_id_5018	Bin_1	200.46	164.584
47	gene_id_5019	Bin_1	237.683	200.958
6	gene_id_502	Bin_1	435.236	344.105
47	gene_id_5020	Bin_1	376.735	248.504
47	gene_id_5021	Bin_1	191.358	105.026
47	gene_id_5022	Bin_1	571.77	356.503
47	gene_id_5023	Bin_1	1015.86	678.131
47	gene_id_5024	Bin_1	114.551	119.442
47	gene_id_5025	Bin_1	104.614	122.467
47	gene_id_5026	Bin_1	92.8774	92.0491
47	gene_id_5027	Bin_1	185.066	150.777
47	gene_id_5028	Bin_1	411.065	334.702
47	gene_id_5029	Bin_1	147.544	233.669
6	gene_id_503	Bin_1	373.262	242.873
47	gene_id_5030	Bin_1	88.6688	121.254
47	gene_id_5031	Bin_1	246.687	257.003
47	gene_id_5032	Bin_1	113.894	129.229
47	gene_id_5033	Bin_1	541.123	465.28
47	gene_id_5034	Bin_1	196.656	253.614
47	gene_id_5035	Bin_1	110.809	123.354
47	gene_id_5036	Bin_1	190.315	231.271
47	gene_id_5037	Bin_1	179.379	206.451
47	gene_id_5038	Bin_1	229.231	248.871

47	gene_id_5039	Bin_1	379.608	395.157
6	gene_id_504	Bin_1	310.041	227.627
47	gene_id_5040	Bin_1	203.244	215.461
47	gene_id_5041	Bin_1	164.999	210.556
47	gene_id_5042	Bin_1	171.776	169.343
47	gene_id_5043	Bin_1	219.343	165.105
47	gene_id_5044	Bin_1	106.035	113.486
47	gene_id_5045	Bin_1	227.588	204.938
47	gene_id_5046	Bin_1	87.5978	113.926
47	gene_id_5047	Bin_1	115.71	96.6311
47	gene_id_5048	Bin_1	161.066	173.743
47	gene_id_5049	Bin_1	175.957	175.988
6	gene_id_505	Bin_1	353.225	213.922
47	gene_id_5050	Bin_1	91.937	77.8041
47	gene_id_5051	Bin_1	140.578	146.979
47	gene_id_5052	Bin_1	59.24	63.5167
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47	gene_id_5054	Bin_1	247.353	136.457
47	gene_id_5055	Bin_1	100.344	68.9115
47	gene_id_5056	Bin_1	184.967	127.041
47	gene_id_5057	Bin_1	210.049	203.054
47	gene_id_5058	Bin_1	30.9461	45.0346
47	gene_id_5059	Bin_1	73.7038	54.2269
6	gene_id_506	Bin_1	308.448	205.605
47	gene_id_5060	Bin_1	15.2058	22.8268
47	gene_id_5061	Bin_1	18.0115	18.1244
47	gene_id_5062	Bin_1	50.3077	59.1299
47	gene_id_5063	Bin_1	22.9656	21.6895
47	gene_id_5064	Bin_1	1545.59	1144.92
47	gene_id_5065	Bin_1	62.6768	77.8762
47	gene_id_5066	Bin_1	85.8861	119.646
47	gene_id_5067	Bin_1	196.704	114.015
47	gene_id_5068	Bin_1	145.001	89.9077
47	gene_id_5069	Bin_1	406.548	274.366
6	gene_id_507	Bin_1	363.019	311.272
47	gene_id_5070	Bin_1	133.653	142.353
47	gene_id_5071	Bin_1	126.671	97.5392
47	gene_id_5072	Bin_1	138.435	120.168
47	gene_id_5073	Bin_1	64.7251	78.0267
47	gene_id_5074	Bin_1	145.287	151.026
47	gene_id_5075	Bin_1	128.193	163.79
47	gene_id_5076	Bin_1	114.829	111.397
47	gene_id_5077	Bin_1	131.664	109.387
47	gene_id_5078	Bin_1	260.437	285.87
47	gene_id_5079	Bin_1	201.929	205.316
6	gene_id_508	Bin_1	167.402	204.909
47	gene_id_5080	Bin_1	56.2548	61.0377
47	gene_id_5081	Bin_1	100.386	71.1512
47	gene_id_5082	Bin_1	163.938	143.078
47	gene_id_5083	Bin_1	126.305	103.305

47	gene_id_5084	Bin_1	173.778	118.712
47	gene_id_5085	Bin_1	36.2801	37.3076
47	gene_id_5086	Bin_1	95.6423	65.6495
47	gene_id_5087	Bin_1	129.412	110.874
47	gene_id_5088	Bin_1	89.0749	103.913
47	gene_id_5089	Bin_1	656.014	355.634
6	gene_id_509	Bin_1	164.468	180.748
47	gene_id_5090	Bin_1	15.8962	25.1872
47	gene_id_5091	Bin_1	98.5096	129.901
47	gene_id_5092	Bin_1	186.981	160.674
47	gene_id_5093	Bin_1	3151.4	2237.65
47	gene_id_5094	Bin_1	229.187	508.269
47	gene_id_5095	Bin_1	491.225	300.816
47	gene_id_5097	Bin_1	713.215	387.238
47	gene_id_5098	Bin_1	164.47	134.583
47	gene_id_5099	Bin_1	186.185	126.329
6	gene_id_510	Bin_1	674.112	365.12
47	gene_id_5100	Bin_1	236.324	286.21
47	gene_id_5101	Bin_1	97.0651	112.464
47	gene_id_5102	Bin_1	55.7702	83.7319
47	gene_id_5103	Bin_1	99.438	129.943
47	gene_id_5104	Bin_1	740.592	417.368
47	gene_id_5105	Bin_1	211.462	199.456
47	gene_id_5106	Bin_1	312.137	324.794
47	gene_id_5107	Bin_1	421.472	355.29
47	gene_id_5108	Bin_1	7083.45	6530.09
47	gene_id_5109	Bin_1	826.489	1138.23
6	gene_id_511	Bin_1	93.8335	55.1379
47	gene_id_5110	Bin_1	151.505	142.579
47	gene_id_5111	Bin_1	48.3378	43.6236
47	gene_id_5112	Bin_1	189.89	223.856
47	gene_id_5113	Bin_1	223.423	231.554
47	gene_id_5114	Bin_1	158.644	194.18
47	gene_id_5115	Bin_1	186.279	227.062
47	gene_id_5116	Bin_1	170.107	157.415
47	gene_id_5117	Bin_1	221.767	175.028
47	gene_id_5118	Bin_1	159.398	186.253
47	gene_id_5119	Bin_1	460.789	468.324
6	gene_id_512	Bin_1	65.8859	70.1145
47	gene_id_5120	Bin_1	108.251	86.2564
47	gene_id_5121	Bin_1	2754	1259.13
47	gene_id_5122	Bin_1	1219.73	1136.13
47	gene_id_5123	Bin_1	81.965	68.0014
47	gene_id_5124	Bin_1	283.022	211.433
47	gene_id_5125	Bin_1	233.038	219.283
47	gene_id_5126	Bin_1	271.618	248.154
47	gene_id_5127	Bin_1	215.117	188.017
47	gene_id_5128	Bin_1	94.1695	116.594
47	gene_id_5129	Bin_1	526.137	396.356
6	gene_id_513	Bin_1	175.614	91.7818

47	gene_id_5130	Bin_1	261.645	217.837
47	gene_id_5131	Bin_1	144.325	206.079
47	gene_id_5132	Bin_1	139.885	139.265
47	gene_id_5133	Bin_1	104.005	95.6081
47	gene_id_5134	Bin_1	112.521	81.2124
47	gene_id_5135	Bin_1	89.7069	93.2046
47	gene_id_5136	Bin_1	142.161	99.2628
47	gene_id_5137	Bin_1	173.249	136.718
47	gene_id_5138	Bin_1	150.623	125.757
47	gene_id_5139	Bin_1	118.998	103.269
6	gene_id_514	Bin_1	193.612	131.755
47	gene_id_5140	Bin_1	650.577	422.861
47	gene_id_5141	Bin_1	207.596	195.195
47	gene_id_5142	Bin_1	104.799	99.7144
47	gene_id_5143	Bin_1	152.643	106.524
47	gene_id_5144	Bin_1	165.652	154.894
47	gene_id_5145	Bin_1	519.204	529.394
47	gene_id_5145	Bin_1	752.28	930.177
47	gene_id_5146	Bin_1	461	468.362
47	gene_id_5147	Bin_1	420.898	437.313
47	gene_id_5148	Bin_1	396.528	424.421
47	gene_id_5149	Bin_1	416.823	426.153
6	gene_id_515	Bin_1	127.817	87.7749
47	gene_id_5150	Bin_1	611.401	642.846
47	gene_id_5151	Bin_1	324.836	361.297
47	gene_id_5152	Bin_1	424.721	544.53
47	gene_id_5153	Bin_1	492.382	319.727
47	gene_id_5154	Bin_1	209.838	267.675
47	gene_id_5155	Bin_1	1911.66	1559.31
47	gene_id_5156	Bin_1	122.164	149.437
47	gene_id_5157	Bin_1	86.5324	122.831
47	gene_id_5158	Bin_1	159.516	152.068
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6	gene_id_516	Bin_1	114.29	124.846
47	gene_id_5160	Bin_1	37.9014	61.4315
47	gene_id_5161	Bin_1	16.305	30.5202
47	gene_id_5162	Bin_1	35.1385	54.6454
47	gene_id_5163	Bin_1	65.0283	116.493
47	gene_id_5164	Bin_1	46.5269	65.681
47	gene_id_5165	Bin_1	129.775	114.267
47	gene_id_5166	Bin_1	325.745	344.112
47	gene_id_5167	Bin_1	38.9574	60.8025
47	gene_id_5168	Bin_1	131.137	96.104
47	gene_id_5169	Bin_1	171.052	181.049
6	gene_id_517	Bin_1	275.624	192.755
47	gene_id_5170	Bin_1	84.2795	121.407
47	gene_id_5171	Bin_1	129.35	166.641
47	gene_id_5172	Bin_1	148.009	186.957
47	gene_id_5173	Bin_1	241.753	210.026
47	gene_id_5174	Bin_1	264.457	208.847

47	gene_id_5175	Bin_1	4064.51	2993.4
47	gene_id_5176	Bin_1	328.57	264.34
47	gene_id_5177	Bin_1	394.983	327.365
47	gene_id_5178	Bin_1	290.784	378.882
47	gene_id_5179	Bin_1	89.5944	103.807
6	gene_id_518	Bin_1	373.862	355.111
47	gene_id_5180	Bin_1	92.0398	56.837
47	gene_id_5181	Bin_1	152.462	150.637
47	gene_id_5182	Bin_1	313.524	236.858
47	gene_id_5183	Bin_1	101.253	152.089
47	gene_id_5184	Bin_1	121.515	144.996
47	gene_id_5185	Bin_1	246.436	163.327
47	gene_id_5186	Bin_1	456.774	283.486
47	gene_id_5187	Bin_1	34.5991	29.5202
47	gene_id_5188	Bin_1	113.165	135.616
47	gene_id_5189	Bin_1	110.64	119.365
6	gene_id_519	Bin_1	227.651	230.395
47	gene_id_5190	Bin_1	129.105	190.562
47	gene_id_5191	Bin_1	62.7905	38.9918
47	gene_id_5192	Bin_1	89.0542	93.1158
47	gene_id_5193	Bin_1	113.004	101.62
47	gene_id_5194	Bin_1	292.521	254.145
47	gene_id_5195	Bin_1	944.294	828.642
47	gene_id_5196	Bin_1	511.89	439.754
47	gene_id_5197	Bin_1	570.561	480.288
47	gene_id_5198	Bin_1	788.152	613.69
47	gene_id_5199	Bin_1	42.7734	43.1534
6	gene_id_520	Bin_1	74.8113	62.2143
47	gene_id_5200	Bin_1	133.801	102.016
47	gene_id_5201	Bin_1	338.323	274.246
47	gene_id_5202	Bin_1	1260.73	1066.42
47	gene_id_5203	Bin_1	152.776	170.45
47	gene_id_5204	Bin_1	201.745	195.516
47	gene_id_5205	Bin_1	258.328	186.525
47	gene_id_5206	Bin_1	88.5595	131.563
47	gene_id_5207	Bin_1	134.446	163.715
47	gene_id_5208	Bin_1	47918.2	59555
47	gene_id_5209	Bin_1	163.563	180.687
6	gene_id_521	Bin_1	237.46	117.992
47	gene_id_5210	Bin_1	73.1475	69.8155
47	gene_id_5211	Bin_1	178.154	206.399
47	gene_id_5212	Bin_1	196.95	214.269
47	gene_id_5213	Bin_1	38.9905	68.5072
47	gene_id_5214	Bin_1	453.688	445.209
47	gene_id_5215	Bin_1	110.436	97.8618
47	gene_id_5216	Bin_1	238.84	278.798
47	gene_id_5217	Bin_1	308.146	299.661
47	gene_id_5218	Bin_1	117.367	128.419
47	gene_id_5219	Bin_1	104.181	126.677
6	gene_id_522	Bin_1	70.4026	86.968

47	gene_id_5220	Bin_1	147.055	200.199
47	gene_id_5221	Bin_1	383.202	409.599
47	gene_id_5222	Bin_1	397.626	147.804
47	gene_id_5223	Bin_1	215.307	75.3018
47	gene_id_5224	Bin_1	445.128	177.218
47	gene_id_5225	Bin_1	240.138	335.533
47	gene_id_5226	Bin_1	1859.62	2157.41
47	gene_id_5227	Bin_1	159.339	145.679
47	gene_id_5228	Bin_1	116.008	95.5576
47	gene_id_5229	Bin_1	93.7208	75.4888
6	gene_id_523	Bin_1	313.658	365.155
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47	gene_id_5232	Bin_1	142.494	155.138
47	gene_id_5233	Bin_1	103.261	93.1692
47	gene_id_5234	Bin_1	52.3924	59.0004
47	gene_id_5235	Bin_1	158.791	216.635
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47	gene_id_5237	Bin_1	92.8954	107.626
47	gene_id_5238	Bin_1	77.3297	95.0852
47	gene_id_5239	Bin_1	115.764	103.418
6	gene_id_524	Bin_1	168.796	151.743
47	gene_id_5240	Bin_1	175.39	113.559
47	gene_id_5241	Bin_1	3004.19	3006.41
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47	gene_id_5243	Bin_1	121.153	142.566
47	gene_id_5244	Bin_1	297.681	616.459
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47	gene_id_5247	Bin_1	299.803	379.292
47	gene_id_5248	Bin_1	512.118	727.797
47	gene_id_5249	Bin_1	562.138	713.332
6	gene_id_525	Bin_1	1051.51	827.32
47	gene_id_5250	Bin_1	1052.65	1357.02
47	gene_id_5251	Bin_1	590.804	937.546
47	gene_id_5252	Bin_1	2620.71	4225.68
47	gene_id_5253	Bin_1	363.365	277.518
47	gene_id_5254	Bin_1	263.276	396.27
47	gene_id_5255	Bin_1	62.4175	111.823
47	gene_id_5256	Bin_1	117.527	148.884
47	gene_id_5257	Bin_1	160.609	167.209
47	gene_id_5258	Bin_1	126.446	101.87
47	gene_id_5259	Bin_1	533.916	465.492
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47	gene_id_5260	Bin_1	73.7293	61.5416
47	gene_id_5261	Bin_1	86.9235	72.388
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47	gene_id_5264	Bin_1	134.421	97.9424
47	gene_id_5265	Bin_1	144.145	162.941
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47	gene_id_5267	Bin_1	263.022	191.949
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6	gene_id_527	Bin_1	208.866	168.192
47	gene_id_5270	Bin_1	483.663	216.722
47	gene_id_5271	Bin_1	134.041	180.78
47	gene_id_5272	Bin_1	150.802	165.409
47	gene_id_5273	Bin_1	354.683	300.768
47	gene_id_5274	Bin_1	131.415	142.118
47	gene_id_5275	Bin_1	242.318	218.312
47	gene_id_5276	Bin_1	79.8356	91.3742
47	gene_id_5277	Bin_1	73.7548	97.5514
47	gene_id_5278	Bin_1	136.751	116.896
47	gene_id_5279	Bin_1	231.997	259.552
6	gene_id_528	Bin_1	81.8007	68.1064
47	gene_id_5280	Bin_1	123.663	119.237
47	gene_id_5281	Bin_1	108.988	106.199
47	gene_id_5282	Bin_1	83.8952	105.113
47	gene_id_5283	Bin_1	163.848	155.566
47	gene_id_5284	Bin_1	58.9239	64.4332
47	gene_id_5285	Bin_1	129.646	191.572
47	gene_id_5286	Bin_1	208.517	152.403
47	gene_id_5287	Bin_1	116.979	89.1778
47	gene_id_5288	Bin_1	164.415	115.932
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47	gene_id_5291	Bin_1	180.938	226.814
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47	gene_id_5293	Bin_1	342.548	329.798
47	gene_id_5294	Bin_1	1240.36	901.831
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47	gene_id_5296	Bin_1	217.163	259.658
47	gene_id_5297	Bin_1	7851.77	8542.5
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6	gene_id_530	Bin_1	169.656	144.234
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47	gene_id_5301	Bin_1	335.857	453.334
47	gene_id_5302	Bin_1	135.152	188.562
47	gene_id_5303	Bin_1	308.662	414.329
47	gene_id_5304	Bin_1	368.518	368.096
47	gene_id_5305	Bin_1	332.954	497.239
47	gene_id_5306	Bin_1	1104.58	1327.58
47	gene_id_5307	Bin_1	283.044	368.744
47	gene_id_5308	Bin_1	503.165	522.653
47	gene_id_5309	Bin_1	134.692	187.007
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47	gene_id_5310	Bin_1	468.495	604.074
47	gene_id_5311	Bin_1	770.728	1314.13

47	gene_id_5312	Bin_1	303.254	433.7
47	gene_id_5313	Bin_1	326.699	375.265
47	gene_id_5314	Bin_1	178.182	274.228
47	gene_id_5315	Bin_1	210.614	260.278
47	gene_id_5316	Bin_1	314.233	408.727
47	gene_id_5317	Bin_1	260.966	364.628
47	gene_id_5318	Bin_1	223.92	347.998
47	gene_id_5319	Bin_1	292.887	475.957
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47	gene_id_5320	Bin_1	304.274	665.949
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47	gene_id_5322	Bin_1	177.734	280.872
47	gene_id_5323	Bin_1	273.729	508.017
47	gene_id_5324	Bin_1	640.319	769.199
47	gene_id_5325	Bin_1	282.648	345.166
47	gene_id_5326	Bin_1	2411.18	3352.01
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47	gene_id_5329	Bin_1	876.969	1121.91
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47	gene_id_5330	Bin_1	186.322	247.757
47	gene_id_5331	Bin_1	345.391	402.479
47	gene_id_5332	Bin_1	433.937	442.867
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6	gene_id_540	Bin_1	302.778	270.607
6	gene_id_541	Bin_1	1366.22	1273.64
6	gene_id_542	Bin_1	60.2813	80.9001
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6	gene_id_544	Bin_1	99.9167	82.7331
6	gene_id_545	Bin_1	477.813	459.049
6	gene_id_546	Bin_1	305.184	370.208
6	gene_id_547	Bin_1	91.8726	91.0732
6	gene_id_548	Bin_1	101.418	77.553
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6	gene_id_550	Bin_1	2539.5	2281.87
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6	gene_id_554	Bin_1	195.689	79.8649
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6	gene_id_556	Bin_1	6335.39	15261.6
6	gene_id_557	Bin_1	132.09	135.322
6	gene_id_558	Bin_1	1458.34	1448.53
6	gene_id_559	Bin_1	31.8937	42.6774
6	gene_id_560	Bin_1	157.543	123.538
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6	gene_id_562	Bin_1	64.325	93.704
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6	gene_id_565	Bin_1	179.549	105.896
6	gene_id_566	Bin_1	513.79	340.803
6	gene_id_567	Bin_1	281.648	372.104
6	gene_id_568	Bin_1	477.902	315.018
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117	gene_id_9301	Bin_1	133.859	131.253
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131	gene_id_10005	Bin_2	73.9276	376.338
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131	gene_id_10007	Bin_2	46.9666	512.211
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131	gene_id_10011	Bin_2	5.03379	139.32
13	gene_id_1002	Bin_2	1.42342	19.0199
131	gene_id_10020	Bin_2	0	16.8974
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131	gene_id_10041	Bin_2	26.916	81.0659
131	gene_id_10042	Bin_2	12.3443	87.3503
13	gene_id_1009	Bin_2	0	15.2023
13	gene_id_1013	Bin_2	5.87486	11.1892
13	gene_id_1016	Bin_2	59.5065	274.617
13	gene_id_1018	Bin_2	63.7119	114.46
13	gene_id_1023	Bin_2	45.0141	288.703
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138	gene_id_10400	Bin_2	4.04092	47.203
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154	gene_id_11054	Bin_2	43.6261	13.165
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154	gene_id_11058	Bin_2	11.6203	17.2893

154	gene_id_11059	Bin_2	46.0105	34.1365
154	gene_id_11060	Bin_2	25.1781	15.8002
154	gene_id_11061	Bin_2	15.731	17.9337
156	gene_id_11126	Bin_2	7.84752	34.3017
156	gene_id_11127	Bin_2	4.72508	38.6608
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156	gene_id_11138	Bin_2	342.155	477.331
156	gene_id_11140	Bin_2	51.1721	147.848
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156	gene_id_11145	Bin_2	0.739055	13.6164
156	gene_id_11152	Bin_2	62.7417	102.409
156	gene_id_11154	Bin_2	0	46.1037
156	gene_id_11155	Bin_2	44.7268	375.792
156	gene_id_11156	Bin_2	120.681	1097.62
156	gene_id_11160	Bin_2	0	23.3487
156	gene_id_11161	Bin_2	3.58422	19.7603
156	gene_id_11166	Bin_2	0	19.9991
156	gene_id_11169	Bin_2	1.12869	23.4192
156	gene_id_11170	Bin_2	25.3323	77.2858
156	gene_id_11176	Bin_2	76.4278	565.129
156	gene_id_11179	Bin_2	7.64355	23.0315
156	gene_id_11184	Bin_2	61.9329	116.808
156	gene_id_11186	Bin_2	2.34873	23.8593
156	gene_id_11187	Bin_2	88.8368	701.763
156	gene_id_11191	Bin_2	12.1435	31.2987
156	gene_id_11221	Bin_2	1.80387	21.779
156	gene_id_11226	Bin_2	0	35.8807
156	gene_id_11227	Bin_2	63.5923	204.515
156	gene_id_11235	Bin_2	13.8082	47.734
156	gene_id_11237	Bin_2	5.87147	38.0576
156	gene_id_11238	Bin_2	0	24.4995
156	gene_id_11239	Bin_2	4.80273	15.1821
156	gene_id_11240	Bin_2	33.4736	75.2302
156	gene_id_11241	Bin_2	5.17403	15.7457
158	gene_id_11267	Bin_2	270.396	492.294
158	gene_id_11268	Bin_2	15.3152	99.9959
158	gene_id_11269	Bin_2	5.58107	59.7224
158	gene_id_11270	Bin_2	10.99	25.0512
158	gene_id_11271	Bin_2	190.244	624.125
15	gene_id_1128	Bin_2	1.86768	13.7206
163	gene_id_11334	Bin_2	3.78707	11.9998
163	gene_id_11338	Bin_2	3.82096	14.0302
15	gene_id_1134	Bin_2	2.22547	16.3018
163	gene_id_11343	Bin_2	0.572016	11.9766
15	gene_id_1135	Bin_2	13.9312	113.008
15	gene_id_1141	Bin_2	4.12925	20.0791
15	gene_id_1141	Bin_2	3.30192	17.4717
15	gene_id_1144	Bin_2	171.98	746.519
15	gene_id_1145	Bin_2	11.0588	56.2521

15	gene_id_1148	Bin_2	3.31751	11.2652
15	gene_id_1150	Bin_2	1.82243	35.1943
15	gene_id_1151	Bin_2	1.80351	20.9889
15	gene_id_1154	Bin_2	20.4153	51.9182
15	gene_id_1159	Bin_2	3.24645	17.1833
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177	gene_id_11631	Bin_2	10.4548	22.3721
177	gene_id_11635	Bin_2	7.53975	18.5552
177	gene_id_11636	Bin_2	3.76198	29.5663
177	gene_id_11637	Bin_2	2.66484	58.3531
15	gene_id_1164	Bin_2	0	11.9571
177	gene_id_11640	Bin_2	32.5282	635.935
177	gene_id_11641	Bin_2	2.8035	24.1745
177	gene_id_11641	Bin_2	9.48831	82.2834
177	gene_id_11644	Bin_2	0	20.5358
177	gene_id_11647	Bin_2	0	13.2979
177	gene_id_11648	Bin_2	18.099	34.7629
15	gene_id_1165	Bin_2	57.7898	193.363
1	gene_id_117	Bin_2	32.2237	283.763
15	gene_id_1174	Bin_2	43.8772	470.907
15	gene_id_1175	Bin_2	1.36056	26.4704
15	gene_id_1177	Bin_2	2.09689	32.645
183	gene_id_11778	Bin_2	10.0696	43.5417
183	gene_id_11779	Bin_2	0.696215	7.70166
15	gene_id_1178	Bin_2	2.42335	62.0299
183	gene_id_11786	Bin_2	35.8239	156.867
183	gene_id_11795	Bin_2	19.7479	204.486
183	gene_id_11800	Bin_2	9.86139	175.571
187	gene_id_11820	Bin_2	10.3354	38.2379
187	gene_id_11820	Bin_2	12.6968	147.932
187	gene_id_11827	Bin_2	0	13.5275
15	gene_id_1190	Bin_2	9.39337	24.0791
15	gene_id_1192	Bin_2	0	10.1311
15	gene_id_1195	Bin_2	1.23688	15.2222
15	gene_id_1196	Bin_2	24.0127	172.586
15	gene_id_1209	Bin_2	10.6072	83.2907
15	gene_id_1237	Bin_2	5.76203	47.8929
15	gene_id_1238	Bin_2	40.2483	406.559
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15	gene_id_1242	Bin_2	0	9.91538
15	gene_id_1257	Bin_2	224.872	349.093
15	gene_id_1259	Bin_2	9.22041	22.4989
15	gene_id_1260	Bin_2	13.6107	19.1934
15	gene_id_1262	Bin_2	37.8751	124.24
15	gene_id_1266	Bin_2	0	12.81
1	gene_id_127	Bin_2	9.72949	39.5225
15	gene_id_1272	Bin_2	0	16.8473

15	gene_id_1279	Bin_2	14.8923	21.6853
1	gene_id_128	Bin_2	71.9885	573.003
15	gene_id_1280	Bin_2	120.342	324.201
15	gene_id_1281	Bin_2	227.848	452.874
199	gene_id_12842	Bin_2	140.206	324.915
199	gene_id_12843	Bin_2	2.26821	27.6818
199	gene_id_12844	Bin_2	3.75708	19.8314
199	gene_id_12849	Bin_2	4.55381	25.7754
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15	gene_id_1289	Bin_2	62.1217	224.135
15	gene_id_1290	Bin_2	8.48171	57.5992
15	gene_id_1293	Bin_2	16.2391	51.444
15	gene_id_1295	Bin_2	5.17983	10.5823
15	gene_id_1296	Bin_2	174.488	1704.04
15	gene_id_1297	Bin_2	9.25732	17.6999
1	gene_id_130	Bin_2	17.5255	123.746
15	gene_id_1302	Bin_2	5.08187	30.3249
15	gene_id_1305	Bin_2	10.6324	44.6609
15	gene_id_1306	Bin_2	7.00162	50.7636
15	gene_id_1307	Bin_2	14.4063	39.9643
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15	gene_id_1312	Bin_2	43.2859	124.24
15	gene_id_1314	Bin_2	1.29587	17.3513
1	gene_id_133	Bin_2	0	25.0725
1	gene_id_135	Bin_2	35.8634	74.6958
1	gene_id_136	Bin_2	21.6415	86.3429
1	gene_id_137	Bin_2	41.194	200.393
1	gene_id_138	Bin_2	69.8119	665.088
221	gene_id_13808	Bin_2	1.56115	10.5392
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221	gene_id_13821	Bin_2	9.47776	38.8489
221	gene_id_13828	Bin_2	267.533	1706.39
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241	gene_id_14425	Bin_2	26.2195	50.8158
241	gene_id_14426	Bin_2	53.546	70.3604
241	gene_id_14427	Bin_2	4.30872	85.2554
246	gene_id_14465	Bin_2	1.93924	16.611
246	gene_id_14470	Bin_2	32.9928	57.9052
247	gene_id_14474	Bin_2	0	13.8592
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1	gene_id_145	Bin_2	19.7614	29.5123
250	gene_id_14610	Bin_2	12.9478	41.1573
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2	gene_id_147	Bin_2	462.729	686.887
2	gene_id_148	Bin_2	2.15771	18.4497
1	gene_id_15	Bin_2	2.06647	25.261
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367	gene_id_17117	Bin_2	9.88192	16.6088
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367	gene_id_17119	Bin_2	14.7088	41.6565
367	gene_id_17126	Bin_2	2.26098	40.0129
20	gene_id_1772	Bin_2	59.3949	292.84
3	gene_id_180	Bin_2	2.71942	19.8581
3	gene_id_181	Bin_2	4.61772	14.0843
20	gene_id_1813	Bin_2	38.7436	59.254
3	gene_id_182	Bin_2	1.35277	18.0965
20	gene_id_1826	Bin_2	17.3393	50.4365
20	gene_id_1834	Bin_2	11.7181	18.8188
3	gene_id_186	Bin_2	9.25496	147.385
3	gene_id_187	Bin_2	1.13852	28.7469
20	gene_id_1874	Bin_2	2.12854	14.3037
20	gene_id_1879	Bin_2	3.36771	22.406
3	gene_id_188	Bin_2	16.4781	189.007
20	gene_id_1882	Bin_2	11.3617	32.6781
20	gene_id_1884	Bin_2	1.50504	18.2584
20	gene_id_1890	Bin_2	1.1251	15.1063
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20	gene_id_1902	Bin_2	19.4568	22.7971
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20	gene_id_1904	Bin_2	2.10376	40.4454
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20	gene_id_1907	Bin_2	191.184	2498.34
20	gene_id_1914	Bin_2	1.22423	17.9029
20	gene_id_1917	Bin_2	45.5528	63.4184
20	gene_id_1918	Bin_2	133.115	585.066
20	gene_id_1919	Bin_2	13.844	62.5693
20	gene_id_1928	Bin_2	2.18818	49.8899
20	gene_id_1935	Bin_2	40.4983	41.211
20	gene_id_1937	Bin_2	37.4786	328.558
20	gene_id_1938	Bin_2	33.9762	350.208
20	gene_id_1939	Bin_2	1.11522	13.7386
20	gene_id_1947	Bin_2	3.49218	31.6513
20	gene_id_1949	Bin_2	9.53408	55.1557
20	gene_id_1954	Bin_2	1.42176	24.4596
3	gene_id_196	Bin_2	10.7403	51.1606
565	gene_id_19611	Bin_2	0	12.2309
20	gene_id_1970	Bin_2	1.1913	14.5255
20	gene_id_1992	Bin_2	19.4667	181.644
20	gene_id_1994	Bin_2	0	13.0868
3	gene_id_200	Bin_2	577.857	640.825
20	gene_id_2005	Bin_2	17.1352	113.173
20	gene_id_2013	Bin_2	7.06468	40.2074

20	gene_id_2018	Bin_2	4.41205	48.1988
20	gene_id_2019	Bin_2	7.7476	30.214
20	gene_id_2020	Bin_2	10.5816	53.391
21	gene_id_2021	Bin_2	19.4765	21.1148
21	gene_id_2024	Bin_2	21.5621	67.3929
21	gene_id_2025	Bin_2	2.69484	27.3366
21	gene_id_2029	Bin_2	0	127.183
3	gene_id_203	Bin_2	3.90519	32.2527
21	gene_id_2031	Bin_2	86.9019	762.853
21	gene_id_2034	Bin_2	5.36905	28.8948
21	gene_id_2041	Bin_2	0	19.1356
3	gene_id_205	Bin_2	7.84165	20.9075
21	gene_id_2050	Bin_2	24.149	108.416
3	gene_id_207	Bin_2	24.376	40.5051
21	gene_id_2071	Bin_2	0	11.9225
21	gene_id_2075	Bin_2	1.10752	14.8745
21	gene_id_2084	Bin_2	18.0506	27.8094
21	gene_id_2086	Bin_2	0	20.2753
22	gene_id_2092	Bin_2	1.85099	62.5268
22	gene_id_2093	Bin_2	148.859	873.214
22	gene_id_2095	Bin_2	20.7249	48.8139
22	gene_id_2096	Bin_2	2.10016	24.3824
22	gene_id_2099	Bin_2	2.52831	11.3675
22	gene_id_2101	Bin_2	2.7181	10.0254
22	gene_id_2103	Bin_2	2.65486	17.7647
22	gene_id_2105	Bin_2	6.19004	12.348
22	gene_id_2106	Bin_2	6.32861	51.5568
22	gene_id_2108	Bin_2	1.80811	12.182
22	gene_id_2114	Bin_2	26.3482	167.717
22	gene_id_2124	Bin_2	28.1995	157.184
22	gene_id_2127	Bin_2	41.4571	460.486
22	gene_id_2132	Bin_2	1.99661	12.2104
22	gene_id_2136	Bin_2	133.639	836.686
22	gene_id_2138	Bin_2	2.37504	12.3051
22	gene_id_2140	Bin_2	18.5667	34.6788
22	gene_id_2141	Bin_2	14.2628	1.73248
22	gene_id_2145	Bin_2	2.18431	13.338
22	gene_id_2147	Bin_2	2.01077	14.7547
22	gene_id_2155	Bin_2	1.62561	15.9544
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22	gene_id_2158	Bin_2	4.11264	16.0102
22	gene_id_2163	Bin_2	12.5458	15.2814
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22	gene_id_2166	Bin_2	4.91699	18.9923
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22	gene_id_2168	Bin_2	17.6421	44.6795
22	gene_id_2169	Bin_2	3.01188	17.1898
22	gene_id_2174	Bin_2	17.0662	44.4305

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25	gene_id_2320	Bin_2	0	13.2325
25	gene_id_2322	Bin_2	0.828969	13.2173
25	gene_id_2328	Bin_2	3.5175	14.0095
25	gene_id_2329	Bin_2	33.7842	114.812
3	gene_id_235	Bin_2	0	11.5982
25	gene_id_2352	Bin_2	8.16083	42.4851
3	gene_id_236	Bin_2	1.61318	10.6023
25	gene_id_2390	Bin_2	2.10327	14.1367
25	gene_id_2397	Bin_2	22.2324	73.9228
25	gene_id_2400	Bin_2	3.23035	11.9213
25	gene_id_2407	Bin_2	1.40091	20.4282
25	gene_id_2408	Bin_2	1.37642	18.4058
25	gene_id_2411	Bin_2	0.834828	15.357
25	gene_id_2413	Bin_2	0	18.7985
25	gene_id_2421	Bin_2	14.013	143.861
25	gene_id_2422	Bin_2	25.3459	116.866
25	gene_id_2424	Bin_2	4.42316	31.0535
25	gene_id_2426	Bin_2	2.10016	17.966
25	gene_id_2427	Bin_2	52.7112	676.607
25	gene_id_2429	Bin_2	13.9896	32.4809
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25	gene_id_2431	Bin_2	1.56487	26.5522
25	gene_id_2432	Bin_2	12.188	31.504
25	gene_id_2439	Bin_2	4362.48	57290.2
25	gene_id_2442	Bin_2	46.7143	228.073
25	gene_id_2446	Bin_2	385.777	969.679
25	gene_id_2447	Bin_2	232.211	1509.18
26	gene_id_2448	Bin_2	29.8445	66.415
26	gene_id_2449	Bin_2	37.3122	92.2586
26	gene_id_2471	Bin_2	4.68154	22.9272
26	gene_id_2472	Bin_2	21.5295	50.8744
26	gene_id_2484	Bin_2	4.52398	15.7401
26	gene_id_2487	Bin_2	31.3901	93.5502
26	gene_id_2497	Bin_2	1.72032	21.0887
26	gene_id_2508	Bin_2	0	26.7248
26	gene_id_2520	Bin_2	0	17.359
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26	gene_id_2546	Bin_2	0.780573	12.4554
26	gene_id_2548	Bin_2	216.767	1209
26	gene_id_2558	Bin_2	10.7106	64.4136
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26	gene_id_2599	Bin_2	2.17426	19.9165
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26	gene_id_2614	Bin_2	1.6002	19.3831
1	gene_id_37	Bin_2	0	17.0843
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34	gene_id_3711	Bin_2	1.42034	13.0904
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5	gene_id_412	Bin_2	20.1804	98.3124
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5	gene_id_415	Bin_2	2.12854	18.2047
5	gene_id_419	Bin_2	20.2236	41.2498
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42	gene_id_4367	Bin_2	1.28162	8.6719
42	gene_id_4373	Bin_2	4.93101	15.0208
5	gene_id_438	Bin_2	23.9943	133.204
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5	gene_id_444	Bin_2	3.81874	9.37715
5	gene_id_447	Bin_2	181.75	687.327
5	gene_id_452	Bin_2	6.48873	19.6424
5	gene_id_461	Bin_2	3.81463	11.2406
1	gene_id_47	Bin_2	2.64798	19.4692
46	gene_id_4705	Bin_2	3.22958	23.4663
46	gene_id_4708	Bin_2	17.1922	46.6632
46	gene_id_4713	Bin_2	236.141	2788.66
46	gene_id_4723	Bin_2	46.4541	90.3047
46	gene_id_4729	Bin_2	6.53915	31.8327
46	gene_id_4730	Bin_2	9.25732	33.7906
46	gene_id_4733	Bin_2	0	20.11
46	gene_id_4734	Bin_2	8.77369	25.4429
46	gene_id_4737	Bin_2	0	23.3226
46	gene_id_4746	Bin_2	19.9037	9.28309
46	gene_id_4750	Bin_2	17.6893	7.69407
46	gene_id_4752	Bin_2	10.3162	19.6764
46	gene_id_4754	Bin_2	15.2966	86.0598
46	gene_id_4760	Bin_2	2.81853	23.9719
46	gene_id_4765	Bin_2	3.20765	31.0814
5	gene_id_477	Bin_2	3.09164	14.2324
46	gene_id_4779	Bin_2	1.62218	23.5709
46	gene_id_4780	Bin_2	193.509	628.826
46	gene_id_4781	Bin_2	13.7171	39.4613
46	gene_id_4788	Bin_2	2.97363	28.7246
46	gene_id_4789	Bin_2	3.76198	10.1634
46	gene_id_4796	Bin_2	4.61772	28.1686
46	gene_id_4797	Bin_2	4.56831	23.2789
46	gene_id_4799	Bin_2	10.1429	13.2596
46	gene_id_4800	Bin_2	11.9116	18.7184
46	gene_id_4801	Bin_2	7.58114	33.8539
46	gene_id_4802	Bin_2	9.24193	51.0628
46	gene_id_4807	Bin_2	24.0629	104.956
46	gene_id_4819	Bin_2	4.67398	54.1429
46	gene_id_4820	Bin_2	1.38719	18.5467
46	gene_id_4823	Bin_2	1.87015	12.5936
46	gene_id_4824	Bin_2	8.94602	45.5894
46	gene_id_4825	Bin_2	2.72112	26.4704
46	gene_id_4827	Bin_2	18.0196	97.8283
46	gene_id_4828	Bin_2	21.9397	86.7318
46	gene_id_4855	Bin_2	0	13.1937
46	gene_id_4856	Bin_2	0	10.1789
5	gene_id_491	Bin_2	6.31762	20.0046
5	gene_id_492	Bin_2	4.12395	15.9586
5	gene_id_495	Bin_2	0	13.1981
5	gene_id_496	Bin_2	1.2888	15.6896

5	gene_id_501	Bin_2	1.64638	12.1167
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48	gene_id_5340	Bin_2	1.78569	21.5657
48	gene_id_5343	Bin_2	3.84514	58.5476
48	gene_id_5344	Bin_2	10.4129	40.8666
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50	gene_id_5431	Bin_2	6.90892	25.1945
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50	gene_id_5435	Bin_2	0	23.1698
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50	gene_id_5441	Bin_2	15.3647	47.4054
50	gene_id_5442	Bin_2	11.4038	153.509
50	gene_id_5449	Bin_2	10.393	13.9737
50	gene_id_5450	Bin_2	12.488	85.273
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50	gene_id_5452	Bin_2	66.363	368.744
50	gene_id_5457	Bin_2	3.08209	22.4212
50	gene_id_5461	Bin_2	11.4659	19.1101
50	gene_id_5485	Bin_2	4.51574	35.1838
50	gene_id_5496	Bin_2	1.84137	22.2184
50	gene_id_5501	Bin_2	2.11243	12.367
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50	gene_id_5508	Bin_2	1.07232	19.65
50	gene_id_5510	Bin_2	1.37109	43.34
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50	gene_id_5521	Bin_2	1.66019	30.1355
50	gene_id_5525	Bin_2	0	26.8653
53	gene_id_5571	Bin_2	2.19786	20.1289
53	gene_id_5579	Bin_2	93.6965	1848.14
53	gene_id_5581	Bin_2	4.08168	23.1616
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62	gene_id_5875	Bin_2	93.4287	691.095
62	gene_id_5876	Bin_2	9.20738	44.1163
62	gene_id_5877	Bin_2	59.257	116.952
62	gene_id_5878	Bin_2	2.75804	32.8086
62	gene_id_5882	Bin_2	2.40688	14.6707
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62	gene_id_5886	Bin_2	7.72567	86.886

62	gene_id_5892	Bin_2	4.49328	13.7117
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62	gene_id_5901	Bin_2	2.21948	14.5392
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1	gene_id_6	Bin_2	0.84177	13.4186
7	gene_id_604	Bin_2	4.39764	26.1099
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7	gene_id_612	Bin_2	3.28955	27.8723
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67	gene_id_6190	Bin_2	20.6443	140.169
67	gene_id_6194	Bin_2	1.54751	9.49846
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67	gene_id_6198	Bin_2	292.698	607.161
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1	gene_id_62	Bin_2	62.465	64.6545
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69	gene_id_6253	Bin_2	6.48873	25.5352
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69	gene_id_6282	Bin_2	0	15.8955
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69	gene_id_6305	Bin_2	7.72523	16.5442
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69	gene_id_6311	Bin_2	14.8283	36.2791
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69	gene_id_6315	Bin_2	1.96384	26.0148
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69	gene_id_6323	Bin_2	12.1917	56.9479
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70	gene_id_6330	Bin_2	25.0595	8.72971
70	gene_id_6331	Bin_2	43.293	22.1629
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72	gene_id_6421	Bin_2	108.159	1042.63
7	gene_id_643	Bin_2	1.74575	12.8376
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7	gene_id_647	Bin_2	6.6621	16.2092
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73	gene_id_6582	Bin_2	271.084	1367.76
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73	gene_id_6603	Bin_2	0	13.8935
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77	gene_id_6848	Bin_2	443.904	1502.52
77	gene_id_6855	Bin_2	0	25.6495
9	gene_id_690	Bin_2	134.628	581.41
9	gene_id_693	Bin_2	6.76759	42.9737
9	gene_id_698	Bin_2	0	15.2814
9	gene_id_708	Bin_2	0	42.1087
9	gene_id_716	Bin_2	720.022	6245.81
9	gene_id_721	Bin_2	7.01277	37.1855
9	gene_id_722	Bin_2	2.13818	19.5918
9	gene_id_724	Bin_2	6.41454	22.204
9	gene_id_728	Bin_2	1.45087	17.8247
9	gene_id_742	Bin_2	4.62314	29.8949
9	gene_id_752	Bin_2	55.1498	221.665
9	gene_id_755	Bin_2	9.03026	34.6909
9	gene_id_756	Bin_2	157.881	491.656
9	gene_id_757	Bin_2	135.198	615.367
9	gene_id_759	Bin_2	1.18915	17.5685
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9	gene_id_761	Bin_2	0.80902	25.4781
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87	gene_id_7729	Bin_2	0	31.1089
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9	gene_id_782	Bin_2	6.28723	20.9527
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91	gene_id_7859	Bin_2	214.923	420.798
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9	gene_id_789	Bin_2	5.18715	58.5217
91	gene_id_7893	Bin_2	10.6133	56.0953
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91	gene_id_7895	Bin_2	13.651	21.8159
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92	gene_id_8085	Bin_2	10.513	27.3309
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95	gene_id_8200	Bin_2	0	12.2273
95	gene_id_8203	Bin_2	1.83185	28.7389
95	gene_id_8204	Bin_2	15.3577	41.4802
95	gene_id_8205	Bin_2	138.059	351.143
95	gene_id_8207	Bin_2	0.738285	10.8819
110	gene_id_8694	Bin_2	2.2507	97.1337
110	gene_id_8707	Bin_2	52.5362	217.534
110	gene_id_8709	Bin_2	3.41432	20.4531
110	gene_id_8712	Bin_2	18.4339	95.9426
110	gene_id_8713	Bin_2	7.2842	50.1118
110	gene_id_8714	Bin_2	4.62652	67.9855
110	gene_id_8715	Bin_2	1.44349	16.8482
110	gene_id_8716	Bin_2	6.56455	36.761
110	gene_id_8716	Bin_2	4.75812	31.3099
110	gene_id_8717	Bin_2	1.06175	19.6284
110	gene_id_8718	Bin_2	6.57909	29.8631
110	gene_id_8721	Bin_2	0	46.2672
110	gene_id_8722	Bin_2	0	12.0158
110	gene_id_8724	Bin_2	0	21.6569
110	gene_id_8725	Bin_2	6.6259	34.4431
110	gene_id_8725	Bin_2	1.68787	20.4163
110	gene_id_8726	Bin_2	4.2709	28.211
110	gene_id_8727	Bin_2	13.9527	116.127
110	gene_id_8737	Bin_2	24.6349	128.49
110	gene_id_8742	Bin_2	0	17.0982
110	gene_id_8745	Bin_2	3.00002	28.5525
110	gene_id_8746	Bin_2	0.615221	9.84342
110	gene_id_8748	Bin_2	4.90541	22.4166
110	gene_id_8749	Bin_2	0.835813	14.3499
110	gene_id_8754	Bin_2	13.9518	53.3738
110	gene_id_8755	Bin_2	35.3442	184.938
110	gene_id_8759	Bin_2	1.62964	21.7035
110	gene_id_8765	Bin_2	0	10.3812
110	gene_id_8767	Bin_2	4.15345	16.8284
110	gene_id_8769	Bin_2	3.85212	17.6785
110	gene_id_8778	Bin_2	1.88758	17.3307
11	gene_id_884	Bin_2	18.92	119.766
11	gene_id_885	Bin_2	5.10506	88.2317
11	gene_id_886	Bin_2	2.47881	29.6115
11	gene_id_891	Bin_2	17.5509	117.727
11	gene_id_898	Bin_2	19.207	50.642

11	gene_id_903	Bin_2	14.1759	58.1952
11	gene_id_910	Bin_2	28.4278	92.2808
11	gene_id_911	Bin_2	15.7694	354.338
11	gene_id_913	Bin_2	0	36.2243
11	gene_id_915	Bin_2	11.5275	50.9357
11	gene_id_917	Bin_2	2.57112	17.8613
11	gene_id_918	Bin_2	7.32302	40.8925
11	gene_id_919	Bin_2	12.7883	67.036
1	gene_id_92	Bin_2	6.91531	15.468
11	gene_id_922	Bin_2	29.3358	17.5312
12	gene_id_927	Bin_2	1.71824	16.8508
12	gene_id_928	Bin_2	1.65988	15.2683
12	gene_id_934	Bin_2	78.0446	228.091
12	gene_id_935	Bin_2	0	26.8173
12	gene_id_939	Bin_2	3.18188	16.5947
12	gene_id_940	Bin_2	10.9854	113.404
12	gene_id_944	Bin_2	10.2155	58.976
12	gene_id_946	Bin_2	0	14.3735
120	gene_id_9474	Bin_2	0.690113	8.48324
120	gene_id_9478	Bin_2	240.334	2428.51
120	gene_id_9490	Bin_2	3124.67	11003.2
120	gene_id_9491	Bin_2	7.30852	30.8721
12	gene_id_950	Bin_2	12.3656	34.6929
122	gene_id_9504	Bin_2	3.44968	22.9363
12	gene_id_955	Bin_2	1.48299	17.9973
12	gene_id_965	Bin_2	6.17903	28.1368
12	gene_id_966	Bin_2	9.86139	109.732
12	gene_id_968	Bin_2	14.1753	107.796
1	gene_id_97	Bin_2	18.8228	18.6781
12	gene_id_971	Bin_2	203.904	849.455
128	gene_id_9711	Bin_2	12.0845	26.6589
128	gene_id_9715	Bin_2	8.69662	39.4389
128	gene_id_9716	Bin_2	0	21.4606
128	gene_id_9729	Bin_2	7.50194	47.4971
129	gene_id_9732	Bin_2	1.01985	27.4331
129	gene_id_9738	Bin_2	0	19.9088
129	gene_id_9748	Bin_2	0	29.941
129	gene_id_9750	Bin_2	12.8127	38.4695
129	gene_id_9751	Bin_2	1.5966	40.6152
129	gene_id_9752	Bin_2	83.9867	423.343
129	gene_id_9753	Bin_2	36.277	76.312
129	gene_id_9755	Bin_2	37.273	47.9301
129	gene_id_9761	Bin_2	9.60122	32.9513
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12	gene_id_989	Bin_2	1.01402	12.3994
131	gene_id_9931	Bin_2	7.52232	22.5498
131	gene_id_9934	Bin_2	7.67055	24.4848
131	gene_id_9935	Bin_2	232.521	2080.42
131	gene_id_9937	Bin_2	21.9444	159.474
131	gene_id_9938	Bin_2	2.81293	42.724

131	gene_id_9943	Bin_2	1.4674	11.7164
131	gene_id_9950	Bin_2	1.04082	17.8104
131	gene_id_9951	Bin_2	14.0631	53.4893
131	gene_id_9952	Bin_2	126.109	1540.2
131	gene_id_9954	Bin_2	0	27.4311
131	gene_id_9957	Bin_2	2.98738	15.5926
12	gene_id_996	Bin_2	0	41.5176
131	gene_id_9960	Bin_2	14.8698	43.6548
131	gene_id_9962	Bin_2	7.54186	34.1016
131	gene_id_9963	Bin_2	2.6546	14.0957
131	gene_id_9965	Bin_2	1021.02	2780.6
131	gene_id_9966	Bin_2	132.979	136.091
131	gene_id_9967	Bin_2	0.800863	22.6019
131	gene_id_9982	Bin_2	25.9378	104.362
131	gene_id_9985	Bin_2	0	25.9451
131	gene_id_9987	Bin_2	3.30976	50.7749
131	gene_id_9990	Bin_2	18.8549	63.0398
131	gene_id_9991	Bin_2	2.95279	45.5321
131	gene_id_9995	Bin_2	0	12.4919
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135	gene_id_10381	Bin_3	55.4839	86.4891
14	gene_id_1057	Bin_3	68.2633	37.5529
14	gene_id_1062	Bin_3	43.1123	22.9189
14	gene_id_1064	Bin_3	115.117	93.7002
14	gene_id_1065	Bin_3	432.859	211.208
14	gene_id_1077	Bin_3	219.765	191.486
149	gene_id_10871	Bin_3	19.4737	12.6417
14	gene_id_1123	Bin_3	106.328	35.4006
185	gene_id_11807	Bin_3	31.9501	27.5814
210	gene_id_13432	Bin_3	66.0115	103.343
210	gene_id_13436	Bin_3	2.99735	21.8196
218	gene_id_13786	Bin_3	151.103	16.6223
218	gene_id_13787	Bin_3	246.535	307.25
220	gene_id_13792	Bin_3	20.3724	0
220	gene_id_13796	Bin_3	468.42	432.179
228	gene_id_14055	Bin_3	5.6946	7.01983
228	gene_id_14057	Bin_3	66.4661	122.243
235	gene_id_14243	Bin_3	25.6254	29.8498
235	gene_id_14244	Bin_3	241.432	93.2363
235	gene_id_14292	Bin_3	138.906	102.12
235	gene_id_14293	Bin_3	34.5145	15.8155
238	gene_id_14359	Bin_3	93.6535	17.5455
244	gene_id_14443	Bin_3	463.093	433.759
244	gene_id_14449	Bin_3	58.6242	4.57364
244	gene_id_14455	Bin_3	107.716	59.7459
249	gene_id_14583	Bin_3	140.617	37.9462
249	gene_id_14586	Bin_3	246.535	219.464
259	gene_id_14851	Bin_3	10.0915	36.1411
259	gene_id_14853	Bin_3	24.531	5.86318
261	gene_id_15029	Bin_3	59.3347	45.8689

261	gene_id_15033	Bin_3	8364.07	12575.5
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278	gene_id_15177	Bin_3	152.722	196.16
278	gene_id_15178	Bin_3	40.5735	43.5988
278	gene_id_15179	Bin_3	15.6347	20.2279
285	gene_id_15239	Bin_3	17.1402	30.825
285	gene_id_15250	Bin_3	18.1769	13.9994
286	gene_id_15255	Bin_3	73.2468	41.0568
294	gene_id_15544	Bin_3	12.568	1.53079
303	gene_id_15783	Bin_3	45.8898	86.0598
313	gene_id_16269	Bin_3	14.5381	23.8608
313	gene_id_16270	Bin_3	11.0895	22.3743
313	gene_id_16270	Bin_3	4.89536	11.6318
313	gene_id_16270	Bin_3	3.57067	17.4993
313	gene_id_16270	Bin_3	5.37061	34.5898
325	gene_id_16413	Bin_3	124.24	9.91637
325	gene_id_16413	Bin_3	11.6545	3.8838
325	gene_id_16413	Bin_3	24.7644	24.3931
327	gene_id_16445	Bin_3	283.269	135.941
327	gene_id_16455	Bin_3	529.259	256.454
331	gene_id_16573	Bin_3	45.2021	45.5416
331	gene_id_16574	Bin_3	24.3709	10.6299
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331	gene_id_16577	Bin_3	430.297	236.825
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331	gene_id_16580	Bin_3	36.0529	30.1534
333	gene_id_16607	Bin_3	24.0929	16.9863
348	gene_id_16943	Bin_3	94.711	222.627
348	gene_id_16944	Bin_3	56.717	65.0458
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348	gene_id_16947	Bin_3	33.5714	16.6442
355	gene_id_17001	Bin_3	24.6886	42.6099
355	gene_id_17025	Bin_3	439.05	734.619
420	gene_id_17679	Bin_3	165.706	95.3806
422	gene_id_17695	Bin_3	142.942	52.939
424	gene_id_17718	Bin_3	148.178	97.3453
427	gene_id_17750	Bin_3	1886.5	1669.96
427	gene_id_17751	Bin_3	465.244	423.558
430	gene_id_17769	Bin_3	32.1558	37.1281
430	gene_id_17770	Bin_3	13.0593	27.0025
430	gene_id_17805	Bin_3	44.1362	39.3473
433	gene_id_17836	Bin_3	3076	1775.48
434	gene_id_17871	Bin_3	49.1153	46.1634
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435	gene_id_17876	Bin_3	102.344	22.7458
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468	gene_id_18380	Bin_3	27.4514	1.95552
468	gene_id_18385	Bin_3	57.3949	34.592
468	gene_id_18387	Bin_3	20.1012	15.5441
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476	gene_id_18565	Bin_3	30.4333	49.04
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499	gene_id_18806	Bin_3	21.0198	23.0315
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508	gene_id_18976	Bin_3	655.816	326.517
517	gene_id_19063	Bin_3	4.43433	14.5242
517	gene_id_19064	Bin_3	28.5212	33.561
522	gene_id_19145	Bin_3	20.916	2.83499
559	gene_id_19481	Bin_3	175.478	221.503
561	gene_id_19513	Bin_3	44.7551	56.2084
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564	gene_id_19582	Bin_3	65.1965	81.4085
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582	gene_id_19872	Bin_3	132.902	29.6381
582	gene_id_19873	Bin_3	33.4928	2.24448
582	gene_id_19874	Bin_3	81.3366	5.92453
582	gene_id_19875	Bin_3	31.0278	15.4245
582	gene_id_19876	Bin_3	10.0696	39.5834
583	gene_id_19889	Bin_3	5.88116	34.8861
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583	gene_id_19905	Bin_3	8.33886	36.3602
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583	gene_id_19933	Bin_3	73.6772	34.9725
597	gene_id_20167	Bin_3	48.2184	65.7329
652	gene_id_20644	Bin_3	45.1225	44.9533
653	gene_id_20657	Bin_3	8.6664	43.9956
653	gene_id_20679	Bin_3	210.093	197.287
664	gene_id_20729	Bin_3	36.6337	28.4595
664	gene_id_20737	Bin_3	64.0674	43.6806
689	gene_id_21094	Bin_3	87.6807	140.994
712	gene_id_21268	Bin_3	16.9634	8.86142
712	gene_id_21269	Bin_3	235.362	298.016

713	gene_id_21272	Bin_3	11.6037	4.73326
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720	gene_id_21317	Bin_3	9.77583	30.0384
720	gene_id_21330	Bin_3	7.5418	30.015
720	gene_id_21336	Bin_3	447.426	848.302
736	gene_id_21424	Bin_3	17.1756	7.57005
742	gene_id_21491	Bin_3	135.545	64.9714
742	gene_id_21494	Bin_3	96.5958	162.624
751	gene_id_21564	Bin_3	42.6485	128.649
766	gene_id_21711	Bin_3	94.092	250.591
766	gene_id_21716	Bin_3	398.96	310.172
769	gene_id_21731	Bin_3	63.5955	266.819
769	gene_id_21735	Bin_3	84.4304	75.0422
769	gene_id_21741	Bin_3	65.8828	34.167
774	gene_id_21768	Bin_3	48.4134	29.2608
778	gene_id_21782	Bin_3	370.338	86.4738
799	gene_id_21975	Bin_3	10.8021	2.89704
816	gene_id_22079	Bin_3	140.48	96.5002
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825	gene_id_22165	Bin_3	13.9106	6.83928
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895	gene_id_22671	Bin_3	829.253	497.524
895	gene_id_22672	Bin_3	1104.12	1919.95
895	gene_id_22673	Bin_3	89.6491	203.157
895	gene_id_22683	Bin_3	62.957	43.7505
907	gene_id_22770	Bin_3	22.5035	30.7612
941	gene_id_22896	Bin_3	1151.52	1981.84
942	gene_id_22905	Bin_3	218.135	156.941
980	gene_id_23150	Bin_3	126.197	75.8
984	gene_id_23166	Bin_3	23.8758	22.1625
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1017	gene_id_23350	Bin_3	2.88156	24.4956
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1032	gene_id_23444	Bin_3	42.3227	64.1039
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1267	gene_id_24626	Bin_3	219.308	193.122
1268	gene_id_24630	Bin_3	14.9481	33.3402
1268	gene_id_24631	Bin_3	10.1082	18.4658
1268	gene_id_24632	Bin_3	6.57152	12.6429
1268	gene_id_24633	Bin_3	22.3239	26.1959
1331	gene_id_24846	Bin_3	79.9625	92.9061
1333	gene_id_24851	Bin_3	97.8093	39.4829
1421	gene_id_25181	Bin_3	29.0841	32.9125
1421	gene_id_25182	Bin_3	1681.02	640.113
1421	gene_id_25183	Bin_3	10.6484	18.4495
1458	gene_id_25287	Bin_3	20.2049	10.8328
1463	gene_id_25325	Bin_3	17.3328	4.19006
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1508	gene_id_25495	Bin_3	108.428	501.955
1643	gene_id_25958	Bin_3	96.3401	15.5744
1660	gene_id_26024	Bin_3	180.361	185.831
1706	gene_id_26223	Bin_3	31.8399	7.64936
1848	gene_id_26634	Bin_3	21.1893	65.2583
1848	gene_id_26637	Bin_3	99.8398	36.3821
1924	gene_id_26851	Bin_3	245.748	352.38
2401	gene_id_27915	Bin_3	146.3	75.9306
2401	gene_id_27917	Bin_3	44.4236	46.4531
2750	gene_id_28608	Bin_3	8.81563	7.56206
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49	gene_id_5394	Bin_3	35.9557	28.141
51	gene_id_5543	Bin_3	76.6303	78.1588
57	gene_id_5654	Bin_3	341.826	735.937
78	gene_id_6888	Bin_3	94.4175	38.4206
78	gene_id_6893	Bin_3	55202.8	28504.4
78	gene_id_6894	Bin_3	1194.24	877.349
78	gene_id_6895	Bin_3	16842	15502.1
103	gene_id_8510	Bin_3	39.9093	176.07
103	gene_id_8516	Bin_3	17.4838	26.9585
103	gene_id_8517	Bin_3	25.8098	18.7217
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132	gene_id_10044	Bin_4	104.067	96.9493
132	gene_id_10048	Bin_4	17.844	21.6067
132	gene_id_10062	Bin_4	72.6662	76.1737
132	gene_id_10068	Bin_4	51.649	37.4847
132	gene_id_10076	Bin_4	9.24627	26.158
132	gene_id_10077	Bin_4	48.2184	46.9521
132	gene_id_10084	Bin_4	908.249	921.558
132	gene_id_10090	Bin_4	10.8786	39.3969
132	gene_id_10108	Bin_4	10.0462	27.2537

132	gene_id_10122	Bin_4	13.8984	9.89064
133	gene_id_10137	Bin_4	25.0448	44.0235
133	gene_id_10141	Bin_4	0	12.4344
133	gene_id_10143	Bin_4	55.347	14.8762
133	gene_id_10149	Bin_4	15.5638	3.43792
133	gene_id_10149	Bin_4	49.719	22.404
133	gene_id_10149	Bin_4	49.4225	22.303
133	gene_id_10153	Bin_4	103.033	160.718
133	gene_id_10162	Bin_4	137.74	155.964
133	gene_id_10164	Bin_4	18.9463	43.5385
133	gene_id_10172	Bin_4	81.8657	5.01503
133	gene_id_10184	Bin_4	19.2525	23.7004
133	gene_id_10201	Bin_4	53.164	118.002
133	gene_id_10203	Bin_4	13.0044	50.4365
133	gene_id_10216	Bin_4	27.444	24.6611
133	gene_id_10235	Bin_4	85.2439	48.5799
133	gene_id_10254	Bin_4	1.76347	21.305
143	gene_id_10598	Bin_4	26.746	43.0497
143	gene_id_10605	Bin_4	36.5651	61.0925
143	gene_id_10606	Bin_4	13.9236	21.5811
143	gene_id_10607	Bin_4	25.0336	19.2387
143	gene_id_10608	Bin_4	378.716	289.375
143	gene_id_10615	Bin_4	3.1596	12.8704
143	gene_id_10618	Bin_4	29.651	28.1315
143	gene_id_10623	Bin_4	1273.33	2434.76
143	gene_id_10624	Bin_4	7.89267	27.122
143	gene_id_10630	Bin_4	437.599	1433.57
143	gene_id_10631	Bin_4	457.22	1109.85
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178	gene_id_11669	Bin_4	69.7344	30.6174
178	gene_id_11683	Bin_4	67.4427	38.6242
178	gene_id_11688	Bin_4	29.6945	26.8563
178	gene_id_11690	Bin_4	43.4667	27.729
178	gene_id_11698	Bin_4	21.8103	51.914
178	gene_id_11713	Bin_4	19.9419	8.15252
192	gene_id_12039	Bin_4	12.0403	21.91
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196	gene_id_12677	Bin_4	2.22947	26.7359
196	gene_id_12681	Bin_4	28.61	95.4258
196	gene_id_12687	Bin_4	24.4473	34.6516
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196	gene_id_12692	Bin_4	18.0506	35.755
196	gene_id_12794	Bin_4	21.2903	7.67157
196	gene_id_12809	Bin_4	164.47	269.167
196	gene_id_12815	Bin_4	15.753	3.81783
196	gene_id_12818	Bin_4	5.21208	15.8591
196	gene_id_12828	Bin_4	6.5336	27.6846

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205	gene_id_13056	Bin_4	11.9509	19.1395
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205	gene_id_13088	Bin_4	6.43908	13.4199
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208	gene_id_13219	Bin_4	20.3079	17.8196
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209	gene_id_13262	Bin_4	42.3227	54.2418
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209	gene_id_13273	Bin_4	18.0387	15.2453
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209	gene_id_13281	Bin_4	72.1797	89.1696
209	gene_id_13295	Bin_4	11.8953	28.4635
209	gene_id_13307	Bin_4	72.9993	37.627
209	gene_id_13322	Bin_4	494.523	1105.36
209	gene_id_13330	Bin_4	52.9207	48.6727
209	gene_id_13332	Bin_4	153.659	50.6947
209	gene_id_13349	Bin_4	30.6346	10.5031
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209	gene_id_13366	Bin_4	57.0333	129.309
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209	gene_id_13379	Bin_4	347.205	367.376
211	gene_id_13439	Bin_4	12.5817	7.20008
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217	gene_id_13703	Bin_4	10.1924	4.81148
217	gene_id_13721	Bin_4	53.0356	67.2999
217	gene_id_13738	Bin_4	217.165	1165.19
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16	gene_id_1444	Bin_4	23.4957	51.4584
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248	gene_id_14522	Bin_4	19.7421	13.0031
248	gene_id_14525	Bin_4	56.824	77.4127
248	gene_id_14530	Bin_4	76.355	75.9658
248	gene_id_14542	Bin_4	78.436	128.371
248	gene_id_14559	Bin_4	2.10327	12.8516
248	gene_id_14568	Bin_4	295.358	150.97
248	gene_id_14582	Bin_4	51.4552	43.6458
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292	gene_id_15432	Bin_4	14.554	36.4479
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292	gene_id_15498	Bin_4	125.001	186.337
299	gene_id_15590	Bin_4	36.8439	46.9529
299	gene_id_15594	Bin_4	27.9885	20.1944
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299	gene_id_15599	Bin_4	52.7866	83.0383
299	gene_id_15606	Bin_4	4.01235	16.2691
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345	gene_id_16850	Bin_4	50.4437	302.539
345	gene_id_16878	Bin_4	205.934	668.546
354	gene_id_16978	Bin_4	46.5703	52.4549
357	gene_id_17034	Bin_4	14.2289	20.7033
357	gene_id_17035	Bin_4	52.0178	15.1309
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638	gene_id_20539	Bin_4	27.3423	16.4665
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782	gene_id_21801	Bin_4	221.861	318.46
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102	gene_id_8413	Bin_4	149.591	138.19
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119	gene_id_9421	Bin_4	26.9526	12.8367
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344	gene_id_16810	Bin_5	6.72554	9.86087
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372	gene_id_17181	Bin_5	8.93389	10.9723
372	gene_id_17185	Bin_5	11.9871	8.97827
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1067	gene_id_23631	Bin_5	25.1626	1.71816
1067	gene_id_23632	Bin_5	21.615	2.59485
1076	gene_id_23677	Bin_5	9.5587	11.7952
1076	gene_id_23681	Bin_5	29.7457	23.6892
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567	gene_id_19662	Bin_6	162.098	59.5743
567	gene_id_19663	Bin_6	2012.49	2389.54
567	gene_id_19665	Bin_6	23.3657	10.5163
567	gene_id_19668	Bin_6	16.2561	11.9658
567	gene_id_19669	Bin_6	13.0302	7.92953
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567	gene_id_19676	Bin_6	124.547	48.7027
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567	gene_id_19680	Bin_6	46.1973	15.4386
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676	gene_id_20987	Bin_6	33265.4	5942.86
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966	gene_id_23049	Bin_6	13.2027	3.90538
966	gene_id_23050	Bin_6	16.591	4.98981
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966	gene_id_23058	Bin_6	14.4931	8.01611
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84	gene_id_7177	Bin_6	19.5868	9.80356

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84	gene_id_7189	Bin_6	31.1052	20.012
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84	gene_id_7516	Bin_6	14.7907	13.8845

84	gene_id_7531	Bin_6	12.422	8.48324
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84	gene_id_7590	Bin_6	90.2891	23.5662
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4	gene_id_301	Bin_9	292.359	827.011
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32	gene_id_3464	Bin_9	284152	684433
32	gene_id_3477	Bin_9	5.41073	74.5438
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32	gene_id_3653	Bin_9	135.535	383.848
33	gene_id_3701	Bin_9	21.144	25.8946
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33	gene_id_3702	Bin_9	44.0004	37.4878
33	gene_id_3702	Bin_9	30.166	36.4955
38	gene_id_3790	Bin_9	9.47776	70.8422
39	gene_id_3815	Bin_9	0	12.927
39	gene_id_3830	Bin_9	232.358	256.454
39	gene_id_3846	Bin_9	332.523	248.828
39	gene_id_3883	Bin_9	10.532	7.72222
39	gene_id_3897	Bin_9	3418.07	7566.68
39	gene_id_3933	Bin_9	8.12559	48.874
39	gene_id_3949	Bin_9	4418.52	12584.4
39	gene_id_3978	Bin_9	4.28294	59.8407
39	gene_id_4056	Bin_9	37.4549	35.3532
44	gene_id_4548	Bin_9	0	18.5662
44	gene_id_4551	Bin_9	17.1154	19.0573
44	gene_id_4551	Bin_9	26.8703	62.1264
44	gene_id_4568	Bin_9	136.319	805.175
44	gene_id_4616	Bin_9	5.0086	18.5276
44	gene_id_4661	Bin_9	0	11.4481
63	gene_id_5908	Bin_9	9.8124	29.3159
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63	gene_id_5929	Bin_9	227.275	812.388
63	gene_id_5930	Bin_9	3.61695	50.2157
63	gene_id_5936	Bin_9	1.66573	13.2786
68	gene_id_6203	Bin_9	102.812	62.3012
68	gene_id_6248	Bin_9	3.16277	67.3228
75	gene_id_6765	Bin_9	41.2499	87.4899
79	gene_id_6979	Bin_9	5.96946	21.7299
79	gene_id_6988	Bin_9	4.2709	38.4695
82	gene_id_7082	Bin_9	38.3909	61.0518
82	gene_id_7104	Bin_9	5.92306	16.907
82	gene_id_7159	Bin_9	546.679	158.06
82	gene_id_7160	Bin_9	718.701	832.166
82	gene_id_7163	Bin_9	692.458	1561.46
85	gene_id_7621	Bin_9	53.8511	210.511
85	gene_id_7643	Bin_9	141.292	282.767
85	gene_id_7662	Bin_9	14.9954	101.342
90	gene_id_7844	Bin_9	19.1161	3.85964
107	gene_id_8652	Bin_9	10.4794	16.3252
107	gene_id_8662	Bin_9	7.03123	41.4784
107	gene_id_8663	Bin_9	6.81641	30.9109
107	gene_id_8665	Bin_9	7.97086	43.2937
107	gene_id_8666	Bin_9	7.31281	24.003
107	gene_id_8667	Bin_9	3.07344	27.2353
112	gene_id_8817	Bin_9	7.87653	40.6824
113	gene_id_8876	Bin_9	35.0742	106.871
116	gene_id_9196	Bin_9	189.236	2782.43
127	gene_id_9636	Bin_9	96145.8	218963

127	gene_id_9706	Bin_9	1731.14	3643.42

Contig	Gene_ID	Bin_genome	RPKM HiTCE_T1	RPKM HiTCE_T2	RPKM HiTCE_T3
31	gene_id_2801	Bin_1	22.1142	10.5824	10.5349
31	gene_id_2802	Bin_1	141.517	182.589	111.968
31	gene_id_2803	Bin_1	56.1944	94.8165	58.2977
31	gene_id_2804	Bin_1	71.0215	100.023	110.549
31	gene_id_2805	Bin_1	110.066	171.031	359.368
31	gene_id_2806	Bin_1	37.5705	41.2584	47.3634
31	gene_id_2807	Bin_1	36.9538	56.1004	41.2717
31	gene_id_2808	Bin_1	42.6222	63.447	40.6852
31	gene_id_2809	Bin_1	86.067	126.413	74.5673
31	gene_id_2810	Bin_1	48.7429	41.3293	37.2203
31	gene_id_2811	Bin_1	51.6361	53.0966	36.4023
31	gene_id_2812	Bin_1	49.9492	44.5219	28.3428
31	gene_id_2813	Bin_1	66.9265	58.0826	71.6351
31	gene_id_2815	Bin_1	31.3989	36.2208	51.4062
31	gene_id_2816	Bin_1	26.4197	8.53427	8.95788
31	gene_id_2817	Bin_1	6.56882	15.4005	11.8319
31	gene_id_2818	Bin_1	21.1598	9.60281	19.4714
31	gene_id_2819	Bin_1	40.7627	38.8559	65.3117
31	gene_id_2820	Bin_1	96.2974	76.344	354.028
31	gene_id_2821	Bin_1	15.6297	5.12578	26.3852
31	gene_id_2822	Bin_1	13.9651	8.57072	32.4472
31	gene_id_2823	Bin_1	13.7595	2.88293	6.66931
31	gene_id_2824	Bin_1	15.2206	4.54893	11.9755
31	gene_id_2825	Bin_1	10.4244	4.77579	13.3955
31	gene_id_2826	Bin_1	17.0294	5.72488	14.9564
31	gene_id_2827	Bin_1	125.059	127.53	653.728
31	gene_id_2828	Bin_1	22621.3	25311	25772.1
31	gene_id_2829	Bin_1	9651.69	11763.6	60914.7
31	gene_id_2830	Bin_1	104.199	103.528	141.078
31	gene_id_2831	Bin_1	69.3102	75.5828	426.031
31	gene_id_2832	Bin_1	84.8173	16.6987	40.9716
31	gene_id_2833	Bin_1	205.821	28.5225	350.646
31	gene_id_2834	Bin_1	90.9576	125.344	3526.25
31	gene_id_2835	Bin_1	17.8729	16.6068	539.477
31	gene_id_2836	Bin_1	109.863	169.744	282.314
31	gene_id_2837	Bin_1	52.0432	65.7706	79.7371
31	gene_id_2838	Bin_1	38.0711	45.7686	372.215
31	gene_id_2839	Bin_1	70.7393	89.1757	5814.89
31	gene_id_2840	Bin_1	36.5021	21.2218	169.825
31	gene_id_2841	Bin_1	12.5143	4.18309	13.5342
31	gene_id_2842	Bin_1	20.4551	28.8631	213.223
31	gene_id_2843	Bin_1	26.3974	17.4536	22.4725
31	gene_id_2844	Bin_1	73.5848	129.311	40.261
31	gene_id_2845	Bin_1	341.428	456.442	95.1119
31	gene_id_2847	Bin_1	9.37913	5.93587	17.9931
31	gene_id_2848	Bin_1	35.5879	61.0026	2270.27

31	gene_id_2849	Bin_1	20.3277	34.024	419.645
31	gene_id_2850	Bin_1	145.537	200.288	246.804
31	gene_id_2851	Bin_1	193.884	149.52	198.973
31	gene_id_2852	Bin_1	547.896	178.285	266.52
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31	gene_id_2862	Bin_1	5.55033	3.50226	11.8947
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31	gene_id_2880	Bin_1	200.968	165.534	311.441
31	gene_id_2883	Bin_1	12.4524	1.95912	8.55651
31	gene_id_2884	Bin_1	9.47411	0.543063	2.29967
31	gene_id_2885	Bin_1	12.5626	1.32253	0.933477
31	gene_id_2891	Bin_1	15.7155	0.495862	3.26953
31	gene_id_2893	Bin_1	15.7573	0.748981	1.45055
31	gene_id_2894	Bin_1	21.052	0	0
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31	gene_id_2902	Bin_1	37.3798	43.3586	90.1454
31	gene_id_2903	Bin_1	87.605	33.9549	393.939
31	gene_id_2904	Bin_1	16.7388	23.8726	67.7939
31	gene_id_2905	Bin_1	18.8995	28.618	23.6583
31	gene_id_2906	Bin_1	25.0832	33.0008	31.5125
31	gene_id_2907	Bin_1	38.4443	23.4255	72.8259
31	gene_id_2908	Bin_1	22.9051	23.5061	17.6301
31	gene_id_2909	Bin_1	24.2792	20.8997	36.349
31	gene_id_2910	Bin_1	18.8465	21.0829	5.73739
31	gene_id_2911	Bin_1	64.1295	43.0413	88.8293
31	gene_id_2912	Bin_1	43.4916	33.0128	109.409
31	gene_id_2914	Bin_1	73.0416	52.8625	1533.45
31	gene_id_2915	Bin_1	86.7188	549.61	570.665
31	gene_id_2916	Bin_1	18.1166	217.979	137.727
31	gene_id_2917	Bin_1	27.3376	8.44522	12.2984
31	gene_id_2918	Bin_1	30.5114	21.2142	14.0448
31	gene_id_2919	Bin_1	31.4645	29.5197	15.4671
31	gene_id_2920	Bin_1	19.1645	19.7424	3.09634
31	gene_id_2921	Bin_1	20.1747	13.9171	12.7718
31	gene_id_2922	Bin_1	28.3952	36.9912	18.0912
31	gene_id_2923	Bin_1	23.5898	21.0788	78.7253
31	gene_id_2924	Bin_1	2266.99	1833.96	1535.38

31	gene_id_2925	Bin_1	115.772	181.396	353.928
31	gene_id_2926	Bin_1	339.188	451.7	2473.37
31	gene_id_2927	Bin_1	338.505	1056.86	5951.87
31	gene_id_2928	Bin_1	2585.19	5361.13	14648.1
31	gene_id_2929	Bin_1	139.351	249.588	1185.47
31	gene_id_2930	Bin_1	164.209	403.935	678.707
31	gene_id_2931	Bin_1	110.825	206.013	534.516
31	gene_id_2932	Bin_1	313.84	432.964	716.33
31	gene_id_2933	Bin_1	176.81	172.114	695.063
31	gene_id_2934	Bin_1	283.105	295.717	1583.5
31	gene_id_2935	Bin_1	1250	1522.47	603.499
31	gene_id_2936	Bin_1	620.697	980.668	533.693
31	gene_id_2937	Bin_1	192.592	216.248	151.872
31	gene_id_2938	Bin_1	598.07	623.907	375.804
31	gene_id_2939	Bin_1	433.356	736.531	420.831
31	gene_id_2940	Bin_1	22358.4	14910.5	19254.5
31	gene_id_2941	Bin_1	298.037	215.466	161.297
31	gene_id_2942	Bin_1	238.341	231.804	164.162
31	gene_id_2943	Bin_1	914.06	1502.93	1002.25
31	gene_id_2944	Bin_1	489.333	752.366	593.816
31	gene_id_2945	Bin_1	1870.22	1089.77	1605.23
31	gene_id_2946	Bin_1	81.0903	93.1566	578.925
31	gene_id_2947	Bin_1	133.534	125.491	222.635
31	gene_id_2948	Bin_1	66.0215	83.0622	191.454
31	gene_id_2949	Bin_1	700.983	943.676	1621.75
31	gene_id_2950	Bin_1	239.877	303.31	283.084
31	gene_id_2951	Bin_1	203.93	241.1	158.375
31	gene_id_2952	Bin_1	100.903	143.426	108.154
31	gene_id_2953	Bin_1	132.455	188.884	154.984
31	gene_id_2954	Bin_1	129.637	125.345	103.949
31	gene_id_2955	Bin_1	78.1981	32.0767	64.3556
31	gene_id_2956	Bin_1	44.5104	29.1115	39.6081
31	gene_id_2957	Bin_1	136.503	228.154	211.978
31	gene_id_2958	Bin_1	574.01	560.438	1003.92
31	gene_id_2959	Bin_1	248.617	361.707	7112.66
31	gene_id_2960	Bin_1	178.188	188.389	7446.8
31	gene_id_2961	Bin_1	275.448	232.846	4342.41
31	gene_id_2962	Bin_1	53.5232	111.893	659.736
31	gene_id_2963	Bin_1	71.9163	101.331	462.486
31	gene_id_2964	Bin_1	302.906	515.926	1696.27
31	gene_id_2965	Bin_1	93.6354	140.477	245.059
31	gene_id_2966	Bin_1	1275.12	1142.42	5750.06
31	gene_id_2967	Bin_1	1403.99	1647.64	2744.47
31	gene_id_2968	Bin_1	187.944	223.918	224.244
31	gene_id_2969	Bin_1	146.117	215.87	141.496
31	gene_id_2970	Bin_1	56.0926	87.0676	83.6459
31	gene_id_2971	Bin_1	49.9156	47.3059	38.9334

31	gene_id_2972	Bin_1	158.742	238.23	290.479
31	gene_id_2973	Bin_1	367.493	369.462	718.779
31	gene_id_2974	Bin_1	11726.1	9446.05	41375.7
31	gene_id_2975	Bin_1	261.25	411.054	1170.49
31	gene_id_2976	Bin_1	335.257	263.982	4428.65
31	gene_id_2977	Bin_1	135.483	274.93	578.054
31	gene_id_2978	Bin_1	94.4282	124.296	311.914
31	gene_id_2979	Bin_1	99.741	191.03	2127.29
31	gene_id_2980	Bin_1	1497.84	1251.07	676.99
31	gene_id_2981	Bin_1	300.481	195.85	268.953
31	gene_id_2982	Bin_1	303.878	217.059	416.406
31	gene_id_2983	Bin_1	83.1732	108.23	416.551
31	gene_id_2984	Bin_1	185.804	406.926	231.145
31	gene_id_2985	Bin_1	90.777	172.55	794.067
31	gene_id_2986	Bin_1	125.796	185.325	587.41
31	gene_id_2987	Bin_1	301.824	328.266	291.284
31	gene_id_2988	Bin_1	79.2607	82.8193	96.7462
31	gene_id_2989	Bin_1	259.649	409.943	279.45
31	gene_id_2990	Bin_1	134.858	173.885	137.088
31	gene_id_2991	Bin_1	272.954	282.078	745.214
31	gene_id_2992	Bin_1	296.066	596.085	1386.2
31	gene_id_2993	Bin_1	51.7494	55.6567	130.777
31	gene_id_2994	Bin_1	333.969	331.67	917.377
31	gene_id_2995	Bin_1	208.224	245.197	881.797
31	gene_id_2996	Bin_1	48.1954	121.788	980.222
31	gene_id_2997	Bin_1	88.3269	154.475	422.382
31	gene_id_2998	Bin_1	87.9382	72.7432	257.127
31	gene_id_2999	Bin_1	4496.95	1483.79	2841.14
31	gene_id_3000	Bin_1	3436.07	2646.92	5728.48
31	gene_id_3001	Bin_1	76.8757	45.9016	112.088
31	gene_id_3002	Bin_1	85.8038	351.419	534.276
31	gene_id_3003	Bin_1	97.876	147.6	507.129
31	gene_id_3004	Bin_1	137.526	259.607	497.065
31	gene_id_3005	Bin_1	669.146	804.33	9850.28
31	gene_id_3006	Bin_1	21.742	13.7912	38.2605
31	gene_id_3007	Bin_1	47.8962	24.6193	53.2056
31	gene_id_3008	Bin_1	305.689	589.675	892.244
31	gene_id_3009	Bin_1	501.513	855.087	941.477
31	gene_id_3010	Bin_1	1200.8	1211.42	2175.23
31	gene_id_3011	Bin_1	66.9864	74.4294	83.3687
31	gene_id_3012	Bin_1	111.908	143.392	167.319
31	gene_id_3013	Bin_1	49.1885	67.0803	66.3403
31	gene_id_3014	Bin_1	335.095	377.231	314.839
31	gene_id_3015	Bin_1	120.149	109.757	123.037
31	gene_id_3016	Bin_1	138.69	174.593	154.548
31	gene_id_3017	Bin_1	539.85	928.872	372.538
31	gene_id_3018	Bin_1	194.976	186.326	467.534

31	gene_id_3019	Bin_1	100.787	115.331	172.049
31	gene_id_3020	Bin_1	466.712	206.553	274.68
31	gene_id_3021	Bin_1	367.641	446.838	638.914
31	gene_id_3022	Bin_1	62.1482	50.8368	100.503
31	gene_id_3023	Bin_1	1153.44	1937.28	1215.92
31	gene_id_3024	Bin_1	33.1671	61.0531	827.672
31	gene_id_3025	Bin_1	93.8643	161.852	352.696
31	gene_id_3026	Bin_1	105.084	141.103	87.4915
31	gene_id_3027	Bin_1	543.662	439.371	299.227
31	gene_id_3028	Bin_1	73.9537	74.5533	105.774
31	gene_id_3029	Bin_1	100.823	65.0374	86.0771
31	gene_id_3030	Bin_1	63.4994	68.0037	154.317
31	gene_id_3031	Bin_1	108.614	139.275	126.958
31	gene_id_3032	Bin_1	120.962	129.684	144.368
31	gene_id_3033	Bin_1	113.698	67.9339	79.696
31	gene_id_3034	Bin_1	224.807	339.223	1014.06
31	gene_id_3035	Bin_1	284.571	413.14	1916.49
31	gene_id_3036	Bin_1	56.3293	49.6674	77.775
31	gene_id_3037	Bin_1	78.932	88.7562	53.6751
31	gene_id_3038	Bin_1	166.077	231.148	3129.09
31	gene_id_3039	Bin_1	100.637	119.304	420.282
31	gene_id_3040	Bin_1	24.7965	6.63471	27.217
31	gene_id_3041	Bin_1	347.596	153.317	265.622
31	gene_id_3042	Bin_1	69.4896	48.1203	39.347
31	gene_id_3043	Bin_1	103.581	79.5725	92.5711
31	gene_id_3044	Bin_1	42.8177	21.1797	20.8609
31	gene_id_3045	Bin_1	34.8815	23.6294	11.3063
31	gene_id_3046	Bin_1	69.9634	48.2411	41.5924
31	gene_id_3047	Bin_1	112.503	178.951	142.623
31	gene_id_3048	Bin_1	25.6303	20.4218	11.1332
31	gene_id_3049	Bin_1	35.4523	26.3463	16.0988
31	gene_id_3050	Bin_1	28.0096	32.5572	68.3782
31	gene_id_3051	Bin_1	35.6562	33.2308	17.0094
31	gene_id_3052	Bin_1	31.1023	31.2481	15.2737
31	gene_id_3053	Bin_1	32.6172	18.9708	5.95062
31	gene_id_3059	Bin_1	11.4641	1.27821	3.04175
31	gene_id_3061	Bin_1	78.5739	74.5637	79.749
31	gene_id_3062	Bin_1	40.8058	35.6052	26.0604
31	gene_id_3063	Bin_1	40.8277	19.6785	40.3737
31	gene_id_3064	Bin_1	12.6904	0.422031	1.22561
31	gene_id_3067	Bin_1	26.5089	3.27869	1.15607
31	gene_id_3071	Bin_1	17.8529	2.64319	11.5616
31	gene_id_3074	Bin_1	7.88169	2.2625	8.48639
31	gene_id_3081	Bin_1	13.2938	12.4641	85.0927
31	gene_id_3082	Bin_1	105.363	75.8981	343.203
31	gene_id_3083	Bin_1	20.733	23.3766	181.458
31	gene_id_3084	Bin_1	147.09	191.771	1550.73

31	gene_id_3088	Bin_1	17.4555	3.9143	13.756
31	gene_id_3089	Bin_1	7.3813	6.39512	14.7337
31	gene_id_3092	Bin_1	12.713	5.66485	13.8014
31	gene_id_3093	Bin_1	49.048	28.2649	78.1308
31	gene_id_3094	Bin_1	728.953	241.747	741.173
31	gene_id_3095	Bin_1	311.7	435.01	5385.15
31	gene_id_3096	Bin_1	28.1201	34.8716	183.959
31	gene_id_3097	Bin_1	59.7569	54.2331	86.4454
31	gene_id_3098	Bin_1	95.9568	72.442	148.607
31	gene_id_3099	Bin_1	94.9126	95.6261	441.649
31	gene_id_3100	Bin_1	389.939	295.662	2183.24
31	gene_id_3101	Bin_1	33.9599	20.8427	14.8523
31	gene_id_3102	Bin_1	59.432	46.0794	60.3673
31	gene_id_3105	Bin_1	18.4983	5.69151	19.0178
31	gene_id_3106	Bin_1	93.9562	42.0558	48.833
31	gene_id_3107	Bin_1	92.1705	65.1269	32.3304
31	gene_id_3108	Bin_1	13.8197	4.89616	23.468
31	gene_id_3110	Bin_1	14.4232	1.80737	5.953
31	gene_id_3112	Bin_1	14.2224	8.1141	12.4746
31	gene_id_3113	Bin_1	407.958	200.174	642.117
31	gene_id_3114	Bin_1	12.1776	4.23235	35.358
31	gene_id_3115	Bin_1	18.6466	5.61591	763.308
31	gene_id_3116	Bin_1	70.3239	33.1132	1081.51
31	gene_id_3117	Bin_1	2905.45	4330.12	8237.75
31	gene_id_3118	Bin_1	82.0662	14.1773	41.0273
31	gene_id_3119	Bin_1	164.586	40.8006	99.646
31	gene_id_3120	Bin_1	214.34	44.101	98.0301
31	gene_id_3121	Bin_1	194.139	37.5718	187.841
31	gene_id_3122	Bin_1	298.195	72.2451	1042.82
31	gene_id_3123	Bin_1	609.09	337.304	1222.36
31	gene_id_3124	Bin_1	2355.15	507.543	8064.52
31	gene_id_3125	Bin_1	154.965	160.594	61.5117
31	gene_id_3126	Bin_1	54.4505	97.477	207.229
31	gene_id_3127	Bin_1	35.0213	55.99	76.1565
31	gene_id_3128	Bin_1	262.399	80.1852	111.484
31	gene_id_3129	Bin_1	1184.27	489.044	443.067
31	gene_id_3130	Bin_1	1248.32	593.219	1392.37
31	gene_id_3131	Bin_1	1014.32	420.678	708.667
31	gene_id_3132	Bin_1	98.009	130.447	99.3163
31	gene_id_3133	Bin_1	121.25	105.15	84.6126
31	gene_id_3134	Bin_1	135.719	184.006	229.281
31	gene_id_3135	Bin_1	155.67	199.923	140.95
31	gene_id_3136	Bin_1	27.852	31.7543	37.1013
31	gene_id_3137	Bin_1	100.281	139.671	183.317
31	gene_id_3138	Bin_1	89.2457	87.1115	133.168
31	gene_id_3139	Bin_1	763.005	743.305	3448.07
31	gene_id_3141	Bin_1	388.136	627.424	601.303

31	gene_id_3142	Bin_1	47.646	19.87	17.1149
31	gene_id_3143	Bin_1	51.667	21.5969	46.9526
31	gene_id_3144	Bin_1	55.3512	54.2573	104.357
31	gene_id_3145	Bin_1	79.4636	267.124	166.798
31	gene_id_3146	Bin_1	110.785	100.204	279.109
31	gene_id_3147	Bin_1	241.998	367.42	1553.03
31	gene_id_3148	Bin_1	433.089	144.743	192.934
31	gene_id_3149	Bin_1	132.77	146.763	196.671
31	gene_id_3150	Bin_1	2919.94	2985.03	25775
31	gene_id_3151	Bin_1	208.348	89.1807	276.392
31	gene_id_3152	Bin_1	123.674	171.016	578.546
31	gene_id_3153	Bin_1	76.2732	91.043	270.177
31	gene_id_3154	Bin_1	183.792	152.723	34769.5
31	gene_id_3155	Bin_1	245.153	130.953	3853.16
31	gene_id_3156	Bin_1	32.2956	12.0712	182.187
31	gene_id_3157	Bin_1	43.46	36.2654	145.296
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31	gene_id_3160	Bin_1	96.9008	94.8381	399.732
31	gene_id_3161	Bin_1	194.829	252.119	308.835
31	gene_id_3162	Bin_1	904.228	77.5925	152.966
31	gene_id_3163	Bin_1	553.824	66.1395	66.2232
31	gene_id_3164	Bin_1	594.426	57.3123	77.1181
31	gene_id_3165	Bin_1	947.112	82.0732	121.507
31	gene_id_3166	Bin_1	62.3546	94.1761	631.915
31	gene_id_3167	Bin_1	1073.66	1430.73	14595.2
31	gene_id_3168	Bin_1	31.3383	17.3143	17.7163
31	gene_id_3169	Bin_1	32.7087	31.5075	53.9074
31	gene_id_3170	Bin_1	168.195	221.144	391.859
31	gene_id_3171	Bin_1	66.1998	98.8143	91.0991
31	gene_id_3172	Bin_1	83.0846	154.169	141.307
31	gene_id_3173	Bin_1	9.33738	2.95479	14.5093
31	gene_id_3174	Bin_1	45.1074	63.1097	517.598
31	gene_id_3175	Bin_1	357.787	410.178	635.895
31	gene_id_3176	Bin_1	408.998	552.168	534.056
31	gene_id_3177	Bin_1	1092.58	1708.92	5645.78
31	gene_id_3178	Bin_1	4490.73	10361.8	9438.86
31	gene_id_3179	Bin_1	42361.2	59459.3	232944
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31	gene_id_3183	Bin_1	111.661	33.8657	46.9157
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31	gene_id_3193	Bin_1	79.6278	138.563	528.282
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31	gene_id_3198	Bin_1	10.2626	0.462854	4.68556
31	gene_id_3199	Bin_1	11.9555	4.39087	5.07027
31	gene_id_3200	Bin_1	13.6522	1.3216	6.27355
31	gene_id_3202	Bin_1	15.1386	1.27065	1.39592
31	gene_id_3204	Bin_1	20.5105	3.22732	3.24022
31	gene_id_3205	Bin_1	13.7854	2.89553	9.13083
31	gene_id_3207	Bin_1	12.1933	3.17072	28.6546
31	gene_id_3209	Bin_1	15.6232	7.50605	17.21
31	gene_id_3210	Bin_1	44.9438	7.88963	78.1455
31	gene_id_3211	Bin_1	14.4249	2.37878	4.85346
31	gene_id_3212	Bin_1	41.2085	54.6246	94.6039
31	gene_id_3213	Bin_1	120.58	153.687	264.333
31	gene_id_3214	Bin_1	205.8	223.756	334.634
31	gene_id_3215	Bin_1	89.5451	64.7877	490.4
31	gene_id_3216	Bin_1	46.775	53.4326	566.17
31	gene_id_3217	Bin_1	16.813	37.0038	208.296
31	gene_id_3218	Bin_1	134.345	79.898	64.6464
31	gene_id_3219	Bin_1	79.8571	63.2109	46.1466
31	gene_id_3220	Bin_1	176.813	159.585	187.075
31	gene_id_3221	Bin_1	43.4056	67.4621	79.8299
31	gene_id_3222	Bin_1	53.822	56.2213	393.459
31	gene_id_3223	Bin_1	158.821	154.139	988.164
31	gene_id_3224	Bin_1	240.198	201.811	1067.16
31	gene_id_3225	Bin_1	29.6592	14.164	8.45519
31	gene_id_3227	Bin_1	77.3788	30.3113	21.7031
31	gene_id_3228	Bin_1	191.614	190.352	151.8
31	gene_id_3229	Bin_1	204.178	263.125	932.546
31	gene_id_3230	Bin_1	189.43	253.006	705.901
31	gene_id_3231	Bin_1	47.1137	28.8356	119.33
31	gene_id_3232	Bin_1	86.6447	69.5089	197.68
31	gene_id_3243	Bin_1	202.556	254.139	1061.01
31	gene_id_3244	Bin_1	106.587	117.926	317.837
31	gene_id_3245	Bin_1	115.497	184.631	863.369
31	gene_id_3246	Bin_1	89.4014	79.9338	257.793
31	gene_id_3247	Bin_1	75.0422	57.6911	91.6979
31	gene_id_3248	Bin_1	170.464	85.0973	113.937
31	gene_id_3249	Bin_1	75.147	111.217	151.656
31	gene_id_3250	Bin_1	264.528	424.637	820.51
31	gene_id_3251	Bin_1	181.921	353.089	655.578

31	gene_id_3252	Bin_1	244.216	197.152	207.056
31	gene_id_3253	Bin_1	80.694	86.3851	65.7337
31	gene_id_3254	Bin_1	94.8762	50.6829	62.6892
31	gene_id_3255	Bin_1	191.675	185.557	140.413
31	gene_id_3256	Bin_1	144.213	176.448	153.261
31	gene_id_3257	Bin_1	89.5147	74.9762	140.933
31	gene_id_3258	Bin_1	329.849	451.208	2878.43
31	gene_id_3259	Bin_1	65.0638	37.3995	43.8823
31	gene_id_3260	Bin_1	482.117	775.477	552.423
31	gene_id_3261	Bin_1	99.3854	154.013	441.849
31	gene_id_3262	Bin_1	1753.54	1195.6	9507.82
31	gene_id_3263	Bin_1	632.433	1003.84	2500.84
31	gene_id_3264	Bin_1	616.069	763.324	1114.65
31	gene_id_3265	Bin_1	728.1	862.806	926.573
31	gene_id_3266	Bin_1	332.461	754.529	676.812
31	gene_id_3267	Bin_1	129.667	305.009	159.419
31	gene_id_3269	Bin_1	167.112	225.353	1392.82
31	gene_id_3270	Bin_1	53.0958	57.3352	144.707
31	gene_id_3271	Bin_1	464.099	507.61	1115.95
31	gene_id_3272	Bin_1	15222.4	30105.7	21458.4
31	gene_id_3273	Bin_1	512.778	714.518	750.174
31	gene_id_3274	Bin_1	146.894	94.1914	278.474
31	gene_id_3275	Bin_1	81.3108	82.374	194.328
31	gene_id_3276	Bin_1	261.159	386.184	416.207
31	gene_id_3277	Bin_1	3092.39	2497.22	3884.94
31	gene_id_3278	Bin_1	28.7467	31.7595	88.249
31	gene_id_3279	Bin_1	2444.85	3443.5	6275.34
31	gene_id_3280	Bin_1	112.609	160.348	458.374
31	gene_id_3281	Bin_1	91.0105	112.33	146.496
31	gene_id_3282	Bin_1	188.817	174.294	181.508
31	gene_id_3283	Bin_1	384.887	801.21	3139.22
31	gene_id_3284	Bin_1	116.316	160.476	231.39
31	gene_id_3285	Bin_1	129.012	125.593	205.604
31	gene_id_3286	Bin_1	76.1901	94.1182	76.4016
31	gene_id_3287	Bin_1	139.431	158.305	187.292
31	gene_id_3288	Bin_1	132.235	96.227	40.4325
31	gene_id_3289	Bin_1	66.96	59.818	34.5177
31	gene_id_3290	Bin_1	335.812	237.011	181.936
31	gene_id_3291	Bin_1	247.599	244.101	192.917
31	gene_id_3292	Bin_1	438.065	656.586	695.085
31	gene_id_3293	Bin_1	343.699	528.005	305.417
31	gene_id_3294	Bin_1	91.8806	116.948	173.742
31	gene_id_3295	Bin_1	131.357	158.869	293.209
31	gene_id_3296	Bin_1	100.743	125.064	1403.93
31	gene_id_3297	Bin_1	852.124	1727.59	2474.11
31	gene_id_3298	Bin_1	176.857	209.436	632.457
31	gene_id_3299	Bin_1	294.748	348.151	482.781

31	gene_id_3300	Bin_1	61.1856	101.555	340.232
31	gene_id_3301	Bin_1	1601.97	1937.89	3656.19
31	gene_id_3302	Bin_1	94.8452	113.942	152.042
31	gene_id_3303	Bin_1	177.813	231.386	411.343
31	gene_id_3304	Bin_1	58618.9	38227.1	27500.3
31	gene_id_3305	Bin_1	363.334	858.493	3618.35
31	gene_id_3306	Bin_1	60.0401	65.6139	93.4388
31	gene_id_3307	Bin_1	606.176	438.378	348.329
31	gene_id_3308	Bin_1	567.146	565.013	288.199
31	gene_id_3309	Bin_1	90.23	136.453	85.5084
31	gene_id_3310	Bin_1	128.783	128.123	88.5746
31	gene_id_3311	Bin_1	140.369	195.408	133.646
31	gene_id_3312	Bin_1	285.67	416.189	181.731
31	gene_id_3313	Bin_1	195.246	253.387	144.236
31	gene_id_3314	Bin_1	243.57	258.955	123.119
31	gene_id_3315	Bin_1	241.033	175.037	123.736
31	gene_id_3316	Bin_1	246.623	218.756	219.637
31	gene_id_3317	Bin_1	126.173	140.017	513.2
31	gene_id_3318	Bin_1	134.988	115.804	504.054
31	gene_id_3319	Bin_1	63.5825	64.5463	206.199
31	gene_id_3320	Bin_1	325.152	709.583	1496.39
31	gene_id_3321	Bin_1	1816.66	1339.41	6535.06
31	gene_id_3322	Bin_1	45.2312	67.989	97.5815
31	gene_id_3323	Bin_1	103.481	145.026	220.626
31	gene_id_3324	Bin_1	143.034	235.835	172.934
31	gene_id_3325	Bin_1	56.4624	75.3221	124.418
31	gene_id_3326	Bin_1	150.302	139.611	122.215
31	gene_id_3327	Bin_1	155.005	92.1839	115.344
31	gene_id_3328	Bin_1	477.786	659.17	504.073
31	gene_id_3329	Bin_1	94.8708	112.041	176.573
31	gene_id_3330	Bin_1	4298.62	3630.02	4043.75
31	gene_id_3331	Bin_1	243.235	134.576	289.038
31	gene_id_3332	Bin_1	129.756	55.0917	92.6852
31	gene_id_3333	Bin_1	855.917	1015.59	361.884
31	gene_id_3334	Bin_1	106.096	182.168	34.7365
31	gene_id_3335	Bin_1	158.18	283.997	127.516
31	gene_id_3336	Bin_1	96.7261	124.776	57.192
31	gene_id_3337	Bin_1	80.4863	82.6677	46.2844
31	gene_id_3338	Bin_1	95.9169	107.707	295.226
31	gene_id_3339	Bin_1	67.9384	91.041	186.169
31	gene_id_3340	Bin_1	91.2743	91.4776	285.919
31	gene_id_3341	Bin_1	127.999	157.79	207.918
31	gene_id_3342	Bin_1	413.798	133.487	213.29
31	gene_id_3343	Bin_1	396.933	135.505	417.073
31	gene_id_3344	Bin_1	44.1363	44.4641	39.0838
31	gene_id_3345	Bin_1	110.099	131.21	86.7379
31	gene_id_3346	Bin_1	126.845	223.736	102.198

31	gene_id_3347	Bin_1	202.356	233.105	168.526
31	gene_id_3348	Bin_1	194.905	205.27	379.239
31	gene_id_3349	Bin_1	153.574	137.749	151.05
31	gene_id_3350	Bin_1	134.875	165.678	195.853
31	gene_id_3351	Bin_1	226.715	1173.28	5290.9
31	gene_id_3352	Bin_1	114.832	179.209	338.7
31	gene_id_3353	Bin_1	86.8328	88.0927	219.155
31	gene_id_3354	Bin_1	103.506	146.861	510.092
31	gene_id_3355	Bin_1	263.17	360.159	1402.72
31	gene_id_3356	Bin_1	183.61	197.317	163.958
31	gene_id_3357	Bin_1	227.135	51.2755	414.632
31	gene_id_3358	Bin_1	120.233	179.602	155.888
31	gene_id_3359	Bin_1	125.746	167.469	158.464
31	gene_id_3360	Bin_1	118.661	147.727	154.491
31	gene_id_3361	Bin_1	139.258	157.071	145.62
31	gene_id_3362	Bin_1	92.6996	97.1632	132.332
31	gene_id_3363	Bin_1	373.021	372.767	433.171
31	gene_id_3364	Bin_1	161.759	129.613	142.221
31	gene_id_3365	Bin_1	80.9883	99.0255	129.096
31	gene_id_3366	Bin_1	450.899	418.984	339.751
31	gene_id_3367	Bin_1	121.02	100.218	140.089
31	gene_id_3368	Bin_1	104.075	151.347	96.7031
31	gene_id_3369	Bin_1	68.2342	91.5992	99.8586
31	gene_id_3370	Bin_1	1386.41	1341.15	1044.37
31	gene_id_3371	Bin_1	94.648	308.615	131.499
31	gene_id_3372	Bin_1	64.6826	244.493	91.8628
31	gene_id_3373	Bin_1	100.225	392.386	169.173
31	gene_id_3374	Bin_1	81.7114	489.673	256.833
31	gene_id_3375	Bin_1	83.2014	481.044	200.708
31	gene_id_3376	Bin_1	71.6311	502.986	181.576
31	gene_id_3377	Bin_1	67.0756	468.667	124.398
31	gene_id_3378	Bin_1	65.3014	1021.4	579.119
31	gene_id_3379	Bin_1	55.9095	964.697	585.18
40	gene_id_4082	Bin_1	14.1465	7.80284	15.3501
40	gene_id_4083	Bin_1	827.664	743.191	44234.3
40	gene_id_4084	Bin_1	112.255	111.878	2425.16
40	gene_id_4085	Bin_1	16.4585	6.8488	52.0429
40	gene_id_4088	Bin_1	17.0689	12.5409	239.732
40	gene_id_4089	Bin_1	750.572	630.737	14728.6
40	gene_id_4090	Bin_1	122.731	153.479	12698.4
40	gene_id_4091	Bin_1	70.6769	63.5129	3114.05
40	gene_id_4092	Bin_1	40.9749	44.2906	439.368
40	gene_id_4093	Bin_1	73.2795	132.592	99.5077
40	gene_id_4094	Bin_1	100.782	91.7951	177.584
40	gene_id_4095	Bin_1	165.507	222.348	465.498
40	gene_id_4096	Bin_1	50.2531	54.1601	49.4177
40	gene_id_4097	Bin_1	16.9857	22.9056	33.4105

40	gene_id_4098	Bin_1	114.64	50.3608	17.1714
40	gene_id_4099	Bin_1	31.9369	95.7742	66.2505
40	gene_id_4100	Bin_1	90.1096	101.409	186.629
40	gene_id_4101	Bin_1	80.3955	243.281	326.071
40	gene_id_4102	Bin_1	36.3103	142.325	217.654
40	gene_id_4103	Bin_1	27.0875	121.68	243.406
40	gene_id_4104	Bin_1	51.8676	133.563	276.394
40	gene_id_4105	Bin_1	42.7307	216.339	480.355
40	gene_id_4106	Bin_1	46.1909	112.985	308.567
40	gene_id_4107	Bin_1	107.14	192.223	561.877
40	gene_id_4108	Bin_1	102.214	141.327	824.25
40	gene_id_4109	Bin_1	5796.61	14512.9	19295.3
40	gene_id_4110	Bin_1	248.772	353.01	3706.42
40	gene_id_4111	Bin_1	137.602	139.155	642.287
40	gene_id_4112	Bin_1	241.053	315.832	163.326
40	gene_id_4113	Bin_1	686.239	534.79	537.472
40	gene_id_4114	Bin_1	101.288	97.26	160.021
40	gene_id_4115	Bin_1	307.556	206.499	302.058
40	gene_id_4116	Bin_1	108.439	103.76	647.519
40	gene_id_4117	Bin_1	236.263	348.523	4077.38
40	gene_id_4118	Bin_1	75.1296	52.838	91.0378
40	gene_id_4119	Bin_1	3051.63	1389.68	1324.49
40	gene_id_4120	Bin_1	23.2089	10.3626	59.3859
40	gene_id_4121	Bin_1	41.324	66.9684	245.71
40	gene_id_4122	Bin_1	73.4844	147.026	643.423
40	gene_id_4123	Bin_1	200.777	346.811	3629.05
40	gene_id_4124	Bin_1	107.725	131.005	170.876
40	gene_id_4125	Bin_1	117.689	163.667	1010.82
40	gene_id_4126	Bin_1	174.117	221.811	1099.74
40	gene_id_4127	Bin_1	605768	584344	685021
40	gene_id_4128	Bin_1	1080.32	1174.8	363.79
40	gene_id_4129	Bin_1	73.1744	49.02	104.008
40	gene_id_4130	Bin_1	344.765	455.443	6422.44
40	gene_id_4131	Bin_1	105.987	71.9342	333.035
40	gene_id_4132	Bin_1	39.4537	29.4495	157.99
40	gene_id_4133	Bin_1	68.2895	55.5325	123.725
40	gene_id_4134	Bin_1	106.208	113.797	342.146
40	gene_id_4135	Bin_1	194.525	275.014	1697.52
40	gene_id_4136	Bin_1	54.7438	51.9758	289.414
40	gene_id_4137	Bin_1	93.0805	152.038	2367.74
40	gene_id_4138	Bin_1	374.387	749.672	15275.4
40	gene_id_4139	Bin_1	38.5916	42.0436	399.185
40	gene_id_4140	Bin_1	2254.33	7279.1	5240.79
40	gene_id_4141	Bin_1	16589.7	43955.2	78542.6
40	gene_id_4142	Bin_1	211.355	275.746	575.096
40	gene_id_4143	Bin_1	134.094	191.717	424.591
40	gene_id_4144	Bin_1	157.995	109.836	159.226

40	gene_id_4145	Bin_1	62.0692	44.8736	101.451
40	gene_id_4146	Bin_1	57.6631	31.3495	80.2208
40	gene_id_4147	Bin_1	70.7065	86.8662	154.991
40	gene_id_4148	Bin_1	40.1131	36.2511	117.255
40	gene_id_4149	Bin_1	169.121	160.172	143.822
40	gene_id_4150	Bin_1	130.921	91.9868	160.247
40	gene_id_4151	Bin_1	152.742	134.583	152.26
40	gene_id_4152	Bin_1	152.4	178.21	288.557
40	gene_id_4153	Bin_1	227.362	299.257	411.288
40	gene_id_4154	Bin_1	177.04	84.7742	177.29
40	gene_id_4155	Bin_1	78.5419	115.219	693.189
40	gene_id_4156	Bin_1	80.3133	68.2356	2465.3
40	gene_id_4157	Bin_1	190.961	169.564	5570.22
40	gene_id_4158	Bin_1	253.022	159.012	179.581
40	gene_id_4159	Bin_1	231.27	116.298	164.086
40	gene_id_4160	Bin_1	273.828	242.419	202.221
40	gene_id_4161	Bin_1	5261.21	6117.73	10717.3
40	gene_id_4162	Bin_1	31686.3	16786.3	10619
40	gene_id_4163	Bin_1	205.793	183.16	297.496
40	gene_id_4164	Bin_1	112.29	115.658	134.911
40	gene_id_4165	Bin_1	476.345	502.752	738.839
40	gene_id_4166	Bin_1	191.525	420.215	4801.23
40	gene_id_4167	Bin_1	143.022	274.473	4698.6
40	gene_id_4168	Bin_1	128.94	323.969	1398.16
40	gene_id_4168	Bin_1	38.8859	323.969	1398.16
40	gene_id_4168	Bin_1	128.94	180.992	194.312
40	gene_id_4168	Bin_1	38.8859	180.992	194.312
40	gene_id_4169	Bin_1	95.1894	168.615	321.923
40	gene_id_4170	Bin_1	197.092	212.791	295.068
40	gene_id_4171	Bin_1	406.63	487.387	613.191
40	gene_id_4172	Bin_1	469.984	600.06	2947.16
40	gene_id_4173	Bin_1	173.942	227.775	274.808
40	gene_id_4174	Bin_1	318.145	569.487	3474.51
40	gene_id_4175	Bin_1	35.3696	50.0636	155.966
40	gene_id_4176	Bin_1	92.678	118.322	226.132
40	gene_id_4177	Bin_1	58.7977	57.5803	81.8582
40	gene_id_4178	Bin_1	91.0424	69.402	91.4492
40	gene_id_4179	Bin_1	59.5389	45.4895	150.994
40	gene_id_4180	Bin_1	86.9108	83.0122	91.6061
40	gene_id_4181	Bin_1	46.4909	55.5013	56.0245
40	gene_id_4182	Bin_1	502.545	661.303	1167.91
40	gene_id_4183	Bin_1	155.559	247.289	488.56
40	gene_id_4184	Bin_1	230.132	253.232	861.143
40	gene_id_4185	Bin_1	137.575	127.204	108.069
40	gene_id_4186	Bin_1	549.346	472.208	379.415
40	gene_id_4187	Bin_1	98.0715	131.836	77.718
40	gene_id_4188	Bin_1	521.401	1067.42	3459.39

40	gene_id_4189	Bin_1	2580.52	2706.33	3157.42
40	gene_id_4190	Bin_1	98.9779	122.365	340.515
40	gene_id_4191	Bin_1	108.653	112.118	380.065
40	gene_id_4192	Bin_1	574.978	713.945	3643.43
40	gene_id_4193	Bin_1	137.687	151.125	188.319
40	gene_id_4194	Bin_1	158.845	183.732	403.131
40	gene_id_4195	Bin_1	228.844	195.542	367.375
40	gene_id_4196	Bin_1	2798.95	3360.38	514.31
40	gene_id_4197	Bin_1	208.725	206.653	300.909
40	gene_id_4198	Bin_1	792.143	993.991	1631.1
40	gene_id_4200	Bin_1	79.6212	98.1651	103.008
40	gene_id_4201	Bin_1	136.674	128.257	116.231
40	gene_id_4202	Bin_1	91.8024	153.669	284
40	gene_id_4203	Bin_1	207.629	219.428	109.5
40	gene_id_4204	Bin_1	4503.1	3846.63	7542.05
40	gene_id_4205	Bin_1	189.922	225.887	102.379
40	gene_id_4206	Bin_1	232.372	348.993	222.839
40	gene_id_4207	Bin_1	898.753	1252.07	1401.66
40	gene_id_4208	Bin_1	645.788	762.229	1330.76
43	gene_id_4420	Bin_1	35.3282	32.5006	34.8431
43	gene_id_4421	Bin_1	295.624	442.899	299.042
43	gene_id_4422	Bin_1	2322.88	1256.83	1235.27
43	gene_id_4423	Bin_1	684.494	893.351	961.366
43	gene_id_4424	Bin_1	129.528	176.837	381.251
43	gene_id_4425	Bin_1	533.328	379.352	586.79
43	gene_id_4426	Bin_1	1808.06	2010.32	1474.54
43	gene_id_4427	Bin_1	229.16	276.374	150.215
43	gene_id_4428	Bin_1	309.448	579.479	570.813
43	gene_id_4429	Bin_1	193.936	386.292	298.768
43	gene_id_4430	Bin_1	739.866	1065.53	4880.91
43	gene_id_4431	Bin_1	119.395	201.337	139.582
43	gene_id_4432	Bin_1	34.3146	29.8086	28.7675
43	gene_id_4433	Bin_1	56.0584	48.8986	70.9629
43	gene_id_4434	Bin_1	195.467	192.245	102.507
43	gene_id_4435	Bin_1	443.698	366.35	247.544
43	gene_id_4436	Bin_1	149.437	132.458	63.9056
43	gene_id_4437	Bin_1	138.157	137.826	88.096
43	gene_id_4438	Bin_1	192.342	187.489	70.6714
43	gene_id_4439	Bin_1	145.352	59.0622	137.887
43	gene_id_4439	Bin_1	32.9162	59.0622	137.887
43	gene_id_4439	Bin_1	145.352	216.134	81.6692
43	gene_id_4439	Bin_1	32.9162	216.134	81.6692
43	gene_id_4440	Bin_1	159.955	232.644	174.549
43	gene_id_4441	Bin_1	103.33	91.6001	132.207
43	gene_id_4442	Bin_1	127.208	122.474	413.509
43	gene_id_4443	Bin_1	129.877	119.215	112.543
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43	gene_id_4445	Bin_1	87.1346	134.672	340.992
43	gene_id_4446	Bin_1	423.861	479.031	10409.7
43	gene_id_4447	Bin_1	766.62	770.345	9678.22
43	gene_id_4448	Bin_1	74.8335	145.642	271.019
43	gene_id_4449	Bin_1	243.689	308.913	547.931
43	gene_id_4450	Bin_1	34.8361	25.3323	71.2395
43	gene_id_4451	Bin_1	147.445	105.86	222.382
43	gene_id_4452	Bin_1	369.645	201.99	287.973
43	gene_id_4453	Bin_1	53.4968	47.4641	177.448
43	gene_id_4454	Bin_1	190.491	301.282	3017.06
43	gene_id_4455	Bin_1	300.862	475.839	4558.01
43	gene_id_4456	Bin_1	105.04	250.323	2145.22
43	gene_id_4457	Bin_1	349.02	358.305	144.449
43	gene_id_4459	Bin_1	398.911	340.194	152.399
43	gene_id_4460	Bin_1	175.361	214.983	85.8888
43	gene_id_4461	Bin_1	294.993	201.341	339.478
43	gene_id_4462	Bin_1	157.03	152.719	756.525
43	gene_id_4463	Bin_1	11.0594	130.875	327.41
43	gene_id_4464	Bin_1	176.933	196.945	744.563
43	gene_id_4465	Bin_1	50.033	51.7431	50.349
43	gene_id_4466	Bin_1	71.7811	106.745	439.428
43	gene_id_4467	Bin_1	46.0809	53.2946	140.779
43	gene_id_4468	Bin_1	556.456	921.645	1104.91
43	gene_id_4469	Bin_1	55.829	34.8653	56.0273
43	gene_id_4470	Bin_1	283.613	324.647	160.226
43	gene_id_4471	Bin_1	257.656	169.502	96.9416
43	gene_id_4472	Bin_1	201.018	327.234	318.909
43	gene_id_4473	Bin_1	125.336	151.355	188.094
43	gene_id_4474	Bin_1	233.422	155.709	117.19
43	gene_id_4475	Bin_1	74.7903	92.7	53.4387
43	gene_id_4476	Bin_1	124.554	127.252	114.121
43	gene_id_4477	Bin_1	665.583	981.727	902.608
43	gene_id_4478	Bin_1	65.3297	109.219	360.723
43	gene_id_4479	Bin_1	342.706	576.179	822.641
43	gene_id_4480	Bin_1	610.71	454.613	831.746
43	gene_id_4481	Bin_1	77.15	113.87	212.851
43	gene_id_4482	Bin_1	250.718	368.503	340.606
43	gene_id_4483	Bin_1	64.0604	40.9695	27.109
43	gene_id_4484	Bin_1	80.5438	86.5144	59.8367
43	gene_id_4485	Bin_1	284.195	216.296	170.603
43	gene_id_4486	Bin_1	143.337	134.296	79.0825
43	gene_id_4487	Bin_1	216.193	252.872	191.962
43	gene_id_4488	Bin_1	85.0407	123.007	100.467
43	gene_id_4489	Bin_1	82.7856	93.5348	87.2701
43	gene_id_4490	Bin_1	59.7217	109.803	655.858
43	gene_id_4491	Bin_1	103.578	121.855	120.199
43	gene_id_4492	Bin_1	61.312	112.749	68.748

43	gene_id_4493	Bin_1	35.9014	93.0205	75.6695
43	gene_id_4494	Bin_1	51.1071	105.988	131.735
43	gene_id_4495	Bin_1	63.7302	76.1564	120.893
43	gene_id_4496	Bin_1	112.071	111.401	179.236
43	gene_id_4497	Bin_1	88.3871	132.441	64.9258
43	gene_id_4498	Bin_1	65.7955	100.586	174.579
43	gene_id_4499	Bin_1	146.794	159.256	123.046
43	gene_id_4500	Bin_1	225.733	195.898	110.618
43	gene_id_4501	Bin_1	455.355	476.129	305.075
43	gene_id_4502	Bin_1	56.6512	104.153	751.806
43	gene_id_4503	Bin_1	193.177	236.816	234.665
43	gene_id_4504	Bin_1	130.785	147.563	179.075
43	gene_id_4505	Bin_1	139.33	151.768	256.747
43	gene_id_4506	Bin_1	322.788	482.249	773.514
43	gene_id_4507	Bin_1	131.675	230.51	2350.04
43	gene_id_4508	Bin_1	1215.14	1236.5	1496.54
43	gene_id_4509	Bin_1	215.566	149.398	190.957
43	gene_id_4510	Bin_1	14.3454	13.5051	17.0849
43	gene_id_4511	Bin_1	16.5755	33.6793	59.3869
43	gene_id_4512	Bin_1	19.5576	17.5607	754.08
43	gene_id_4513	Bin_1	18.8735	30.0191	149.288
43	gene_id_4514	Bin_1	13.7555	63.9112	48.5687
43	gene_id_4515	Bin_1	25.873	104.234	110.015
43	gene_id_4516	Bin_1	31.0812	141.103	77.9099
43	gene_id_4517	Bin_1	17.1577	218.68	95.1033
43	gene_id_4519	Bin_1	279.647	249.194	176.869
43	gene_id_4520	Bin_1	261.272	372.444	428.077
43	gene_id_4521	Bin_1	13.0745	7.38347	27.3449
43	gene_id_4523	Bin_1	215.109	33.5292	55.2267
43	gene_id_4524	Bin_1	13.5537	1.13894	4.86859
43	gene_id_4528	Bin_1	9.22663	0.581375	3.83262
43	gene_id_4530	Bin_1	8.70222	1.4976	1.40933
43	gene_id_4536	Bin_1	199.185	129.778	252.384
43	gene_id_4537	Bin_1	138.285	126.518	64.7132
43	gene_id_4538	Bin_1	63.1879	117.172	65.0417
43	gene_id_4539	Bin_1	39.2097	50.0054	395.115
43	gene_id_4540	Bin_1	50.5553	54.141	180.261
47	gene_id_4859	Bin_1	1171.42	1284.81	831.434
47	gene_id_4860	Bin_1	688.651	947.121	4876.92
47	gene_id_4861	Bin_1	937.141	970.576	2455.37
47	gene_id_4862	Bin_1	428.734	496.194	969.5
47	gene_id_4863	Bin_1	315.353	341.093	246.209
47	gene_id_4864	Bin_1	418.735	468.2	318.96
47	gene_id_4865	Bin_1	571.142	560.548	508.168
47	gene_id_4866	Bin_1	40.8387	34.5699	195.692
47	gene_id_4867	Bin_1	59.5478	120.143	264.5
47	gene_id_4868	Bin_1	113.735	177.886	804.338

47	gene_id_4869	Bin_1	301.844	520.695	883.558
47	gene_id_4870	Bin_1	184.234	194.341	158.401
47	gene_id_4871	Bin_1	31.1963	42.4457	89.2097
47	gene_id_4872	Bin_1	65.6345	92.1183	186.683
47	gene_id_4873	Bin_1	48.3704	66.5458	107.879
47	gene_id_4874	Bin_1	236.386	340.358	168.96
47	gene_id_4875	Bin_1	419.773	409.378	1504.51
47	gene_id_4876	Bin_1	12124.3	16268.8	8844.77
47	gene_id_4877	Bin_1	365.868	1044.09	1400.85
47	gene_id_4878	Bin_1	245.631	132.672	94.2777
47	gene_id_4879	Bin_1	66.9179	109.327	45.7922
47	gene_id_4884	Bin_1	54.9125	80.9934	48.321
47	gene_id_4885	Bin_1	87.4409	165.245	131.152
47	gene_id_4886	Bin_1	387.868	473.106	1147.08
47	gene_id_4887	Bin_1	235.474	691.866	2196.13
47	gene_id_4889	Bin_1	49.6314	21.7889	114.991
47	gene_id_4890	Bin_1	139.24	165.511	219.242
47	gene_id_4891	Bin_1	104.573	116.035	110.337
47	gene_id_4892	Bin_1	67.4007	77.1074	76.6504
47	gene_id_4893	Bin_1	57.5212	58.9128	44.1207
47	gene_id_4894	Bin_1	191.314	234.185	175.175
47	gene_id_4895	Bin_1	59.3312	84.4816	58.8411
47	gene_id_4896	Bin_1	31.6897	32.7296	19.1452
47	gene_id_4897	Bin_1	121.731	120.058	112.678
47	gene_id_4898	Bin_1	20.3818	8.37608	14.2923
47	gene_id_4899	Bin_1	133.227	180.299	77.5255
47	gene_id_4900	Bin_1	417.455	530.853	267.893
47	gene_id_4901	Bin_1	1991.21	2797.36	8485.64
47	gene_id_4902	Bin_1	4153.16	5377.84	3482.35
47	gene_id_4903	Bin_1	278.28	315.709	558.47
47	gene_id_4904	Bin_1	51.5702	48.6614	229.852
47	gene_id_4905	Bin_1	131.282	99.1581	263.39
47	gene_id_4906	Bin_1	14.436	11.6383	35.7416
47	gene_id_4907	Bin_1	55.3391	31.2649	97.012
47	gene_id_4908	Bin_1	52.603	84.8213	198.892
47	gene_id_4909	Bin_1	38.2639	61.6999	196.023
47	gene_id_4910	Bin_1	119.514	194.293	195.131
47	gene_id_4911	Bin_1	691.947	950.105	525.881
47	gene_id_4912	Bin_1	7073.91	9678.81	9477.84
47	gene_id_4913	Bin_1	1067.07	822.143	1041.03
47	gene_id_4914	Bin_1	461.465	540.83	440.904
47	gene_id_4915	Bin_1	467.435	542.267	451.393
47	gene_id_4916	Bin_1	531.906	773.77	558.369
47	gene_id_4917	Bin_1	170.646	135.949	160.472
47	gene_id_4918	Bin_1	638.562	727.075	515.022
47	gene_id_4919	Bin_1	317.442	330.311	1270.79
47	gene_id_4920	Bin_1	328.432	250.318	535.582

47	gene_id_4921	Bin_1	195.318	302.494	911.317
47	gene_id_4922	Bin_1	71.1117	87.0807	68.4299
47	gene_id_4923	Bin_1	172.561	370.267	433.661
47	gene_id_4924	Bin_1	213.413	495.943	710.275
47	gene_id_4925	Bin_1	92.572	146.204	139.886
47	gene_id_4926	Bin_1	163.156	126.301	177.661
47	gene_id_4927	Bin_1	37.5508	40.2165	38.6556
47	gene_id_4928	Bin_1	11277.6	13567.3	20602.9
47	gene_id_4929	Bin_1	798.183	1192.92	720.741
47	gene_id_4930	Bin_1	220.391	197.644	168.382
47	gene_id_4931	Bin_1	237.659	270.915	316.446
47	gene_id_4932	Bin_1	253.731	262.329	142.452
47	gene_id_4933	Bin_1	100.794	71.5875	112.415
47	gene_id_4934	Bin_1	95.1861	90.8108	86.9279
47	gene_id_4935	Bin_1	139.301	140.381	189.618
47	gene_id_4936	Bin_1	163.241	178.233	181.101
47	gene_id_4937	Bin_1	183.131	152.628	153.041
47	gene_id_4938	Bin_1	242.941	384.713	246.892
47	gene_id_4939	Bin_1	3040.42	4603.92	7703.15
47	gene_id_4940	Bin_1	144.93	139.273	837.526
47	gene_id_4941	Bin_1	24.8783	33.6332	47.797
47	gene_id_4942	Bin_1	108.901	117.88	164.778
47	gene_id_4943	Bin_1	136.961	178.026	286.5
47	gene_id_4944	Bin_1	77.1396	63.513	51.2272
47	gene_id_4945	Bin_1	145.398	140.054	97.1933
47	gene_id_4946	Bin_1	36.0466	35.619	53.2162
47	gene_id_4947	Bin_1	84.9592	113.183	152.702
47	gene_id_4948	Bin_1	23.6906	21.2773	35.8271
47	gene_id_4949	Bin_1	515.571	767.16	663.34
47	gene_id_4950	Bin_1	147.893	294.985	493.938
47	gene_id_4951	Bin_1	80.621	112.003	386.783
47	gene_id_4952	Bin_1	116.17	274.537	2272.76
47	gene_id_4953	Bin_1	103.063	191.388	624.004
47	gene_id_4954	Bin_1	965.608	1785.53	15933.4
47	gene_id_4955	Bin_1	560.499	893.562	8943.62
47	gene_id_4956	Bin_1	2140.68	3517.95	12217.4
47	gene_id_4957	Bin_1	331.093	413.249	1029.15
47	gene_id_4958	Bin_1	162.462	144.04	121.533
47	gene_id_4959	Bin_1	99.0982	162.367	142.674
47	gene_id_4960	Bin_1	40.7205	318.801	32.2663
47	gene_id_4961	Bin_1	64.4554	539.264	106.629
47	gene_id_4962	Bin_1	45.6777	164.497	43.6418
47	gene_id_4963	Bin_1	85.1743	472.539	88.9679
47	gene_id_4964	Bin_1	147.546	185.38	390.971
47	gene_id_4965	Bin_1	138.104	193.987	294.293
47	gene_id_4966	Bin_1	105.729	169.647	115.968
47	gene_id_4967	Bin_1	496.514	647.904	298.429

47	gene_id_4968	Bin_1	166.834	203.182	129.903
47	gene_id_4969	Bin_1	229.594	430.532	323.194
47	gene_id_4970	Bin_1	87.1503	309.739	165.559
47	gene_id_4971	Bin_1	101.542	154.689	130.115
47	gene_id_4972	Bin_1	137.447	74.5817	64.3046
47	gene_id_4973	Bin_1	235.43	50.2256	604.655
47	gene_id_4974	Bin_1	157.474	32.3972	51.9606
47	gene_id_4975	Bin_1	333.697	58.2897	52.1976
47	gene_id_4976	Bin_1	595.263	88.1376	73.9728
47	gene_id_4977	Bin_1	464.322	60.4201	98.0479
47	gene_id_4978	Bin_1	271.308	60.9538	45.7759
47	gene_id_4979	Bin_1	327.548	54.3742	55.6617
47	gene_id_4980	Bin_1	341.136	57.1217	66.6582
47	gene_id_4981	Bin_1	419.39	68.0119	72.3292
47	gene_id_4982	Bin_1	380.435	71.8014	131.87
47	gene_id_4983	Bin_1	1256.35	261.681	492.323
47	gene_id_4984	Bin_1	95.1928	159.938	676.929
47	gene_id_4985	Bin_1	188.4	246.39	342.583
47	gene_id_4986	Bin_1	192.672	250.056	158.407
47	gene_id_4987	Bin_1	53.2337	80.8486	88.5353
47	gene_id_4988	Bin_1	736.382	579.106	1854.88
47	gene_id_4989	Bin_1	446.4	294.899	422.626
47	gene_id_4990	Bin_1	79.2632	79.9021	168.944
47	gene_id_4991	Bin_1	36.5208	43.8439	80.4665
47	gene_id_4992	Bin_1	198.014	268.729	574.758
47	gene_id_4993	Bin_1	239.52	303.047	1025.92
47	gene_id_4994	Bin_1	61.8352	104.112	265.548
47	gene_id_4995	Bin_1	17.1954	27.1911	35.4576
47	gene_id_4996	Bin_1	18.13	19.6427	30.9657
47	gene_id_4997	Bin_1	330.174	452.134	291.537
47	gene_id_4998	Bin_1	269.382	292.173	528.938
47	gene_id_4999	Bin_1	37.6719	22.4778	58.5438
47	gene_id_5000	Bin_1	27.8175	30.6044	73.0867
47	gene_id_5001	Bin_1	584.433	522.924	245.534
47	gene_id_5002	Bin_1	98.0268	48.0967	73.7443
47	gene_id_5003	Bin_1	147.921	226.073	387.761
47	gene_id_5004	Bin_1	98.1654	107.596	98.1974
47	gene_id_5005	Bin_1	106.875	78.1387	61.8453
47	gene_id_5006	Bin_1	125.858	101.176	96.3869
47	gene_id_5007	Bin_1	66.2347	64.8489	63.3283
47	gene_id_5008	Bin_1	64.7892	56.3921	48.3942
47	gene_id_5009	Bin_1	48.4985	78.8422	72.324
47	gene_id_5010	Bin_1	78.5047	120.005	100.894
47	gene_id_5011	Bin_1	80.169	194.812	105.043
47	gene_id_5012	Bin_1	76.4265	73.8357	98.2677
47	gene_id_5013	Bin_1	51.4311	65.4129	186.643
47	gene_id_5014	Bin_1	45.7839	63.0664	77.8869

47	gene_id_5015	Bin_1	111.626	170.128	152.875
47	gene_id_5016	Bin_1	328.087	108.109	361.098
47	gene_id_5017	Bin_1	2051.03	1255.18	5038.27
47	gene_id_5018	Bin_1	130.334	236.207	168.82
47	gene_id_5019	Bin_1	158.723	247.499	290.112
6	gene_id_502	Bin_1	272.283	379.333	1043.23
47	gene_id_5020	Bin_1	197.1	286.003	618.944
47	gene_id_5021	Bin_1	83.0568	173.209	614.133
47	gene_id_5022	Bin_1	282.815	532.281	704.531
47	gene_id_5023	Bin_1	537.328	592.722	537.814
47	gene_id_5024	Bin_1	93.8877	139.136	110.138
47	gene_id_5025	Bin_1	96.9351	106.693	66.0739
47	gene_id_5026	Bin_1	73.033	90.0447	56.236
47	gene_id_5027	Bin_1	118.712	171.001	207.794
47	gene_id_5028	Bin_1	257.482	318.994	482.318
47	gene_id_5029	Bin_1	184.883	97.0682	109.259
6	gene_id_503	Bin_1	192.494	251.768	2627.8
47	gene_id_5030	Bin_1	96.2876	62.7873	46.4397
47	gene_id_5031	Bin_1	204.519	128.262	162.042
47	gene_id_5032	Bin_1	102.425	82.9836	74.3705
47	gene_id_5033	Bin_1	349.666	200.026	201.824
47	gene_id_5034	Bin_1	201.229	187.378	129.804
47	gene_id_5035	Bin_1	97.0355	152.438	483.963
47	gene_id_5036	Bin_1	183.38	327.865	176.813
47	gene_id_5037	Bin_1	162.752	258.133	208.172
47	gene_id_5038	Bin_1	195.483	260.848	252.699
47	gene_id_5039	Bin_1	313.503	454.217	490.521
6	gene_id_504	Bin_1	180.543	172.393	719.033
47	gene_id_5040	Bin_1	171.08	220.148	328.023
47	gene_id_5041	Bin_1	152.27	146.223	454.237
47	gene_id_5042	Bin_1	134.235	180.598	260.206
47	gene_id_5043	Bin_1	129.906	171.319	316.187
47	gene_id_5044	Bin_1	86.3001	98.166	160.306
47	gene_id_5045	Bin_1	161.815	245.201	384.645
47	gene_id_5046	Bin_1	90.1648	71.9894	102.056
47	gene_id_5047	Bin_1	75.7857	112.914	153.69
47	gene_id_5048	Bin_1	136.156	181.728	193.975
47	gene_id_5049	Bin_1	138.945	219.252	2026.84
6	gene_id_505	Bin_1	171.375	231.777	238.905
47	gene_id_5050	Bin_1	61.4926	129.457	822.508
47	gene_id_5051	Bin_1	114.466	161.197	204.964
47	gene_id_5052	Bin_1	49.1839	63.7991	75.1745
47	gene_id_5053	Bin_1	80.6637	175.546	538.588
47	gene_id_5054	Bin_1	107.517	236.817	1998.52
47	gene_id_5055	Bin_1	54.2795	117.752	165.337
47	gene_id_5056	Bin_1	99.9218	170.398	596.872
47	gene_id_5057	Bin_1	155.101	235.418	937.097

47	gene_id_5058	Bin_1	35.7069	38.6158	62.9482
47	gene_id_5059	Bin_1	42.6324	78.8304	121.697
6	gene_id_506	Bin_1	163.283	245.243	364.245
47	gene_id_5060	Bin_1	17.5405	19.305	68.3085
47	gene_id_5061	Bin_1	14.2321	12.7979	63.2584
47	gene_id_5062	Bin_1	46.4339	50.8776	203.294
47	gene_id_5063	Bin_1	17.0586	20.215	107.8
47	gene_id_5064	Bin_1	908.103	1518.75	2715.57
47	gene_id_5065	Bin_1	61.7792	89.4957	60.9006
47	gene_id_5066	Bin_1	93.7266	100.582	116.644
47	gene_id_5067	Bin_1	90.0655	128.518	129.097
47	gene_id_5068	Bin_1	70.858	108.434	80.3964
47	gene_id_5069	Bin_1	208.848	322.926	300.295
6	gene_id_507	Bin_1	246.988	345.094	640.695
47	gene_id_5070	Bin_1	112.606	110.551	224.657
47	gene_id_5071	Bin_1	76.7958	107.807	109.951
47	gene_id_5072	Bin_1	94.655	104.991	130.544
47	gene_id_5073	Bin_1	61.2978	51.0074	48.4225
47	gene_id_5074	Bin_1	119.116	152.528	104.928
47	gene_id_5075	Bin_1	119.443	191.889	111.649
47	gene_id_5076	Bin_1	86.7178	121.34	57.5854
47	gene_id_5077	Bin_1	86.7952	130.672	180.578
47	gene_id_5078	Bin_1	225.323	230.604	240.635
47	gene_id_5079	Bin_1	162.892	203.615	419.178
6	gene_id_508	Bin_1	163.724	136.088	176.945
47	gene_id_5080	Bin_1	47.379	48.9888	41.6767
47	gene_id_5081	Bin_1	56.5582	77.3624	104.511
47	gene_id_5082	Bin_1	112.492	173.745	190.778
47	gene_id_5083	Bin_1	81.7648	138.402	305.275
47	gene_id_5084	Bin_1	93.9157	172.841	1387.41
47	gene_id_5085	Bin_1	28.7102	23.7474	27.5475
47	gene_id_5086	Bin_1	51.9539	71.7483	145.889
47	gene_id_5087	Bin_1	87.9655	80.5366	98.4149
47	gene_id_5088	Bin_1	82.2892	54.7292	77.0906
47	gene_id_5089	Bin_1	449.272	127.207	551.77
6	gene_id_509	Bin_1	141.28	129.075	257.085
47	gene_id_5090	Bin_1	19.9821	9.15842	44.199
47	gene_id_5091	Bin_1	103.05	156.509	148.367
47	gene_id_5092	Bin_1	126.048	177.654	495.032
47	gene_id_5093	Bin_1	1753.06	1608.48	2526.77
47	gene_id_5094	Bin_1	397.328	193.543	97.8487
47	gene_id_5095	Bin_1	238.688	284.03	182.163
47	gene_id_5096	Bin_1	66.7937	82.9174	682.899
47	gene_id_5097	Bin_1	307.17	593.417	1712.06
47	gene_id_5098	Bin_1	98.3265	107.015	112.413
47	gene_id_5099	Bin_1	100.218	91.5983	88.9379
6	gene_id_510	Bin_1	311.141	359.803	753.86

47	gene_id_5100	Bin_1	221.703	284.908	332.716
47	gene_id_5101	Bin_1	88.1384	163.117	143.179
47	gene_id_5102	Bin_1	65.4919	82.9852	153.303
47	gene_id_5103	Bin_1	98.9972	106.694	108.918
47	gene_id_5104	Bin_1	331.147	721.476	1492.34
47	gene_id_5105	Bin_1	158.132	247.823	488.048
47	gene_id_5106	Bin_1	257.547	452.121	259.099
47	gene_id_5107	Bin_1	280.826	305.783	604.004
47	gene_id_5108	Bin_1	5166.21	6425.38	10544.2
47	gene_id_5109	Bin_1	848.764	715.009	743.101
6	gene_id_511	Bin_1	40.5051	55.1327	496.948
47	gene_id_5110	Bin_1	113.126	116.826	323.892
47	gene_id_5111	Bin_1	33.763	15.2065	77.0113
47	gene_id_5112	Bin_1	177.316	167.28	212.123
47	gene_id_5113	Bin_1	183.543	183.749	119.481
47	gene_id_5114	Bin_1	153.474	167.387	119.665
47	gene_id_5115	Bin_1	181.034	147.736	107.018
47	gene_id_5116	Bin_1	123.667	127.461	423.115
47	gene_id_5117	Bin_1	135.66	196.111	525.118
47	gene_id_5118	Bin_1	147.772	144.181	196.323
47	gene_id_5119	Bin_1	364.061	231.339	297.823
6	gene_id_512	Bin_1	53.7234	53.2426	225.517
47	gene_id_5120	Bin_1	68.435	79.6873	67.5206
47	gene_id_5121	Bin_1	998.867	169.085	3149.63
47	gene_id_5122	Bin_1	894.6	994.651	801.981
47	gene_id_5123	Bin_1	53.872	65.4797	389.826
47	gene_id_5124	Bin_1	167.723	166.165	135.528
47	gene_id_5125	Bin_1	173.89	190.631	156.165
47	gene_id_5126	Bin_1	196.799	266.378	582.868
47	gene_id_5127	Bin_1	149.163	182.971	179.083
47	gene_id_5128	Bin_1	92.3231	127.525	127.93
47	gene_id_5129	Bin_1	310.778	538.314	424.022
6	gene_id_513	Bin_1	72.5992	124.858	271.489
47	gene_id_5130	Bin_1	171.948	205.419	279.955
47	gene_id_5131	Bin_1	162.918	268.959	87.4533
47	gene_id_5132	Bin_1	110.052	132.432	440.238
47	gene_id_5133	Bin_1	75.9011	133.925	88.6128
47	gene_id_5134	Bin_1	63.4127	86.2867	96.7422
47	gene_id_5135	Bin_1	73.946	103.254	84.5339
47	gene_id_5136	Bin_1	76.957	119.051	393.323
47	gene_id_5137	Bin_1	107.506	181.061	274.35
47	gene_id_5138	Bin_1	98.5541	110.012	149.75
47	gene_id_5139	Bin_1	82.1279	105.186	143.918
6	gene_id_514	Bin_1	104.036	202.598	374.809
47	gene_id_5140	Bin_1	335.398	425.494	687.199
47	gene_id_5141	Bin_1	154.09	175.184	352.515
47	gene_id_5142	Bin_1	79.1189	115.692	84.4441

47	gene_id_5143	Bin_1	83.0087	139.49	309.997
47	gene_id_5144	Bin_1	120.215	175.316	366.098
47	gene_id_5145	Bin_1	736.922	1473.71	882.746
47	gene_id_5145	Bin_1	421.286	1473.71	882.746
47	gene_id_5145	Bin_1	736.922	797.459	498.299
47	gene_id_5145	Bin_1	421.286	797.459	498.299
47	gene_id_5146	Bin_1	371.417	599.891	869.838
47	gene_id_5147	Bin_1	346.919	484.103	562.078
47	gene_id_5148	Bin_1	334.864	468.848	518.747
47	gene_id_5149	Bin_1	338.088	473.436	591.634
6	gene_id_515	Bin_1	68.7274	128.519	147.703
47	gene_id_5150	Bin_1	508.334	719.533	824.013
47	gene_id_5151	Bin_1	286.419	364.875	352.684
47	gene_id_5152	Bin_1	431.932	396.322	396.431
47	gene_id_5153	Bin_1	253.62	394.185	5559.4
47	gene_id_5154	Bin_1	211.29	190.504	347.088
47	gene_id_5155	Bin_1	1213.63	1088.25	19547
47	gene_id_5156	Bin_1	107.1	75.5282	193.52
47	gene_id_5157	Bin_1	95.8946	95.4073	231.969
47	gene_id_5158	Bin_1	119.839	157.887	396.367
47	gene_id_5159	Bin_1	95.0103	64.8755	163.533
6	gene_id_516	Bin_1	99.0475	83.0886	110.318
47	gene_id_5160	Bin_1	48.7387	148.267	319.701
47	gene_id_5161	Bin_1	23.7076	121.244	195.674
47	gene_id_5162	Bin_1	42.2174	261.795	328.47
47	gene_id_5163	Bin_1	92.415	624.455	667.08
47	gene_id_5164	Bin_1	51.6636	366.332	437.589
47	gene_id_5165	Bin_1	89.6185	3107.94	2669.17
47	gene_id_5166	Bin_1	272.954	225.102	150.945
47	gene_id_5167	Bin_1	47.3826	33.0625	37.5852
47	gene_id_5168	Bin_1	76.2206	121.775	352.821
47	gene_id_5169	Bin_1	143.266	218.716	126.03
6	gene_id_517	Bin_1	152.784	212.629	263.238
47	gene_id_5170	Bin_1	93.4528	63.6867	101.011
47	gene_id_5171	Bin_1	129.49	163.011	182.181
47	gene_id_5172	Bin_1	147.663	188.675	468.869
47	gene_id_5173	Bin_1	165.908	266.464	335.664
47	gene_id_5174	Bin_1	165.668	174.064	939.946
47	gene_id_5175	Bin_1	2368.87	2701.56	2908.23
47	gene_id_5176	Bin_1	209.725	311.456	240.578
47	gene_id_5177	Bin_1	259.46	429.375	306.553
47	gene_id_5178	Bin_1	296.331	302.368	137.478
47	gene_id_5179	Bin_1	80.2086	37.0033	56.4189
6	gene_id_518	Bin_1	280.753	408.172	618.99
47	gene_id_5180	Bin_1	45.2377	40.0948	39.794
47	gene_id_5181	Bin_1	119.504	65.3843	61.1697
47	gene_id_5182	Bin_1	187.131	142.811	516.14

47	gene_id_5183	Bin_1	120.38	97.6346	70.5291
47	gene_id_5184	Bin_1	115.042	127.205	65.7063
47	gene_id_5185	Bin_1	129.476	197.707	380.343
47	gene_id_5186	Bin_1	218.102	264.799	428.93
47	gene_id_5187	Bin_1	23.3652	15.3805	34.2808
47	gene_id_5188	Bin_1	107.593	106.496	88.1143
47	gene_id_5189	Bin_1	94.5955	297.76	256.355
6	gene_id_519	Bin_1	182.761	172.414	181.934
47	gene_id_5190	Bin_1	148.87	340.75	370.168
47	gene_id_5191	Bin_1	23.4661	45.1064	55.8195
47	gene_id_5192	Bin_1	73.425	101.297	107.523
47	gene_id_5193	Bin_1	80.4696	81.626	143.345
47	gene_id_5194	Bin_1	194.553	270.666	2182.76
47	gene_id_5195	Bin_1	673.821	449.999	1244.26
47	gene_id_5196	Bin_1	348.738	307.111	541.058
47	gene_id_5197	Bin_1	380.479	413.769	343.451
47	gene_id_5198	Bin_1	486.246	588.685	711.885
47	gene_id_5199	Bin_1	33.8454	54.7893	118.052
6	gene_id_520	Bin_1	48.9011	42.4404	47.7166
47	gene_id_5200	Bin_1	80.9229	156.524	1190.88
47	gene_id_5201	Bin_1	216.231	279.372	2014.98
47	gene_id_5202	Bin_1	844.252	764.842	2409.11
47	gene_id_5203	Bin_1	133.243	131.569	121.029
47	gene_id_5204	Bin_1	153.881	163.065	326.374
47	gene_id_5205	Bin_1	147.147	249.101	725.709
47	gene_id_5206	Bin_1	104.368	139.398	124.444
47	gene_id_5207	Bin_1	129.838	202.526	160.056
47	gene_id_5208	Bin_1	47030.3	77903	38138.5
47	gene_id_5209	Bin_1	143.012	245.592	105.601
6	gene_id_521	Bin_1	91.1884	133.221	25.4279
47	gene_id_5210	Bin_1	54.7407	91.211	43.6233
47	gene_id_5211	Bin_1	163.753	225.718	200.321
47	gene_id_5212	Bin_1	169.89	279.64	260.856
47	gene_id_5213	Bin_1	52.1828	65.2569	73.6224
47	gene_id_5214	Bin_1	352.632	507.956	369.037
47	gene_id_5215	Bin_1	77.4434	88.7441	93.2256
47	gene_id_5216	Bin_1	208.173	180.162	164.884
47	gene_id_5217	Bin_1	241.445	351.357	192.693
47	gene_id_5218	Bin_1	100.077	127.32	75.6088
47	gene_id_5219	Bin_1	100.144	74.1295	95.4925
6	gene_id_522	Bin_1	67.2901	55.706	38.7671
47	gene_id_5220	Bin_1	158.078	144.083	232.689
47	gene_id_5221	Bin_1	324.656	402.844	385.296
47	gene_id_5222	Bin_1	116.102	144.623	931.873
47	gene_id_5223	Bin_1	61.3506	111.626	365.947
47	gene_id_5224	Bin_1	134.685	148.633	575.966
47	gene_id_5225	Bin_1	266.053	383.975	375.392

47	gene_id_5226	Bin_1	1709.6	1958.4	1657.27
47	gene_id_5227	Bin_1	115.038	142.033	188.631
47	gene_id_5228	Bin_1	75.6456	77.9483	86.1351
47	gene_id_5229	Bin_1	58.8105	51.0656	63.2213
6	gene_id_523	Bin_1	299.918	306.537	576.639
47	gene_id_5230	Bin_1	44.0778	28.4309	114.885
47	gene_id_5231	Bin_1	684.308	403.323	727.185
47	gene_id_5232	Bin_1	122.724	189.049	385.312
47	gene_id_5233	Bin_1	73.2355	98.7136	112.073
47	gene_id_5234	Bin_1	46.7156	54.5395	50.4853
47	gene_id_5235	Bin_1	174.458	103.384	128.938
47	gene_id_5236	Bin_1	107.916	136.954	165.088
47	gene_id_5237	Bin_1	85.3727	107.057	131.548
47	gene_id_5238	Bin_1	75.7251	88.6317	100.778
47	gene_id_5239	Bin_1	81.8696	112.044	450.83
6	gene_id_524	Bin_1	120.675	195.668	132.62
47	gene_id_5240	Bin_1	89.5374	151.716	1056.33
47	gene_id_5241	Bin_1	2380.96	2198.96	1149.24
47	gene_id_5242	Bin_1	2482.61	1961.74	2762.47
47	gene_id_5243	Bin_1	107.177	95.691	167.042
47	gene_id_5244	Bin_1	486.957	146.44	181.817
47	gene_id_5245	Bin_1	331.804	143.985	135.316
47	gene_id_5246	Bin_1	320.248	138.445	129.292
47	gene_id_5247	Bin_1	300.054	145.781	171.836
47	gene_id_5248	Bin_1	575.736	188.719	400.278
47	gene_id_5249	Bin_1	562.523	257.519	239.942
6	gene_id_525	Bin_1	655.54	890.685	452.557
47	gene_id_5250	Bin_1	1074.38	382.689	363.17
47	gene_id_5251	Bin_1	743.801	354.016	183.502
47	gene_id_5252	Bin_1	3344.48	1549.32	822.257
47	gene_id_5253	Bin_1	219.048	357.546	468.759
47	gene_id_5254	Bin_1	314.134	323.744	207.143
47	gene_id_5255	Bin_1	89.1243	82.5738	63.3724
47	gene_id_5256	Bin_1	118.206	115.901	112.707
47	gene_id_5257	Bin_1	132.575	150.182	217.395
47	gene_id_5258	Bin_1	80.8994	110.36	227.297
47	gene_id_5259	Bin_1	373.401	233.813	363.144
6	gene_id_526	Bin_1	99.0322	196.513	1963.18
47	gene_id_5260	Bin_1	48.6852	34.8862	96.9422
47	gene_id_5261	Bin_1	57.4608	62.4959	96.7623
47	gene_id_5262	Bin_1	165.823	304.416	363.101
47	gene_id_5263	Bin_1	51.8454	70.3884	74.9996
47	gene_id_5264	Bin_1	77.6167	136.934	153.275
47	gene_id_5265	Bin_1	123.474	145.735	209.281
47	gene_id_5266	Bin_1	378.066	419.604	756.679
47	gene_id_5267	Bin_1	152.55	263.666	213.676
47	gene_id_5268	Bin_1	236.55	304.156	184.954

47	gene_id_5269	Bin_1	106.958	165.28	108.503
6	gene_id_527	Bin_1	133.019	205.148	805.258
47	gene_id_5270	Bin_1	169.312	315.53	757.805
47	gene_id_5271	Bin_1	143.416	130.8	354.656
47	gene_id_5272	Bin_1	130.621	141.777	239.352
47	gene_id_5273	Bin_1	237.172	382.999	365.188
47	gene_id_5274	Bin_1	112.736	143.93	118.748
47	gene_id_5275	Bin_1	170.739	178.935	317.805
47	gene_id_5276	Bin_1	71.6065	93.1853	213.249
47	gene_id_5277	Bin_1	77.1701	91.8971	107.907
47	gene_id_5278	Bin_1	91.8554	129.21	243.047
47	gene_id_5279	Bin_1	204.656	317.403	557.648
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47	gene_id_5280	Bin_1	94.5281	118.506	485.625
47	gene_id_5281	Bin_1	83.9641	113.534	175.854
47	gene_id_5282	Bin_1	83.3874	78.0555	97.0435
47	gene_id_5283	Bin_1	122.634	126.034	221.302
47	gene_id_5284	Bin_1	52.4267	39.4875	48.3725
47	gene_id_5285	Bin_1	151.317	131.935	182.847
47	gene_id_5286	Bin_1	121.061	158.688	153.222
47	gene_id_5287	Bin_1	70.6768	104.742	53.1165
47	gene_id_5288	Bin_1	91.7589	137.657	90.5872
47	gene_id_5289	Bin_1	230.558	253.356	261.706
6	gene_id_529	Bin_1	406.789	358.377	871.225
47	gene_id_5290	Bin_1	201.082	333.714	250.574
47	gene_id_5291	Bin_1	178.959	161.771	54.7017
47	gene_id_5292	Bin_1	272.586	353.85	302.782
47	gene_id_5293	Bin_1	261.663	337.782	348.572
47	gene_id_5294	Bin_1	713.56	654.132	1289.3
47	gene_id_5295	Bin_1	129.768	132.536	109.648
47	gene_id_5296	Bin_1	204.421	178.499	120.374
47	gene_id_5297	Bin_1	6758.31	7202.08	5035.3
47	gene_id_5298	Bin_1	1071.56	1056.54	2754.65
47	gene_id_5299	Bin_1	707.481	836.429	592.521
6	gene_id_530	Bin_1	114.577	180.212	362.526
47	gene_id_5300	Bin_1	234.794	122.747	158.043
47	gene_id_5301	Bin_1	356.791	283.965	418.33
47	gene_id_5302	Bin_1	146.738	115.837	104.025
47	gene_id_5303	Bin_1	326.359	342.519	248.813
47	gene_id_5304	Bin_1	291.854	401.838	720.141
47	gene_id_5305	Bin_1	392.526	307.226	307.235
47	gene_id_5306	Bin_1	1065.49	1234.42	923.742
47	gene_id_5307	Bin_1	292.026	342.576	272.834
47	gene_id_5308	Bin_1	414.582	617.822	287.669
47	gene_id_5309	Bin_1	148.773	135.711	83.0314
6	gene_id_531	Bin_1	1473.22	1801.83	1149.04
47	gene_id_5310	Bin_1	480.654	445.831	348.094

47	gene_id_5311	Bin_1	1039.41	610.897	825.783
47	gene_id_5312	Bin_1	343.011	239.241	467.121
47	gene_id_5313	Bin_1	297.505	240.435	348.063
47	gene_id_5314	Bin_1	217.5	123.288	204.354
47	gene_id_5315	Bin_1	202.899	135.941	254.171
47	gene_id_5316	Bin_1	324.175	266.249	235.737
47	gene_id_5317	Bin_1	253.033	188.606	514.387
47	gene_id_5318	Bin_1	273.264	147.195	276.568
47	gene_id_5319	Bin_1	370.397	125.701	211.981
6	gene_id_532	Bin_1	1288.03	896.008	1329.44
47	gene_id_5320	Bin_1	469.481	289.872	247.095
47	gene_id_5321	Bin_1	174.336	161.301	272.478
47	gene_id_5322	Bin_1	222.82	122.704	157.588
47	gene_id_5323	Bin_1	402.674	264.374	381.198
47	gene_id_5324	Bin_1	608.999	336.343	533.45
47	gene_id_5325	Bin_1	270.944	247.139	303.725
47	gene_id_5326	Bin_1	2655.93	2454.73	2020.97
47	gene_id_5327	Bin_1	234.159	198.32	245.342
47	gene_id_5328	Bin_1	192.184	241.54	175.424
47	gene_id_5329	Bin_1	889.137	739.53	599.519
6	gene_id_533	Bin_1	1564.71	1888.94	1030.9
47	gene_id_5330	Bin_1	195.36	330.967	144.923
47	gene_id_5331	Bin_1	319.131	565.161	235.069
47	gene_id_5332	Bin_1	349.908	643.701	319.594
47	gene_id_5333	Bin_1	86.8427	1855.29	625.774
6	gene_id_534	Bin_1	56.8072	91.5315	386.25
6	gene_id_535	Bin_1	153.132	209.683	222.402
6	gene_id_536	Bin_1	31.9646	23.9694	186.04
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6	gene_id_538	Bin_1	82.7331	103.099	59.6331
6	gene_id_540	Bin_1	214.596	264.889	127.791
6	gene_id_541	Bin_1	953.717	748.051	584.817
6	gene_id_542	Bin_1	64.0082	90.7283	79.0009
6	gene_id_543	Bin_1	70.8095	95.383	1615.88
6	gene_id_544	Bin_1	65.2767	103.752	354.273
6	gene_id_545	Bin_1	369.894	551.514	387.667
6	gene_id_546	Bin_1	293.626	287.295	174.034
6	gene_id_547	Bin_1	72.2593	65.2339	72.0593
6	gene_id_548	Bin_1	60.1307	63.7205	128.93
6	gene_id_549	Bin_1	255.998	1211.75	2855.99
6	gene_id_550	Bin_1	1808.87	1326.68	1797.15
6	gene_id_551	Bin_1	331.663	304.271	446.673
6	gene_id_552	Bin_1	222.81	724.37	11146.3
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6	gene_id_554	Bin_1	63.4176	43.6684	99.5913
6	gene_id_555	Bin_1	50.7869	68.4844	77.0149
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6	gene_id_557	Bin_1	107.475	170.577	193.641
6	gene_id_558	Bin_1	1133.94	1158.91	2829.57
6	gene_id_559	Bin_1	33.7599	20.4563	92.1532
6	gene_id_560	Bin_1	86.6881	114.324	453.659
6	gene_id_561	Bin_1	54.6753	94.5865	236.913
6	gene_id_562	Bin_1	74.3329	91.8428	107.036
6	gene_id_563	Bin_1	150.656	233.725	527.41
6	gene_id_564	Bin_1	27.1287	48.9151	479.769
6	gene_id_565	Bin_1	84.0094	184.772	386.447
6	gene_id_566	Bin_1	269.334	636.13	1048.98
6	gene_id_567	Bin_1	281.549	147.965	454.064
6	gene_id_568	Bin_1	242.838	172.86	179.811
6	gene_id_569	Bin_1	257.684	204.656	354.805
6	gene_id_570	Bin_1	62.7039	125.159	146.192
117	gene_id_9243	Bin_1	71.2772	53.4152	249.302
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117	gene_id_9245	Bin_1	149.512	103.625	275.088
117	gene_id_9246	Bin_1	244.272	482.319	680.733
117	gene_id_9247	Bin_1	254.039	228.939	119.155
117	gene_id_9249	Bin_1	76.5754	98.4009	178.167
117	gene_id_9250	Bin_1	25.7568	26.1975	69.0978
117	gene_id_9251	Bin_1	63.1227	70.0738	310.007
117	gene_id_9252	Bin_1	78.0207	151.025	851.127
117	gene_id_9253	Bin_1	54.1772	62.1871	133.719
117	gene_id_9254	Bin_1	81.4261	116.608	120.955
117	gene_id_9255	Bin_1	5999.05	2347.7	51389.7
117	gene_id_9256	Bin_1	59.1672	84.9696	80.613
117	gene_id_9257	Bin_1	55.3566	101.919	151.358
117	gene_id_9258	Bin_1	66.4695	97.098	85.4173
117	gene_id_9259	Bin_1	114.371	183.411	683.389
117	gene_id_9260	Bin_1	138.046	181.94	286.884
117	gene_id_9261	Bin_1	58.6027	90.2309	85.1506
117	gene_id_9262	Bin_1	81.7306	82.2199	143.755
117	gene_id_9263	Bin_1	38.4868	64.2303	112.253
117	gene_id_9265	Bin_1	19.7046	4.41093	8.92399
117	gene_id_9267	Bin_1	14.9063	7.7824	18.8672
117	gene_id_9270	Bin_1	41.5634	55.9581	400.432
117	gene_id_9271	Bin_1	220.154	276.94	2540.15
117	gene_id_9272	Bin_1	5064.58	8298.66	9120.74
117	gene_id_9273	Bin_1	32690.5	23961.4	22589.5
117	gene_id_9274	Bin_1	62.1546	31.4476	103.979
117	gene_id_9275	Bin_1	9.51787	6.94648	23.73
117	gene_id_9276	Bin_1	109.546	25.577	90.5503
117	gene_id_9277	Bin_1	13.2341	4.39973	11.4636
117	gene_id_9279	Bin_1	21.5495	15.8078	29.0186
117	gene_id_9280	Bin_1	38.1051	12.8014	35.0008
117	gene_id_9281	Bin_1	91.6467	63.4561	96.2991

117	gene_id_9282	Bin_1	59.9355	83.6843	64.7679
117	gene_id_9283	Bin_1	145.237	414.604	179.384
117	gene_id_9284	Bin_1	16.3646	29.8125	75.6832
117	gene_id_9285	Bin_1	27.475	45.888	50.2241
117	gene_id_9286	Bin_1	78.4878	68.2054	67.6391
117	gene_id_9287	Bin_1	305.647	321.646	314.952
117	gene_id_9288	Bin_1	127.234	127.386	198.379
117	gene_id_9289	Bin_1	199.342	145.787	188.887
117	gene_id_9290	Bin_1	235.968	168.578	267.229
117	gene_id_9291	Bin_1	93.0361	136.488	251.192
117	gene_id_9292	Bin_1	153.596	156.131	582.543
117	gene_id_9293	Bin_1	375.64	420.409	5307.4
117	gene_id_9294	Bin_1	116.598	134.303	66.0283
117	gene_id_9295	Bin_1	185.049	190.066	265.062
117	gene_id_9296	Bin_1	434.501	570.172	322.105
117	gene_id_9297	Bin_1	366.561	529.551	118.925
117	gene_id_9298	Bin_1	101.264	132.35	24.2784
117	gene_id_9299	Bin_1	190.643	147.05	521.326
117	gene_id_9300	Bin_1	101.55	64.5522	226.169
117	gene_id_9301	Bin_1	103.763	125.221	146.341
131	gene_id_10006	Bin_2	255.998	9.85159	0
131	gene_id_10007	Bin_2	406.217	3.96814	0
131	gene_id_10009	Bin_2	31.6224	38.4799	1.69677
131	gene_id_10010	Bin_2	14.5193	12.2137	0
131	gene_id_10011	Bin_2	110.414	27.7361	8.24948
13	gene_id_1002	Bin_2	15.0873	0	0
131	gene_id_10020	Bin_2	13.4043	0.765357	1.14104
131	gene_id_10022	Bin_2	59.861	5.78254	1.64155
131	gene_id_10023	Bin_2	16.7241	0	0
131	gene_id_10024	Bin_2	21.3263	0	0
131	gene_id_10028	Bin_2	7.94875	9.97333	0
131	gene_id_10033	Bin_2	21.0129	43.927	0
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13	gene_id_1009	Bin_2	12.0596	0	0
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13	gene_id_1013	Bin_2	6.61357	31.7631	0.277988
13	gene_id_1016	Bin_2	217.769	3.03305	1.06954
13	gene_id_1018	Bin_2	84.7178	24.9928	1.24822
13	gene_id_1023	Bin_2	177.804	13.5028	1.4656
13	gene_id_1026	Bin_2	13.8962	8.73366	0
1	gene_id_103	Bin_2	15.4212	7.32298	0.455531
13	gene_id_1030	Bin_2	18.6848	58.4665	0
13	gene_id_1031	Bin_2	19.7135	52.4366	0
138	gene_id_10389	Bin_2	9.63352	0.25437	0
138	gene_id_10390	Bin_2	12.8873	0.302223	1.32908
138	gene_id_10395	Bin_2	55.6528	2.41788	1.70589

138	gene_id_10397	Bin_2	33.6953	2.46928	0
138	gene_id_10399	Bin_2	31.8753	4.13444	0.833676
1	gene_id_104	Bin_2	29.498	63.8643	0
138	gene_id_10400	Bin_2	37.4183	0	0
138	gene_id_10406	Bin_2	22342.3	13.326	4.69013
138	gene_id_10408	Bin_2	17.4882	7.30364	0
138	gene_id_10411	Bin_2	10.5276	28.4822	0
138	gene_id_10412	Bin_2	11.835	2.97446	1.04949
138	gene_id_10414	Bin_2	16.0821	0	0
138	gene_id_10418	Bin_2	3146.17	0	0
138	gene_id_10424	Bin_2	20.465	46.5512	0
138	gene_id_10425	Bin_2	1.26716	8.75001	1.18581
138	gene_id_10426	Bin_2	37.092	39.8368	1.08058
138	gene_id_10433	Bin_2	54.8373	1.61556	0
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138	gene_id_10439	Bin_2	13.1333	1.03557	0
138	gene_id_10440	Bin_2	11289.3	63.0762	44.038
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138	gene_id_10442	Bin_2	182.147	0	0
138	gene_id_10444	Bin_2	366.686	0	0
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150	gene_id_10915	Bin_2	322.042	97.0764	0
150	gene_id_10917	Bin_2	1.43051	27.7885	0
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150	gene_id_10920	Bin_2	4.0278	18.5266	0.594212
150	gene_id_10921	Bin_2	36.137	117.756	0
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150	gene_id_10926	Bin_2	46.9082	10.2184	1.13872
150	gene_id_10927	Bin_2	64.7986	17.6432	2.26224
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150	gene_id_10943	Bin_2	21.7176	92.7604	2.11036
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150	gene_id_10945	Bin_2	56.8294	60.815	0

150	gene_id_10949	Bin_2	14.5949	2.11761	0.498122
150	gene_id_10950	Bin_2	41.3034	2.90777	1.76539
150	gene_id_10951	Bin_2	23.989	1.245	0.878228
150	gene_id_10952	Bin_2	19.0828	0.778363	0
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150	gene_id_10959	Bin_2	139.468	444.076	2.5298
150	gene_id_10965	Bin_2	9.96466	9.19839	0.807226
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150	gene_id_10966	Bin_2	161.503	9.73343	1.37276
150	gene_id_10967	Bin_2	9.26843	17.2575	0
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150	gene_id_10981	Bin_2	34.5964	2.32216	3.35901
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150	gene_id_10986	Bin_2	80.5729	2.63759	3.82333
150	gene_id_10992	Bin_2	166.172	341.926	0
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1	gene_id_110	Bin_2	13.6677	2.87583	0
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153	gene_id_11029	Bin_2	16.0033	11.107	8.12355
153	gene_id_11030	Bin_2	1458.51	0	0
153	gene_id_11031	Bin_2	28.4246	6.91563	5.03492
153	gene_id_11034	Bin_2	59.5595	0	2.27883
153	gene_id_11035	Bin_2	439.014	0	0
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153	gene_id_11040	Bin_2	53.9999	0	0
154	gene_id_11058	Bin_2	13.7151	0	0.552422
154	gene_id_11060	Bin_2	15.397	0.511244	0.76278
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156	gene_id_11125	Bin_2	8.7804	9.11865	0
156	gene_id_11126	Bin_2	27.2008	7.66091	0
156	gene_id_11127	Bin_2	30.6726	1.93599	0
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156	gene_id_11129	Bin_2	89.495	0	0

156	gene_id_11133	Bin_2	10.5762	13.2432	0
156	gene_id_11138	Bin_2	378.232	21.9635	36.6397
156	gene_id_11140	Bin_2	26.9073	16.8151	0.741446
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156	gene_id_11221	Bin_2	17.2741	1.07897	0
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156	gene_id_11226	Bin_2	28.4609	22.5113	1.3236
156	gene_id_11227	Bin_2	162.161	98.3094	13.8853
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156	gene_id_11235	Bin_2	37.8673	24.511	1.48261
156	gene_id_11237	Bin_2	30.1936	1.54438	0.768066
156	gene_id_11238	Bin_2	19.4326	0	0
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158	gene_id_11267	Bin_2	312.987	366.603	0
158	gene_id_11268	Bin_2	79.2479	11.2318	0
158	gene_id_11269	Bin_2	47.357	8.13683	2.29527
158	gene_id_11270	Bin_2	19.8719	0	0.586448
158	gene_id_11271	Bin_2	493.711	39.4064	43.279
15	gene_id_1128	Bin_2	8.35003	101.094	0.655937
15	gene_id_1132	Bin_2	7.9136	11.8818	0
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15	gene_id_1150	Bin_2	27.3013	12.7926	0
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183	gene_id_11786	Bin_2	124.418	1.12536	2.38171
15	gene_id_1179	Bin_2	2.8334	20.9837	1.23309
183	gene_id_11795	Bin_2	162.182	8.2314	0.829536
15	gene_id_1180	Bin_2	2.98039	6.25503	0
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183	gene_id_11802	Bin_2	33.1176	116.786	0
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187	gene_id_11820	Bin_2	117.262	2.74423	7.51604
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15	gene_id_1209	Bin_2	66.0633	1.05844	0
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15	gene_id_1239	Bin_2	457.678	122.839	0
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1	gene_id_127	Bin_2	31.2588	30.2963	0
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15	gene_id_1279	Bin_2	24.5506	0	0
1	gene_id_128	Bin_2	411.356	158.388	0
15	gene_id_1280	Bin_2	257.207	3.7968	5.10725
15	gene_id_1281	Bin_2	359.239	12.7525	20.3353
199	gene_id_12842	Bin_2	257.394	0	0
199	gene_id_12843	Bin_2	21.96	0	0
199	gene_id_12844	Bin_2	13.2734	15.424	0.958484
199	gene_id_12848	Bin_2	11.6187	19.7152	0
199	gene_id_12849	Bin_2	20.4455	2.74449	0
201	gene_id_12869	Bin_2	20.1004	0.840529	0

201	gene_id_12872	Bin_2	11.6642	17.9795	1.26785
15	gene_id_1289	Bin_2	179.846	1.25808	1.82606
15	gene_id_1290	Bin_2	45.6926	0	0
15	gene_id_1293	Bin_2	40.8126	14.0263	0.871781
15	gene_id_1295	Bin_2	8.39562	1.58848	0
15	gene_id_1296	Bin_2	1335.98	263.151	0
15	gene_id_1297	Bin_2	14.0406	2.40355	0
15	gene_id_1298	Bin_2	9.37861	11.6973	0
1	gene_id_130	Bin_2	92.4913	189.717	0
15	gene_id_1302	Bin_2	24.0477	2.98225	0
15	gene_id_1305	Bin_2	35.4291	0.718405	0
15	gene_id_1306	Bin_2	40.2641	2.09694	0
15	gene_id_1307	Bin_2	31.7053	2.93758	0.414638
15	gene_id_1309	Bin_2	45.2665	2.49811	0
15	gene_id_1312	Bin_2	98.4547	20.6791	0
15	gene_id_1314	Bin_2	13.7642	0.785625	0.554371
1	gene_id_133	Bin_2	19.886	1.12821	0
1	gene_id_135	Bin_2	59.2955	6.11049	1.39475
1	gene_id_136	Bin_2	68.8736	6.21091	2.02324
1	gene_id_137	Bin_2	158.928	8.99174	6.5424
1	gene_id_138	Bin_2	527.397	10.99	11.5547
221	gene_id_13808	Bin_2	8.36159	0	0
221	gene_id_13811	Bin_2	654.189	0	0
221	gene_id_13821	Bin_2	30.8126	3.39324	1.59587
221	gene_id_13828	Bin_2	1349.36	180.583	0
221	gene_id_13834	Bin_2	12.0264	0	0
221	gene_id_13837	Bin_2	19.9492	0	0.552422
1	gene_id_140	Bin_2	20.9705	0	0
1	gene_id_141	Bin_2	13.2225	6.95728	1.67423
1	gene_id_144	Bin_2	22.2138	22.603	3.35924
241	gene_id_14425	Bin_2	39.253	114.734	2.93519
241	gene_id_14426	Bin_2	55.8722	68.4372	1.86787
241	gene_id_14427	Bin_2	49.9896	18.1254	0
246	gene_id_14465	Bin_2	13.1782	0	2.60608
246	gene_id_14470	Bin_2	46.8221	0	0.271383
247	gene_id_14471	Bin_2	127.999	206.883	0
247	gene_id_14474	Bin_2	10.9957	1.38856	0
247	gene_id_14477	Bin_2	26.1578	0	0
247	gene_id_14478	Bin_2	17.4862	0.732597	0
247	gene_id_14479	Bin_2	73.531	1.00858	3.24389
247	gene_id_14480	Bin_2	90.9995	3.77728	0
1	gene_id_145	Bin_2	23.1711	54.6488	0
1	gene_id_146	Bin_2	8.77408	27.2647	0
250	gene_id_14610	Bin_2	31.3895	132.912	4.03636
250	gene_id_14611	Bin_2	182.856	0	0
250	gene_id_14613	Bin_2	64.7138	7.64551	1.54108
250	gene_id_14614	Bin_2	32.8991	1.84244	0

2	gene_id_147	Bin_2	548.02	8.52945	30.9648
2	gene_id_148	Bin_2	14.6364	0.657868	0
1	gene_id_15	Bin_2	20.0401	0	0.940854
2	gene_id_170	Bin_2	41.3942	10.048	0
367	gene_id_17117	Bin_2	14.7499	0.398136	0.281064
367	gene_id_17117	Bin_2	14.6345	0.398136	0.281064
367	gene_id_17117	Bin_2	14.7499	0.916716	0
367	gene_id_17117	Bin_2	14.6345	0.916716	0
367	gene_id_17118	Bin_2	20.1128	0	0
367	gene_id_17119	Bin_2	39.0912	0	0.469117
367	gene_id_17126	Bin_2	31.7423	4.81879	0
382	gene_id_17298	Bin_2	5.79666	11.4843	0.667274
2	gene_id_176	Bin_2	7.28908	37.855	0
20	gene_id_1772	Bin_2	214.061	39.705	5.37518
2	gene_id_178	Bin_2	1.11552	7.71561	0
2	gene_id_179	Bin_2	1.56852	13.7398	0
3	gene_id_180	Bin_2	15.6259	7.39589	1.46514
3	gene_id_181	Bin_2	11.173	0.702527	0
20	gene_id_1813	Bin_2	49.8617	0	0
3	gene_id_182	Bin_2	14.3551	0	0
20	gene_id_1826	Bin_2	39.9786	0	0
20	gene_id_1834	Bin_2	14.9257	3.49084	0
20	gene_id_1844	Bin_2	0	21.6014	0
3	gene_id_186	Bin_2	116.898	30.962	0
20	gene_id_1861	Bin_2	9.11804	8.17371	0
3	gene_id_187	Bin_2	21.4917	12.2743	0
20	gene_id_1874	Bin_2	11.3473	0	0
20	gene_id_1877	Bin_2	10.7108	21.8353	0
20	gene_id_1879	Bin_2	17.772	0	0
3	gene_id_188	Bin_2	149.778	98.7714	0
20	gene_id_1880	Bin_2	7.42606	50.2269	0
20	gene_id_1882	Bin_2	25.9157	0	1.89411
20	gene_id_1883	Bin_2	1.4539	9.63972	0.323993
20	gene_id_1884	Bin_2	6.81445	6.303	0
20	gene_id_1887	Bin_2	4.45399	7.74878	0.24862
20	gene_id_1890	Bin_2	10.7599	9.23968	0
20	gene_id_1894	Bin_2	8.97249	18.4244	0
20	gene_id_1902	Bin_2	18.0883	9.34353	2.60205
20	gene_id_1903	Bin_2	165.932	45.6371	10.6927
20	gene_id_1904	Bin_2	32.077	4.99398	0
20	gene_id_1905	Bin_2	24.0175	2.42036	0.427036
20	gene_id_1907	Bin_2	1976.69	16.4864	0
20	gene_id_1912	Bin_2	2.46882	23.0221	0
20	gene_id_1914	Bin_2	14.2021	2.23085	0
20	gene_id_1917	Bin_2	48.5276	27.0308	0
20	gene_id_1918	Bin_2	458.39	283.028	6.69689
20	gene_id_1919	Bin_2	49.6147	0	0

20	gene_id_1928	Bin_2	39.5665	2.59151	0
20	gene_id_1935	Bin_2	37.1602	0	0
20	gene_id_1937	Bin_2	259.935	8.82608	0
20	gene_id_1938	Bin_2	277.736	101.736	0.944208
20	gene_id_1939	Bin_2	10.9006	0.344848	0.243419
20	gene_id_1947	Bin_2	25.1048	4.18401	0
20	gene_id_1949	Bin_2	13.7715	6.81349	0
20	gene_id_1954	Bin_2	19.4061	0.437809	0.309017
3	gene_id_196	Bin_2	40.569	1.57	2.21444
565	gene_id_19611	Bin_2	9.7043	0.361077	1.33282
20	gene_id_1970	Bin_2	11.5229	0	0
20	gene_id_1992	Bin_2	144.098	1.39405	0
20	gene_id_1994	Bin_2	10.3822	1.18916	0.886896
3	gene_id_200	Bin_2	510.492	14.509	39.1031
20	gene_id_2005	Bin_2	89.7561	3.80961	0
20	gene_id_2013	Bin_2	31.8962	0	0
20	gene_id_2018	Bin_2	32.2825	9.01375	0
20	gene_id_2019	Bin_2	23.9737	6.07708	0.357496
3	gene_id_202	Bin_2	0	22.8623	0
20	gene_id_2020	Bin_2	42.2222	28.7962	0
21	gene_id_2024	Bin_2	53.4406	0	0
21	gene_id_2025	Bin_2	21.689	1.246	0.293159
21	gene_id_2029	Bin_2	100.709	0	0
3	gene_id_203	Bin_2	25.5873	0	0
21	gene_id_2031	Bin_2	603.571	8.24319	0
21	gene_id_2034	Bin_2	22.9264	0.907285	0.45151
21	gene_id_2041	Bin_2	15.18	0	0
3	gene_id_205	Bin_2	16.584	1.88788	0.666007
21	gene_id_2050	Bin_2	85.8689	12.5024	0
3	gene_id_207	Bin_2	32.1374	0.376345	1.38913
21	gene_id_2071	Bin_2	9.45926	0	0
21	gene_id_2075	Bin_2	11.8	0	0
21	gene_id_2084	Bin_2	22.0582	0.985759	0
21	gene_id_2086	Bin_2	16.0821	0	0
22	gene_id_2090	Bin_2	4.26523	33.5888	3.64676
22	gene_id_2091	Bin_2	5.70564	14.9117	0
22	gene_id_2092	Bin_2	49.5929	0	0.780105
22	gene_id_2093	Bin_2	691.338	10.6303	0
22	gene_id_2095	Bin_2	34.2785	63.4485	0
22	gene_id_2096	Bin_2	18.3796	15.84	0.429957
22	gene_id_2099	Bin_2	9.01858	4.65467	0
22	gene_id_2101	Bin_2	7.95419	0.418853	0.625107
22	gene_id_2103	Bin_2	14.0921	1.60816	0
22	gene_id_2105	Bin_2	9.79667	1.90288	0.335765
22	gene_id_2106	Bin_2	40.8412	39.2027	0
22	gene_id_2108	Bin_2	9.66461	1.66163	0
22	gene_id_2110	Bin_2	10.8338	12.5917	0

22	gene_id_2113	Bin_2	18.2227	55.6691	0
22	gene_id_2114	Bin_2	132.96	2.14192	0
22	gene_id_2124	Bin_2	124.467	14.3113	0
22	gene_id_2127	Bin_2	364.588	10.3937	7.75108
22	gene_id_2132	Bin_2	9.68686	1.8302	0.430547
22	gene_id_2136	Bin_2	662.761	11.656	10.9784
22	gene_id_2138	Bin_2	9.76347	0.883273	0
22	gene_id_2140	Bin_2	27.7208	17.4397	0
22	gene_id_2145	Bin_2	10.5812	0	0
22	gene_id_2147	Bin_2	11.7053	0.614278	0
22	gene_id_2154	Bin_2	34.3279	63.9567	0
22	gene_id_2155	Bin_2	12.6578	1.4976	0
22	gene_id_2156	Bin_2	63.0387	0	0
22	gene_id_2158	Bin_2	12.7025	1.26729	1.22677
22	gene_id_2162	Bin_2	10.8925	45.4321	0
22	gene_id_2163	Bin_2	10.8945	30.1496	0
22	gene_id_2164	Bin_2	35.6787	0	0.663195
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22	gene_id_2165	Bin_2	19.4456	0	0.321014
22	gene_id_2166	Bin_2	15.0684	0.4327	0
22	gene_id_2167	Bin_2	26.5457	0	0
22	gene_id_2168	Bin_2	35.4398	0	0
22	gene_id_2169	Bin_2	13.6372	4.90745	0
22	gene_id_2171	Bin_2	2.99949	6.34078	0
22	gene_id_2174	Bin_2	33.2558	8.50201	0.461537
22	gene_id_2175	Bin_2	11.4636	2.17529	0
22	gene_id_2177	Bin_2	4.98858	26.3824	0
22	gene_id_2178	Bin_2	12.5573	33.5909	0.789911
3	gene_id_230	Bin_2	12.8925	3.37926	0
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25	gene_id_2320	Bin_2	10.4983	3.05693	0.760164
25	gene_id_2322	Bin_2	10.4862	10.3146	0
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25	gene_id_2328	Bin_2	11.1145	9.16496	0
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25	gene_id_2345	Bin_2	3.9971	9.19373	0.58975
3	gene_id_235	Bin_2	9.20177	0	0
25	gene_id_2352	Bin_2	33.7082	7.36226	2.2194
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25	gene_id_2390	Bin_2	11.215	0	0
25	gene_id_2397	Bin_2	58.604	14.782	2.97857
25	gene_id_2400	Bin_2	9.45848	1.99297	0.876254
25	gene_id_2406	Bin_2	3.71588	13.6068	0

25	gene_id_2407	Bin_2	16.2046	4.23464	0
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25	gene_id_2421	Bin_2	114.124	0.710377	0
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25	gene_id_2426	Bin_2	14.2528	2.56326	0
25	gene_id_2427	Bin_2	536.449	1.89717	0
25	gene_id_2429	Bin_2	25.8223	0.638017	0.317595
25	gene_id_2430	Bin_2	32.3323	0	0
25	gene_id_2431	Bin_2	21.0614	0	0
25	gene_id_2432	Bin_2	24.9533	69.5063	0.265198
25	gene_id_2433	Bin_2	5.49865	9.68252	0
25	gene_id_2437	Bin_2	3.01761	13.3344	0
25	gene_id_2439	Bin_2	45328.2	8.24319	5.78925
25	gene_id_2440	Bin_2	5.12762	21.3003	0
25	gene_id_2441	Bin_2	2.56219	15.2775	0
25	gene_id_2442	Bin_2	181.683	45.3901	1.455
25	gene_id_2446	Bin_2	773.31	7.88633	21.1997
25	gene_id_2447	Bin_2	1193.33	0	48.2056
26	gene_id_2448	Bin_2	53.4784	0	0
26	gene_id_2449	Bin_2	73.1744	2.22818	2.35788
3	gene_id_246	Bin_2	3.00366	40.7015	0
26	gene_id_2471	Bin_2	18.1892	1.14628	0.404495
26	gene_id_2472	Bin_2	40.3649	0	0.253842
26	gene_id_2484	Bin_2	12.488	4.17437	0.692121
26	gene_id_2487	Bin_2	548.567	68.9611	0
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26	gene_id_2508	Bin_2	21.1983	6.63573	0
26	gene_id_2520	Bin_2	13.7698	0.86336	0
26	gene_id_2521	Bin_2	10.2941	1.73417	0
26	gene_id_2522	Bin_2	18.8747	4.61873	0.465641
26	gene_id_2523	Bin_2	21.8581	6.10187	0
3	gene_id_253	Bin_2	5.19097	13.0301	0
26	gene_id_2530	Bin_2	9.90102	0	0
26	gene_id_2546	Bin_2	9.88188	1.91929	0.338661
26	gene_id_2548	Bin_2	956.259	11.1072	65.4381
26	gene_id_2550	Bin_2	13.3557	18.1664	0
26	gene_id_2558	Bin_2	51.1113	3.15022	0.930848
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26	gene_id_2560	Bin_2	11.072	0.269791	0
26	gene_id_2561	Bin_2	9.33027	52.1093	0
26	gene_id_2570	Bin_2	52.9766	5.16495	6.33338
26	gene_id_2573	Bin_2	12.7535	9.84488	0
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26	gene_id_2585	Bin_2	13.4512	1.536	0
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26	gene_id_2597	Bin_2	34.1131	0.897697	4.22708
26	gene_id_2599	Bin_2	15.8	0.662767	1.45612
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34	gene_id_3707	Bin_2	64.2573	20.5359	11.4627
34	gene_id_3708	Bin_2	6.85725	10.7761	0
34	gene_id_3709	Bin_2	11.8384	2.86939	0
34	gene_id_3711	Bin_2	10.3859	4.81116	0
34	gene_id_3714	Bin_2	17.8545	1.01499	0
34	gene_id_3728	Bin_2	6.61595	3.76259	0.623934
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1	gene_id_42	Bin_2	28.1946	5.05272	0.594212
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42	gene_id_4260	Bin_2	26.8006	6.72423	0
42	gene_id_4263	Bin_2	3.16544	10.8916	0
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42	gene_id_4270	Bin_2	15.2049	0.683115	0
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42	gene_id_4281	Bin_2	13.4683	0	0
42	gene_id_4282	Bin_2	15.5153	0.81141	0.572555
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42	gene_id_4289	Bin_2	11.262	18.368	0.144077
5	gene_id_429	Bin_2	66.6495	3.17357	3.47896
42	gene_id_4290	Bin_2	161.645	12.4646	2.20061
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42	gene_id_4309	Bin_2	26.4715	4.84616	5.91679
5	gene_id_431	Bin_2	57.8981	26.5031	23.6881
42	gene_id_4317	Bin_2	9.21835	21.0033	0
42	gene_id_4318	Bin_2	3.10223	16.502	0
42	gene_id_4328	Bin_2	51.0983	0	0
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42	gene_id_4332	Bin_2	14.6917	3.24673	0
42	gene_id_4333	Bin_2	62.7409	1.46039	0
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42	gene_id_4347	Bin_2	8.58307	13.446	0
42	gene_id_4349	Bin_2	64.6417	16.5943	0
5	gene_id_435	Bin_2	47.6496	0	0
42	gene_id_4367	Bin_2	6.88037	1.18622	0
42	gene_id_4373	Bin_2	11.9157	0.748619	0
5	gene_id_438	Bin_2	105.573	34.5756	27.2815
5	gene_id_439	Bin_2	164.313	41.2132	36.3793
1	gene_id_44	Bin_2	3.40006	10.7538	0.535071
5	gene_id_444	Bin_2	7.43966	0.939387	0.331514
5	gene_id_447	Bin_2	464.072	1914.21	24.1028
5	gene_id_448	Bin_2	64.2151	1292.35	0
1	gene_id_45	Bin_2	1.99043	36.0553	0
5	gene_id_450	Bin_2	16.2667	36.1387	0
5	gene_id_451	Bin_2	5.6423	25.8019	0
5	gene_id_452	Bin_2	13.4518	31.2175	0.595338
1	gene_id_46	Bin_2	4.52962	10.2768	0.402939
5	gene_id_461	Bin_2	8.91811	0.938397	0
1	gene_id_47	Bin_2	12.2806	14.2238	0
46	gene_id_4705	Bin_2	18.6134	0	1.4463
46	gene_id_4708	Bin_2	37.0161	5.60829	9.8654
46	gene_id_4711	Bin_2	5.96286	15.0406	0
46	gene_id_4713	Bin_2	2209.18	18.3373	0
46	gene_id_4723	Bin_2	67.563	86.971	0
46	gene_id_4729	Bin_2	25.2517	0.792622	0
5	gene_id_473	Bin_2	3.37152	18.9618	0
46	gene_id_4730	Bin_2	26.8048	0	0
46	gene_id_4733	Bin_2	14.4327	16.7548	1.04101
46	gene_id_4734	Bin_2	20.1805	5.25472	9.3928
46	gene_id_4737	Bin_2	18.4988	6.30566	1.56547
46	gene_id_4744	Bin_2	24.0129	107.193	0
46	gene_id_4746	Bin_2	5.13033	31.4976	0.484754
46	gene_id_4747	Bin_2	16.8638	39.906	0
46	gene_id_4748	Bin_2	6.02156	19.5264	0
46	gene_id_4749	Bin_2	16.9037	72.545	0

46	gene_id_4750	Bin_2	5.70431	34.3136	0.212473
46	gene_id_4751	Bin_2	5.76874	47.8048	0.604645
46	gene_id_4752	Bin_2	14.2224	12.1711	2.9272
46	gene_id_4754	Bin_2	68.1674	3.98664	0
46	gene_id_4760	Bin_2	19.0155	0	0.601032
46	gene_id_4765	Bin_2	24.6538	1.92879	0
5	gene_id_477	Bin_2	11.2917	2.37605	0
46	gene_id_4772	Bin_2	4.28529	5.94467	0
46	gene_id_4779	Bin_2	18.6964	7.79969	0
46	gene_id_4780	Bin_2	468.688	717.428	11.3967
46	gene_id_4781	Bin_2	30.9798	26.773	4.49611
46	gene_id_4782	Bin_2	6.92581	8.68414	0
46	gene_id_4783	Bin_2	12.8172	22.964	0
46	gene_id_4783	Bin_2	2.17306	22.964	0
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46	gene_id_4789	Bin_2	7.7329	16.0748	0
46	gene_id_4795	Bin_2	0	7.06991	0
46	gene_id_4796	Bin_2	22.3461	0	0
46	gene_id_4797	Bin_2	18.4528	16.0878	0.283888
46	gene_id_4799	Bin_2	10.539	10.9739	1.69152
1	gene_id_48	Bin_2	5.04124	14.2418	0
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46	gene_id_4801	Bin_2	21.2522	7.90919	1.76621
46	gene_id_4802	Bin_2	40.4874	10.7015	7.81827
46	gene_id_4807	Bin_2	83.2453	12.1636	2.42699
46	gene_id_4813	Bin_2	5.15271	47.6992	1.20515
46	gene_id_4814	Bin_2	3.58358	19.0095	0
46	gene_id_4815	Bin_2	8.04103	21.122	0
46	gene_id_4816	Bin_2	3.5245	18.7054	0
46	gene_id_4817	Bin_2	6.18946	35.0584	0
46	gene_id_4819	Bin_2	42.9131	0	0
46	gene_id_4820	Bin_2	14.7121	0	0
46	gene_id_4823	Bin_2	9.99106	1.7172	0
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46	gene_id_4825	Bin_2	20.9977	0.823421	0
46	gene_id_4827	Bin_2	77.6132	5.78998	1.11449
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46	gene_id_4836	Bin_2	4.03276	12.5554	0
46	gene_id_4855	Bin_2	10.467	0.599385	0
46	gene_id_4856	Bin_2	8.07559	0	0.760164
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5	gene_id_492	Bin_2	12.6619	2.91224	0.800335
5	gene_id_495	Bin_2	10.4703	0	0
5	gene_id_496	Bin_2	12.4461	2.34446	0

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48	gene_id_5340	Bin_2	17.1051	3.20583	0
48	gene_id_5343	Bin_2	46.4134	10.9177	0
48	gene_id_5344	Bin_2	32.3998	13.9295	0
48	gene_id_5345	Bin_2	15.7854	5.00404	0
48	gene_id_5362	Bin_2	74.2658	2.37963	0
48	gene_id_5378	Bin_2	8.59903	10.2309	0.424727
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50	gene_id_5457	Bin_2	9.09445	6.71614	0.477445
50	gene_id_5461	Bin_2	8.27486	9.77539	0.524335
50	gene_id_5485	Bin_2	27.9029	1.33462	0
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50	gene_id_5496	Bin_2	17.6225	1.10032	0
50	gene_id_5498	Bin_2	20.0563	20.7666	0
50	gene_id_5501	Bin_2	9.81243	2.28805	0.97591
50	gene_id_5504	Bin_2	6.06634	10.9279	0
50	gene_id_5506	Bin_2	20.3398	5.06503	0
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50	gene_id_5508	Bin_2	15.5887	4.578	0.461537
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50	gene_id_5509	Bin_2	6.17902	38.7857	5.25007
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50	gene_id_5510	Bin_2	22.6077	20.9316	0.335765
50	gene_id_5511	Bin_2	13.4343	15.5491	0
50	gene_id_5512	Bin_2	19.523	2.03462	0
50	gene_id_5516	Bin_2	5.23823	4.96548	0.61756
50	gene_id_5521	Bin_2	23.9031	0	0
50	gene_id_5525	Bin_2	21.3081	1.10854	0
53	gene_id_5564	Bin_2	15.852	15.4695	0
53	gene_id_5571	Bin_2	15.9684	4.68825	0.472645
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53	gene_id_5579	Bin_2	1462.13	0	0
53	gene_id_5581	Bin_2	18.373	0	0
53	gene_id_5582	Bin_2	32.7823	0.530124	0
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62	gene_id_5866	Bin_2	4.86887	31.1693	0
62	gene_id_5867	Bin_2	5.51326	39.493	0.290417
62	gene_id_5868	Bin_2	12.651	36.4017	0.662472
62	gene_id_5869	Bin_2	8.61578	26.9091	0
62	gene_id_5870	Bin_2	9.55157	17.241	0.608459
62	gene_id_5871	Bin_2	9.6199	14.6487	0
62	gene_id_5873	Bin_2	21.5418	4.77273	2.93292
62	gene_id_5874	Bin_2	16.902	13.054	0
62	gene_id_5875	Bin_2	548.195	88.5655	55.706
62	gene_id_5876	Bin_2	34.9865	12.2316	0
62	gene_id_5877	Bin_2	92.7534	0	0.885654
62	gene_id_5878	Bin_2	26.0159	9.65835	0
62	gene_id_5882	Bin_2	11.638	2.4017	0.339026
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62	gene_id_5886	Bin_2	59.6199	56.4156	0
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1	gene_id_6	Bin_2	10.6458	0	0
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1	gene_id_61	Bin_2	23.9266	112.389	0
7	gene_id_610	Bin_2	14.6521	1.23025	0
7	gene_id_612	Bin_2	14.6553	58.2988	0.962124
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7	gene_id_614	Bin_2	12.7594	37.1788	0
7	gene_id_617	Bin_2	229.057	23.2463	0.68339
7	gene_id_619	Bin_2	6.55997	13.5907	0
67	gene_id_6190	Bin_2	111.044	0	0
67	gene_id_6194	Bin_2	7.5359	1.42716	0
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67	gene_id_6202	Bin_2	315.958	1.67834	7.68153
69	gene_id_6253	Bin_2	20.2544	4.8748	0
69	gene_id_6255	Bin_2	153.071	8.90706	1.57063
69	gene_id_6258	Bin_2	34.1684	177.487	0
69	gene_id_6265	Bin_2	68.1824	41.6896	0
69	gene_id_6267	Bin_2	15.7915	10.8674	1.47191
69	gene_id_6268	Bin_2	70.5832	35.3308	0.692426
69	gene_id_6277	Bin_2	362.265	23.9694	13.1642
69	gene_id_6282	Bin_2	12.6104	1.83272	0
69	gene_id_6290	Bin_2	9.80724	3.3336	0
69	gene_id_6291	Bin_2	17.5825	27.9783	0
69	gene_id_6292	Bin_2	13.6317	4.61873	0
69	gene_id_6305	Bin_2	13.1251	1.18127	0
69	gene_id_6309	Bin_2	12.9294	0	0
69	gene_id_6311	Bin_2	28.7814	0	1.32778
69	gene_id_6313	Bin_2	21.9517	1.83343	2.6597
69	gene_id_6314	Bin_2	16.2339	2.773	0
69	gene_id_6315	Bin_2	20.6329	8.18812	2.56697
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69	gene_id_6323	Bin_2	45.1429	0	0

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70	gene_id_6332	Bin_2	32.6559	0	1.0209
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70	gene_id_6338	Bin_2	642.036	9.25486	40.299
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72	gene_id_6407	Bin_2	6.71301	8.4212	0
72	gene_id_6408	Bin_2	118.063	308.969	0
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72	gene_id_6410	Bin_2	10.875	39.5878	0
72	gene_id_6411	Bin_2	7.73249	11.9183	1.19055
72	gene_id_6413	Bin_2	5.4853	13.8265	0.859387
72	gene_id_6414	Bin_2	3.09537	14.5289	0
72	gene_id_6416	Bin_2	144.074	292.958	0
72	gene_id_6418	Bin_2	17.1112	6.72787	0
72	gene_id_6421	Bin_2	825.849	132.712	2.84072
72	gene_id_6426	Bin_2	25.5619	60.125	2.65459
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7	gene_id_643	Bin_2	10.1848	1.07045	0
72	gene_id_6432	Bin_2	24.4426	143.818	2.07231
72	gene_id_6436	Bin_2	10.4234	1.31186	0
72	gene_id_6438	Bin_2	35.6398	3.97986	1.40328
7	gene_id_644	Bin_2	16.9425	1.62477	0.485107
72	gene_id_6444	Bin_2	15.5763	0	0
72	gene_id_6447	Bin_2	1675.73	0	0
72	gene_id_6449	Bin_2	9.93762	11.4438	2.49318
72	gene_id_6450	Bin_2	6.57413	9.89937	0
72	gene_id_6452	Bin_2	18.0766	43.1507	2.25413
72	gene_id_6457	Bin_2	18.1864	4.17142	0

72	gene_id_6459	Bin_2	11.7752	0.739906	1.04426
72	gene_id_6465	Bin_2	14.178	5.19662	3.20233
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72	gene_id_6468	Bin_2	136.071	0	4.4813
7	gene_id_647	Bin_2	12.8581	5.64897	0
72	gene_id_6474	Bin_2	7.73892	0.444366	0
72	gene_id_6477	Bin_2	136.661	2.03462	0
72	gene_id_6479	Bin_2	10.3059	10.2253	0.656106
72	gene_id_6480	Bin_2	4.25178	14.7123	0
72	gene_id_6481	Bin_2	10.5378	30.1536	0
72	gene_id_6483	Bin_2	10.9062	15.5994	0
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72	gene_id_6484	Bin_2	18.7801	13.7095	0
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7	gene_id_651	Bin_2	46.2584	1.20131	0
72	gene_id_6513	Bin_2	33.4477	188.089	0
72	gene_id_6514	Bin_2	19.7686	4.64165	0.163835
72	gene_id_6515	Bin_2	33.8905	2.55049	0.599884
72	gene_id_6516	Bin_2	6.21698	31.3	0
72	gene_id_6517	Bin_2	27.453	11.9981	5.35132
72	gene_id_6519	Bin_2	97.0958	11.6648	18.7505
72	gene_id_6521	Bin_2	111.929	6.80981	11.3655
72	gene_id_6522	Bin_2	20.3451	2.93775	0
72	gene_id_6523	Bin_2	11.768	6.36148	0
72	gene_id_6524	Bin_2	11.0237	7.39907	0.614408
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72	gene_id_6527	Bin_2	45.6404	1.43449	1.06947
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7	gene_id_654	Bin_2	9.95631	5.83973	0.343474
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72	gene_id_6540	Bin_2	13.9337	31.3559	0.487597
72	gene_id_6541	Bin_2	45.8138	36.2811	12.2848
72	gene_id_6543	Bin_2	96.859	82.1572	0
72	gene_id_6544	Bin_2	27.1457	4.46572	5.25906
72	gene_id_6545	Bin_2	27.6551	2.17275	1.02217
72	gene_id_6546	Bin_2	68.8208	8.04314	5.68145
7	gene_id_655	Bin_2	19.5312	1.53335	2.82702
7	gene_id_655	Bin_2	9.54226	1.53335	2.82702

7	gene_id_655	Bin_2	19.5312	0.430607	0
7	gene_id_655	Bin_2	9.54226	0.430607	0
72	gene_id_6555	Bin_2	23.9206	0	0
72	gene_id_6556	Bin_2	52.1549	43.2406	0
72	gene_id_6558	Bin_2	32.5504	0	0
7	gene_id_656	Bin_2	2683.92	0	16.2824
73	gene_id_6563	Bin_2	61.5844	5.31932	1.87716
73	gene_id_6570	Bin_2	13.4984	1.54132	0
73	gene_id_6571	Bin_2	19.8451	25.5452	0
73	gene_id_6572	Bin_2	354.239	160.37	1.91722
73	gene_id_6579	Bin_2	9.89246	0	0
7	gene_id_658	Bin_2	2499.67	489.155	0
73	gene_id_6582	Bin_2	1051.96	473.378	12.9932
73	gene_id_6587	Bin_2	11.348	4.47945	0.316169
7	gene_id_659	Bin_2	61.4434	149.43	2.34543
73	gene_id_6603	Bin_2	11.0221	1.89247	0
73	gene_id_6605	Bin_2	19.6213	5.07802	0
73	gene_id_6607	Bin_2	556.841	34.5141	36.4024
7	gene_id_661	Bin_2	461.334	1.9299	2.72183
73	gene_id_6612	Bin_2	10.1234	0	0
74	gene_id_6613	Bin_2	924.898	5.31513	0
7	gene_id_662	Bin_2	2694.36	173.427	30.9308
74	gene_id_6621	Bin_2	22.7369	8.38945	0
74	gene_id_6628	Bin_2	61.7188	0.806995	0
74	gene_id_6629	Bin_2	27.2744	0	1.29876
7	gene_id_663	Bin_2	183.446	6.24699	0
74	gene_id_6636	Bin_2	55.3357	5.99642	0
74	gene_id_6637	Bin_2	9.10933	0	0
74	gene_id_6640	Bin_2	12.6013	0.567293	0
74	gene_id_6648	Bin_2	8.96576	1.41506	0.332919
74	gene_id_6663	Bin_2	45.2665	0	0
74	gene_id_6667	Bin_2	6.91494	8.70808	0
74	gene_id_6672	Bin_2	7.81759	0.897697	0
74	gene_id_6673	Bin_2	116.169	95.4084	0
74	gene_id_6674	Bin_2	255.098	56.1471	0
74	gene_id_6675	Bin_2	56.2872	0	1.41926
74	gene_id_6676	Bin_2	10.5036	18.7618	0.823215
74	gene_id_6682	Bin_2	12.8467	4.0527	0
74	gene_id_6694	Bin_2	8.94992	0	0
1	gene_id_67	Bin_2	18.6466	42.1193	0
74	gene_id_6700	Bin_2	4.39035	9.16716	0
74	gene_id_6703	Bin_2	17.0318	0	0
1	gene_id_68	Bin_2	10.7872	30.0283	0.799725
77	gene_id_6847	Bin_2	27.3293	0	3.29702
77	gene_id_6847	Bin_2	15.8983	0	3.29702
77	gene_id_6847	Bin_2	27.3293	1.81105	0.63892
77	gene_id_6847	Bin_2	15.8983	1.81105	0.63892

77	gene_id_6848	Bin_2	1188.56	19.7032	36.3726
77	gene_id_6855	Bin_2	20.3451	6.85476	0
1	gene_id_69	Bin_2	6.01755	31.0841	0.664598
9	gene_id_690	Bin_2	460.424	0	3.23489
9	gene_id_693	Bin_2	34.086	4.05995	0
9	gene_id_698	Bin_2	12.1223	0	0.537307
9	gene_id_708	Bin_2	25.076	10.7642	0
9	gene_id_709	Bin_2	0	63.7816	0
1	gene_id_71	Bin_2	27.1771	62.4699	0
9	gene_id_716	Bin_2	4934.37	1156.39	0
9	gene_id_721	Bin_2	29.5052	1.02451	3.17783
9	gene_id_722	Bin_2	15.4508	7.13112	1.88185
9	gene_id_724	Bin_2	17.6148	4.56459	7.46722
9	gene_id_728	Bin_2	14.1419	6.25235	0
9	gene_id_739	Bin_2	4.29153	12.5496	0.632489
1	gene_id_74	Bin_2	10.5983	21.6089	0.586448
9	gene_id_742	Bin_2	23.713	2.78457	0
9	gene_id_744	Bin_2	0	86.6191	0
1	gene_id_75	Bin_2	9.16437	36.3321	0
9	gene_id_751	Bin_2	161.254	589.652	0
9	gene_id_752	Bin_2	175.372	8.67351	18.2647
9	gene_id_755	Bin_2	27.5175	2.72211	2.63263
9	gene_id_756	Bin_2	389.984	4.74992	2.75605
9	gene_id_757	Bin_2	486.754	532.767	38.5784
9	gene_id_758	Bin_2	12.7244	19.5519	1.37876
9	gene_id_759	Bin_2	13.5673	8.58228	0.252415
1	gene_id_76	Bin_2	3.34597	18.1818	0.631039
9	gene_id_761	Bin_2	20.2159	0.502421	0.354671
9	gene_id_762	Bin_2	17.0927	11.5493	0
9	gene_id_763	Bin_2	19.7268	3.79994	0
9	gene_id_764	Bin_2	23.6854	9.09488	0
9	gene_id_765	Bin_2	8.25693	7.22647	0.599196
86	gene_id_7665	Bin_2	11.1197	248.921	0
86	gene_id_7666	Bin_2	105.792	209.045	0
86	gene_id_7668	Bin_2	38.3289	3.43345	0
86	gene_id_7671	Bin_2	7.28463	0	0
86	gene_id_7674	Bin_2	11.7752	0.739906	0
86	gene_id_7676	Bin_2	13.5813	0	0
86	gene_id_7678	Bin_2	8.58062	0	0
86	gene_id_7680	Bin_2	22.4584	0.672787	0
86	gene_id_7686	Bin_2	8.1856	0.739556	0
86	gene_id_7689	Bin_2	8.11455	37.7266	0
9	gene_id_769	Bin_2	62.2088	1.9134	0
86	gene_id_7692	Bin_2	6.76497	11.0311	0
1	gene_id_77	Bin_2	7.80476	25.7556	0
86	gene_id_7701	Bin_2	48.2658	14.8621	1.31002
86	gene_id_7702	Bin_2	36.6212	3.60393	0.847435

86	gene_id_7703	Bin_2	15.8655	0.903685	0
86	gene_id_7704	Bin_2	45.1195	1.93079	0.454198
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86	gene_id_7705	Bin_2	483.541	30.1719	33.1439
86	gene_id_7706	Bin_2	8945	36.9415	108.434
86	gene_id_7707	Bin_2	851.519	6.85315	10.2297
86	gene_id_7708	Bin_2	3068.26	34.6357	62.4614
86	gene_id_7709	Bin_2	24.5159	1.17591	1.65907
86	gene_id_7710	Bin_2	13.3557	18.1664	0
86	gene_id_7711	Bin_2	5.15788	25.32	0
86	gene_id_7712	Bin_2	31.9947	38.5945	0
86	gene_id_7714	Bin_2	56.2641	4.30435	7.9147
86	gene_id_7717	Bin_2	17.3777	26.2878	0
86	gene_id_7718	Bin_2	15.015	1.01798	1.01308
87	gene_id_7724	Bin_2	3.93064	26.3147	0
87	gene_id_7729	Bin_2	24.6705	6.96554	0
87	gene_id_7731	Bin_2	55.2974	18.7747	1.39936
87	gene_id_7737	Bin_2	255.136	68.0644	0
87	gene_id_7738	Bin_2	13.6494	2.65786	0.938067
87	gene_id_7739	Bin_2	37.7345	0	0
9	gene_id_775	Bin_2	45.1074	88.3536	0
9	gene_id_778	Bin_2	45.7808	0	1.09472
9	gene_id_779	Bin_2	23.0295	0	0
9	gene_id_780	Bin_2	22.8679	0	3.11391
9	gene_id_782	Bin_2	16.6198	0.945946	0
9	gene_id_783	Bin_2	24.1269	0	0
9	gene_id_784	Bin_2	24.1502	0	0
91	gene_id_7856	Bin_2	20.1287	43.4394	1.11464
91	gene_id_7859	Bin_2	329.188	1367.48	3.58712
91	gene_id_7860	Bin_2	1040.29	351.951	319.838
91	gene_id_7861	Bin_2	935.979	18.9329	0
91	gene_id_7862	Bin_2	10.3195	1.50266	0
91	gene_id_7864	Bin_2	29.3995	10.7706	0
91	gene_id_7865	Bin_2	12.3139	0.4096	0
91	gene_id_7868	Bin_2	12.1736	2.78374	0
91	gene_id_7882	Bin_2	18.0782	0	0
91	gene_id_7888	Bin_2	11.1651	38.278	0.55471
9	gene_id_789	Bin_2	46.4178	7.25382	0
91	gene_id_7892	Bin_2	450.662	1255.46	0
91	gene_id_7893	Bin_2	44.4886	1.25909	0.888158
91	gene_id_7894	Bin_2	21.1525	0	0
91	gene_id_7895	Bin_2	15.4407	74.4121	0
1	gene_id_79	Bin_2	10.699	23.9513	0.938567
91	gene_id_7901	Bin_2	19.719	11.6639	0
91	gene_id_7902	Bin_2	20.1994	1.14564	0

91	gene_id_7903	Bin_2	23.815	45.816	0
91	gene_id_7905	Bin_2	8.29226	3.49216	0
91	gene_id_7922	Bin_2	38.5846	9.12897	2.58726
91	gene_id_7923	Bin_2	33.7334	13.4939	1.54865
91	gene_id_7926	Bin_2	5.81901	12.4337	0.516124
91	gene_id_7927	Bin_2	12.9906	18.521	0
91	gene_id_7928	Bin_2	20.3398	0	0
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91	gene_id_7929	Bin_2	8.83483	0	0
91	gene_id_7934	Bin_2	789.839	290.544	9.51091
91	gene_id_7935	Bin_2	20.4985	24.7834	0.339716
91	gene_id_7940	Bin_2	12.457	1.12172	0
91	gene_id_7941	Bin_2	47.4427	5.88563	1.03776
91	gene_id_7947	Bin_2	12.8088	0.538463	1.18336
91	gene_id_7951	Bin_2	10.1128	0	0
91	gene_id_7972	Bin_2	8.07506	16.6383	0
91	gene_id_7974	Bin_2	1268.44	0	0
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1	gene_id_8	Bin_2	13.3449	53.4814	0
1	gene_id_80	Bin_2	9.81073	28.1086	0
91	gene_id_8014	Bin_2	11.3641	0	0
91	gene_id_8016	Bin_2	16.3644	0	0.383278
91	gene_id_8020	Bin_2	12.2123	0	0
91	gene_id_8025	Bin_2	11.7685	0.783158	0.860846
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91	gene_id_8027	Bin_2	58.7618	4.58256	0.808198
91	gene_id_8029	Bin_2	10.8852	6.28832	0.403456
91	gene_id_8032	Bin_2	19.9433	1.92047	0
91	gene_id_8034	Bin_2	26.8989	29.7808	0
91	gene_id_8039	Bin_2	6.24734	23.3236	0
91	gene_id_8040	Bin_2	6.856	0	0
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91	gene_id_8055	Bin_2	10.5968	3.0337	2.715
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92	gene_id_8082	Bin_2	23.9232	20.5547	1.43146
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92	gene_id_8085	Bin_2	21.6795	8.14971	0
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1	gene_id_81	Bin_2	5.61211	23.3333	0
1	gene_id_82	Bin_2	3.27024	20.0776	0
95	gene_id_8200	Bin_2	9.7003	0.610905	0
95	gene_id_8203	Bin_2	22.7943	0	0.772433
95	gene_id_8204	Bin_2	32.9096	9.9159	11.2643
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1	gene_id_83	Bin_2	9.85676	40.3359	0
110	gene_id_8694	Bin_2	77.0331	1.33063	0
110	gene_id_8707	Bin_2	168.94	251.464	1.99464
110	gene_id_8709	Bin_2	16.2284	3.02223	0.213338
110	gene_id_8712	Bin_2	76.1159	1.12883	5.26903
110	gene_id_8713	Bin_2	39.7582	2.69038	1.30211
110	gene_id_8714	Bin_2	53.9361	0.566571	0
110	gene_id_8715	Bin_2	13.3672	0	1.32627
110	gene_id_8716	Bin_2	29.1542	0	0
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110	gene_id_8721	Bin_2	36.6857	0	0
110	gene_id_8722	Bin_2	9.53282	1.09279	0
110	gene_id_8724	Bin_2	17.1798	4.62395	0
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110	gene_id_8726	Bin_2	22.3737	1.26626	0
110	gene_id_8727	Bin_2	92.083	8.13683	0
110	gene_id_8737	Bin_2	101.931	6.82068	0
110	gene_id_8742	Bin_2	13.5657	0	0
110	gene_id_8745	Bin_2	22.6532	0	0
110	gene_id_8746	Bin_2	7.80992	2.27928	0
110	gene_id_8748	Bin_2	17.7827	0	1.63618
110	gene_id_8749	Bin_2	11.3847	2.05205	0.362077
110	gene_id_8754	Bin_2	42.3155	17.9893	2.97058
110	gene_id_8755	Bin_2	132.071	65.7313	0
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110	gene_id_8767	Bin_2	13.3491	7.53629	0
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1	gene_id_88	Bin_2	12.1187	27.9827	0
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11	gene_id_884	Bin_2	94.9457	0	1.51788
11	gene_id_885	Bin_2	69.9247	2.80796	4.17605
11	gene_id_886	Bin_2	23.4824	0	1.02758
1	gene_id_89	Bin_2	7.1234	24.1058	0
11	gene_id_891	Bin_2	93.232	26.9551	0
11	gene_id_893	Bin_2	1.11552	8.41703	0
11	gene_id_894	Bin_2	4.74427	16.1855	0
11	gene_id_898	Bin_2	91.9509	19.4472	15.6191
1	gene_id_9	Bin_2	11.9835	33.7669	0
1	gene_id_90	Bin_2	13.8928	36.2788	0
11	gene_id_900	Bin_2	15.9429	173.47	0
11	gene_id_901	Bin_2	0	77.5905	0
11	gene_id_903	Bin_2	46.1679	3.09274	2.23216
1	gene_id_91	Bin_2	81.2297	97.0868	6.19423
11	gene_id_910	Bin_2	75.0202	2.17908	2.39143
11	gene_id_911	Bin_2	280.656	4.09326	0
11	gene_id_913	Bin_2	28.7243	1.61556	0
11	gene_id_915	Bin_2	40.3988	52.6995	2.51424
11	gene_id_917	Bin_2	14.1705	1.05148	0.784374
11	gene_id_918	Bin_2	29.6281	33.1469	0
11	gene_id_919	Bin_2	53.1865	7.884	3.90805
1	gene_id_92	Bin_2	11.5001	17.1046	0
12	gene_id_927	Bin_2	13.3688	1.05397	0
12	gene_id_928	Bin_2	12.1134	2.03795	0
1	gene_id_93	Bin_2	5.63025	83.626	0
12	gene_id_934	Bin_2	177.235	67.7729	0
12	gene_id_935	Bin_2	21.2679	0	0
12	gene_id_939	Bin_2	13.1658	0.977564	0
1	gene_id_94	Bin_2	6.35968	12.9294	0
12	gene_id_940	Bin_2	89.2335	50.5493	4.42344
12	gene_id_944	Bin_2	35.9506	18.7594	0.661798
12	gene_id_946	Bin_2	11.403	1.79574	0
120	gene_id_9474	Bin_2	6.73059	0.850514	0
120	gene_id_9478	Bin_2	1919.19	0	0
120	gene_id_9490	Bin_2	8696.58	38.7177	260.121
120	gene_id_9491	Bin_2	24.4863	0	0
1	gene_id_95	Bin_2	1.7147	26.7796	0
12	gene_id_950	Bin_2	27.5151	0	0
122	gene_id_9504	Bin_2	18.1924	0	0

12	gene_id_955	Bin_2	14.2759	0.894601	0
1	gene_id_96	Bin_2	14.9778	41.903	0
12	gene_id_965	Bin_2	22.3242	0.381508	0
12	gene_id_966	Bin_2	86.8861	0	0
12	gene_id_968	Bin_2	83.2507	45.0723	0
1	gene_id_97	Bin_2	14.3694	39.3375	1.25535
12	gene_id_970	Bin_2	4.13909	9.51542	0
12	gene_id_971	Bin_2	693.337	15.7971	52.753
128	gene_id_9711	Bin_2	21.1435	5.99038	0
128	gene_id_9715	Bin_2	31.4032	0	0.755496
128	gene_id_9716	Bin_2	17.0218	1.0635	0
128	gene_id_9729	Bin_2	37.6719	0	0
129	gene_id_9732	Bin_2	21.7634	0.622877	0
129	gene_id_9738	Bin_2	15.7915	0	0.697034
129	gene_id_9748	Bin_2	23.7472	9.11818	0
129	gene_id_9750	Bin_2	30.5097	2.53252	1.88497
129	gene_id_9751	Bin_2	32.2161	2.8807	0
129	gene_id_9752	Bin_2	335.281	30.2684	15.6062
129	gene_id_9753	Bin_2	59.8365	27.3653	8.19339
129	gene_id_9755	Bin_2	38.0006	9.73343	2.89324
129	gene_id_9757	Bin_2	3.45119	7.95382	0
129	gene_id_9761	Bin_2	26.137	5.77386	0
1	gene_id_98	Bin_2	10.6462	37.115	0.170134
12	gene_id_989	Bin_2	9.83678	0	0.437136
1	gene_id_99	Bin_2	16.7964	27.6532	2.56954
131	gene_id_9931	Bin_2	17.8903	0	0
131	gene_id_9934	Bin_2	21.0208	1.02014	0.360003
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131	gene_id_9937	Bin_2	126.444	1.81254	0
131	gene_id_9938	Bin_2	33.8905	0	0
131	gene_id_9943	Bin_2	9.29567	0	0
131	gene_id_9950	Bin_2	14.1293	0	0
131	gene_id_9951	Bin_2	42.4142	1.63934	0
131	gene_id_9952	Bin_2	1218.17	23.1798	8.11356
131	gene_id_9954	Bin_2	18.4832	24.0575	3.98366
131	gene_id_9955	Bin_2	27.7855	27.9068	1.97001
131	gene_id_9957	Bin_2	12.371	0	0.685698
12	gene_id_996	Bin_2	32.9268	1.28084	0
131	gene_id_9960	Bin_2	34.6328	6.66506	0.427617
131	gene_id_9962	Bin_2	27.0473	0	0.793903
131	gene_id_9963	Bin_2	11.1829	4.3392	2.384
131	gene_id_9965	Bin_2	2196.89	165.413	319.355
131	gene_id_9966	Bin_2	107.255	101.132	93.3449
131	gene_id_9967	Bin_2	17.9318	0	0
131	gene_id_9982	Bin_2	72.0879	27.751	1.3046
131	gene_id_9985	Bin_2	20.5777	0	0
131	gene_id_9987	Bin_2	40.2568	1.90525	4.1753

131	gene_id_9990	Bin_2	50.0134	5.78314	10.2298
131	gene_id_9991	Bin_2	36.1032	1.71503	0
131	gene_id_9992	Bin_2	5.20798	13.0108	0
131	gene_id_9995	Bin_2	9.91154	0.313729	0.221458
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135	gene_id_10364	Bin_3	0	662.389	0
135	gene_id_10366	Bin_3	0	12.9477	0
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135	gene_id_10373	Bin_3	1.14851	15.8818	0
135	gene_id_10374	Bin_3	15.083	35.2974	14.8342
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135	gene_id_10380	Bin_3	19.8719	4.98666	2.99817
135	gene_id_10381	Bin_3	68.7877	17.1423	23.9894
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14	gene_id_1055	Bin_3	3.95295	14.7747	0
14	gene_id_1057	Bin_3	29.6736	27.5793	3.35962
14	gene_id_1062	Bin_3	6.74595	9.46379	9.65645
14	gene_id_1064	Bin_3	69.4057	17.9219	22.8895
14	gene_id_1065	Bin_3	167.373	23.6332	265.329
14	gene_id_1077	Bin_3	151.794	74.59	499.068
149	gene_id_10875	Bin_3	0	26.6512	0
149	gene_id_10878	Bin_3	12.3541	14.4974	7.57719
14	gene_id_1117	Bin_3	4.63092	33.4881	1.97001
14	gene_id_1119	Bin_3	0	2186.87	0
14	gene_id_1121	Bin_3	0	12.117	0
14	gene_id_1122	Bin_3	0	16.4614	0
14	gene_id_1123	Bin_3	3.36229	32.8677	0
14	gene_id_1124	Bin_3	0	7.60757	0.413002
14	gene_id_1127	Bin_3	4.50213	38.8429	1.37551
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185	gene_id_11813	Bin_3	0	360.206	0
185	gene_id_11814	Bin_3	1.41994	209.849	0.632975
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188	gene_id_11843	Bin_3	1.65136	7.81226	0
188	gene_id_11851	Bin_3	0	22.9359	1.01105
188	gene_id_11852	Bin_3	1.32194	34.6669	0.589619
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210	gene_id_13394	Bin_3	0	13.2858	0
210	gene_id_13431	Bin_3	0	35.9169	0
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218	gene_id_13780	Bin_3	22.2306	99.6537	0
218	gene_id_13783	Bin_3	0	60.1248	3.57472
218	gene_id_13786	Bin_3	9.34241	127.563	34.1731
218	gene_id_13787	Bin_3	237.694	1587.81	505.542
220	gene_id_13790	Bin_3	1.59122	7.02822	0
220	gene_id_13793	Bin_3	0	6.91608	0
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228	gene_id_14022	Bin_3	38.8256	207.585	0
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228	gene_id_14030	Bin_3	0	12.9253	0
228	gene_id_14034	Bin_3	5.8634	52.0852	12.5281
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228	gene_id_14038	Bin_3	5.76011	19.5414	0
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228	gene_id_14043	Bin_3	2.36412	14.6656	0
228	gene_id_14044	Bin_3	0.516391	12.2909	0.115694
228	gene_id_14046	Bin_3	0	200.174	19.9976
228	gene_id_14048	Bin_3	1.13177	14.2303	0

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228	gene_id_14055	Bin_3	5.17591	6.22412	0.231237
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244	gene_id_14440	Bin_3	7.81745	40.4537	0
244	gene_id_14443	Bin_3	343.109	1331.37	59.349
244	gene_id_14446	Bin_3	1.2811	13.6693	0
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244	gene_id_14449	Bin_3	3.33249	75.642	0
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249	gene_id_14586	Bin_3	173.772	194.02	0
249	gene_id_14588	Bin_3	1.61191	22.178	2.21306
249	gene_id_14589	Bin_3	45.1074	63.1097	0
249	gene_id_14593	Bin_3	0	7.88763	0
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261	gene_id_15036	Bin_3	0	19.8645	0
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261	gene_id_15043	Bin_3	2.72838	41.266	0.854968

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278	gene_id_15164	Bin_3	8.94655	58.0781	1.57586
278	gene_id_15171	Bin_3	0	19.0853	0
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278	gene_id_15177	Bin_3	129.7	946.924	7.1941
278	gene_id_15178	Bin_3	33.7911	153.521	28.0385
278	gene_id_15179	Bin_3	10.3107	62.6207	2.63443
278	gene_id_15180	Bin_3	2.54059	51.3882	2.3319
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287	gene_id_15272	Bin_3	13.7658	22.7891	25.1008
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317	gene_id_16311	Bin_3	0	19.1095	0
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325	gene_id_16407	Bin_3	0	21.1708	0
325	gene_id_16408	Bin_3	1.23362	25.5646	0
325	gene_id_16409	Bin_3	2.04079	61.8876	1.24808
325	gene_id_16410	Bin_3	0.358024	66.2817	0.819691
325	gene_id_16411	Bin_3	1.23659	94.9865	0
325	gene_id_16412	Bin_3	1.14355	86.076	0.795136
325	gene_id_16413	Bin_3	4.60908	154.382	0.739641
325	gene_id_16414	Bin_3	0	20.5038	0.371057
325	gene_id_16415	Bin_3	1.95985	1359.16	85.9458
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327	gene_id_16452	Bin_3	0.716517	56.11	5.93133
327	gene_id_16455	Bin_3	202.983	50.4878	59.8975
327	gene_id_16456	Bin_3	0	36.2632	0

327	gene_id_16460	Bin_3	0	87.7399	0
327	gene_id_16462	Bin_3	0	8.65547	0
327	gene_id_16464	Bin_3	1.27609	10.8888	0.28466
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327	gene_id_16467	Bin_3	0	7.43615	0
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331	gene_id_16574	Bin_3	5.06865	8.75001	0.561304
331	gene_id_16576	Bin_3	9.11469	83.1499	3.6665
331	gene_id_16577	Bin_3	190.784	49.3637	77.4077
331	gene_id_16578	Bin_3	41.2317	152.364	21.2404
331	gene_id_16579	Bin_3	6.43282	407.354	1.41926
331	gene_id_16580	Bin_3	23.9228	406.043	2.13072
331	gene_id_16581	Bin_3	7.97352	48.4196	12.7446
331	gene_id_16585	Bin_3	6.22878	34.8838	0.911343
331	gene_id_16586	Bin_3	0	12.9407	11.4522
333	gene_id_16594	Bin_3	0	9.49251	0
333	gene_id_16597	Bin_3	2.01848	7.62392	0.448364
333	gene_id_16598	Bin_3	6.96312	38.3716	0
333	gene_id_16600	Bin_3	2.48479	23.4035	1.163
333	gene_id_16601	Bin_3	2.33538	38.1579	0
333	gene_id_16606	Bin_3	0	29.6039	0
333	gene_id_16607	Bin_3	13.176	148.465	5.09352
333	gene_id_16611	Bin_3	53.2482	70.5076	34.9207
333	gene_id_16614	Bin_3	21.658	35.4926	0
333	gene_id_16615	Bin_3	0	9.03685	1.34671
333	gene_id_16624	Bin_3	0.964676	6.07569	0
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348	gene_id_16942	Bin_3	10.3521	55.7091	0
348	gene_id_16943	Bin_3	171.563	1089.22	0
348	gene_id_16944	Bin_3	28.673	50.9601	0.413481
348	gene_id_16945	Bin_3	2.30185	22.8623	2.12603
348	gene_id_16946	Bin_3	0	19.9636	0.485799
348	gene_id_16947	Bin_3	12.4932	77.9863	0.785959
348	gene_id_16948	Bin_3	0	123.565	0
348	gene_id_16962	Bin_3	0	10.1365	0
348	gene_id_16964	Bin_3	0	9.94572	0
348	gene_id_16966	Bin_3	10.5089	82.8431	0
348	gene_id_16967	Bin_3	0	15.1347	0
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355	gene_id_17002	Bin_3	7.39226	16.7962	0
355	gene_id_17014	Bin_3	0	34.2179	0.58703
355	gene_id_17016	Bin_3	3.04284	41.2132	5.56888

355	gene_id_17020	Bin_3	128.288	1766.13	0
355	gene_id_17024	Bin_3	7.89573	85.9515	0.697034
355	gene_id_17025	Bin_3	488.065	827.67	55.7658
377	gene_id_17235	Bin_3	44.7334	11.2734	71.0352
378	gene_id_17238	Bin_3	3.26167	17.727	1.19725
378	gene_id_17239	Bin_3	27.8525	21.3176	18.2026
378	gene_id_17244	Bin_3	1.71532	10.8499	4.96755
378	gene_id_17245	Bin_3	1.1542	15.2341	1.08165
378	gene_id_17253	Bin_3	1.71412	10.8085	0
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388	gene_id_17383	Bin_3	1.86074	33.6568	0
391	gene_id_17449	Bin_3	0	17.6432	0
417	gene_id_17669	Bin_3	1.15229	29.6943	0
417	gene_id_17674	Bin_3	23.3082	36.5034	0
420	gene_id_17676	Bin_3	4.44083	10.4718	0
420	gene_id_17679	Bin_3	71.7303	51.4396	5.73287
420	gene_id_17682	Bin_3	1.19157	8.98343	0
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422	gene_id_17694	Bin_3	0	18.4048	0
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424	gene_id_17710	Bin_3	7.99573	75.3577	3.61332
424	gene_id_17715	Bin_3	1.21014	106.418	1.13327
424	gene_id_17718	Bin_3	85.9724	3.2039	11.7989
424	gene_id_17719	Bin_3	0	11.4207	0.503712

424	gene_id_17720	Bin_3	0	15.9617	0
424	gene_id_17722	Bin_3	9.70405	71.532	0
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433	gene_id_17835	Bin_3	3.38672	6.40728	1.55027
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434	gene_id_17872	Bin_3	70.2935	71.1282	3.03406
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440	gene_id_17984	Bin_3	28.9598	345.388	2.2755
453	gene_id_18143	Bin_3	2.19352	17.7221	0
453	gene_id_18145	Bin_3	0.947677	8.35762	0
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461	gene_id_18247	Bin_3	0.693764	13.1472	0.654002
465	gene_id_18299	Bin_3	17.5833	55.3152	0
465	gene_id_18336	Bin_3	4.20548	25.4824	0.620008
468	gene_id_18378	Bin_3	1.6731	9.49697	0
468	gene_id_18379	Bin_3	4.72431	36.9609	0
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468	gene_id_18400	Bin_3	8.23028	99.9243	0
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468	gene_id_18402	Bin_3	3.22383	25.2023	0
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496	gene_id_18785	Bin_3	0	11.9414	0
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499	gene_id_18810	Bin_3	0	12.9522	0
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508	gene_id_18979	Bin_3	0.317246	13.2811	0.300516
510	gene_id_19015	Bin_3	0.828616	12.021	0
517	gene_id_19048	Bin_3	0	10.4909	0
517	gene_id_19049	Bin_3	756.901	5714.21	0
517	gene_id_19050	Bin_3	0	157.625	6.90648
517	gene_id_19059	Bin_3	5.55267	12.7001	0
517	gene_id_19062	Bin_3	3.50307	7.33805	1.09411
517	gene_id_19063	Bin_3	11.5233	5.45775	0
517	gene_id_19064	Bin_3	52.0317	32.1945	5.7995
517	gene_id_19065	Bin_3	4.69502	18.6058	0
517	gene_id_19068	Bin_3	0	18.2245	0
517	gene_id_19077	Bin_3	0.960515	19.7653	0.453976
522	gene_id_19145	Bin_3	8.08793	34.4029	10.5881
522	gene_id_19150	Bin_3	2.37214	27.9567	0

522	gene_id_19152	Bin_3	0	14.6279	1.09052
522	gene_id_19153	Bin_3	0	14.812	0
522	gene_id_19154	Bin_3	0	15.2171	0
522	gene_id_19155	Bin_3	0.566218	9.67061	0
523	gene_id_19162	Bin_3	0	17.5552	3.84778
525	gene_id_19168	Bin_3	0	48.7058	0
525	gene_id_19172	Bin_3	0	13.0301	0
525	gene_id_19175	Bin_3	0	8.6348	0
539	gene_id_19310	Bin_3	3.56948	164.885	2.35788
539	gene_id_19317	Bin_3	2.4981	9.41088	1.16913
539	gene_id_19318	Bin_3	7.2274	50.467	2.9704
542	gene_id_19331	Bin_3	2.7553	18.7213	2.53046
542	gene_id_19332	Bin_3	0	5.34582	0.377295
542	gene_id_19333	Bin_3	3.11044	22.9608	0
542	gene_id_19334	Bin_3	2.51731	23.3851	1.09947
542	gene_id_19336	Bin_3	1.80782	11.2821	0
548	gene_id_19396	Bin_3	2.57287	20.702	25.4403
557	gene_id_19455	Bin_3	1.90309	13.7859	2.16308
557	gene_id_19458	Bin_3	10.107	22.2682	0
557	gene_id_19459	Bin_3	1.38242	16.4677	0
557	gene_id_19463	Bin_3	1.2005	18.5982	0.267912
557	gene_id_19465	Bin_3	3.29991	671.478	2.99194
559	gene_id_19474	Bin_3	0	8.29561	0
559	gene_id_19476	Bin_3	0	16.2304	0
559	gene_id_19478	Bin_3	0	13.3462	0
559	gene_id_19479	Bin_3	4.81673	20.0224	2.715
559	gene_id_19481	Bin_3	180.43	132.53	18.308
559	gene_id_19486	Bin_3	2.73376	16.8904	1.19109
559	gene_id_19488	Bin_3	0	62.8506	11.0125
559	gene_id_19489	Bin_3	0	15.9376	0
559	gene_id_19492	Bin_3	0	11.9265	0
559	gene_id_19493	Bin_3	2.92985	11.7478	0.436456
559	gene_id_19493	Bin_3	0.581283	11.7478	0.436456
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559	gene_id_19498	Bin_3	0	5.63058	0.646373
559	gene_id_19500	Bin_3	2.28202	7.17247	2.13895
561	gene_id_19513	Bin_3	44.5823	35.349	7.72531
561	gene_id_19525	Bin_3	4.04442	23.9228	1.77632
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561	gene_id_19526	Bin_3	1.53747	15.397	0
561	gene_id_19533	Bin_3	8.05957	13.1052	7.19171
561	gene_id_19534	Bin_3	11.164	21.1323	5.76289
561	gene_id_19540	Bin_3	8.29857	298.981	3.74489

561	gene_id_19541	Bin_3	0	69.8748	0
561	gene_id_19542	Bin_3	9.13355	139.052	0
561	gene_id_19543	Bin_3	2.07651	109.08	1.67671
561	gene_id_19544	Bin_3	1.9757	54.7365	0
561	gene_id_19545	Bin_3	2.23769	107.231	0
561	gene_id_19546	Bin_3	0	66.5241	0
561	gene_id_19547	Bin_3	17.5833	236.347	103.784
561	gene_id_19548	Bin_3	128.899	71.9685	22.5485
561	gene_id_19549	Bin_3	22.9351	0.898212	0
561	gene_id_19550	Bin_3	2.84492	19.3108	0
561	gene_id_19555	Bin_3	5.25322	181.983	2.21583
563	gene_id_19565	Bin_3	0	16.5381	0
563	gene_id_19567	Bin_3	3.51651	25.8261	0
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563	gene_id_19569	Bin_3	0	20.1503	0
563	gene_id_19570	Bin_3	0	44.4677	1.12369
564	gene_id_19580	Bin_3	10.6869	10.4027	0.683124
564	gene_id_19581	Bin_3	31.219	38.6334	44.743
564	gene_id_19582	Bin_3	61.9327	210.737	236.289
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564	gene_id_19585	Bin_3	2.19352	19.0853	0
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564	gene_id_19589	Bin_3	0	9.56256	0
564	gene_id_19590	Bin_3	0	14.7629	2.19625
564	gene_id_19591	Bin_3	44.5292	118.453	0
564	gene_id_19592	Bin_3	1.07109	12.1285	0
564	gene_id_19593	Bin_3	1.00778	9.51631	0.447725
564	gene_id_19596	Bin_3	1.3609	426.713	1.20437
564	gene_id_19597	Bin_3	112.952	248.744	14.4407
564	gene_id_19598	Bin_3	1.03463	6.5113	0
564	gene_id_19599	Bin_3	1.05972	9.33435	0
564	gene_id_19600	Bin_3	11.0485	57.809	0
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564	gene_id_19601	Bin_3	0	7.56594	0
564	gene_id_19602	Bin_3	5.55798	15.1752	7.50815
564	gene_id_19604	Bin_3	0	77.9531	0

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568	gene_id_19701	Bin_3	1.11021	7.6793	0
568	gene_id_19702	Bin_3	12.9119	18.2049	1.04181
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568	gene_id_19705	Bin_3	29.4056	103.315	15.8899
570	gene_id_19719	Bin_3	1.96536	24.489	0
570	gene_id_19720	Bin_3	8.36472	53.3712	0
570	gene_id_19723	Bin_3	3.48156	21.3176	7.67841
574	gene_id_19764	Bin_3	2.41585	8.31604	1.73504
574	gene_id_19765	Bin_3	4.96957	23.4035	4.52794
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574	gene_id_19767	Bin_3	4.99863	23.2225	0
574	gene_id_19768	Bin_3	0	47.2289	0
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579	gene_id_19827	Bin_3	1.00758	20.4096	0.476077
579	gene_id_19828	Bin_3	9.031	31.5859	2.72547
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581	gene_id_19837	Bin_3	0	11.8976	0
581	gene_id_19847	Bin_3	3.01526	13.2152	0
581	gene_id_19848	Bin_3	0	11.3989	1.46219
581	gene_id_19854	Bin_3	0	20.1503	2.60106
581	gene_id_19855	Bin_3	1.54721	9.76491	0
582	gene_id_19869	Bin_3	24.3443	0.384807	0.271617
582	gene_id_19871	Bin_3	12.3483	0.410734	0.289913
582	gene_id_19875	Bin_3	21.5822	3.36756	0
582	gene_id_19876	Bin_3	18.6074	13.927	0
582	gene_id_19878	Bin_3	2.14515	10.5398	0
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582	gene_id_19879	Bin_3	2.60516	13.8953	0.576759
582	gene_id_19880	Bin_3	10.8653	45.9279	13.6534
583	gene_id_19883	Bin_3	2.42984	40.6691	0
583	gene_id_19884	Bin_3	6.03322	81.7414	0
583	gene_id_19885	Bin_3	0	53.026	0
583	gene_id_19888	Bin_3	3.27024	60.2328	0
583	gene_id_19889	Bin_3	25.9194	158.789	0
583	gene_id_19892	Bin_3	8.83214	53.1917	0.357545

583	gene_id_19893	Bin_3	5.08361	34.6589	0
583	gene_id_19899	Bin_3	0	15.5078	0
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583	gene_id_19902	Bin_3	0	13.1434	0
583	gene_id_19905	Bin_3	12.1544	24.3197	0.490348
583	gene_id_19906	Bin_3	18.667	18.4272	0.565344
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583	gene_id_19907	Bin_3	1.33583	12.6609	0
583	gene_id_19911	Bin_3	2.23104	8.41703	6.10767
583	gene_id_19915	Bin_3	1.44232	9.94053	0
583	gene_id_19916	Bin_3	15.958	10.8449	3.07557
583	gene_id_19917	Bin_3	303.962	108.171	681.534
583	gene_id_19920	Bin_3	24.2553	64.4627	10.3924
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588	gene_id_19983	Bin_3	1.22147	6.56442	0.27256
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593	gene_id_20082	Bin_3	1.67558	10.2467	0.776841
593	gene_id_20089	Bin_3	8.66595	16.3252	1.15894
593	gene_id_20090	Bin_3	3.91023	27.7221	0
593	gene_id_20091	Bin_3	0	39.9669	0.854348
596	gene_id_20153	Bin_3	20.2577	47.4275	2.79187
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597	gene_id_20167	Bin_3	47.3304	64.2542	22.3966
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597	gene_id_20170	Bin_3	1.4727	11.069	0
600	gene_id_20211	Bin_3	2.16633	26.9347	0
600	gene_id_20214	Bin_3	5.76926	15.3626	0
600	gene_id_20215	Bin_3	0.679602	6.86976	0
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600	gene_id_20217	Bin_3	0.726193	9.17123	0.32366
600	gene_id_20219	Bin_3	0	16.0792	0
600	gene_id_20223	Bin_3	4.4638	14.0908	0
607	gene_id_20263	Bin_3	4.80252	40.0514	7.22206
607	gene_id_20264	Bin_3	7.98291	36.1987	0
607	gene_id_20266	Bin_3	0	10.5869	0
611	gene_id_20304	Bin_3	32.175	569.994	0
611	gene_id_20306	Bin_3	25.1549	292.255	18.5851
618	gene_id_20382	Bin_3	19.0616	1116.3	15.3203
618	gene_id_20384	Bin_3	0	31.1615	0
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620	gene_id_20393	Bin_3	4.03555	15.1869	0.595338
620	gene_id_20395	Bin_3	2.99588	13.1316	0
637	gene_id_20531	Bin_3	4.21511	51.1299	2.8761
649	gene_id_20630	Bin_3	1.15229	19.5548	0
649	gene_id_20631	Bin_3	1.307	13.7991	1.01894
652	gene_id_20644	Bin_3	44.7416	9.88315	8.71681
652	gene_id_20646	Bin_3	7.86128	45.4527	0
652	gene_id_20647	Bin_3	5.29265	50.5508	2.23126
653	gene_id_20653	Bin_3	0	18.2468	0
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653	gene_id_20660	Bin_3	1.35825	11.0733	3.14018
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661	gene_id_20719	Bin_3	0	40.021	0
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661	gene_id_20722	Bin_3	5.9535	34.4868	0
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664	gene_id_20729	Bin_3	22.5047	35.6582	3.59326
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664	gene_id_20731	Bin_3	5.25085	21.1456	0.466332
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664	gene_id_20737	Bin_3	33.5146	654.173	0
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665	gene_id_20743	Bin_3	0	17.7809	1.65508

689	gene_id_21073	Bin_3	0	21.2265	0
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689	gene_id_21082	Bin_3	1.25804	11.0573	0
689	gene_id_21089	Bin_3	0	88.0394	0
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689	gene_id_21092	Bin_3	7.76933	80.8653	3.17229
689	gene_id_21093	Bin_3	2.18666	17.6679	0
689	gene_id_21094	Bin_3	6.37114	18.6739	0.376803
689	gene_id_21099	Bin_3	9.32329	47.7352	10.3343
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689	gene_id_21099	Bin_3	9.32329	14.5561	0.302181
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689	gene_id_21100	Bin_3	5.92756	16.3869	0
689	gene_id_21101	Bin_3	3.13001	15.668	0
689	gene_id_21102	Bin_3	3.32344	92.4424	0.732799
689	gene_id_21103	Bin_3	0.725439	7.78752	0
689	gene_id_21105	Bin_3	2.51157	29.1711	1.17533
689	gene_id_21107	Bin_3	1.03924	13.734	0
712	gene_id_21267	Bin_3	0	34.0809	0
712	gene_id_21268	Bin_3	7.33701	8.44799	2.7708
712	gene_id_21269	Bin_3	239.029	0	117.511
713	gene_id_21272	Bin_3	3.39437	12.9031	1.58362
713	gene_id_21273	Bin_3	2.08867	24.6912	0
713	gene_id_21275	Bin_3	0	10.5208	0
713	gene_id_21276	Bin_3	1.93276	14.4547	0.849726
713	gene_id_21277	Bin_3	0	42.9458	1.59435
720	gene_id_21292	Bin_3	0	28.2102	0
720	gene_id_21296	Bin_3	7.36631	41.0861	4.40993
720	gene_id_21297	Bin_3	2.03991	19.0481	0
720	gene_id_21298	Bin_3	23.0994	3.09437	0
720	gene_id_21299	Bin_3	44.007	8.0048	4.42826
720	gene_id_21299	Bin_3	23.4795	8.0048	4.42826
720	gene_id_21299	Bin_3	44.007	2.11545	0.373261
720	gene_id_21299	Bin_3	23.4795	2.11545	0.373261
720	gene_id_21300	Bin_3	117.126	3.82052	22.4709
720	gene_id_21307	Bin_3	1.48253	12.8267	0.220836
720	gene_id_21308	Bin_3	3.84443	32.7957	0
720	gene_id_21312	Bin_3	4.43199	24.5848	0
720	gene_id_21317	Bin_3	20.8476	52.7329	16.7666
720	gene_id_21318	Bin_3	1.307	20.9746	0.194819
720	gene_id_21322	Bin_3	0	6.22877	0.929024
720	gene_id_21323	Bin_3	0	14.6425	0.543817
720	gene_id_21328	Bin_3	0	32.1477	0
720	gene_id_21330	Bin_3	20.4588	21.6496	57.38
720	gene_id_21332	Bin_3	0.678283	5.57093	0
720	gene_id_21334	Bin_3	3.59309	9.02899	2.71465
720	gene_id_21336	Bin_3	734.731	94.7628	34.327

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741	gene_id_21483	Bin_3	0	454.073	9.0762
741	gene_id_21485	Bin_3	2.42027	17.4829	0
741	gene_id_21486	Bin_3	0	22.9452	0
741	gene_id_21487	Bin_3	5.50043	44.1318	0.349978
741	gene_id_21490	Bin_3	10.1204	0.706991	30.2253
742	gene_id_21491	Bin_3	53.7977	43.3175	19.7211
742	gene_id_21494	Bin_3	128.803	83.3496	27.1386
745	gene_id_21506	Bin_3	0	15.3681	0
745	gene_id_21509	Bin_3	0	12.3972	0
751	gene_id_21560	Bin_3	5.71923	39.2197	0.83839
751	gene_id_21561	Bin_3	7.39618	39.3977	1.09761
751	gene_id_21564	Bin_3	97.2494	759.065	28.6312
751	gene_id_21566	Bin_3	1.68576	11.5878	0
766	gene_id_21711	Bin_3	152.568	150.598	35.523
766	gene_id_21714	Bin_3	1.13177	14.2303	0.502102
766	gene_id_21715	Bin_3	5.21436	124.646	9.03801
766	gene_id_21716	Bin_3	12.9703	13.1912	18.1846
769	gene_id_21727	Bin_3	0	8.267	0.822197
769	gene_id_21728	Bin_3	1.99828	13.8389	0.44393
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769	gene_id_21730	Bin_3	27.7855	66.9763	0
769	gene_id_21731	Bin_3	140.122	72.8255	27.8967
769	gene_id_21732	Bin_3	5.04512	18.917	4.6964
769	gene_id_21735	Bin_3	54.8373	108.243	108.93
769	gene_id_21738	Bin_3	0	12.6516	0
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769	gene_id_21741	Bin_3	17.2365	29.564	15.2123
769	gene_id_21742	Bin_3	7.09119	299.488	2.4109
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774	gene_id_21765	Bin_3	0.645112	28.9484	0
774	gene_id_21768	Bin_3	22.0582	166.593	5.71928
774	gene_id_21770	Bin_3	5.78391	64.209	0
774	gene_id_21771	Bin_3	13.4494	395.273	4.02577

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786	gene_id_21858	Bin_3	0	9.19089	0
786	gene_id_21860	Bin_3	5.3001	13.2365	1.64282
799	gene_id_21975	Bin_3	2.54004	8.54304	0
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816	gene_id_22077	Bin_3	0	35.107	0
816	gene_id_22078	Bin_3	0	21.1171	0
816	gene_id_22079	Bin_3	54.1501	233.378	6.48037
816	gene_id_22081	Bin_3	25.6037	8.04533	27.596
816	gene_id_22084	Bin_3	8.85892	25.479	0
816	gene_id_22088	Bin_3	3.22383	16.1294	0
825	gene_id_22162	Bin_3	24.8922	73.349	0
825	gene_id_22165	Bin_3	4.65801	6.26022	0
825	gene_id_22169	Bin_3	0	38.7651	0
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825	gene_id_22181	Bin_3	1.21857	8.41893	2.2212
848	gene_id_22321	Bin_3	1.56669	12.2287	0.233298
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864	gene_id_22439	Bin_3	0	14.643	0
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864	gene_id_22445	Bin_3	0	83.2937	0

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864	gene_id_22447	Bin_3	2.02894	87.5963	0.904803
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879	gene_id_22516	Bin_3	12.642	91.9645	1.80271
879	gene_id_22517	Bin_3	7.14053	6.5506	37.7859
879	gene_id_22519	Bin_3	3.71024	9.35086	0
883	gene_id_22548	Bin_3	13.418	34.6509	0.842888
883	gene_id_22549	Bin_3	0	25.0957	0
883	gene_id_22550	Bin_3	131.331	222.773	6.88476
883	gene_id_22551	Bin_3	100.08	1.41398	56.2338
883	gene_id_22552	Bin_3	29.6293	20.5814	2.17808
883	gene_id_22554	Bin_3	23.2169	0	38.2392
888	gene_id_22593	Bin_3	0.842598	14.8789	0
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888	gene_id_22598	Bin_3	0.895895	32.0609	1.0475
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895	gene_id_22672	Bin_3	1267.18	1738.74	0
895	gene_id_22673	Bin_3	161.093	63.7	0
895	gene_id_22674	Bin_3	0	25.8375	0
895	gene_id_22682	Bin_3	2.70076	24.0231	1.98632
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907	gene_id_22776	Bin_3	0.761801	10.098	0.717513
941	gene_id_22896	Bin_3	1566.06	177.898	165.628
942	gene_id_22901	Bin_3	3.02741	32.0101	3.1888
942	gene_id_22904	Bin_3	0	486.132	2.79187
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942	gene_id_22906	Bin_3	14.4252	33.7608	11.2909
942	gene_id_22908	Bin_3	5.3677	27.1039	1.74701
942	gene_id_22909	Bin_3	0	8.1438	0
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944	gene_id_22916	Bin_3	0	38.3046	0
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957	gene_id_23015	Bin_3	0	157.717	0
957	gene_id_23017	Bin_3	1.2358	8.53638	0
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961	gene_id_23032	Bin_3	2.94764	14.4235	0
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972	gene_id_23089	Bin_3	1.26259	7.92622	0
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984	gene_id_23163	Bin_3	288.238	73.5912	1884.92
984	gene_id_23164	Bin_3	2.55284	12.0178	0
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984	gene_id_23171	Bin_3	0.717989	16.7766	0.320033
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998	gene_id_23253	Bin_3	1.93812	15.7018	0
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1006	gene_id_23294	Bin_3	2.9147	11.8684	0
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1106	gene_id_23827	Bin_3	45.1074	75.7316	22.7529
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1116	gene_id_23911	Bin_3	0	66.0296	3.88037
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1164	gene_id_24133	Bin_3	0	15.7642	0
1167	gene_id_24142	Bin_3	2.73243	35.9819	0
1167	gene_id_24144	Bin_3	9.47677	15.5213	13.4433
1167	gene_id_24146	Bin_3	0	6.12086	0
1167	gene_id_24147	Bin_3	0	26.3263	0
1170	gene_id_24157	Bin_3	0	10.0142	0
1194	gene_id_24270	Bin_3	866.08	117.325	277.324
1194	gene_id_24274	Bin_3	19.0616	112.655	0
1194	gene_id_24275	Bin_3	1.22929	11.5799	0.544759
1194	gene_id_24276	Bin_3	40.1272	138.823	0
1194	gene_id_24276	Bin_3	8.32798	138.823	0
1194	gene_id_24276	Bin_3	40.1272	25.2603	0
1194	gene_id_24276	Bin_3	8.32798	25.2603	0
1194	gene_id_24277	Bin_3	45.0651	88.5245	25.936
1204	gene_id_24323	Bin_3	4.20244	13.0717	0
1204	gene_id_24325	Bin_3	46.9047	35.6944	0
1253	gene_id_24555	Bin_3	0	8.56711	0
1262	gene_id_24589	Bin_3	7.62033	14.3109	0
1262	gene_id_24590	Bin_3	3.37853	14.3819	0
1262	gene_id_24591	Bin_3	1.10996	4.21327	0

1267	gene_id_24620	Bin_3	0.808493	8.67122	1.52207
1267	gene_id_24621	Bin_3	0.712138	7.64585	0
1267	gene_id_24624	Bin_3	0.544181	9.98511	0.486086
1267	gene_id_24626	Bin_3	121.103	153.974	65.7287
1267	gene_id_24627	Bin_3	0	7.21838	0.391883
1268	gene_id_24630	Bin_3	26.4417	2.53252	0
1268	gene_id_24631	Bin_3	14.6484	8.43343	0.541007
1268	gene_id_24632	Bin_3	10.0302	2.87309	0
1268	gene_id_24633	Bin_3	20.7824	3.41683	1.20572
1268	gene_id_24634	Bin_3	8.08884	32.7364	0
1273	gene_id_24667	Bin_3	136.783	399.662	26.6238
1273	gene_id_24668	Bin_3	2.32374	16.0642	0
1273	gene_id_24675	Bin_3	3.50811	21.4471	0.261012
1273	gene_id_24675	Bin_3	1.50439	21.4471	0.261012
1273	gene_id_24675	Bin_3	3.50811	12.2452	0
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1278	gene_id_24684	Bin_3	5.88113	19.938	0
1278	gene_id_24686	Bin_3	0	11.2368	0
1278	gene_id_24687	Bin_3	3.75386	15.7125	0
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1278	gene_id_24689	Bin_3	2.24278	18.1104	6.11121
1278	gene_id_24690	Bin_3	0	28.9125	0
1295	gene_id_24728	Bin_3	0	7.26879	0
1295	gene_id_24729	Bin_3	2.71256	21.7924	1.18214
1330	gene_id_24842	Bin_3	1.7939	15.6758	0
1331	gene_id_24846	Bin_3	76.3104	25.6908	7.44536
1333	gene_id_24850	Bin_3	7.16722	66.4677	0
1333	gene_id_24851	Bin_3	14.3792	80.2519	21.6503
1333	gene_id_24851	Bin_3	6.16609	80.2519	21.6503
1333	gene_id_24851	Bin_3	1.02103	80.2519	21.6503
1333	gene_id_24851	Bin_3	14.3792	13.496	1.86557
1333	gene_id_24851	Bin_3	6.16609	13.496	1.86557
1333	gene_id_24851	Bin_3	1.02103	13.496	1.86557
1333	gene_id_24851	Bin_3	14.3792	28.4575	0
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1333	gene_id_24851	Bin_3	1.02103	28.4575	0
1358	gene_id_24968	Bin_3	1.79852	22.4504	0
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1358	gene_id_24968	Bin_3	1.36318	10.3346	0
1360	gene_id_24975	Bin_3	0	27.9833	1.40955
1390	gene_id_25067	Bin_3	1.18955	8.22098	0
1412	gene_id_25141	Bin_3	0	16.7228	0
1421	gene_id_25181	Bin_3	34.0789	4.23232	9.17358
1421	gene_id_25182	Bin_3	507.602	64.131	955.586

1421	gene_id_25183	Bin_3	14.6345	5.5003	6.68547
1458	gene_id_25281	Bin_3	2.49365	8.01872	0.797544
1458	gene_id_25281	Bin_3	0	8.01872	0.797544
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1458	gene_id_25284	Bin_3	2.85654	33.4867	0
1458	gene_id_25287	Bin_3	14.7382	8.37493	4.34414
1458	gene_id_25287	Bin_3	3.8428	8.37493	4.34414
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1458	gene_id_25290	Bin_3	26.3334	25.2433	3.41066
1458	gene_id_25294	Bin_3	1.62314	22.3297	0.716098
1458	gene_id_25295	Bin_3	6.27791	166.369	5.22338
1463	gene_id_25324	Bin_3	8.26036	34.1228	4.17451
1463	gene_id_25326	Bin_3	13.5628	25.1451	0
1463	gene_id_25326	Bin_3	11.3095	25.1451	0
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1463	gene_id_25327	Bin_3	3.15525	15.221	0.93405
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1463	gene_id_25328	Bin_3	6.11269	12.7538	0.576845
1464	gene_id_25334	Bin_3	3.00232	14.0993	0
1464	gene_id_25335	Bin_3	14.8559	76.9616	8.53753
1501	gene_id_25480	Bin_3	0.650514	7.40005	0.613571
1501	gene_id_25481	Bin_3	5.12689	23.8018	1.11904
1508	gene_id_25495	Bin_3	396.984	222.973	70.5776
1508	gene_id_25497	Bin_3	0	7.41227	0
1513	gene_id_25522	Bin_3	2.26457	15.4695	0
1549	gene_id_25610	Bin_3	3.07657	7.74556	0
1569	gene_id_25668	Bin_3	1.45735	161.322	0
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1580	gene_id_25708	Bin_3	0	167.35	0
1580	gene_id_25709	Bin_3	1.99908	31.125	0
1580	gene_id_25710	Bin_3	3.49246	21.4676	0
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1592	gene_id_25746	Bin_3	0	39.3114	0
1592	gene_id_25752	Bin_3	4.91087	25.869	14.303
1635	gene_id_25934	Bin_3	1.50556	10.9299	2.38613
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1635	gene_id_25935	Bin_3	1.85089	12.7001	0
1635	gene_id_25937	Bin_3	0	16.0503	0
1635	gene_id_25938	Bin_3	4.51452	18.2245	0
1643	gene_id_25956	Bin_3	0	31.4951	3.63381
1643	gene_id_25960	Bin_3	0	57.897	0
1643	gene_id_25961	Bin_3	3.10127	6.36115	0
1660	gene_id_26024	Bin_3	134.911	687.078	12.6325
1671	gene_id_26067	Bin_3	5.34226	28.0754	0
1690	gene_id_26174	Bin_3	4.45696	17.9977	0
1706	gene_id_26223	Bin_3	3.75984	9.01938	0
1706	gene_id_26224	Bin_3	2.12867	7.40867	0
1706	gene_id_26225	Bin_3	0	28.8044	0
1706	gene_id_26227	Bin_3	4.95742	306.269	2.09954
1706	gene_id_26229	Bin_3	0	8.53638	0
1706	gene_id_26230	Bin_3	4.17733	27.2903	0
1706	gene_id_26231	Bin_3	4.23093	25.6342	0
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1706	gene_id_26232	Bin_3	27.1972	443.243	0
1706	gene_id_26233	Bin_3	1.0486	34.9704	0
28	gene_id_2631	Bin_3	0	16.3175	0
1741	gene_id_26313	Bin_3	0	44.0094	0
28	gene_id_2633	Bin_3	3.37152	15.8015	2.2296
1747	gene_id_26332	Bin_3	2.37102	14.8972	10.2834
1747	gene_id_26332	Bin_3	0.775318	14.8972	10.2834
1747	gene_id_26332	Bin_3	2.37102	5.87183	0
1747	gene_id_26332	Bin_3	0.775318	5.87183	0
1747	gene_id_26333	Bin_3	2.00124	7.60934	0.179054
1779	gene_id_26445	Bin_3	3.80711	140.702	0.778535
1833	gene_id_26596	Bin_3	0	11.498	0
1848	gene_id_26633	Bin_3	0	4.18459	0
1848	gene_id_26634	Bin_3	51.5368	932.958	9.6719
1848	gene_id_26635	Bin_3	7.31345	276.162	2.34728
1848	gene_id_26637	Bin_3	28.6346	50.4488	232.48
1848	gene_id_26638	Bin_3	0	18.9717	0
1848	gene_id_26639	Bin_3	2.39501	16.1191	6.99809
1924	gene_id_26851	Bin_3	269.876	2442.69	143.125
1924	gene_id_26852	Bin_3	2.4712	15.0684	1.14196
1924	gene_id_26853	Bin_3	1.25804	13.4267	0.557321
1947	gene_id_26898	Bin_3	0.322514	35.9669	1.91207
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2084	gene_id_27227	Bin_3	0	29.0889	0
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2084	gene_id_27229	Bin_3	5.39154	21.3694	0.31912

2084	gene_id_27230	Bin_3	4.54936	18.483	0.613005
2161	gene_id_27434	Bin_3	0	4.62969	0
2161	gene_id_27435	Bin_3	11.1069	29.384	0
2222	gene_id_27577	Bin_3	2.18666	21.7452	0
2224	gene_id_27583	Bin_3	0.952843	10.2033	0
2224	gene_id_27584	Bin_3	0	38.7192	0
2274	gene_id_27679	Bin_3	1.24005	11.419	0
2307	gene_id_27738	Bin_3	0	14.6125	0
2307	gene_id_27739	Bin_3	2.02432	37.1394	0
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2307	gene_id_27740	Bin_3	2.10667	9.27874	0
2401	gene_id_27915	Bin_3	60.1905	29.833	8.26705
2401	gene_id_27917	Bin_3	38.8594	26.136	54.8686
2401	gene_id_27920	Bin_3	1.51207	15.272	0.673691
2493	gene_id_28089	Bin_3	0	17.6944	0
2493	gene_id_28090	Bin_3	1.3609	23.8959	0
2493	gene_id_28091	Bin_3	0	31.7137	0
2493	gene_id_28092	Bin_3	0	790.056	0
2648	gene_id_28397	Bin_3	11.1153	149.481	9.29469
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2648	gene_id_28399	Bin_3	1.06456	8.03699	0
2750	gene_id_28607	Bin_3	2.83205	32.8362	0
2750	gene_id_28608	Bin_3	5.78397	22.6812	1.0625
2750	gene_id_28609	Bin_3	7.72906	21.8285	1.20515
2750	gene_id_28610	Bin_3	0	11.0304	0
2775	gene_id_28656	Bin_3	0	13.1879	0
3169	gene_id_29364	Bin_3	0	32.3892	0
3169	gene_id_29365	Bin_3	0	17.5823	1.60928
3169	gene_id_29366	Bin_3	0	127.572	0
3169	gene_id_29367	Bin_3	1.57559	497.808	0.695491
3169	gene_id_29368	Bin_3	0.788434	92.5398	0.351151
3169	gene_id_29369	Bin_3	11.0839	214.282	0
3225	gene_id_29452	Bin_3	3.02967	20.5206	1.31549
3678	gene_id_30270	Bin_3	0	13.7271	0.744962
3678	gene_id_30271	Bin_3	3.41745	7.87702	0.505333
4054	gene_id_30880	Bin_3	3.12432	28.8242	1.35507
49	gene_id_5384	Bin_3	9.22726	89.3412	0
49	gene_id_5393	Bin_3	0	17.6581	0
49	gene_id_5394	Bin_3	22.011	33.7919	62.8277
49	gene_id_5397	Bin_3	6.27665	28.9485	0
49	gene_id_5401	Bin_3	3.16672	35.0403	4.11827
49	gene_id_5402	Bin_3	0	5.35869	0
49	gene_id_5410	Bin_3	2.84492	19.3108	0
51	gene_id_5530	Bin_3	0	80.4829	1.66997
51	gene_id_5531	Bin_3	0	23.4482	0

51	gene_id_5534	Bin_3	7.18958	31.2091	3.259
51	gene_id_5537	Bin_3	11.2863	21.0283	0.988778
51	gene_id_5539	Bin_3	0	32.1044	0
51	gene_id_5542	Bin_3	11.3456	36.5499	14.6
51	gene_id_5543	Bin_3	63.6224	23.9184	112.115
57	gene_id_5638	Bin_3	0	115.899	0
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57	gene_id_5638	Bin_3	0	7.41138	0
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57	gene_id_5639	Bin_3	0	11.6231	0
57	gene_id_5642	Bin_3	2.00183	10.1191	0.297602
57	gene_id_5654	Bin_3	582.384	780.233	10.6863
57	gene_id_5656	Bin_3	1.10669	16.7024	0
57	gene_id_5659	Bin_3	4.14023	14.94	4.58512
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57	gene_id_5665	Bin_3	0	9.29851	0
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57	gene_id_5667	Bin_3	31.2458	163.052	0
8	gene_id_675	Bin_3	1.42759	10.7352	0.631218
8	gene_id_676	Bin_3	9.08498	17.0633	0
8	gene_id_677	Bin_3	0	8.01897	0
8	gene_id_679	Bin_3	0.878601	22.1252	0
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78	gene_id_6874	Bin_3	0	16.0132	0
8	gene_id_688	Bin_3	0.717252	6.79441	1.35188
78	gene_id_6881	Bin_3	0.729984	5.53124	0
78	gene_id_6882	Bin_3	5.06081	13.3801	0.950266
78	gene_id_6885	Bin_3	1.01954	8.98436	0.452888
78	gene_id_6886	Bin_3	0	12.7316	0
8	gene_id_689	Bin_3	10.5089	59.1737	0
78	gene_id_6893	Bin_3	22505.9	3764.76	2365.21
78	gene_id_6894	Bin_3	695.84	318.512	591.75
78	gene_id_6895	Bin_3	161.469	28.3416	184.832
78	gene_id_6902	Bin_3	273.723	336.103	867.956
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103	gene_id_8510	Bin_3	76.6858	394.571	0
103	gene_id_8512	Bin_3	0	9.28188	0
103	gene_id_8516	Bin_3	13.7136	16.6545	4.93667
103	gene_id_8517	Bin_3	37.2931	5.61591	104.268

103	gene_id_8527	Bin_3	0	15.8115	0
103	gene_id_8528	Bin_3	6.24864	20.1262	3.27551
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103	gene_id_8529	Bin_3	0	75.8807	1.44945
103	gene_id_8530	Bin_3	0	19.4215	1.60708
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103	gene_id_8534	Bin_3	1.65331	14.6	1.14596
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118	gene_id_9303	Bin_3	339.128	1155.78	121.815
118	gene_id_9310	Bin_3	0	18.7801	0
118	gene_id_9312	Bin_3	0	18.0028	0
118	gene_id_9313	Bin_3	2.3995	58.7879	2.24738
118	gene_id_9314	Bin_3	1.88584	198.729	0
118	gene_id_9315	Bin_3	6.39124	68.7316	0
118	gene_id_9316	Bin_3	0.740813	29.934	0
118	gene_id_9317	Bin_3	5.97896	118.872	4.11027
118	gene_id_9318	Bin_3	2.76485	68.4711	0
118	gene_id_9319	Bin_3	0	46.5139	2.3853
118	gene_id_9320	Bin_3	0.92633	37.9381	0.41192
118	gene_id_9321	Bin_3	0.577194	38.8613	0.258828
118	gene_id_9323	Bin_3	2.01557	6.97863	0
118	gene_id_9325	Bin_3	3.99786	31.6016	3.61332
132	gene_id_10044	Bin_4	76.8757	31.1475	2.43775
132	gene_id_10048	Bin_4	131.062	159.544	0
132	gene_id_10062	Bin_4	50.2005	25.479	0
132	gene_id_10068	Bin_4	29.7229	10.0204	0
132	gene_id_10076	Bin_4	20.7489	19.492	0
132	gene_id_10077	Bin_4	53.3267	38.1781	2.2469
132	gene_id_10084	Bin_4	730.392	37.4552	15.7107
132	gene_id_10090	Bin_4	31.2479	4.33693	0
132	gene_id_10107	Bin_4	8.94242	22.2202	0
132	gene_id_10108	Bin_4	21.6205	20.3995	8.0036
133	gene_id_10137	Bin_4	34.9268	4.09937	0.36166
133	gene_id_10141	Bin_4	9.86454	0	0
133	gene_id_10149	Bin_4	11.5672	16.2649	0.791664
133	gene_id_10149	Bin_4	5.62128	16.2649	0.791664

133	gene_id_10149	Bin_4	11.5672	19.0855	0
133	gene_id_10149	Bin_4	5.62128	19.0855	0
133	gene_id_10153	Bin_4	127.528	14.3223	0.803038
133	gene_id_10162	Bin_4	122.01	32.0889	0
133	gene_id_10164	Bin_4	34.5394	3.39473	0
133	gene_id_10184	Bin_4	18.8837	2.98551	0
133	gene_id_10201	Bin_4	36.6359	24.6162	0
133	gene_id_10203	Bin_4	39.9786	4.86179	0
133	gene_id_10254	Bin_4	16.8984	5.27966	0
143	gene_id_10598	Bin_4	34.1542	11.7993	1.53083
143	gene_id_10600	Bin_4	10.4447	21.3176	0
143	gene_id_10605	Bin_4	48.8593	37.7501	0
143	gene_id_10606	Bin_4	28.3379	9.48454	0
143	gene_id_10607	Bin_4	16.2046	11.857	0
143	gene_id_10608	Bin_4	232.999	31.9089	0
143	gene_id_10614	Bin_4	6.18198	8.29108	0
143	gene_id_10615	Bin_4	10.2103	5.784	0
143	gene_id_10623	Bin_4	1924.07	158.26	82.1149
143	gene_id_10624	Bin_4	21.518	3.88042	0.72376
143	gene_id_10630	Bin_4	1133.93	53.294	0
143	gene_id_10631	Bin_4	992.979	83.5713	0
143	gene_id_10660	Bin_4	50.8736	2.56908	0
176	gene_id_11607	Bin_4	0	197.009	0
176	gene_id_11614	Bin_4	20.3043	7.8695	0.391673
176	gene_id_11614	Bin_4	12.8338	7.8695	0.391673
176	gene_id_11614	Bin_4	20.3043	13.4808	0
176	gene_id_11614	Bin_4	12.8338	13.4808	0
178	gene_id_11669	Bin_4	76.8731	35.5938	0
178	gene_id_11683	Bin_4	24.2638	24.5735	0
178	gene_id_11688	Bin_4	21.5654	0	0
178	gene_id_11698	Bin_4	41.166	9.55475	0
192	gene_id_12039	Bin_4	17.3795	3.62948	0
196	gene_id_12675	Bin_4	15.7176	0	0
196	gene_id_12677	Bin_4	21.2034	0	0
196	gene_id_12681	Bin_4	75.6441	0	0
196	gene_id_12687	Bin_4	73.3923	0	0
196	gene_id_12687	Bin_4	73.3923	0	0
196	gene_id_12687	Bin_4	27.5644	0	0
196	gene_id_12687	Bin_4	27.5644	0	0
196	gene_id_12692	Bin_4	135.069	0	0
196	gene_id_12809	Bin_4	211.51	112.89	0
196	gene_id_12815	Bin_4	3.3184	7.849	0
196	gene_id_12818	Bin_4	12.5804	4.73885	0
196	gene_id_12828	Bin_4	21.9592	2.94423	0
205	gene_id_13006	Bin_4	5.20317	16.0973	0
205	gene_id_13011	Bin_4	27.9073	6.20764	0
205	gene_id_13012	Bin_4	15.403	19.1439	0

205	gene_id_13030	Bin_4	19.886	0	0
205	gene_id_13045	Bin_4	9.56912	0	0
205	gene_id_13048	Bin_4	76.9038	2.88312	0
205	gene_id_13051	Bin_4	29.6314	0	0
205	gene_id_13056	Bin_4	15.1843	4.5039	0
205	gene_id_13058	Bin_4	40.2995	2.23784	0
205	gene_id_13059	Bin_4	19.1435	0	0
205	gene_id_13088	Bin_4	50.8736	5.13816	0
205	gene_id_13088	Bin_4	9.81249	5.13816	0
205	gene_id_13088	Bin_4	50.8736	2.48043	0
205	gene_id_13088	Bin_4	9.81249	2.48043	0
205	gene_id_13089	Bin_4	121.715	14.0225	0
208	gene_id_13201	Bin_4	23.8021	22.1443	0
208	gene_id_13216	Bin_4	40.3876	1.09478	0
208	gene_id_13225	Bin_4	54.1434	0	0
209	gene_id_13262	Bin_4	43.7272	4.83575	0
209	gene_id_13267	Bin_4	12.7159	2.2896	0
209	gene_id_13270	Bin_4	0	10.267	0
209	gene_id_13275	Bin_4	22.6935	0.837366	0
209	gene_id_13281	Bin_4	70.711	6.0455	0
209	gene_id_13295	Bin_4	22.5726	0	0
209	gene_id_13322	Bin_4	594.588	159.73	0
209	gene_id_13355	Bin_4	189.37	111.766	0
209	gene_id_13366	Bin_4	58.9777	12.9003	0.606836
209	gene_id_13369	Bin_4	141.903	59.4339	2.94435
209	gene_id_13379	Bin_4	290.542	109.579	1.83301
211	gene_id_13449	Bin_4	592.874	300.004	12.1113
211	gene_id_13482	Bin_4	198.067	12.3407	1.13009
211	gene_id_13499	Bin_4	2672.31	1266.08	1713.91
216	gene_id_13537	Bin_4	29.8236	0	0
216	gene_id_13539	Bin_4	42.337	1.5428	0
216	gene_id_13543	Bin_4	4295.92	670.086	17.519
216	gene_id_13546	Bin_4	16.8984	9.50338	0.744962
216	gene_id_13557	Bin_4	29.2937	9.68728	0
216	gene_id_13572	Bin_4	12.3362	6.19747	0
216	gene_id_13573	Bin_4	5.98166	20.2669	0
216	gene_id_13574	Bin_4	17.2722	8.11668	0
216	gene_id_13576	Bin_4	45.7146	8.60871	0
217	gene_id_13594	Bin_4	24.6817	150.769	10.2297
16	gene_id_1361	Bin_4	30.7299	100.587	0
217	gene_id_13614	Bin_4	0	51.3961	11.2918
16	gene_id_1364	Bin_4	103.013	47.8056	0
217	gene_id_13671	Bin_4	190.616	0	0
217	gene_id_13676	Bin_4	53.5624	78.2798	1.92042
217	gene_id_13677	Bin_4	39.596	14.6977	2.73778
217	gene_id_13693	Bin_4	314.617	8.98352	0
217	gene_id_13721	Bin_4	23.8526	18.5711	0

217	gene_id_13738	Bin_4	921.042	247.707	0
217	gene_id_13768	Bin_4	42.3155	7.99522	0
217	gene_id_13770	Bin_4	1535.07	897.938	133.833
16	gene_id_1444	Bin_4	40.7983	0	0
248	gene_id_14525	Bin_4	61.4232	9.02166	0
248	gene_id_14530	Bin_4	60.2332	7.07778	0
248	gene_id_14542	Bin_4	101.747	23.1217	0
248	gene_id_14559	Bin_4	10.1954	1.28348	0
248	gene_id_14568	Bin_4	92.2477	173.52	3.14185
248	gene_id_14575	Bin_4	33.7628	75.0936	190.355
248	gene_id_14582	Bin_4	35.0741	4.60628	0
281	gene_id_15216	Bin_4	0	55.6772	0
292	gene_id_15432	Bin_4	291.035	222.144	32.1836
292	gene_id_15432	Bin_4	27.763	222.144	32.1836
292	gene_id_15432	Bin_4	291.035	1.78784	0.210339
292	gene_id_15432	Bin_4	27.763	1.78784	0.210339
292	gene_id_15465	Bin_4	89.1169	1.99297	0.594908
292	gene_id_15465	Bin_4	22.7004	1.99297	0.594908
292	gene_id_15465	Bin_4	89.1169	3.24289	0
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292	gene_id_15470	Bin_4	19.3769	33.4658	0.944208
292	gene_id_15484	Bin_4	3746.08	320.029	0
292	gene_id_15485	Bin_4	57.3487	15.4916	2.61495
292	gene_id_15496	Bin_4	340.073	558.706	0
292	gene_id_15498	Bin_4	149.2	39.3779	1.46219
299	gene_id_15590	Bin_4	37.2526	0	0.291527
299	gene_id_15594	Bin_4	16.0216	0	0
299	gene_id_15595	Bin_4	36.2568	0.56585	0
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299	gene_id_15596	Bin_4	30.9874	0.695935	0
299	gene_id_15598	Bin_4	84.3869	0.392269	0
299	gene_id_15599	Bin_4	65.8822	0.867087	0
299	gene_id_15606	Bin_4	12.9056	0.809933	0
311	gene_id_15999	Bin_4	0	189.982	14.9059
311	gene_id_16000	Bin_4	44.547	2.69126	0
311	gene_id_16045	Bin_4	132.958	11.5452	0
311	gene_id_16068	Bin_4	2.74449	110.205	55.4881
311	gene_id_16078	Bin_4	39.6076	27.3485	0
311	gene_id_16094	Bin_4	11.9565	6.76032	0
312	gene_id_16095	Bin_4	3.91401	35.0418	0
312	gene_id_16147	Bin_4	264.873	13.9459	0
312	gene_id_16177	Bin_4	15.3829	2.58185	0.962647
312	gene_id_16183	Bin_4	3245.85	258.923	0
312	gene_id_16184	Bin_4	12.811	7.23671	1.19863
312	gene_id_16209	Bin_4	9.01253	0.568017	0

328	gene_id_16488	Bin_4	22.3431	33.2067	2.34543
328	gene_id_16490	Bin_4	64.4017	58.3447	0
328	gene_id_16506	Bin_4	36.6574	30.6657	3.03824
328	gene_id_16508	Bin_4	19.3447	49.2559	8.32028
328	gene_id_16519	Bin_4	19.2743	7.20786	0
328	gene_id_16525	Bin_4	28.8668	4.24387	0
328	gene_id_16539	Bin_4	39.9786	12.1545	0
328	gene_id_16540	Bin_4	9.97032	10.3868	0.732799
328	gene_id_16543	Bin_4	6.80872	18.0795	0
328	gene_id_16549	Bin_4	30.9171	8.67522	1.22351
345	gene_id_16819	Bin_4	99.8383	356.18	0
345	gene_id_16831	Bin_4	34.6434	4.24338	0
345	gene_id_16832	Bin_4	127.984	6.36302	0
345	gene_id_16838	Bin_4	52.8775	4.65621	0
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345	gene_id_16845	Bin_4	5.98014	12.4153	0
345	gene_id_16846	Bin_4	19.738	44.157	2.79488
345	gene_id_16847	Bin_4	7.26803	20.889	0.719181
345	gene_id_16850	Bin_4	10.4905	36.3748	1.16692
345	gene_id_16851	Bin_4	1.93737	20.1322	0
345	gene_id_16857	Bin_4	14.1965	13.8893	0
345	gene_id_16878	Bin_4	528.609	18.2774	12.7708
354	gene_id_16978	Bin_4	41.5963	21.2313	0
354	gene_id_16987	Bin_4	2.62919	7.18253	0
354	gene_id_16992	Bin_4	7.56514	6.89161	0
357	gene_id_17029	Bin_4	0	100.169	5.44312
357	gene_id_17034	Bin_4	18.4562	0.611745	0
357	gene_id_17036	Bin_4	430.528	71.8682	6.30358
357	gene_id_17041	Bin_4	0	2206.88	0
357	gene_id_17060	Bin_4	20.6708	25.479	0
361	gene_id_17088	Bin_4	19.1225	0.9968	1.40655
361	gene_id_17092	Bin_4	457.968	33.3398	0
361	gene_id_17093	Bin_4	247.4	54.1601	3.32244
361	gene_id_17094	Bin_4	495.602	122.896	21.5312
361	gene_id_17099	Bin_4	222.82	191.858	32.2171
429	gene_id_17764	Bin_4	42.337	9.25681	0
451	gene_id_18054	Bin_4	21.4577	2.68921	0
451	gene_id_18106	Bin_4	21.978	0	0
451	gene_id_18118	Bin_4	13.714	5.9738	0
503	gene_id_18876	Bin_4	30.5648	7.42677	0
503	gene_id_18940	Bin_4	18.0478	57.196	1.92249
503	gene_id_18941	Bin_4	72.15	17.767	0
503	gene_id_18942	Bin_4	26.1823	11.8103	0
540	gene_id_19319	Bin_4	3.34123	11.2051	1.04428
540	gene_id_19321	Bin_4	0	13.8876	0

572	gene_id_19736	Bin_4	9.34241	58.4665	7.49859
572	gene_id_19748	Bin_4	16.4905	0	0
591	gene_id_20007	Bin_4	3.81532	14.3696	0
591	gene_id_20008	Bin_4	61.8785	42.1858	0
625	gene_id_20416	Bin_4	70.3608	20.8341	0
638	gene_id_20544	Bin_4	53.0177	18.0328	0
681	gene_id_21006	Bin_4	22.2675	2.54858	0
728	gene_id_21375	Bin_4	17.7097	9.24332	0
728	gene_id_21377	Bin_4	38.1237	5.04801	1.1866
782	gene_id_21801	Bin_4	235.07	136.911	0
849	gene_id_22370	Bin_4	40.8811	0	0
912	gene_id_22818	Bin_4	194.744	130.876	0
912	gene_id_22819	Bin_4	23447.6	1.1427	0
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952	gene_id_22989	Bin_4	34.3379	3.19324	0
1401	gene_id_25106	Bin_4	0	68.9708	0
1401	gene_id_25107	Bin_4	1.87572	11.6973	1.65036
1401	gene_id_25108	Bin_4	13.0565	46.8513	5.94438
1401	gene_id_25109	Bin_4	19.8045	84.6148	3.39757
1570	gene_id_25673	Bin_4	33.2986	1.35938	0
1570	gene_id_25677	Bin_4	138.086	48.2475	5.59017
1791	gene_id_26476	Bin_4	12.5865	17.1491	0
1791	gene_id_26477	Bin_4	4.31172	6.52471	0.383746
1791	gene_id_26478	Bin_4	30.3192	39.3939	2.5298
1791	gene_id_26478	Bin_4	5.01003	39.3939	2.5298
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1791	gene_id_26478	Bin_4	30.3192	10.0932	0
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30	gene_id_2771	Bin_4	3952.71	2298.34	112.999
2306	gene_id_27737	Bin_4	12.2273	8.10146	4.24833
30	gene_id_2781	Bin_4	24.1307	14.9614	0
30	gene_id_2783	Bin_4	16.2987	20.6292	0.469735
30	gene_id_2784	Bin_4	10.9044	9.20835	0
56	gene_id_5623	Bin_4	17.3706	0	0
56	gene_id_5624	Bin_4	19.1485	1.72386	0
56	gene_id_5628	Bin_4	39.1277	5.84092	0.951379
56	gene_id_5632	Bin_4	19.8343	0.829561	0
61	gene_id_5761	Bin_4	20.2342	0.905523	0
61	gene_id_5762	Bin_4	25.85	1.7191	0
61	gene_id_5763	Bin_4	15.7683	0	0

61	gene_id_5764	Bin_4	382.502	11.1001	1.19393
61	gene_id_5766	Bin_4	28.0949	11.0681	0
61	gene_id_5772	Bin_4	20.0415	2.27372	0
61	gene_id_5778	Bin_4	18.7801	3.91701	0
61	gene_id_5781	Bin_4	122.544	33.2451	2.70627
61	gene_id_5786	Bin_4	169.153	25.2439	0
61	gene_id_5787	Bin_4	9.02917	2.58894	0
61	gene_id_5788	Bin_4	487.985	184.942	0
61	gene_id_5792	Bin_4	5.10437	16.5349	0.28466
61	gene_id_5804	Bin_4	23.2317	34.024	7.84956
61	gene_id_5808	Bin_4	183.238	96.9828	2.53375
61	gene_id_5815	Bin_4	11.5234	1.53392	0
61	gene_id_5817	Bin_4	25143.9	8119.31	0
100	gene_id_8272	Bin_4	29.0571	31.5248	2.23313
100	gene_id_8273	Bin_4	2.22848	13.8444	0
100	gene_id_8296	Bin_4	105.5	10.0573	3.54864
101	gene_id_8333	Bin_4	5.02096	11.506	0
101	gene_id_8347	Bin_4	17.3772	74.6231	0
101	gene_id_8347	Bin_4	15.5113	74.6231	0
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101	gene_id_8348	Bin_4	23.8956	12.5646	0
101	gene_id_8349	Bin_4	12.5408	7.8984	0
101	gene_id_8350	Bin_4	131.203	20.0409	0
101	gene_id_8351	Bin_4	40.2568	15.242	0
101	gene_id_8359	Bin_4	0.62943	15.5174	0
101	gene_id_8360	Bin_4	15.286	91.178	6.40088
101	gene_id_8361	Bin_4	15.998	38.1781	6.7407
101	gene_id_8366	Bin_4	20.9687	19.4573	0
101	gene_id_8367	Bin_4	33.5673	14.3396	1.64282
102	gene_id_8386	Bin_4	12.4697	4.27591	1.06264
102	gene_id_8396	Bin_4	47.8289	23.3851	0
102	gene_id_8412	Bin_4	13.3086	23.7062	0
102	gene_id_8413	Bin_4	110.318	106.68	0
102	gene_id_8436	Bin_4	36.6359	29.0919	0
102	gene_id_8437	Bin_4	7319.84	574.586	0
102	gene_id_8440	Bin_4	14.9699	0	1.272
102	gene_id_8452	Bin_4	0	190.303	0
102	gene_id_8453	Bin_4	4.06742	24.7079	0
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102	gene_id_8455	Bin_4	0	50.6416	0
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102	gene_id_8458	Bin_4	0	25.222	0
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102	gene_id_8467	Bin_4	91.1884	121.11	0
102	gene_id_8469	Bin_4	1727.32	538.638	0
102	gene_id_8491	Bin_4	156.465	0	0
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109	gene_id_8671	Bin_4	16.2154	2.03995	0
109	gene_id_8672	Bin_4	52.6667	25.2433	0
114	gene_id_8915	Bin_4	26.3753	9.58153	0
114	gene_id_8923	Bin_4	10.3678	20.8511	0
114	gene_id_8992	Bin_4	15.9575	7.20984	0
114	gene_id_9003	Bin_4	277.603	236.71	35.8902
119	gene_id_9379	Bin_4	15.3712	3.63054	0
119	gene_id_9421	Bin_4	10.1422	15.7	2.33506
119	gene_id_9422	Bin_4	191.363	38.848	0
119	gene_id_9438	Bin_4	0	5.41082	0
119	gene_id_9441	Bin_4	20.1392	0.889749	0
119	gene_id_9442	Bin_4	14.4089	0	0
119	gene_id_9465	Bin_4	0	32.6262	0
119	gene_id_9468	Bin_4	641.51	100.607	0
119	gene_id_9469	Bin_4	9.97277	19.6417	0.629953
123	gene_id_9510	Bin_4	53.9999	22.3597	0
123	gene_id_9520	Bin_4	9.1405	15.9195	0
123	gene_id_9555	Bin_4	9.24838	3.59441	0
123	gene_id_9571	Bin_4	32.8738	61.4777	0
123	gene_id_9619	Bin_4	85.3326	4.50276	0.2119
139	gene_id_10484	Bin_5	10.7656	24.1361	0
139	gene_id_10491	Bin_5	26.2965	4.12474	0
139	gene_id_10491	Bin_5	16.5424	4.12474	0
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139	gene_id_10492	Bin_5	25.6567	7.30855	0.778862
142	gene_id_10557	Bin_5	23.9133	15.9304	7.98255
142	gene_id_10563	Bin_5	107.972	46.9987	2.18703
142	gene_id_10564	Bin_5	18.9133	3.98977	0
142	gene_id_10565	Bin_5	57.0176	15.6927	0
142	gene_id_10567	Bin_5	11.7357	2.94981	0
142	gene_id_10572	Bin_5	15.3144	4.82864	0.757317
142	gene_id_10573	Bin_5	11.6287	12.0783	2.65034
142	gene_id_10575	Bin_5	16.3712	3.69778	0.261012
142	gene_id_10576	Bin_5	14.9589	8.02715	0.666545
157	gene_id_11246	Bin_5	48.9852	32.1288	24.6558
157	gene_id_11255	Bin_5	13.0551	2.93758	1.29101
159	gene_id_11277	Bin_5	2.64958	9.14221	0
159	gene_id_11284	Bin_5	30.8414	45.1616	3.36524
159	gene_id_11286	Bin_5	102.206	8.48873	0
159	gene_id_11287	Bin_5	54.3858	89.8724	22.3654

159	gene_id_11289	Bin_5	1.12515	7.11758	1.06245
159	gene_id_11290	Bin_5	4.25919	14.3368	2.85931
159	gene_id_11290	Bin_5	0	14.3368	2.85931
159	gene_id_11290	Bin_5	4.25919	6.98312	0
159	gene_id_11290	Bin_5	0	6.98312	0
161	gene_id_11297	Bin_5	14.2503	6.43043	0.799462
161	gene_id_11297	Bin_5	12.7465	6.43043	0.799462
161	gene_id_11297	Bin_5	14.2503	7.46109	0.526502
161	gene_id_11297	Bin_5	12.7465	7.46109	0.526502
161	gene_id_11299	Bin_5	132.226	56.1342	5.24104
161	gene_id_11300	Bin_5	242.404	73.4781	15.3624
161	gene_id_11302	Bin_5	146.381	74.2402	30.4155
161	gene_id_11307	Bin_5	17.9342	2.11426	11.2786
161	gene_id_11308	Bin_5	275.248	0	0
161	gene_id_11309	Bin_5	179.423	38.8305	3.91583
161	gene_id_11319	Bin_5	272.582	52.2321	0
161	gene_id_11320	Bin_5	96.7754	26.5966	7.7089
161	gene_id_11321	Bin_5	18.7801	2.93775	0
161	gene_id_11323	Bin_5	37.6599	4.04231	1.77563
161	gene_id_11323	Bin_5	25.5746	4.04231	1.77563
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161	gene_id_11323	Bin_5	37.6599	7.7196	0
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161	gene_id_11324	Bin_5	17.9798	5.10991	0
161	gene_id_11325	Bin_5	18.5247	6.27099	0.623934
161	gene_id_11326	Bin_5	19.1503	1.95274	0
161	gene_id_11327	Bin_5	67.2763	7.21909	2.5498
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164	gene_id_11346	Bin_5	0.704247	10.2306	1.32759
164	gene_id_11347	Bin_5	37.6836	13.3106	2.47401
164	gene_id_11349	Bin_5	178.651	82.8431	0
164	gene_id_11350	Bin_5	31.5879	0	0
164	gene_id_11351	Bin_5	159.53	113.006	26.0096
164	gene_id_11352	Bin_5	225.536	69.1935	13.2248
164	gene_id_11355	Bin_5	31.3356	8.07782	0
164	gene_id_11356	Bin_5	13.5394	6.41564	0.301891
164	gene_id_11357	Bin_5	9.50253	0	0
164	gene_id_11359	Bin_5	9.55336	0	40.9534
164	gene_id_11359	Bin_5	8.03845	0	40.9534
164	gene_id_11359	Bin_5	9.55336	1.52149	0
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174	gene_id_11579	Bin_5	3.83407	14.0359	2.4692
174	gene_id_11582	Bin_5	11.4362	1.6637	0

174	gene_id_11584	Bin_5	43.8225	12.0643	1.089
174	gene_id_11585	Bin_5	13.5593	9.2349	0
174	gene_id_11586	Bin_5	16.4048	4.89952	0
190	gene_id_11875	Bin_5	7.21933	7.39366	0
190	gene_id_11877	Bin_5	2.49041	21.5992	2.29477
190	gene_id_11878	Bin_5	12.3047	21.9521	1.63474
190	gene_id_11881	Bin_5	11.7232	8.99108	0
190	gene_id_11890	Bin_5	21.7984	1.35493	0
190	gene_id_11892	Bin_5	90.3017	39.6226	5.73849
190	gene_id_11893	Bin_5	39.9884	29.0609	4.41171
190	gene_id_11897	Bin_5	43.5779	23.2974	2.04363
190	gene_id_11901	Bin_5	7.71054	0.750153	0
190	gene_id_11908	Bin_5	30.5246	16.9755	3.59419
190	gene_id_11909	Bin_5	15.267	3.48045	0
190	gene_id_11910	Bin_5	11.6269	4.5536	0.52287
190	gene_id_11911	Bin_5	40.9114	9.9375	0
190	gene_id_11914	Bin_5	29.092	9.52843	1.744
190	gene_id_11915	Bin_5	36.1355	20.2483	9.53009
190	gene_id_11916	Bin_5	5690.26	1017.75	9.67499
190	gene_id_11920	Bin_5	13.4815	9.37971	1.3236
190	gene_id_11921	Bin_5	12.1177	5.45726	0.814144
190	gene_id_11922	Bin_5	10.4276	3.70687	0.290718
191	gene_id_11926	Bin_5	10.9374	3.02302	0.644494
191	gene_id_11927	Bin_5	9.48963	3.58665	3.89268
191	gene_id_11928	Bin_5	21.7984	6.77467	2.86709
191	gene_id_11931	Bin_5	55.3631	13.6301	8.46626
191	gene_id_11932	Bin_5	92.8678	30.5265	5.89481
191	gene_id_11933	Bin_5	1667.74	630.762	0
191	gene_id_11941	Bin_5	11.6728	0	0
191	gene_id_11948	Bin_5	49.6357	19.4141	8.52471
191	gene_id_11952	Bin_5	9.50253	2.39432	0
191	gene_id_11955	Bin_5	20.7755	5.80345	1.02384
191	gene_id_11958	Bin_5	940.279	251.004	0
191	gene_id_11960	Bin_5	40.0829	28.4215	0.802009
191	gene_id_11961	Bin_5	67.2922	21.6297	1.17332
191	gene_id_11962	Bin_5	41.8618	3.38771	0
191	gene_id_11963	Bin_5	33.4934	4.64232	1.72821
191	gene_id_11964	Bin_5	172.73	9.17438	1.29389
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191	gene_id_11971	Bin_5	165.932	54.2325	4.25494

191	gene_id_11972	Bin_5	81.157	16.2398	2.22817
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191	gene_id_11978	Bin_5	80.2086	15.4741	0
191	gene_id_11979	Bin_5	76.0012	11.6801	0
191	gene_id_11980	Bin_5	256.518	24.7296	0
191	gene_id_11981	Bin_5	160.549	3.91853	8.6058
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191	gene_id_11986	Bin_5	38.6456	1.26626	0
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191	gene_id_11990	Bin_5	58.2743	6.2052	0
191	gene_id_11991	Bin_5	108.184	10.3636	3.08033
191	gene_id_11992	Bin_5	84.8307	18.6551	2.77285
191	gene_id_11993	Bin_5	39.9311	5.55754	0.653539
191	gene_id_11994	Bin_5	36.3911	6.4896	0
191	gene_id_11995	Bin_5	137.846	14.7541	2.43775
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191	gene_id_12004	Bin_5	13.6739	6.28787	0.221928
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301	gene_id_15700	Bin_5	12.7776	1.07433	0
301	gene_id_15708	Bin_5	27.1017	4.8596	0.571514
301	gene_id_15721	Bin_5	15.2613	0.798309	1.68995
301	gene_id_15729	Bin_5	4.27404	2.67842	7.63007
301	gene_id_15740	Bin_5	11.9035	5.16663	15.2966
301	gene_id_15742	Bin_5	24.9932	21.6743	1.09184
301	gene_id_15743	Bin_5	23.8526	27.2376	2.71652

301	gene_id_15745	Bin_5	19.5437	15.8307	0.859019
301	gene_id_15745	Bin_5	10.9277	15.8307	0.859019
301	gene_id_15745	Bin_5	19.5437	8.03428	0
301	gene_id_15745	Bin_5	10.9277	8.03428	0
301	gene_id_15746	Bin_5	11.8441	7.78058	1.02593
301	gene_id_15748	Bin_5	12.6814	3.05468	2.2797
301	gene_id_15749	Bin_5	97.6048	19.6557	0
301	gene_id_15749	Bin_5	65.263	19.6557	0
301	gene_id_15749	Bin_5	97.6048	7.64105	0
301	gene_id_15749	Bin_5	65.263	7.64105	0
301	gene_id_15752	Bin_5	30.9589	15.1354	1.01721
301	gene_id_15753	Bin_5	12.9359	20.4029	4.00106
301	gene_id_15753	Bin_5	4.42638	20.4029	4.00106
301	gene_id_15753	Bin_5	12.9359	13.9511	2.36309
301	gene_id_15753	Bin_5	4.42638	13.9511	2.36309
304	gene_id_15795	Bin_5	23.7834	17.5394	3.2328
304	gene_id_15796	Bin_5	15.6788	34.1905	2.58412
304	gene_id_15797	Bin_5	16.1321	26.7973	1.07989
304	gene_id_15798	Bin_5	7.9111	25.4592	1.09717
304	gene_id_15799	Bin_5	46.4511	187.993	4.56441
304	gene_id_15800	Bin_5	4.70016	30.2025	0.417947
304	gene_id_15801	Bin_5	11.063	36.4008	7.59134
304	gene_id_15802	Bin_5	21.7671	6.55791	2.19928
304	gene_id_15806	Bin_5	12.9686	0.583662	0.823839
304	gene_id_15807	Bin_5	16.8955	1.85528	1.71161
304	gene_id_15809	Bin_5	63.5509	5.87012	0
304	gene_id_15811	Bin_5	45.8418	3.76242	0
304	gene_id_15818	Bin_5	12.9515	6.41188	0.41138
304	gene_id_15819	Bin_5	32.5867	25.092	0
304	gene_id_15828	Bin_5	27.7968	3.86596	1.44003
304	gene_id_15830	Bin_5	101.5	26.2768	46.608
304	gene_id_15838	Bin_5	53.4835	12.46	0
304	gene_id_15840	Bin_5	16.2314	4.05995	0
304	gene_id_15843	Bin_5	165.452	235.063	58.1307
304	gene_id_15844	Bin_5	29.0754	24.9472	0
304	gene_id_15845	Bin_5	19.8758	11.0846	0.177838
304	gene_id_15846	Bin_5	40.6742	7.41237	0
304	gene_id_15847	Bin_5	24.3511	6.72477	0
304	gene_id_15850	Bin_5	48.1299	2.2603	1.59435
304	gene_id_15851	Bin_5	20.1562	6.21497	0.230898
304	gene_id_15853	Bin_5	26.2329	11.3384	1.3016
304	gene_id_15854	Bin_5	35.4757	29.717	0
304	gene_id_15855	Bin_5	19.9786	15.5942	0.646979
304	gene_id_15856	Bin_5	20.8109	23.0296	0
304	gene_id_15857	Bin_5	31.9688	22.4736	2.95932
306	gene_id_15870	Bin_5	14.0464	2.96951	1.75896
306	gene_id_15870	Bin_5	10.6526	2.96951	1.75896

306	gene_id_15870	Bin_5	8.46334	2.96951	1.75896
306	gene_id_15870	Bin_5	14.0464	4.85244	1.10249
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306	gene_id_15870	Bin_5	10.6526	0.880441	0
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306	gene_id_15873	Bin_5	12.8095	2.20949	0.809599
306	gene_id_15878	Bin_5	17.9762	8.6363	5.88776
306	gene_id_15884	Bin_5	33.9969	18.9871	0
306	gene_id_15886	Bin_5	4.35968	10.8395	87.0425
306	gene_id_15888	Bin_5	9.36614	0.985138	0
309	gene_id_15916	Bin_5	1.27493	12.0877	3.86002
309	gene_id_15917	Bin_5	1.30956	11.5861	5.42435
309	gene_id_15918	Bin_5	6.66183	25.9096	26.6782
309	gene_id_15920	Bin_5	652.184	61.899	85.3914
309	gene_id_15921	Bin_5	16.2204	3.00502	0
309	gene_id_15922	Bin_5	22.0086	20.2454	2.51898
309	gene_id_15922	Bin_5	18.8735	20.2454	2.51898
309	gene_id_15922	Bin_5	22.0086	18.688	0
309	gene_id_15922	Bin_5	18.8735	18.688	0
309	gene_id_15929	Bin_5	38.7155	27.5388	10.4772
309	gene_id_15930	Bin_5	17.8942	4.35869	0
309	gene_id_15934	Bin_5	79.5015	24.267	2.42099
309	gene_id_15940	Bin_5	56.9367	30.9495	4.60508
309	gene_id_15953	Bin_5	49.3383	81.316	13.1072
309	gene_id_15954	Bin_5	12.2084	11.5452	0
309	gene_id_15955	Bin_5	15.9705	14.4314	0.254665
309	gene_id_15956	Bin_5	19.042	18.5547	1.62829
309	gene_id_15957	Bin_5	18.1535	10.8327	0
310	gene_id_15987	Bin_5	12.2039	18.9939	25.8968
310	gene_id_15992	Bin_5	24.1307	0	1.05518
330	gene_id_16559	Bin_5	44.7604	14.6879	7.23724
334	gene_id_16634	Bin_5	26.634	7.68545	0
334	gene_id_16635	Bin_5	11.1013	10.4922	0
334	gene_id_16636	Bin_5	16.7664	7.49251	0.220371
334	gene_id_16637	Bin_5	127.391	66.9348	4.69049
334	gene_id_16638	Bin_5	25.2836	12.3262	6.42143
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334	gene_id_16641	Bin_5	37.8221	6.91979	3.25422
334	gene_id_16645	Bin_5	83.7688	113.271	14.0704
334	gene_id_16647	Bin_5	122.368	194.724	392.791
334	gene_id_16650	Bin_5	16.0092	2.51972	0.939525
334	gene_id_16651	Bin_5	27.2354	3.59285	0
334	gene_id_16655	Bin_5	5.20062	8.15873	0

334	gene_id_16656	Bin_5	35.1594	5.98579	0.89285
334	gene_id_16657	Bin_5	18.8584	8.2314	0
334	gene_id_16659	Bin_5	8.96576	1.41506	0
334	gene_id_16662	Bin_5	49.1012	28.0171	96.1992
337	gene_id_16680	Bin_5	101.288	51.5614	13.0793
337	gene_id_16681	Bin_5	11.365	21.345	2.48988
337	gene_id_16682	Bin_5	13.1519	32.4914	3.2268
337	gene_id_16683	Bin_5	25.4672	53.5764	28.6638
337	gene_id_16685	Bin_5	20.5697	9.0192	2.03442
337	gene_id_16686	Bin_5	25.3087	8.67689	2.60891
337	gene_id_16687	Bin_5	23.7214	29.4281	7.37782
337	gene_id_16688	Bin_5	36.7601	14.2509	1.67625
338	gene_id_16691	Bin_5	12.8999	2.14473	0
338	gene_id_16694	Bin_5	12.6279	23.2463	1.34418
340	gene_id_16705	Bin_5	34.677	7.75303	2.88074
340	gene_id_16707	Bin_5	36.4222	5.3139	2.75341
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340	gene_id_16709	Bin_5	12.3852	3.1249	0.777041
340	gene_id_16711	Bin_5	14.1188	1.36623	0
340	gene_id_16716	Bin_5	11.835	20.0776	1.63345
340	gene_id_16717	Bin_5	37.4614	46.6749	2.5634
340	gene_id_16718	Bin_5	14.1085	19.3912	2.83155
340	gene_id_16719	Bin_5	37.6599	42.4578	12.6878
340	gene_id_16720	Bin_5	44.5543	26.1048	7.01482
340	gene_id_16721	Bin_5	67.575	1.35493	0
340	gene_id_16723	Bin_5	8.8336	0.929576	0.328053
340	gene_id_16725	Bin_5	31.5358	9.97023	0
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344	gene_id_16803	Bin_5	237.813	275.96	18.8641
344	gene_id_16804	Bin_5	3.79659	4.79306	4.51367
344	gene_id_16807	Bin_5	20.153	13.1578	1.86606
344	gene_id_16808	Bin_5	9.1473	2.6225	0.740364
344	gene_id_16809	Bin_5	15.7476	8.17127	0.41192

344	gene_id_16810	Bin_5	14.5514	4.01197	0
344	gene_id_16812	Bin_5	105.792	14.6698	0
344	gene_id_16813	Bin_5	95.8072	10.8773	0
372	gene_id_17178	Bin_5	25.5436	5.5526	3.22422
372	gene_id_17180	Bin_5	31.7878	13.7004	77.4956
372	gene_id_17181	Bin_5	7.67267	5.07744	11.9136
372	gene_id_17185	Bin_5	7.47882	6.76074	0.477226
372	gene_id_17186	Bin_5	18.5434	16.8549	3.05556
374	gene_id_17194	Bin_5	11.3932	1.65751	0
374	gene_id_17195	Bin_5	14.6039	1.82966	1.36328
374	gene_id_17199	Bin_5	15.4292	8.71575	1.01259
374	gene_id_17200	Bin_5	78.7132	8.33496	2.94356
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374	gene_id_17203	Bin_5	24.0284	10.8858	3.08712
374	gene_id_17204	Bin_5	522.307	56.8337	8.32028
374	gene_id_17205	Bin_5	26.6704	5.87969	0.711704
374	gene_id_17206	Bin_5	13.2155	1.27979	0
374	gene_id_17208	Bin_5	10.732	0	0
374	gene_id_17211	Bin_5	16.3442	5.27372	1.17429
374	gene_id_17212	Bin_5	50.7596	8.8632	4.85589
374	gene_id_17215	Bin_5	10.4813	1.80058	0.895254
374	gene_id_17217	Bin_5	21.1472	10.1931	3.25692
374	gene_id_17220	Bin_5	10.7002	0.964847	0
386	gene_id_17352	Bin_5	27.7389	7.95186	1.16505
386	gene_id_17353	Bin_5	44.1651	16.9633	49.9249
386	gene_id_17354	Bin_5	23.9949	3.6137	0
390	gene_id_17390	Bin_5	96.2947	155.686	139.834
390	gene_id_17391	Bin_5	18.7381	14.6565	10.7259
390	gene_id_17393	Bin_5	13.6699	3.63478	1.31938
390	gene_id_17400	Bin_5	40.0899	2.22676	0
390	gene_id_17401	Bin_5	23.3704	4.8748	0
390	gene_id_17405	Bin_5	17.0143	17.1953	2.90167
390	gene_id_17413	Bin_5	42.3622	21.8294	3.00699
390	gene_id_17414	Bin_5	18.2784	5.45323	0
390	gene_id_17415	Bin_5	17.2151	2.93775	1.45899
390	gene_id_17416	Bin_5	38.5931	11.1472	1.12304
390	gene_id_17417	Bin_5	213.95	73.7582	215.13
390	gene_id_17425	Bin_5	20.7364	16.728	9.55164
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390	gene_id_17432	Bin_5	17.4274	8.61452	2.02959
390	gene_id_17433	Bin_5	12.2883	6.44528	0
390	gene_id_17438	Bin_5	12.2264	2.57099	0.362913

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390	gene_id_17446	Bin_5	22.5586	11.1314	0.664458
392	gene_id_17458	Bin_5	8.67996	10.8423	5.60958
392	gene_id_17459	Bin_5	162.459	7.10682	77.7414
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402	gene_id_17523	Bin_5	35.9605	46.1284	112.638
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402	gene_id_17536	Bin_5	249.105	595.644	486.532
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402	gene_id_17542	Bin_5	42.3825	2.59116	0
402	gene_id_17543	Bin_5	55.0535	2.14753	0.757535
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403	gene_id_17568	Bin_5	43.401	6.70537	0
405	gene_id_17587	Bin_5	129.201	139.761	194.918
405	gene_id_17588	Bin_5	11.1909	4.92546	0.496548
411	gene_id_17602	Bin_5	43.3223	16.4	4.3291
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411	gene_id_17608	Bin_5	23.2761	7.31393	0
411	gene_id_17623	Bin_5	169.716	40.1919	0
411	gene_id_17626	Bin_5	26.6745	35.3218	18.9833
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411	gene_id_17638	Bin_5	4.78259	10.516	1.11991
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426	gene_id_17730	Bin_5	39.297	17.2599	0
426	gene_id_17732	Bin_5	101.263	36.7551	6.75184
426	gene_id_17737	Bin_5	23.2527	2.2548	0.840912
426	gene_id_17738	Bin_5	38.4763	4.47337	0
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432	gene_id_17831	Bin_5	114.583	42.2451	2.29513
439	gene_id_17975	Bin_5	7.04899	13.2038	3.19127
439	gene_id_17976	Bin_5	4.5566	7.16093	0
439	gene_id_17979	Bin_5	5.99733	12.8939	1.66745
454	gene_id_18153	Bin_5	8.1312	3.30602	1.32617
454	gene_id_18154	Bin_5	7.3326	1.83722	18.2985
454	gene_id_18159	Bin_5	179.998	104.975	15.5517
454	gene_id_18160	Bin_5	8.5165	15.4042	5.41311
454	gene_id_18161	Bin_5	15.0183	24.0509	1.3046
454	gene_id_18162	Bin_5	26.8652	18.0311	3.6462
454	gene_id_18163	Bin_5	25.0441	9.93529	0.871781
459	gene_id_18183	Bin_5	29.2707	6.58159	2.32067
459	gene_id_18190	Bin_5	16.9968	2.46116	3.02465
459	gene_id_18191	Bin_5	13.6794	5.93027	0.380493
459	gene_id_18193	Bin_5	8.78601	4.43102	0
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459	gene_id_18200	Bin_5	10.31	0.54174	0.808207
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459	gene_id_18207	Bin_5	32.7951	14.7792	1.69301
459	gene_id_18212	Bin_5	1209.91	176.342	15.492
459	gene_id_18213	Bin_5	18.9596	8.57736	5.72797
459	gene_id_18215	Bin_5	117.955	37.0618	7.15951
459	gene_id_18216	Bin_5	430.489	115.68	6.28369
459	gene_id_18217	Bin_5	14.3724	9.02899	0
459	gene_id_18218	Bin_5	1006.3	257.367	0
471	gene_id_18451	Bin_5	77.3788	0	2.67655
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481	gene_id_18609	Bin_5	111.445	18.1225	4.78456
481	gene_id_18610	Bin_5	17.6813	0.618548	0
481	gene_id_18614	Bin_5	41.166	15.9246	2.24608
481	gene_id_18617	Bin_5	72.5744	68.9689	4.7706
481	gene_id_18618	Bin_5	100.414	58.0732	2.78444
481	gene_id_18620	Bin_5	38.2097	17.4897	4.0424
481	gene_id_18621	Bin_5	35.3425	10.8127	0
481	gene_id_18623	Bin_5	10.7472	1.45357	0
481	gene_id_18624	Bin_5	6.11944	6.06247	1.60014
509	gene_id_18981	Bin_5	27.4449	0	0
509	gene_id_18983	Bin_5	13.5305	4.7997	0
509	gene_id_18986	Bin_5	17.1892	2.14753	0
509	gene_id_18988	Bin_5	15.2663	3.00502	0
509	gene_id_18990	Bin_5	15.0086	5.03944	12.3559
509	gene_id_18991	Bin_5	12.1327	16.3919	3.60232
509	gene_id_18992	Bin_5	10.3822	8.32412	2.09811
509	gene_id_18997	Bin_5	30.4622	5.85843	0
509	gene_id_18998	Bin_5	56.9421	25.8066	4.68351
509	gene_id_18999	Bin_5	14.2745	2.24208	0
509	gene_id_19000	Bin_5	36.6304	11.3625	0
509	gene_id_19001	Bin_5	292.383	216.182	48.5886
509	gene_id_19002	Bin_5	55.3107	3.01292	0
509	gene_id_19003	Bin_5	20.608	3.9212	1.16913
509	gene_id_19003	Bin_5	16.2377	3.9212	1.16913
509	gene_id_19003	Bin_5	20.608	4.56857	0
509	gene_id_19003	Bin_5	16.2377	4.56857	0
509	gene_id_19008	Bin_5	39.0756	8.12406	0
509	gene_id_19010	Bin_5	574.226	161.103	0
509	gene_id_19011	Bin_5	26.9153	6.0661	0
546	gene_id_19372	Bin_5	9.16338	3.62253	0
546	gene_id_19376	Bin_5	13.8831	3.82948	2.01839
546	gene_id_19377	Bin_5	29.7312	3.70392	0
546	gene_id_19378	Bin_5	8.22108	6.36366	1.4528
546	gene_id_19387	Bin_5	135.413	94.7229	0
551	gene_id_19413	Bin_5	76.5943	34.1081	0
551	gene_id_19417	Bin_5	237.607	7.37742	0.647632
551	gene_id_19417	Bin_5	41.9038	7.37742	0.647632
551	gene_id_19417	Bin_5	237.607	40.6102	0
551	gene_id_19417	Bin_5	41.9038	40.6102	0
551	gene_id_19437	Bin_5	8.21102	7.18688	39.1199
575	gene_id_19773	Bin_5	34.049	21.3091	3.49333
575	gene_id_19775	Bin_5	31.0995	35.0649	76.0712
613	gene_id_20316	Bin_5	8.58563	5.41826	0
613	gene_id_20318	Bin_5	48.3854	0	1.60242
614	gene_id_20333	Bin_5	56.1348	12.4849	3.71726
626	gene_id_20436	Bin_5	20.0272	3.58561	1.96838
626	gene_id_20437	Bin_5	99.0508	5.13961	0

626	gene_id_20438	Bin_5	14.6302	12.933	2.68255
629	gene_id_20466	Bin_5	18.3476	16.2144	11.8076
629	gene_id_20469	Bin_5	20.8568	9.45729	0
629	gene_id_20476	Bin_5	61.2132	9.16017	0
629	gene_id_20484	Bin_5	57.358	3.11615	0
629	gene_id_20489	Bin_5	13.6529	9.5758	9.01763
629	gene_id_20490	Bin_5	68.6557	13.5794	29.291
639	gene_id_20553	Bin_5	63.3488	27.8664	2.76135
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639	gene_id_20553	Bin_5	63.3488	4.66717	0
639	gene_id_20553	Bin_5	11.6569	4.66717	0
639	gene_id_20571	Bin_5	0	6.79536	66.0179
666	gene_id_20761	Bin_5	23.2907	14.0332	2.314
666	gene_id_20762	Bin_5	24.9508	14.0099	1.88943
666	gene_id_20763	Bin_5	24.8267	5.48899	0
666	gene_id_20768	Bin_5	12.7553	2.00623	1.99459
666	gene_id_20769	Bin_5	40.3862	28.6396	2.28314
674	gene_id_20923	Bin_5	188.741	109.922	4.31229
674	gene_id_20924	Bin_5	5.51878	8.65038	0
674	gene_id_20926	Bin_5	27.7904	7.82243	0
674	gene_id_20927	Bin_5	7.98592	13.9865	2.19323
674	gene_id_20928	Bin_5	33.7505	31.8736	39.0881
674	gene_id_20929	Bin_5	16.3604	3.21798	1.91974
674	gene_id_20933	Bin_5	14.6321	12.7206	3.66183
685	gene_id_21027	Bin_5	9.34743	2.14348	0
685	gene_id_21031	Bin_5	17.8931	1.11689	0
685	gene_id_21035	Bin_5	64.4084	27.7361	0
685	gene_id_21037	Bin_5	15.2739	0	0
685	gene_id_21041	Bin_5	12.6892	2.67153	0
685	gene_id_21043	Bin_5	35.2235	2.91391	0
686	gene_id_21047	Bin_5	7.78773	1.96592	0.346886
686	gene_id_21054	Bin_5	18.9053	12.7039	31.2834
686	gene_id_21055	Bin_5	49.573	8.98975	58.5602
686	gene_id_21056	Bin_5	189.312	20.4438	261.686
686	gene_id_21056	Bin_5	33.3249	20.4438	261.686
686	gene_id_21056	Bin_5	189.312	95.7266	23.1234
686	gene_id_21056	Bin_5	33.3249	95.7266	23.1234
686	gene_id_21058	Bin_5	13.969	1.76022	0
721	gene_id_21338	Bin_5	116.973	74.072	50.6809
721	gene_id_21339	Bin_5	99.4132	32.7525	4.21732
729	gene_id_21382	Bin_5	30.1796	14.5227	0
729	gene_id_21384	Bin_5	6.91494	1.24401	15.9614
729	gene_id_21385	Bin_5	46.1781	58.6706	58.6758
729	gene_id_21387	Bin_5	9.66009	6.69239	1.33684
729	gene_id_21393	Bin_5	5.00897	11.4791	3.02696
740	gene_id_21473	Bin_5	22.9092	1.10032	1.5525
740	gene_id_21474	Bin_5	13.3048	16.454	60.9417

740	gene_id_21475	Bin_5	5.05035	5.54835	9.13784
740	gene_id_21476	Bin_5	13.3052	3.147	0
750	gene_id_21546	Bin_5	13.6086	9.54499	0.673691
752	gene_id_21572	Bin_5	15.1485	2.65378	1.54104
752	gene_id_21576	Bin_5	12.1352	2.77506	0
752	gene_id_21577	Bin_5	21.2969	1.4095	0
755	gene_id_21594	Bin_5	22.2951	1.74706	0
755	gene_id_21598	Bin_5	79.2117	166.649	7.76461
755	gene_id_21605	Bin_5	21.3487	4.10679	4.50763
755	gene_id_21609	Bin_5	12.4239	9.36139	0
761	gene_id_21652	Bin_5	27.105	15.2693	69.9583
785	gene_id_21828	Bin_5	55.0225	19.6229	1.46096
785	gene_id_21829	Bin_5	38.261	22.7372	0.802009
785	gene_id_21830	Bin_5	307.299	125.734	0
785	gene_id_21831	Bin_5	105.145	33.237	0
785	gene_id_21832	Bin_5	22.4789	4.97737	0.585355
785	gene_id_21833	Bin_5	82.4824	39.2757	0
785	gene_id_21834	Bin_5	194.702	10.4464	0
807	gene_id_22025	Bin_5	51.0082	48.3849	5.53779
807	gene_id_22026	Bin_5	725.441	361.472	30.0537
807	gene_id_22027	Bin_5	25.6217	8.59478	0
807	gene_id_22035	Bin_5	13.6419	9.74335	0.808991
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807	gene_id_22037	Bin_5	11.741	3.85658	0
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821	gene_id_22111	Bin_5	12.7409	1.59949	0
821	gene_id_22114	Bin_5	150.005	53.8221	37.0111
821	gene_id_22119	Bin_5	27.0209	3.34012	2.35543
821	gene_id_22122	Bin_5	84.175	7.10682	0
821	gene_id_22125	Bin_5	97.0405	27.5123	0
821	gene_id_22127	Bin_5	46.1726	18.9885	7.7157
824	gene_id_22156	Bin_5	12.0591	4.13679	7.46337
824	gene_id_22158	Bin_5	22.2865	8.24589	5.25244
824	gene_id_22159	Bin_5	39.6526	9.69759	0
835	gene_id_22208	Bin_5	15.9915	24.3089	0
835	gene_id_22209	Bin_5	11.907	27.9623	4.75073
835	gene_id_22210	Bin_5	5.46426	11.6847	1.02497
835	gene_id_22211	Bin_5	7.45389	9.41866	0.906544
835	gene_id_22213	Bin_5	15.9807	6.17597	0
835	gene_id_22214	Bin_5	11.8112	13.9982	0.581026
835	gene_id_22226	Bin_5	15.6894	8.20385	0.578885
840	gene_id_22259	Bin_5	6.74545	1.77797	0.5308
840	gene_id_22260	Bin_5	12.1857	5.3575	0.540078
840	gene_id_22262	Bin_5	20.8207	4.17321	0
840	gene_id_22263	Bin_5	13.0327	1.36623	0
840	gene_id_22264	Bin_5	28.8692	2.34696	0

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840	gene_id_22269	Bin_5	18.5966	3.58561	0
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851	gene_id_22383	Bin_5	43.2044	24.5058	3.66438
851	gene_id_22385	Bin_5	6.54688	8.23531	0
851	gene_id_22387	Bin_5	20.5189	1.27716	1.80178
885	gene_id_22568	Bin_5	17.2964	7.47982	0.959728
885	gene_id_22571	Bin_5	54.774	59.9414	8.52263
885	gene_id_22575	Bin_5	0	10.1853	1.24347
900	gene_id_22722	Bin_5	25.9194	1.60393	0
909	gene_id_22782	Bin_5	14.2897	6.36148	2.70426
911	gene_id_22796	Bin_5	69.6678	255.016	140.335
911	gene_id_22798	Bin_5	13.1325	45.6442	11.3307
911	gene_id_22799	Bin_5	8.08095	28.2935	9.92874
911	gene_id_22800	Bin_5	5.884	15.3736	2.9932
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920	gene_id_22845	Bin_5	22.2306	74.7403	8.77455
920	gene_id_22846	Bin_5	24.1323	38.1257	33.3655
979	gene_id_23138	Bin_5	26.4525	13.4201	1.05165
979	gene_id_23141	Bin_5	23.3176	0.912954	2.57664
979	gene_id_23142	Bin_5	9.04752	1.7106	0.804846
979	gene_id_23145	Bin_5	44.5271	26.3759	0.930231
985	gene_id_23181	Bin_5	18.6785	0	0
985	gene_id_23186	Bin_5	11.4662	5.04512	1.52581
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1034	gene_id_23456	Bin_5	13.9193	14.5799	0
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1034	gene_id_23464	Bin_5	69.3258	22.6725	4.3283
1034	gene_id_23466	Bin_5	16.4197	10.3661	1.73876
1034	gene_id_23467	Bin_5	19.1662	16.9836	6.42235
1034	gene_id_23469	Bin_5	17.9798	2.04396	1.52246
1034	gene_id_23470	Bin_5	23.937	4.9691	0
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1067	gene_id_23640	Bin_5	33.9562	19.4823	95.1433
1076	gene_id_23677	Bin_5	13.3907	3.8897	0
1076	gene_id_23684	Bin_5	13.0457	15.2946	18.9445
1076	gene_id_23685	Bin_5	22.7949	7.14245	8.4013
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1076	gene_id_23685	Bin_5	22.7949	7.80359	1.69398

1076	gene_id_23685	Bin_5	9.45032	7.80359	1.69398
1079	gene_id_23695	Bin_5	7.61724	0.321433	0.706752
1089	gene_id_23745	Bin_5	24.45	4.69126	0
1089	gene_id_23749	Bin_5	430.387	111.766	34.3799
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1089	gene_id_23753	Bin_5	21.6538	3.12333	0
1089	gene_id_23754	Bin_5	23.3317	12.288	0.289113
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1111	gene_id_23879	Bin_5	12.632	23.4673	11.2738
1235	gene_id_24435	Bin_5	8.49375	1.34113	0
1235	gene_id_24438	Bin_5	8.26774	2.61144	0
1235	gene_id_24443	Bin_5	57.9519	20.0959	14.5586
1311	gene_id_24764	Bin_5	85.5942	13.927	0
1311	gene_id_24765	Bin_5	16.3041	3.24649	0.807226
1311	gene_id_24766	Bin_5	69.2151	3.42029	0
1311	gene_id_24768	Bin_5	593.927	95.852	6.21041
1374	gene_id_25016	Bin_5	15.8718	0.665742	0.469818
1428	gene_id_25195	Bin_5	16.1656	0	0.649486
1557	gene_id_25629	Bin_5	13.4518	1.68743	0
1557	gene_id_25630	Bin_5	12.6962	3.62716	1.08165
1557	gene_id_25631	Bin_5	92.8063	54.3749	19.2231
1557	gene_id_25632	Bin_5	958.366	396.872	174.498
1557	gene_id_25633	Bin_5	4.4718	6.01148	14.4648
1622	gene_id_25874	Bin_5	13.2564	6.63958	15.7746
1622	gene_id_25879	Bin_5	7.71023	7.61953	2.55468
1699	gene_id_26205	Bin_5	15.4507	2.05205	0.362077
1756	gene_id_26362	Bin_5	42.6157	34.42	17.0418
1814	gene_id_26546	Bin_5	17.9111	2.56802	0.766296
1814	gene_id_26549	Bin_5	13.9276	2.56923	0.80693
1913	gene_id_26822	Bin_5	39.3036	15.8605	1.34318
1934	gene_id_26877	Bin_5	35.8072	17.4837	2.08317
1934	gene_id_26878	Bin_5	749.83	283.884	52.5548
2427	gene_id_27968	Bin_5	135.505	30.5551	0
41	gene_id_4224	Bin_5	15.5729	4.0719	0.57465
41	gene_id_4225	Bin_5	24.8585	17.2475	1.88641
41	gene_id_4246	Bin_5	18.2681	4.17562	0
66	gene_id_6175	Bin_5	60.4078	35.1923	1.41928
66	gene_id_6176	Bin_5	18.0223	7.82175	0.716579
66	gene_id_6177	Bin_5	37.8221	4.61319	0
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105	gene_id_8552	Bin_5	32.725	42.0932	20.6293
105	gene_id_8566	Bin_5	87.684	68.1691	17.4714
105	gene_id_8567	Bin_5	28.5862	17.6163	5.11575
105	gene_id_8568	Bin_5	19.967	10.4653	1.9691
105	gene_id_8569	Bin_5	32.4288	14.3219	1.52404
105	gene_id_8571	Bin_5	30.1865	0	1.65097
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105	gene_id_8575	Bin_5	9.76276	2.23779	0
105	gene_id_8576	Bin_5	11.759	2.62169	0
105	gene_id_8579	Bin_5	16.0572	4.58958	1.4416
105	gene_id_8593	Bin_5	16.0084	0	1.49172
105	gene_id_8594	Bin_5	16.2197	14.3813	1.01431
105	gene_id_8597	Bin_5	14.8905	18.3488	2.72743
105	gene_id_8601	Bin_5	26.2695	64.0211	6.04939
105	gene_id_8602	Bin_5	14.7663	10.8579	2.43986
105	gene_id_8607	Bin_5	20.8817	7.47226	1.31804
105	gene_id_8615	Bin_5	47.7304	99.0994	6.55709
105	gene_id_8617	Bin_5	11.5275	11.1562	0.342351
105	gene_id_8619	Bin_5	34.845	8.09933	0
105	gene_id_8620	Bin_5	33.7793	0.882187	0
105	gene_id_8623	Bin_5	200.076	37.3701	0
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111	gene_id_8784	Bin_5	39.6917	0	150.977
111	gene_id_8785	Bin_5	22.3631	13.262	14.9329
111	gene_id_8786	Bin_5	17.621	19.7956	28.6979

111	gene_id_8787	Bin_5	17.5741	11.7797	19.0635
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111	gene_id_8797	Bin_5	101.384	80.8304	12.5405
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111	gene_id_8799	Bin_5	21.469	11.366	0
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111	gene_id_8802	Bin_5	34.9895	14.9934	20.4477
111	gene_id_8803	Bin_5	13.2791	4.46436	4.07286
169	gene_id_11405	Bin_6	28.0445	12.6745	4.20413
169	gene_id_11410	Bin_6	21.1008	5.07494	2.14829
169	gene_id_11411	Bin_6	4.91507	2.04867	17.0247
169	gene_id_11422	Bin_6	8.75301	8.27725	1.16836
169	gene_id_11423	Bin_6	58.9255	17.9921	4.92881
169	gene_id_11434	Bin_6	18.1806	2.01836	0.474788
169	gene_id_11447	Bin_6	19.6502	2.25195	1.6797
169	gene_id_11448	Bin_6	17.0633	4.34181	0
169	gene_id_11448	Bin_6	8.4073	4.34181	0
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169	gene_id_11448	Bin_6	8.4073	3.19815	0
169	gene_id_11450	Bin_6	79.8464	27.4506	11.3692
169	gene_id_11452	Bin_6	15.1386	12.7065	4.18777
169	gene_id_11453	Bin_6	24.749	8.99108	3.52544
169	gene_id_11459	Bin_6	11.0995	5.35168	0.735416
169	gene_id_11460	Bin_6	18.0139	5.63971	1.32639
169	gene_id_11471	Bin_6	6.52285	10.1964	4.55694
169	gene_id_11473	Bin_6	23.1831	9.17717	2.8761
169	gene_id_11474	Bin_6	38.7153	3.66975	14.6517
169	gene_id_11477	Bin_6	23.6217	9.69601	3.24492
169	gene_id_11478	Bin_6	26.5723	11.007	12.9356
169	gene_id_11481	Bin_6	12.2911	3.27078	1.50897
169	gene_id_11484	Bin_6	26.3401	12.0204	11.6327
169	gene_id_11486	Bin_6	15.2464	2.54633	0.74676
169	gene_id_11490	Bin_6	42.1752	10.0219	4.71597
169	gene_id_11491	Bin_6	65.0699	26.7437	22.1776
169	gene_id_11501	Bin_6	74.7371	27.0703	9.12628
169	gene_id_11504	Bin_6	25.1951	7.42551	2.6196
169	gene_id_11505	Bin_6	30.5989	10.7962	3.49093
169	gene_id_11507	Bin_6	18.0361	5.04659	2.77208
169	gene_id_11509	Bin_6	19.2392	5.46108	4.02402
169	gene_id_11512	Bin_6	6.38037	0	22.9053
169	gene_id_11515	Bin_6	14.4634	3.90107	3.82668

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193	gene_id_12070	Bin_6	14.5216	2.28038	2.26653
193	gene_id_12071	Bin_6	19.0246	14.7764	2.595
193	gene_id_12071	Bin_6	10.5812	14.7764	2.595
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193	gene_id_12105	Bin_6	15.4942	22.3744	8.01211
193	gene_id_12126	Bin_6	52.6483	20.4624	5.18582
193	gene_id_12136	Bin_6	21.2034	1.31879	1.86046
193	gene_id_12140	Bin_6	18.8584	5.87957	0
193	gene_id_12143	Bin_6	48.5997	5.42527	1.08826
193	gene_id_12143	Bin_6	12.8522	5.42527	1.08826
193	gene_id_12143	Bin_6	48.5997	21.8892	0
193	gene_id_12143	Bin_6	12.8522	21.8892	0
193	gene_id_12146	Bin_6	95.988	34.9966	13.9629
193	gene_id_12146	Bin_6	17.1202	34.9966	13.9629
193	gene_id_12146	Bin_6	95.988	13.4942	3.8529
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193	gene_id_12147	Bin_6	26.0145	21.9284	12.881
193	gene_id_12148	Bin_6	7.73125	25.9026	20.822
193	gene_id_12152	Bin_6	9.66009	0.6084	0.42937
193	gene_id_12158	Bin_6	74.9451	28.8732	25.1029
193	gene_id_12160	Bin_6	21.3056	30.3504	78.18
193	gene_id_12167	Bin_6	140.647	63.0549	41.135
193	gene_id_12177	Bin_6	16.7647	0.954058	2.76784
193	gene_id_12178	Bin_6	49.0017	2.69126	1.89956
193	gene_id_12216	Bin_6	72.9037	11.656	2.74461
193	gene_id_12259	Bin_6	25.9112	7.55282	5.41311
193	gene_id_12261	Bin_6	24.4689	7.21483	2.61665
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193	gene_id_12274	Bin_6	54.9184	11.9723	0
193	gene_id_12280	Bin_6	12.6974	1.33148	0
193	gene_id_12285	Bin_6	13.173	4.1324	1.23194
193	gene_id_12288	Bin_6	73.5897	155.682	36.3048
193	gene_id_12292	Bin_6	2.88949	2.43932	27.5308
193	gene_id_12293	Bin_6	0	4.5816	69.735
193	gene_id_12300	Bin_6	39.528	7.21498	6.96825
193	gene_id_12303	Bin_6	19.9863	2.6838	0
193	gene_id_12305	Bin_6	30.7934	12.0983	0
193	gene_id_12308	Bin_6	40.0796	9.74074	6.75293
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193	gene_id_12336	Bin_6	11.9097	0	0.480598
193	gene_id_12344	Bin_6	129.663	19.7148	23.6877
193	gene_id_12347	Bin_6	50.2825	9.03875	12.9923
193	gene_id_12350	Bin_6	17.6573	4.25896	1.87061
193	gene_id_12361	Bin_6	22.4719	21.6965	23.3017
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193	gene_id_12365	Bin_6	18.8186	8.26078	1.99815
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193	gene_id_12387	Bin_6	127.336	58.447	46.2399
193	gene_id_12388	Bin_6	13.8604	5.36607	1.47365
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193	gene_id_12390	Bin_6	9.75325	6.0455	15.0392
193	gene_id_12391	Bin_6	66.7022	17.9063	33.9803
193	gene_id_12398	Bin_6	20.3131	5.1294	2.10521
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193	gene_id_12410	Bin_6	17.2276	3.60951	1.0764
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193	gene_id_12419	Bin_6	16.7213	1.74706	1.91825
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193	gene_id_12468	Bin_6	45.042	36.7954	4.72536
193	gene_id_12469	Bin_6	0	16.469	5.16757
193	gene_id_12470	Bin_6	15.7318	8.3614	3.33931
193	gene_id_12529	Bin_6	23.1711	0	0
193	gene_id_12577	Bin_6	8.23735	3.63721	0.733451
193	gene_id_12581	Bin_6	11.0574	2.32246	3.00808
193	gene_id_12582	Bin_6	10.107	3.81741	0.94891
193	gene_id_12583	Bin_6	11.7242	4.35666	2.22284
193	gene_id_12584	Bin_6	30.8617	5.52305	0.649486
193	gene_id_12586	Bin_6	4.88403	9.84204	2.70321
193	gene_id_12605	Bin_6	19.4272	1.74869	3.38452
193	gene_id_12609	Bin_6	240.218	111.838	18.7501
193	gene_id_12610	Bin_6	25.8005	42.385	24.968
193	gene_id_12611	Bin_6	24.7848	13.0616	4.6291
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193	gene_id_12613	Bin_6	75.9663	12.1321	13.3083
193	gene_id_12617	Bin_6	24.2142	10.5083	2.11747
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193	gene_id_12628	Bin_6	59.5015	41.9675	4.93238
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193	gene_id_12640	Bin_6	60.5981	18.3302	4.22027
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203	gene_id_12879	Bin_6	10.2744	3.24691	0.286477
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203	gene_id_12884	Bin_6	25.5073	20.4635	10.9601
203	gene_id_12885	Bin_6	19.5958	22.4682	5.13908
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203	gene_id_12890	Bin_6	28.8813	12.0425	8.02537
203	gene_id_12892	Bin_6	19.2542	20.0709	9.44143
203	gene_id_12893	Bin_6	12.5857	3.18671	2.5261
203	gene_id_12895	Bin_6	20.627	1.07377	12.542
203	gene_id_12897	Bin_6	32.2082	17.9756	9.23573
203	gene_id_12900	Bin_6	11.0428	6.95832	0
203	gene_id_12901	Bin_6	9.55822	2.51291	0.354719
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203	gene_id_12919	Bin_6	20.3153	19.6264	4.06357
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203	gene_id_12934	Bin_6	35.6589	33.9509	3.90921
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232	gene_id_14104	Bin_6	199.895	109.879	8.02966
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232	gene_id_14124	Bin_6	15.7161	0	5.22718
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232	gene_id_14131	Bin_6	31.3896	44.3651	32.4718
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232	gene_id_14153	Bin_6	9.5375	9.33435	0.994314
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260	gene_id_14981	Bin_6	96.6703	36.4621	9.30939
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260	gene_id_14983	Bin_6	100.688	31.4427	14.2788
260	gene_id_14984	Bin_6	114.75	78.2591	34.4863
260	gene_id_14987	Bin_6	3.41745	7.16093	1.57309
260	gene_id_14995	Bin_6	13.2175	2.77074	0
260	gene_id_14997	Bin_6	89.3048	9.41293	45.9775
260	gene_id_14999	Bin_6	14.2321	0	0.451586
260	gene_id_15000	Bin_6	26.149	9.84462	0
260	gene_id_15005	Bin_6	23.8296	2.69347	7.91268
260	gene_id_15006	Bin_6	148.754	44.7697	4.5039
260	gene_id_15008	Bin_6	55.8577	13.2827	2.34543
260	gene_id_15009	Bin_6	105.388	21.7546	8.1129
260	gene_id_15012	Bin_6	219.683	69.4764	8.45851
260	gene_id_15019	Bin_6	12.8138	0	0
18	gene_id_1514	Bin_6	12.5307	2.86437	1.01067
18	gene_id_1520	Bin_6	5.10567	8.81302	0
18	gene_id_1521	Bin_6	23.1931	4.81825	1.79346
18	gene_id_1521	Bin_6	9.20203	4.81825	1.79346
18	gene_id_1521	Bin_6	23.1931	6.33132	1.57432
18	gene_id_1521	Bin_6	9.20203	6.33132	1.57432
18	gene_id_1523	Bin_6	0	0	26.5244
18	gene_id_1524	Bin_6	3.24809	2.04307	9.24011
18	gene_id_1525	Bin_6	293.962	97.7032	76.3444
18	gene_id_1526	Bin_6	12.5948	10.2048	4.40636
18	gene_id_1536	Bin_6	2.92826	0	21.4746
18	gene_id_1536	Bin_6	2.54479	0	21.4746
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18	gene_id_1536	Bin_6	0	0	10.8353

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291	gene_id_15395	Bin_6	11.1013	2.33159	0.41138
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18	gene_id_1559	Bin_6	23.1872	2.42538	4.56381
18	gene_id_1560	Bin_6	5.58577	9.96202	33.3399
18	gene_id_1573	Bin_6	26.9018	10.2902	15.9703
18	gene_id_1577	Bin_6	20.413	2.23779	2.45883
18	gene_id_1586	Bin_6	9.60426	1.65136	0.388491
18	gene_id_1595	Bin_6	55.2426	42.7313	18.2986
18	gene_id_1600	Bin_6	20.7755	4.35259	2.04768
18	gene_id_1602	Bin_6	3.09017	8.42769	0
18	gene_id_1605	Bin_6	26.5677	11.0579	8.06107
18	gene_id_1607	Bin_6	30.2349	14.7694	5.89062
18	gene_id_1612	Bin_6	20.7252	14.3627	15.2835
18	gene_id_1613	Bin_6	34.4886	26.3219	15.3504
18	gene_id_1617	Bin_6	5.34226	3.30299	98.4353
18	gene_id_1625	Bin_6	11.6942	6.13292	1.1239
18	gene_id_1640	Bin_6	15.7084	13.0763	1.25018
18	gene_id_1646	Bin_6	15.6269	14.8138	2.71376
18	gene_id_1653	Bin_6	14.2344	1.79333	3.04893
18	gene_id_1658	Bin_6	4.01239	8.38945	1.25048
18	gene_id_1664	Bin_6	140.095	49.3757	20.4541
18	gene_id_1667	Bin_6	24.7499	0	3.9427
18	gene_id_1668	Bin_6	72.615	9.96202	9.38174
18	gene_id_1670	Bin_6	16.081	7.87945	5.25817
18	gene_id_1678	Bin_6	32.3998	0	2.95741
18	gene_id_1683	Bin_6	98.1004	18.0863	22.6586
18	gene_id_1684	Bin_6	22.6372	2.56167	2.81007
347	gene_id_16894	Bin_6	14.3639	0.900029	0.635046
347	gene_id_16914	Bin_6	20.7882	55.5361	152.069
347	gene_id_16919	Bin_6	37.8888	4.5117	2.32582
347	gene_id_16919	Bin_6	16.9707	4.5117	2.32582
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347	gene_id_16920	Bin_6	17.1387	1.47448	1.4914
347	gene_id_16921	Bin_6	158.545	40.7618	13.3933
347	gene_id_16922	Bin_6	28.4235	4.65621	3.40907
347	gene_id_16923	Bin_6	28.6988	8.36671	2.53761
347	gene_id_16924	Bin_6	40.1368	10.4035	2.39102
347	gene_id_16931	Bin_6	26.5333	6.67739	1.46703
436	gene_id_17890	Bin_6	21.2053	2.92348	23.3577
436	gene_id_17896	Bin_6	5.22004	12.2831	14.3227

436	gene_id_17898	Bin_6	18.9648	12.9115	5.08204
436	gene_id_17899	Bin_6	28.3348	28.1843	7.69437
436	gene_id_17912	Bin_6	2.11944	3.3337	11.6654
436	gene_id_17914	Bin_6	6.86195	5.91532	19.876
436	gene_id_17921	Bin_6	3.08077	12.6389	9.91989
436	gene_id_17926	Bin_6	17.7065	26.7537	15.5092
436	gene_id_17932	Bin_6	8.55985	20.806	25.7283
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436	gene_id_17938	Bin_6	23.261	7.81821	3.93965
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464	gene_id_18277	Bin_6	60.7311	23.1866	11.5914
538	gene_id_19306	Bin_6	18.4102	10.46	4.59219
538	gene_id_19307	Bin_6	22.7617	15.1998	3.42632
567	gene_id_19622	Bin_6	87.8369	17.6654	9.23358
567	gene_id_19623	Bin_6	39.0605	21.9869	8.60877
567	gene_id_19624	Bin_6	11.4341	16.2052	11.8214
567	gene_id_19625	Bin_6	12.1645	4.58426	1.13909
567	gene_id_19639	Bin_6	13.7158	0	1.28181
567	gene_id_19645	Bin_6	16.2645	14.2368	2.90474
567	gene_id_19649	Bin_6	5.91572	11.1151	4.7943
567	gene_id_19650	Bin_6	5.46753	21.9576	36.5078
567	gene_id_19651	Bin_6	1.43935	9.92038	18.9529
567	gene_id_19652	Bin_6	18.0642	0	2.25381
567	gene_id_19653	Bin_6	17.147	3.21355	0.755713
567	gene_id_19654	Bin_6	14.4903	2.47944	2.46389
567	gene_id_19657	Bin_6	5.27352	4.67218	0.235572
567	gene_id_19659	Bin_6	36.3203	14.8192	5.03492
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567	gene_id_19663	Bin_6	1833.98	838.226	313.696
567	gene_id_19665	Bin_6	5.44967	5.72401	3.32364
567	gene_id_19670	Bin_6	21.8148	10.0219	6.00165
567	gene_id_19671	Bin_6	901.324	684.797	0
567	gene_id_19676	Bin_6	60.3868	10.8649	27.039
567	gene_id_19693	Bin_6	12.7009	5.00886	2.16144
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635	gene_id_20521	Bin_6	5.5297	21.6681	24.606
880	gene_id_22538	Bin_6	19.5187	4.67783	2.43562
966	gene_id_23051	Bin_6	294.056	0	12.0555
84	gene_id_7176	Bin_6	19.9492	24.2687	23.7618
84	gene_id_7177	Bin_6	8.75173	4.01613	0.749033
84	gene_id_7178	Bin_6	14.5177	4.96811	0
84	gene_id_7186	Bin_6	8.29989	5.58128	0.953611

84	gene_id_7187	Bin_6	28.548	29.693	33.0441
84	gene_id_7188	Bin_6	6.52285	18.3535	24.3812
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84	gene_id_7189	Bin_6	20.7519	9.96678	2.70504
84	gene_id_7194	Bin_6	57.9844	9.41914	3.49992
84	gene_id_7199	Bin_6	416.124	29.7106	104.233
84	gene_id_7202	Bin_6	45.6327	37.0954	25.4066
84	gene_id_7203	Bin_6	14.42	35.2171	21.0375
84	gene_id_7204	Bin_6	23.5016	19.1796	5.74809
84	gene_id_7212	Bin_6	294.688	32.858	85.498
84	gene_id_7235	Bin_6	14.1367	3.6715	1.52289
84	gene_id_7244	Bin_6	15.2075	3.80807	3.50876
84	gene_id_7246	Bin_6	4.76042	19.1917	34.1153
84	gene_id_7251	Bin_6	22.9301	18.9024	6.93811
84	gene_id_7267	Bin_6	2.74509	8.67087	22.2163
84	gene_id_7270	Bin_6	18.691	7.33231	0.607961
84	gene_id_7276	Bin_6	23.3731	3.99309	1.75565
84	gene_id_7277	Bin_6	23.2816	19.3624	7.78292
84	gene_id_7278	Bin_6	41.9807	42.3301	7.21981
84	gene_id_7279	Bin_6	127.858	29.9617	30.5511
84	gene_id_7281	Bin_6	344.334	0	0
84	gene_id_7289	Bin_6	10.889	6.40847	3.98833
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84	gene_id_7291	Bin_6	19.5246	12.9942	0
84	gene_id_7294	Bin_6	20.5777	9.33332	16.0021
84	gene_id_7302	Bin_6	10.6589	32.5959	35.001
84	gene_id_7303	Bin_6	71.0433	56.4976	10.8923
84	gene_id_7306	Bin_6	2.40049	2.01945	13.5903
84	gene_id_7307	Bin_6	4.81354	12.0425	62.6289
84	gene_id_7323	Bin_6	12.444	17.7911	5.75001
84	gene_id_7329	Bin_6	1.5946	1.51582	22.2714
84	gene_id_7382	Bin_6	7.20951	0.910555	0.321343
84	gene_id_7385	Bin_6	5.3795	4.85053	1.75081
84	gene_id_7386	Bin_6	3.44631	27.9855	14.8503
84	gene_id_7387	Bin_6	10.151	6.38975	5.51348
84	gene_id_7391	Bin_6	6.24864	32.6674	4.21111
84	gene_id_7395	Bin_6	129.073	287.214	0
84	gene_id_7396	Bin_6	159.823	77.9005	12.6679
84	gene_id_7398	Bin_6	58.6309	26.1759	1.67881
84	gene_id_7399	Bin_6	218.829	85.2705	0
84	gene_id_7401	Bin_6	22.6199	14.8382	2.76531
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84	gene_id_7406	Bin_6	40.5785	24.3597	26.6582
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84	gene_id_7415	Bin_6	13.2229	1.65912	0.585355
84	gene_id_7422	Bin_6	44.9703	8.67522	5.02651
84	gene_id_7423	Bin_6	8.04232	13.7721	0
84	gene_id_7424	Bin_6	18.5673	1.67204	1.2248
84	gene_id_7428	Bin_6	45.1429	5.01813	0.442679
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84	gene_id_7429	Bin_6	16.1099	30.1842	45.6051
84	gene_id_7430	Bin_6	6.08495	8.98715	15.1694
84	gene_id_7434	Bin_6	4.89991	12.3092	4.34302
84	gene_id_7438	Bin_6	8.06275	3.19866	2.09764
84	gene_id_7443	Bin_6	9.87936	0.891403	1.33024
84	gene_id_7454	Bin_6	7803.63	2947.56	113.318
84	gene_id_7455	Bin_6	41.0265	16.1458	0.493173
84	gene_id_7456	Bin_6	16.9232	6.87893	1.41058
84	gene_id_7463	Bin_6	43.9888	10.6386	25.0039
84	gene_id_7492	Bin_6	10.0302	0	0
84	gene_id_7495	Bin_6	25.8687	11.0606	10.187
84	gene_id_7496	Bin_6	36.9732	13.8938	14.6706
84	gene_id_7516	Bin_6	11.1374	2.80126	0.988409
84	gene_id_7531	Bin_6	6.9239	0.874757	0.308713
84	gene_id_7533	Bin_6	219.58	93.6611	51.6474
84	gene_id_7543	Bin_6	4.28529	7.02552	5.04524
84	gene_id_7567	Bin_6	34.14	5.87486	2.494
84	gene_id_7568	Bin_6	732.326	0	19.9293
84	gene_id_7578	Bin_6	16.7547	6.12672	7.61875
84	gene_id_7581	Bin_6	20.1465	1.1427	3.40334
84	gene_id_7582	Bin_6	10.0283	16.5273	3.45721
84	gene_id_7584	Bin_6	18.8278	0.90737	1.99241

84	gene_id_7586	Bin_6	32.6914	8.10874	6.36248
84	gene_id_7587	Bin_6	26.1626	25.9008	3.72353
84	gene_id_7591	Bin_6	12.0802	5.93658	3.72857
84	gene_id_7592	Bin_6	13.3746	3.35578	0
84	gene_id_7596	Bin_6	162.083	41.1169	3.6264
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84	gene_id_7599	Bin_6	33.5709	7.99087	0
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84	gene_id_7603	Bin_6	18.3813	10.156	0.511919
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134	gene_id_10256	Bin_9	4.60159	52.7844	0
134	gene_id_10257	Bin_9	5.74982	60.3666	0.32036
134	gene_id_10329	Bin_9	3.90875	13.3952	0
148	gene_id_10864	Bin_9	3.13833	220.009	1.36091
155	gene_id_11101	Bin_9	3.80272	39.4138	0
155	gene_id_11117	Bin_9	2.50869	9.51511	0
155	gene_id_11118	Bin_9	0	36.6745	0
155	gene_id_11120	Bin_9	0	22.8218	0
155	gene_id_11121	Bin_9	0	28.4315	0
170	gene_id_11522	Bin_9	9.22726	110.363	0
170	gene_id_11529	Bin_9	7.15994	29.0523	0
239	gene_id_14362	Bin_9	5.46358	15.7622	0.734959
269	gene_id_15077	Bin_9	11.7262	335.528	3.53692
19	gene_id_1761	Bin_9	9.95953	112.689	7.94535
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24	gene_id_2191	Bin_9	61.4028	681.195	0
24	gene_id_2206	Bin_9	4.11867	11.9508	0
24	gene_id_2220	Bin_9	1.14662	10.811	0
24	gene_id_2234	Bin_9	2.57162	70.2086	0
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24	gene_id_2236	Bin_9	3.70799	37.9251	0.698666
24	gene_id_2237	Bin_9	5.40946	38.8197	0
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24	gene_id_2280	Bin_9	15.706	63.5129	0

24	gene_id_2281	Bin_9	2.68989	10.1724	0
24	gene_id_2282	Bin_9	9.54331	25.4174	0
4	gene_id_262	Bin_9	2.9026	9.09224	0
29	gene_id_2647	Bin_9	2.33596	10.3636	0
4	gene_id_265	Bin_9	3.03648	15.9286	0
29	gene_id_2677	Bin_9	14.5782	48.9888	9.928
29	gene_id_2683	Bin_9	2207.69	985.986	1657.52
29	gene_id_2684	Bin_9	0	9.24582	0
29	gene_id_2686	Bin_9	0	18.0328	0
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4	gene_id_283	Bin_9	38.6563	11.7739	22.3058
4	gene_id_291	Bin_9	6.15566	37.0377	0
4	gene_id_293	Bin_9	0	42.0558	0
4	gene_id_296	Bin_9	331.964	4088.62	30.4174
4	gene_id_301	Bin_9	622.168	304.196	558.724
4	gene_id_302	Bin_9	454.662	177.448	383.884
32	gene_id_3407	Bin_9	182.161	158.669	0
32	gene_id_3438	Bin_9	6.83589	23.7523	1.28899
32	gene_id_3441	Bin_9	0	9.66573	0.620008
32	gene_id_3445	Bin_9	10.1792	15.7556	0
32	gene_id_3464	Bin_9	541815	208903	378309
32	gene_id_3477	Bin_9	59.0728	17.7249	0
32	gene_id_3491	Bin_9	36.9723	6.53333	3.58069
32	gene_id_3504	Bin_9	13.5964	172.256	0
32	gene_id_3518	Bin_9	0	52.2804	0
32	gene_id_3541	Bin_9	39.4613	108.982	0
32	gene_id_3545	Bin_9	5.68985	22.8218	0
4	gene_id_355	Bin_9	0	4604.72	0
32	gene_id_3594	Bin_9	0	41.9749	0
32	gene_id_3595	Bin_9	2.70209	30.0611	1.17771
32	gene_id_3602	Bin_9	4.77668	19.2556	2.20353
32	gene_id_3603	Bin_9	1.54426	15.4639	0
32	gene_id_3604	Bin_9	1.75341	20.8031	0
32	gene_id_3605	Bin_9	6.42055	29.5861	0
32	gene_id_3607	Bin_9	0	236.71	0
32	gene_id_3611	Bin_9	3.45119	11.5692	0
32	gene_id_3612	Bin_9	2.90396	25.0703	0
32	gene_id_3614	Bin_9	2.064	38.536	0
32	gene_id_3615	Bin_9	0	62.7302	0
32	gene_id_3616	Bin_9	3.79214	22.4611	0
32	gene_id_3617	Bin_9	9.16837	37.6242	0
32	gene_id_3618	Bin_9	2.30185	34.2934	1.00781
32	gene_id_3620	Bin_9	3.64454	35.6282	0
32	gene_id_3623	Bin_9	0	72.7549	0
32	gene_id_3624	Bin_9	2.85518	13.419	0

32	gene_id_3625	Bin_9	11.967	66.6301	4.69013
32	gene_id_3627	Bin_9	0	32.5559	0
32	gene_id_3629	Bin_9	0	20.886	0
32	gene_id_3630	Bin_9	1.82195	13.6423	0
32	gene_id_3636	Bin_9	6.36102	14.5067	0
32	gene_id_3647	Bin_9	36.075	35.5341	0
32	gene_id_3653	Bin_9	132.958	75.0441	0
33	gene_id_3701	Bin_9	26.113	0.562987	0
33	gene_id_3701	Bin_9	20.5434	0.562987	0
33	gene_id_3701	Bin_9	26.113	0	0
33	gene_id_3701	Bin_9	20.5434	0	0
33	gene_id_3702	Bin_9	39.8036	0	0.709629
33	gene_id_3702	Bin_9	28.9477	0	0.709629
33	gene_id_3702	Bin_9	39.8036	0	0
33	gene_id_3702	Bin_9	28.9477	0	0
4	gene_id_372	Bin_9	8.43192	43.3761	0
38	gene_id_3743	Bin_9	0	13.3025	0
38	gene_id_3790	Bin_9	25.7823	32.0244	1.1172
39	gene_id_3815	Bin_9	10.2552	0.645463	0
39	gene_id_3830	Bin_9	202.983	132.53	4.44486
39	gene_id_3837	Bin_9	5.28915	10.7843	0
39	gene_id_3846	Bin_9	197.345	8.6907	2.72408
39	gene_id_3851	Bin_9	0	12.4641	0.732799
39	gene_id_3866	Bin_9	2.13844	13.7271	0
39	gene_id_3866	Bin_9	0	13.7271	0
39	gene_id_3866	Bin_9	2.13844	12.1786	0
39	gene_id_3866	Bin_9	0	12.1786	0
39	gene_id_3884	Bin_9	7.31494	71.0347	0
39	gene_id_3885	Bin_9	21.609	157.797	4.27622
39	gene_id_3897	Bin_9	4824.6	2028.51	4165.06
39	gene_id_3906	Bin_9	2.31221	18.892	0
39	gene_id_3916	Bin_9	8.27884	32.6559	0
39	gene_id_3928	Bin_9	4.18868	8.75246	0
39	gene_id_3933	Bin_9	38.7624	9.66265	12.969
39	gene_id_3934	Bin_9	4.22786	28.9278	0
39	gene_id_3935	Bin_9	4.88853	29.3506	2.07231
39	gene_id_3949	Bin_9	9977.51	4338.25	8932.09
39	gene_id_3958	Bin_9	1.34003	8.40529	0
39	gene_id_3978	Bin_9	47.4335	9.61997	0
39	gene_id_3983	Bin_9	0	19.3199	0
39	gene_id_3986	Bin_9	6.11225	26.3369	0
39	gene_id_4017	Bin_9	1.00344	8.21234	0
39	gene_id_4019	Bin_9	2.96012	21.0253	0
39	gene_id_4020	Bin_9	13.5964	277.107	0
39	gene_id_4034	Bin_9	2.2815	12.2667	0
39	gene_id_4035	Bin_9	1.0486	15.8357	0
39	gene_id_4036	Bin_9	2.15964	26.8534	0

39	gene_id_4037	Bin_9	1.7667	11.0304	0
39	gene_id_4039	Bin_9	5.79829	22.8867	0
39	gene_id_4056	Bin_9	28.1057	132.772	2.72347
44	gene_id_4544	Bin_9	11.5333	28.1106	0
44	gene_id_4548	Bin_9	14.727	0	0
44	gene_id_4550	Bin_9	4.67076	16.8775	0.517825
44	gene_id_4551	Bin_9	22.0249	13.5385	32.2121
44	gene_id_4568	Bin_9	654.562	190.497	558.284
44	gene_id_4570	Bin_9	3.09537	13.5603	0
44	gene_id_4571	Bin_9	10.2766	135.257	0
44	gene_id_4580	Bin_9	3.40635	7.13796	0
44	gene_id_4591	Bin_9	3.15567	16.357	0
44	gene_id_4616	Bin_9	14.7006	2.1716	0.901123
44	gene_id_4658	Bin_9	5.54196	138.459	0
44	gene_id_4659	Bin_9	0	41.3597	0
44	gene_id_4660	Bin_9	12.7359	91.6978	0
44	gene_id_4661	Bin_9	9.08248	0	0
44	gene_id_4674	Bin_9	0.955447	8.42544	0
44	gene_id_4675	Bin_9	2.35615	14.6174	0
44	gene_id_4676	Bin_9	0	12.7501	0
44	gene_id_4693	Bin_9	0	146.801	0
60	gene_id_5734	Bin_9	4.29092	20.2448	0
63	gene_id_5908	Bin_9	20.5077	75.1437	22.4787
63	gene_id_5909	Bin_9	4.02905	19.0407	1.18525
63	gene_id_5910	Bin_9	2.9781	25.6883	0
63	gene_id_5911	Bin_9	2.07011	37.3593	0
63	gene_id_5918	Bin_9	3.37805	4.2776	0.456156
63	gene_id_5921	Bin_9	3.9528	96.1997	0
63	gene_id_5922	Bin_9	10.8317	21.5477	0
63	gene_id_5923	Bin_9	5.36011	41.1859	0
63	gene_id_5924	Bin_9	0	28.5556	0
63	gene_id_5925	Bin_9	1.77118	11.0579	0
63	gene_id_5927	Bin_9	0	270.874	0
63	gene_id_5929	Bin_9	295.158	2162.78	10.8
63	gene_id_5930	Bin_9	16.3896	66.7831	0.270915
63	gene_id_5931	Bin_9	844.959	14308.2	0
63	gene_id_5936	Bin_9	10.426	8.6022	0
63	gene_id_5952	Bin_9	5.24026	13.2569	0
63	gene_id_5971	Bin_9	0.880814	6.10786	0
63	gene_id_5978	Bin_9	4.89369	40.9462	0
63	gene_id_5994	Bin_9	8.80814	23.3209	0
63	gene_id_5995	Bin_9	3.24628	20.2998	0
63	gene_id_6065	Bin_9	2.87278	9.00029	0
63	gene_id_6065	Bin_9	2.57162	9.00029	0
63	gene_id_6065	Bin_9	2.87278	8.06995	0
63	gene_id_6065	Bin_9	2.57162	8.06995	0
65	gene_id_6125	Bin_9	12.492	32.8384	0

68	gene_id_6203	Bin_9	61.6598	3.07403	2.17077
68	gene_id_6248	Bin_9	53.3787	0	1.28859
75	gene_id_6710	Bin_9	0	16.5149	1.16463
75	gene_id_6765	Bin_9	69.3247	22.2706	29.932
79	gene_id_6922	Bin_9	1.69953	11.2533	0
79	gene_id_6967	Bin_9	4.20548	28.1185	0
79	gene_id_6968	Bin_9	1.04234	12.4626	0
79	gene_id_6970	Bin_9	11.107	23.4625	0
79	gene_id_6979	Bin_9	17.2367	39.6013	0
79	gene_id_6988	Bin_9	27.4007	61.5477	0
79	gene_id_6995	Bin_9	6.6957	12.6817	0.700875
79	gene_id_6998	Bin_9	6.4079	5.76853	0
79	gene_id_7000	Bin_9	0	21.6965	0
79	gene_id_7011	Bin_9	1.71804	18.84	0
79	gene_id_7011	Bin_9	0	18.84	0
79	gene_id_7011	Bin_9	1.71804	7.61883	0
79	gene_id_7011	Bin_9	0	7.61883	0
79	gene_id_7041	Bin_9	3.93064	66.9829	0
79	gene_id_7045	Bin_9	58.9376	177.433	0
79	gene_id_7050	Bin_9	0	18.6551	0
82	gene_id_7077	Bin_9	31.2862	40.51	4.40122
82	gene_id_7082	Bin_9	48.3877	26.5966	11.263
82	gene_id_7104	Bin_9	13.4129	0.603449	0.900101
82	gene_id_7160	Bin_9	658.281	9.85159	14.733
82	gene_id_7163	Bin_9	1289.46	247.707	0
85	gene_id_7615	Bin_9	3.00602	6.30823	0
85	gene_id_7617	Bin_9	132.436	306.809	0
85	gene_id_7619	Bin_9	24.9946	90.3158	2.85605
85	gene_id_7620	Bin_9	2.53084	5.85228	0
85	gene_id_7621	Bin_9	42.0557	103.674	1.77432
85	gene_id_7643	Bin_9	223.66	130.548	77.2398
85	gene_id_7652	Bin_9	10.9579	264.354	0
85	gene_id_7653	Bin_9	3.33249	28.6213	0
85	gene_id_7654	Bin_9	10.6549	101.87	0
85	gene_id_7656	Bin_9	9.13355	17.0966	1.69733
85	gene_id_7662	Bin_9	72.766	139.669	0
90	gene_id_7774	Bin_9	0	29.4291	0
90	gene_id_7780	Bin_9	2.7553	17.0194	0
90	gene_id_7805	Bin_9	4.08976	13.4156	0
90	gene_id_7806	Bin_9	2.69037	9.28088	0
90	gene_id_7807	Bin_9	14.1146	92.91	1.86908
90	gene_id_7821	Bin_9	3.14662	22.3805	0.293038
90	gene_id_7843	Bin_9	5.03462	23.3851	0
90	gene_id_7844	Bin_9	3.01526	129.32	2.07253
107	gene_id_8651	Bin_9	2.59664	28.9235	0
107	gene_id_8652	Bin_9	12.0431	17.3568	8.30044
107	gene_id_8662	Bin_9	31.6368	7.91351	1.17593

107	gene_id_8663	Bin_9	24.5179	4.08792	0
107	gene_id_8665	Bin_9	34.3494	6.144	0.289113
107	gene_id_8666	Bin_9	19.1258	1.88972	1.12824
107	gene_id_8667	Bin_9	21.6089	4.93422	0
112	gene_id_8817	Bin_9	27.9029	37.3692	0
113	gene_id_8876	Bin_9	84.6824	50.5508	0
116	gene_id_9196	Bin_9	2198.41	1769.81	0
127	gene_id_9636	Bin_9	162209	65765.9	127515
127	gene_id_9671	Bin_9	2.60144	14.4884	0
127	gene_id_9706	Bin_9	2185.21	1257.26	1988.86

Gene ID	Dehao_gene	RPKM Ratio (HiTCE:HiTCEB12)
gene_id_2984	DET0001	0.854242468
gene_id_2999	DET0017	0.775678517
gene_id_3000	DET0018	0.731499956
gene_id_3036	DET0058	1.219100622
gene_id_3037	DET0059	1.083260529
gene_id_3145	DET0128	1.002265006
gene_id_3154	DET0137	1.109542486
gene_id_3155	DET0138	1.122768709
gene_id_3159	DET0142	1.125056088
gene_id_3162	DET0145	0.808347203
gene_id_3164	DET0147	1.075837646
gene_id_3165	DET0148	0.836024714
gene_id_3312	DET0398	1.101615662
gene_id_3334	DET0421	17.97475382
gene_id_3335	DET0424	1.00461874
gene_id_3344	DET0433	1.055381633
gene_id_3358	DET0447	0.903757764
gene_id_5301	DET0503	1.349782794
gene_id_5299	DET0505	1.027311123
gene_id_5291	DET0514	1.253545413
gene_id_5277	DET0530	1.322644763
gene_id_5256	DET0552	1.266806776
gene_id_5254	DET0554	1.505150488
gene_id_5249	DET0560	1.268962426
gene_id_5248	DET0561	1.421150985
gene_id_5245	DET0564	1.409446804
gene_id_5244	DET0565	2.070871167
gene_id_5241	DET0568	1.000738968
gene_id_5228	DET0582	0.823715606
gene_id_5227	DET0583	0.914270831
gene_id_5214	DET0597	0.981310945
gene_id_5209	DET0602	1.104693604
gene_id_5180	DET0632	0.617526331
gene_id_5173	DET0640	0.868762745
gene_id_5165	DET0650	0.880500867
gene_id_5159	DET0657	2.234347626
gene_id_5135	DET0715	1.038990312
gene_id_5131	DET0722	1.427881517
gene_id_5130	DET0724	0.832567028
gene_id_5115	DET0742	1.218935038
gene_id_5113	DET0744	1.036392851
gene_id_5051	DET0819	1.045533441
gene_id_5009	DET0862	2.279655389
gene_id_5001	DET0870	1.267241468
gene_id_4981	DET0925	1.015637813
gene_id_4980	DET0926	1.098836957
gene_id_4973	DET0933	1.032994747
gene_id_4963	DET0943	1.257609709
gene_id_4945	DET0963	1.262902617

gene_id_4944	DET0964	1.426767081
gene_id_4913	DET0995	1.341686488
gene_id_4910	DET1001	0.955315832
gene_id_4870	DET1033	7.716583132
gene_id_4869	DET1035	0.585798971
gene_id_9283	DET1123	1.574132736
gene_id_9297	DET1137	0.892922156
gene_id_4538	DET1144	0.804487668
gene_id_4517	DET1173	0.204584976
gene_id_4516	DET1174	1.841694793
gene_id_4514	DET1176	0.834879969
gene_id_4460	DET1237	1.015627397
gene_id_4451	DET1247	1.420280984
gene_id_4440	DET1260	1.352429161
gene_id_4439	DET1261	1.461540173
gene_id_4437	DET1264	1.502953239
gene_id_4436	DET1265	1.381898762
gene_id_4435	DET1266	1.524727185
gene_id_4434	DET1267	1.133440507
gene_id_4429	DET1272	3.377748021
gene_id_4425	DET1276	1.380945861
gene_id_4422	DET1279	1.445047256
gene_id_547	DET1309	0.99129882
gene_id_516	DET1343	1.092361536
gene_id_4207	DET1357	1.236088657
gene_id_4141	DET1427	1.034438303
gene_id_2845	DET1543	10.33779548
gene_id_2939	DET1596	0.79629522
gene_id_2941	DET1598	0.92725853
gene_id_2953	DET1610	0.835832532
gene_id_4108	DhcVS_1251	0.553050262
gene_id_4107	DhcVS_1252	0.504964602
gene_id_4106	DhcVS_1253	0.367919366
gene_id_4105	DhcVS_1254	0.231768779
gene_id_4104	DhcVS_1255	0.337760341
gene_id_4102	DhcVS_1257	0.265515325

Microarray signal intensity ratio (HiTCE:HiTCEB12)
2.305451002
2.111745857
2.574838829
3.186315112
2.070036437
2.969117592
2.873608414
2.781242329
2.25218641
2.360279427
2.849424585
2.776641019
2.186976079
21.62458611
4.154011808
2.312047934
3.062347535
2.366427741
2.019126242
2.999406927
2.368739236
6.319290677
2.631729823
2.664202446
3.117907833
2.768668452
4.354359426
2.285566742
2.402140519
2.750120184
2.09091479
2.726214619
2.486614496
2.184056135
4.754451887
8.99918897
5.174418783
2.017281582
2.080821516
2.850817689
2.242581317
2.078683358
3.432127305
2.184526387
2.640018696
2.011286791
3.083861923
2.688687202
2.287550736

2.718808734
2.170050833
2.351024793
11.21535719
2.514789438
2.365417491
2.249609883
2.779032896
8.314632401
7.839110533
3.91221408
2.007207051
3.527243061
2.662909405
2.578063708
4.179962456
2.177777916
2.606810714
2.975786871
4.114883588
2.073284213
2.961174401
2.03024874
2.240892262
2.322030615
4.620205523
21.96631488
2.019873279
2.002717233
2.00926593
6.588814369
7.938527652
9.517362315
3.967188328
3.218151617
3.977008733

Gene ID	Dehao_gene	RPKM Ratio (HiTCE:HiTCEB12)
gene_id_4420	DET1281	0.191568561

Microarray signal intensity ratio (HiTCE:HiTCEB12)
0.34124449